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The following Pfam domain model PF00311.9 of the Phosphoenolpyruvate carboxylase is 960 positions long. Its breakpoint score occurs at 11.7 with corresponding E-value of 3.03. Beyond the breakpoint, the E-value underwent an exaggeration where its magnitude increases with large score. In the most extreme case, the largest significant hit Q01647.1 with score of 2796.7 has its EVD E-value of 8e-11 scaled all the way to the logistic E-value of 0. The order of magnitude difference is extremely big.

On the other hand, we also have hits with EVD E-value > 0.1 that shows stretches of impressive sequence matches but deemed as insignificant under the EVD statistical model. Given the length of this particular model, the global-mode can drastically under-sample random sequence matches and thus creates extremely small lambda. This leads to the underestimation of significance for those good hits with large EVD E-value.

For these long domain models, the EVD statistical model can generally underestimate the significance of sequence matches. Yet ironically, it exaggerates the significance for hits with larger scores. In hindsight, the lack of sequence sampling in between the extremes of E-values is just an illusion that is created by the switching between 2 statistical models (EVD and logistic).

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```
hmmsearch - search a sequence database with a profile HMM
HMMER 2.3.2 (Oct 2003)
Copyright (C) 1992-2003 HHMI/Washington University School of Medicine
Freely distributed under the GNU General Public License (GPL)
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
HMM file:                 /home/wongwc/DOMERR/bin/phase6/HMMmodels/globalmode-
hmmpfam/PF00311.9_Phosphoenolpyruvate_carboxylase.hmmmodel
[PF00311.9_Phosphoenolpyruvate_carboxylase]
Sequence database:        /home/wongwc/DOMERR/data/nr-05-04-2010.fasta
per-sequence score cutoff:  [none]
per-domain score cutoff:    [none]
per-sequence Eval cutoff:   <= 10
per-domain Eval cutoff:     [none]
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

Query HMM:   PF00311.9_Phosphoenolpyruvate_carboxylase
Accession:   [none]
Description: [none]
  [HMM has been calibrated; E-values are empirical estimates]

Scores for complete sequences (score includes all domains):
Sequence                              Description       Score    E-value  N
--------                              -----------       -----    ------- ---
gi|231684|sp|Q01647.1|CAPP1_FLAPR     RecName: Full=P  2796.7          0   1
gi|763097|emb|CAA88829.1|             phosphoenolpyru  2791.9          0   1
gi|20162467|gb|AAM14597.1|AF494192_1  phosphoenolpyru  2780.8          0   1
gi|242096062|ref|XP_002438521.1|      hypothetical pr  2766.5          0   1
gi|115578|sp|P15804.2|CAPP3_SORBI     RecName: Full=P  2765.2          0   1
gi|20162465|gb|AAM14596.1|AF494191_1  phosphoenolpyru  2757.4          0   1
gi|10443870|gb|AAG17618.1|AF248079_1  phosphoenolpyru  2725.0          0   1
gi|10185175|emb|CAC08829.1|           putative C4 pho  2715.2          0   1
gi|21464596|emb|CAC85930.1|           putative phosph  2711.4          0   1
gi|23306662|gb|AAN15222.1|            putative C4 pho  2704.1          0   1
gi|231685|sp|Q01648.1|CAPP1_FLATR     RecName: Full=P  2693.2          0   1
gi|1345665|sp|P30694.2|CAPP2_FLATR    RecName: Full=P  2683.7          0   1
gi|2499466|sp|Q42730.1|CAPP_FLAAU     RecName: Full=P  2681.7          0   1
gi|10443872|gb|AAG17619.1|AF248080_1  phosphoenolpyru  2674.9          0   1
gi|228246|prf||1801241A               phosphoenolpyru  2674.3          0   1
gi|27764449|emb|CAD60555.1|           phosphoenolpyru  2649.3          0   1
gi|238624101|ref|NP_001154820.1|      hypothetical pr  2646.7          0   1
gi|162461756|ref|NP_001105418.1|      phosphoenolpyru  2642.2          0   1
gi|212898592|gb|ACJ38542.1|           phosphoenolpyru  2640.0          0   1
gi|295855|emb|CAA33663.1|             P-pyruvate carb  2637.5          0   1
gi|224121514|ref|XP_002330719.1|      predicted prote  2623.3          0   1
gi|224114804|ref|XP_002316861.1|      predicted prote  2618.6          0   1
gi|155967407|gb|ABU41519.1|           phosphoenolpyru  2616.4          0   1
gi|259506726|gb|ABK54024.2|           phosphoenolpyru  2612.4          0   1
gi|2266947|gb|AAB80714.1|             phosphoenolpyru  2610.3          0   1
gi|255553993|ref|XP_002518037.1|      Phosphoenolpyru  2604.3          0   1
```

| | | | | |
|---|---|---|---|---|
| gi\|255579064\|ref\|XP_002530381.1\| | Phosphoenolpyru | 2604.3 | 0 | 1 |
| gi\|972511\|emb\|CAA62469.1\| | phosphoenolpyru | 2602.4 | 0 | 1 |
| gi\|1168761\|sp\|P29196.2\|CAPP_SOLTU | RecName: Full=P | 2602.4 | 0 | 1 |
| gi\|149789414\|gb\|ABR29878.1\| | phosphoenolpyru | 2598.1 | 0 | 1 |
| gi\|157812633\|gb\|ABV80356.1\| | phosphoenolpyru | 2594.7 | 0 | 1 |
| gi\|149789409\|gb\|ABR29876.1\| | phosphoenolpyru | 2593.1 | 0 | 1 |
| gi\|225461660\|ref\|XP_002285441.1\| | PREDICTED: hypo | 2592.5 | 0 | 1 |
| gi\|115581\|sp\|P16097.1\|CAPP2_MESCR | RecName: Full=P | 2585.0 | 0 | 1 |
| gi\|45505269\|gb\|AAS67006.1\| | Phosphoenolpyru | 2584.5 | 0 | 1 |
| gi\|115610\|sp\|P27154.1\|CAPP_TOBAC | RecName: Full=P | 2580.8 | 0 | 1 |
| gi\|223976187\|gb\|ACN32213.1\| | phosphoenolpyru | 2578.6 | 0 | 1 |
| gi\|166714353\|gb\|ABY87944.1\| | phosphoenolpyru | 2573.1 | 0 | 1 |
| gi\|399182\|sp\|Q02909.1\|CAPP1_SOYBN | RecName: Full=P | 2571.3 | 0 | 1 |
| gi\|225446609\|ref\|XP_002280569.1\| | PREDICTED: hypo | 2565.8 | 0 | 1 |
| gi\|242061132\|ref\|XP_002451855.1\| | hypothetical pr | 2565.3 | 0 | 1 |
| gi\|184097733\|gb\|ACC66283.1\| | phosphoenolpyru | 2564.1 | 0 | 1 |
| gi\|115587\|sp\|P29195.1\|CAPP1_SORBI | RecName: Full=P | 2562.2 | 0 | 1 |
| gi\|162458095\|ref\|NP_001105503.1\| | phosphoenolpyru | 2561.5 | 0 | 1 |
| gi\|6688531\|emb\|CAB65170.1\| | phosphoenolpyru | 2560.4 | 0 | 1 |
| gi\|12697498\|emb\|CAC28225.1\| | phosphoenolpyru | 2560.2 | 0 | 1 |
| gi\|218190390\|gb\|EEC72817.1\| | hypothetical pr | 2559.5 | 0 | 1 |
| gi\|40354190\|gb\|AAR84575.1\| | C3 phosphoenolp | 2558.3 | 0 | 1 |
| gi\|15219272\|ref\|NP_175738.1\| | ATPPC1 (PHOSPHO | 2557.3 | 0 | 1 |
| gi\|1705587\|sp\|P51061.1\|CAPP2_SOYBN | RecName: Full=P | 2556.7 | 0 | 1 |
| gi\|37785629\|gb\|AAP43628.1\| | phosphoenolpyru | 2556.2 | 0 | 1 |
| gi\|15232442\|ref\|NP_188112.1\| | ATPPC3 (PHOSPHO | 2555.0 | 0 | 1 |
| gi\|115445275\|ref\|NP_001046417.1\| | Os02g0244700 [O | 2554.8 | 0 | 1 |
| gi\|9828445\|gb\|AAG00180.1\|AF271995_1 | phosphoenolpyru | 2554.8 | 0 | 1 |
| gi\|23503558\|dbj\|BAC20365.1\| | phosphoenolpyru | 2554.8 | 0 | 1 |
| gi\|240254631\|ref\|NP_850373.4\| | ATPPC2 (PHOSPHO | 2554.7 | 0 | 1 |
| gi\|242048870\|ref\|XP_002462179.1\| | hypothetical pr | 2553.8 | 0 | 1 |
| gi\|222423984\|dbj\|BAH19953.1\| | AT1G53310 [Arab | 2553.6 | 0 | 1 |
| gi\|226320260\|gb\|ACO48251.1\| | phosphoenolpyru | 2553.2 | 0 | 1 |
| gi\|20141087\|gb\|AAK58635.2\|AF271161_1 | phosphoenolpyru | 2550.1 | 0 | 1 |
| gi\|399183\|sp\|Q02735.1\|CAPP_MEDSA | RecName: Full=P | 2549.9 | 0 | 1 |
| gi\|25901017\|dbj\|BAC41249.1\| | phosphoenolpyru | 2549.7 | 0 | 1 |
| gi\|28416715\|gb\|AAO42888.1\| | At3g14940 [Arab | 2549.5 | 0 | 1 |
| gi\|2626743\|dbj\|BAA23419.1\| | phosphoenolpyru | 2547.8 | 0 | 1 |
| gi\|26800701\|emb\|CAD58726.1\| | phosphoenolpyru | 2547.1 | 0 | 1 |
| gi\|14279574\|gb\|AAK58637.1\|AF271163_1 | phosphoenolpyru | 2545.4 | 0 | 1 |
| gi\|4033351\|emb\|CAA11415.1\| | phosphoenolpyru | 2545.2 | 0 | 1 |
| gi\|115583\|sp\|P29194.1\|CAPP2_SORBI | RecName: Full=P | 2544.9 | 0 | 1 |
| gi\|242078871\|ref\|XP_002444204.1\| | hypothetical pr | 2540.4 | 0 | 1 |
| gi\|224068767\|ref\|XP_002302820.1\| | predicted prote | 2539.8 | 0 | 1 |
| gi\|51574149\|gb\|AAU07998.1\| | phosphoenolpyru | 2537.8 | 0 | 1 |
| gi\|115476100\|ref\|NP_001061646.1\| | Os08g0366000 [O | 2536.9 | 0 | 1 |
| gi\|25901015\|dbj\|BAC41248.1\| | phosphoenolpyru | 2535.5 | 0 | 1 |
| gi\|829295\|emb\|CAA27270.1\| | PEPCase [Zea ma | 2534.0 | 0 | 1 |
| gi\|24636262\|sp\|Q9AU12.1\|CAPP_PHAVU | RecName: Full=P | 2532.8 | 0 | 1 |
| gi\|4033349\|emb\|CAA11414.1\| | phosphoenolpyro | 2532.7 | 0 | 1 |
| gi\|14279572\|gb\|AAK58636.1\|AF271162_1 | phosphoenolpyru | 2530.3 | 0 | 1 |
| gi\|162458345\|ref\|NP_001105438.1\| | phosphoenolpyru | 2529.8 | 0 | 1 |
| gi\|226320258\|gb\|ACO48250.1\| | phosphoenolpyru | 2528.2 | 0 | 1 |
| gi\|30088841\|gb\|AAP06951.1\| | phosphoenolpyru | 2527.6 | 0 | 1 |
| gi\|51574151\|gb\|AAU07999.1\| | phosphoenolpyru | 2526.5 | 0 | 1 |
| gi\|115577\|sp\|P29193.1\|CAPP1_SACHY | RecName: Full=P | 2524.1 | 0 | 1 |
| gi\|23503556\|dbj\|BAC20364.1\| | phosphoenolpyru | 2520.1 | 0 | 1 |
| gi\|27657589\|emb\|CAC83482.1\| | phosphoenolpyru | 2517.5 | 0 | 1 |
| gi\|5616255\|gb\|AAD45696.1\|AF159051_1 | phosphoenolpyru | 2515.3 | 0 | 1 |
| gi\|148908467\|gb\|ABR17346.1\| | unknown [Picea | 2515.3 | 0 | 1 |
| gi\|125563186\|gb\|EAZ08566.1\| | hypothetical pr | 2515.1 | 0 | 1 |
| gi\|27657587\|emb\|CAC83481.1\| | phosphoenolpyru | 2514.0 | 0 | 1 |
| gi\|27948554\|gb\|AAO25631.1\| | phosphoenolpyru | 2512.6 | 0 | 1 |
| gi\|3341490\|emb\|CAA07610.1\| | phospoenolpyruv | 2512.6 | 0 | 1 |
| gi\|222619275\|gb\|EEE55407.1\| | hypothetical pr | 2512.3 | 0 | 1 |
| gi\|3649776\|emb\|CAA09588.1\| | phosphoenolpyru | 2512.2 | 0 | 1 |
| gi\|51091643\|dbj\|BAD36412.1\| | putative phosph | 2511.8 | 0 | 1 |
| gi\|115478504\|ref\|NP_001062847.1\| | Os09g0315700 [O | 2511.8 | 0 | 1 |
| gi\|157279525\|dbj\|BAF80187.1\| | phosphoenolpyru | 2511.5 | 0 | 1 |
| gi\|1705590\|sp\|P51063.1\|CAPP_PICAB | RecName: Full=P | 2511.4 | 0 | 1 |
| gi\|63053872\|gb\|AAY28731.1\| | phosphoenolpyru | 2510.9 | 0 | 1 |

| | | | | | |
|---|---|---|---|---|---|
| gi\|63053870\|gb\|AAY28730.1\| | phosphoenolpyru | 2510.6 | 0 | 1 |
| gi\|1705589\|sp\|P51062.1\|CAPP_PEA | RecName: Full=P | 2509.4 | 0 | 1 |
| gi\|89363537\|emb\|CAJ84247.1\| | phosphoenolpyru | 2508.7 | 0 | 1 |
| gi\|51574147\|gb\|AAU07997.1\| | phosphoenolpyru | 2504.3 | 0 | 1 |
| gi\|242058751\|ref\|XP_002458521.1\| | hypothetical pr | 2502.5 | 0 | 1 |
| gi\|270232663\|emb\|CBI21984.1\| | unnamed protein | 2495.8 | 0 | 1 |
| gi\|270230868\|emb\|CBI20195.1\| | unnamed protein | 2493.6 | 0 | 1 |
| gi\|3777449\|emb\|CAA09807.1\| | ppc2 [Solanum t | 2490.3 | 0 | 1 |
| gi\|20257597\|gb\|AAM15963.1\|AF495586_1 | putative C4 pho | 2489.3 | 0 | 1 |
| gi\|108742705\|gb\|ABG01962.1\| | phosphoenolpyru | 2480.0 | 0 | 1 |
| gi\|507808\|dbj\|BAA03094.1\| | phosphoenolpyru | 2469.1 | 0 | 1 |
| gi\|6688533\|emb\|CAB65171.1\| | phosphoenolpyru | 2466.8 | 0 | 1 |
| gi\|27462753\|gb\|AAO15570.1\|AF459644_1 | phosphoenolpyru | 2466.2 | 0 | 1 |
| gi\|90652448\|emb\|CAJ86550.1\| | phosphoenolpyro | 2464.6 | 0 | 1 |
| gi\|63053868\|gb\|AAY28729.1\| | phosphoenolpyru | 2460.0 | 0 | 1 |
| gi\|18073908\|emb\|CAC86034.1\| | phosphoenolpyru | 2459.1 | 0 | 1 |
| gi\|23491823\|dbj\|BAC19851.1\| | phosphoenolpyru | 2433.1 | 0 | 1 |
| gi\|115575\|sp\|P10490.1\|CAPP1_MESCR | RecName: Full=P | 2430.6 | 0 | 1 |
| gi\|4877832\|gb\|AAD31452.1\|AF135371_1 | phosphoenol pyr | 2430.1 | 0 | 1 |
| gi\|11991545\|gb\|AAG42288.1\| | phosphoenolpyru | 2427.4 | 0 | 1 |
| gi\|219944332\|gb\|AAX98688.3\| | C4 phosphoenolp | 2427.2 | 0 | 1 |
| gi\|225461662\|ref\|XP_002285442.1\| | PREDICTED: hypo | 2424.8 | 0 | 1 |
| gi\|1870188\|emb\|CAA60627.1\| | phosphoenolpyru | 2416.6 | 0 | 1 |
| gi\|164449187\|gb\|ABY56044.1\| | phosphoenolpyru | 2414.4 | 0 | 1 |
| gi\|225446611\|ref\|XP_002280580.1\| | PREDICTED: hypo | 2412.2 | 0 | 1 |
| gi\|2499465\|sp\|Q43299.1\|CAPP_AMAHP | RecName: Full=P | 2408.9 | 0 | 1 |
| gi\|22347639\|gb\|AAM95946.1\| | phosphoenolpyru | 2399.6 | 0 | 1 |
| gi\|149364113\|gb\|ABR24265.1\| | PhtY [Microbact | 2397.4 | 0 | 1 |
| gi\|2145481\|emb\|CAA62747.1\| | phosphoenolpyru | 2396.7 | 0 | 1 |
| gi\|222622510\|gb\|EEE56642.1\| | hypothetical pr | 2384.8 | 0 | 1 |
| gi\|108782494\|gb\|ABG20459.1\| | phosphoenolpyru | 2382.3 | 0 | 1 |
| gi\|1870190\|emb\|CAA60626.1\| | phosphoenolpyru | 2377.7 | 0 | 1 |
| gi\|4559332\|gb\|AAD22994.1\| | phosphoenolpyru | 2371.1 | 0 | 1 |
| gi\|115440043\|ref\|NP_001044301.1\| | Os01g0758300 [O | 2368.5 | 0 | 1 |
| gi\|115435200\|ref\|NP_001042358.1\| | Os01g0208700 [O | 2286.8 | 0 | 1 |
| gi\|168027443\|ref\|XP_001766239.1\| | predicted prote | 2225.4 | 0 | 1 |
| gi\|168061648\|ref\|XP_001782799.1\| | predicted prote | 2221.4 | 0 | 1 |
| gi\|125524860\|gb\|EAY72974.1\| | hypothetical pr | 2208.1 | 0 | 1 |
| gi\|168010333\|ref\|XP_001757859.1\| | predicted prote | 2189.0 | 0 | 1 |
| gi\|168016115\|ref\|XP_001760595.1\| | predicted prote | 2182.3 | 0 | 1 |
| gi\|168042979\|ref\|XP_001773964.1\| | predicted prote | 2153.6 | 0 | 1 |
| gi\|168044057\|ref\|XP_001774499.1\| | predicted prote | 2109.2 | 0 | 1 |
| gi\|108782496\|gb\|ABG20460.1\| | phosphoenolpyru | 2073.5 | 0 | 1 |
| gi\|290350842\|dbj\|BAI78342.1\| | phosphoenolpyru | 1988.5 | 0 | 1 |
| gi\|20152211\|dbj\|BAB89367.1\| | phosphoenolpyru | 1987.4 | 0 | 1 |
| gi\|108782498\|gb\|ABG20461.1\| | phosphoenolpyru | 1987.3 | 0 | 1 |
| gi\|20152209\|dbj\|BAB89366.1\| | phosphoenolpyru | 1782.0 | 0 | 1 |
| gi\|125527770\|gb\|EAY75884.1\| | hypothetical pr | 1605.5 | 0 | 1 |
| gi\|3649778\|emb\|CAA09589.1\| | pepc2 [Vicia fa | 1566.1 | 0 | 1 |
| gi\|219884355\|gb\|ACL52552.1\| | unknown [Zea ma | 1415.5 | 0 | 1 |
| gi\|38044102\|dbj\|BAB89368.2\| | phosphoenolpyru | 1363.6 | 0 | 1 |
| gi\|2145477\|emb\|CAA62749.1\| | phosphoenolpyru | 1342.0 | 0 | 1 |
| gi\|108782500\|gb\|ABG20462.1\| | phosphoenolpyru | 1341.1 | 0 | 1 |
| gi\|283896826\|emb\|CAX65714.1\| | phosphoenolpyru | 1305.7 | 0 | 1 |
| gi\|254587351\|emb\|CAR63824.1\| | phosphoenolpyru | 1298.7 | 0 | 1 |
| gi\|283898028\|emb\|CAX65715.1\| | phosphoenolpyru | 1277.0 | 0 | 1 |
| gi\|218201055\|gb\|EEC83482.1\| | hypothetical pr | 1259.9 | 0 | 1 |
| gi\|254587353\|emb\|CAR63825.1\| | phosphoenolpyru | 1255.8 | 0 | 1 |
| gi\|154146668\|emb\|CAM83969.1\| | phosphoenolpyru | 1241.8 | 0 | 1 |
| gi\|154146674\|emb\|CAM83972.1\| | phosphoenolpyru | 1240.3 | 0 | 1 |
| gi\|255071487\|ref\|XP_002499417.1\| | phosphoenolpyru | 1222.3 | 0 | 1 |
| gi\|226463760\|gb\|EEH61038.1\| | predicted prote | 1207.4 | 0 | 1 |
| gi\|2145463\|emb\|CAA62748.1\| | phosphoenolpyru | 1179.5 | 0 | 1 |
| gi\|51701301\|sp\|P81831.2\|CAPP1_CHLRE | RecName: Full=P | 1170.8 | 0 | 1 |
| gi\|154146672\|emb\|CAM83971.1\| | phosphoenolpyru | 1144.6 | 0 | 1 |
| gi\|116060913\|emb\|CAL57391.1\| | phosphoenolpyru | 1123.2 | 0 | 1 |
| gi\|145353090\|ref\|XP_001420862.1\| | predicted prote | 1108.1 | 0 | 1 |
| gi\|154146670\|emb\|CAM83970.1\| | phosphoenolpyru | 1051.9 | 0 | 1 |
| gi\|88813079\|ref\|ZP_01128321.1\| | phosphoenolpyru | 899.6 | 1.6e-267 | 1 |
| gi\|281207688\|gb\|EFA81868.1\| | Phosphoenolpyru | 888.9 | 2.7e-264 | 1 |
| gi\|114319423\|ref\|YP_741106.1\| | phosphoenolpyru | 857.8 | 6e-255 | 1 |

| | | | | |
|---|---|---|---|---|
| gi\|255561196\|ref\|XP_002521610.1\| | Phosphoenolpyru | 846.2 | 1.9e-251 | 1 |
| gi\|70671531\|gb\|AAZ06136.1\| | phosphoenolpyru | 825.6 | 3e-245 | 1 |
| gi\|152995284\|ref\|YP_001340119.1\| | phosphoenolpyru | 817.4 | 9.2e-243 | 1 |
| gi\|226320262\|gb\|ACO48252.1\| | phosphoenolpyru | 811.9 | 4e-241 | 1 |
| gi\|83644641\|ref\|YP_433076.1\| | phosphoenolpyru | 808.3 | 4.9e-240 | 1 |
| gi\|12324139\|gb\|AAG52040.1\|AC011914_10 | putative phosph | 807.9 | 6.5e-240 | 1 |
| gi\|87118647\|ref\|ZP_01074546.1\| | phosphoenolpyru | 807.1 | 1.1e-239 | 1 |
| gi\|89094559\|ref\|ZP_01167497.1\| | phosphoenolpyru | 806.6 | 1.6e-239 | 1 |
| gi\|115434082\|ref\|NP_001041799.1\| | Os01g0110700 [O | 804.7 | 6e-239 | 1 |
| gi\|30697740\|ref\|NP_177043.2\| | ATPPC4; phospho | 804.2 | 8.2e-239 | 1 |
| gi\|119476550\|ref\|ZP_01616901.1\| | phosphoenolpyru | 801.7 | 4.9e-238 | 1 |
| gi\|149911768\|ref\|ZP_01900373.1\| | phosphoenolpyru | 798.3 | 4.9e-237 | 1 |
| gi\|149789412\|gb\|ABR29877.1\| | phosphoenolpyru | 798.2 | 5.4e-237 | 1 |
| gi\|224284385\|gb\|ACN39927.1\| | unknown [Picea | 795.9 | 2.6e-236 | 1 |
| gi\|237806868\|ref\|YP_002891308.1\| | Phosphoenolpyru | 795.8 | 2.9e-236 | 1 |
| gi\|254508198\|ref\|ZP_05120323.1\| | phosphoenolpyru | 794.3 | 8.3e-236 | 1 |
| gi\|262370772\|ref\|ZP_06064096.1\| | phosphoenolpyru | 793.1 | 1.8e-235 | 1 |
| gi\|242052357\|ref\|XP_002455324.1\| | hypothetical pr | 790.8 | 9.1e-235 | 1 |
| gi\|156972425\|ref\|YP_001443332.1\| | phosphoenolpyru | 790.7 | 9.7e-235 | 1 |
| gi\|5734703\|gb\|AAD49968.1\|AC008075_1 | Similar to gb\|X | 790.4 | 1.2e-234 | 1 |
| gi\|90407116\|ref\|ZP_01215305.1\| | phosphoenolpyru | 789.9 | 1.6e-234 | 1 |
| gi\|50086573\|ref\|YP_048083.1\| | phosphoenolpyru | 789.6 | 2.1e-234 | 1 |
| gi\|254229794\|ref\|ZP_04923201.1\| | phosphoenolpyru | 788.8 | 3.7e-234 | 1 |
| gi\|145297649\|ref\|YP_001140490.1\| | phosphoenolpyru | 787.7 | 7.7e-234 | 1 |
| gi\|149189173\|ref\|ZP_01867460.1\| | phosphoenolpyru | 787.6 | 8.5e-234 | 1 |
| gi\|262280608\|ref\|ZP_06058392.1\| | phosphoenolpyru | 787.3 | 1e-233 | 1 |
| gi\|45505267\|gb\|AAS67005.1\| | Phosphoenolpyru | 787.1 | 1.2e-233 | 1 |
| gi\|255318037\|ref\|ZP_05359282.1\| | phosphoenolpyru | 787.0 | 1.3e-233 | 1 |
| gi\|90580872\|ref\|ZP_01236674.1\| | phosphoenolpyru | 786.9 | 1.3e-233 | 1 |
| gi\|262380617\|ref\|ZP_06073771.1\| | phosphoenolpyru | 786.7 | 1.5e-233 | 1 |
| gi\|271498759\|ref\|YP_003331784.1\| | Phosphoenolpyru | 786.0 | 2.5e-233 | 1 |
| gi\|292826793\|gb\|EFF85158.1\| | conserved hypot | 785.9 | 2.6e-233 | 1 |
| gi\|149374698\|ref\|ZP_01892472.1\| | phosphoenolpyru | 785.8 | 2.9e-233 | 1 |
| gi\|239502757\|ref\|ZP_04662067.1\| | phosphoenolpyru | 785.7 | 3e-233 | 1 |
| gi\|152972745\|ref\|YP_001337891.1\| | phosphoenolpyru | 785.3 | 4e-233 | 1 |
| gi\|121999069\|ref\|YP_001003856.1\| | phosphoenolpyru | 784.9 | 5.6e-233 | 1 |
| gi\|126643456\|ref\|YP_001086440.1\| | phosphoenolpyru | 784.8 | 5.8e-233 | 1 |
| gi\|169634906\|ref\|YP_001708642.1\| | phosphoenolpyru | 784.8 | 6e-233 | 1 |
| gi\|50119147\|ref\|YP_048314.1\| | phosphoenolpyru | 784.5 | 7e-233 | 1 |
| gi\|226945972\|ref\|YP_002801045.1\| | Phosphoenolpyru | 784.1 | 9.5e-233 | 1 |
| gi\|260553863\|ref\|ZP_05826131.1\| | phosphoenolpyru | 784.0 | 1e-232 | 1 |
| gi\|229588773\|ref\|YP_002870892.1\| | phosphoenolpyru | 783.6 | 1.3e-232 | 1 |
| gi\|169794232\|ref\|YP_001712025.1\| | phosphoenolpyru | 782.9 | 2.2e-232 | 1 |
| gi\|213158772\|ref\|YP_002321193.1\| | phosphoenolpyru | 782.8 | 2.3e-232 | 1 |
| gi\|251791486\|ref\|YP_003006207.1\| | Phosphoenolpyru | 782.7 | 2.5e-232 | 1 |
| gi\|262393083\|ref\|YP_003284937.1\| | phosphoenolpyru | 782.3 | 3.3e-232 | 1 |
| gi\|261823543\|ref\|YP_003261649.1\| | Phosphoenolpyru | 782.0 | 4e-232 | 1 |
| gi\|117621332\|ref\|YP_855124.1\| | phosphoenolpyru | 781.7 | 4.9e-232 | 1 |
| gi\|262273438\|ref\|ZP_06051252.1\| | phosphoenolpyru | 781.7 | 5.1e-232 | 1 |
| gi\|77457296\|ref\|YP_346801.1\| | phosphoenolpyru | 781.6 | 5.3e-232 | 1 |
| gi\|91227300\|ref\|ZP_01261725.1\| | phosphoenolpyru | 781.4 | 6.3e-232 | 1 |
| gi\|71735722\|ref\|YP_276003.1\| | phosphoenolpyru | 781.2 | 7.2e-232 | 1 |
| gi\|89075195\|ref\|ZP_01161626.1\| | phosphoenolpyru | 780.8 | 9.1e-232 | 1 |
| gi\|253690426\|ref\|YP_003019616.1\| | Phosphoenolpyru | 780.7 | 1e-231 | 1 |
| gi\|28807771\|dbj\|BAC61024.1\| | phosphoenolpyru | 780.4 | 1.2e-231 | 1 |
| gi\|70728529\|ref\|YP_258278.1\| | phosphoenolpyru | 779.7 | 2e-231 | 1 |
| gi\|242237649\|ref\|YP_002985830.1\| | Phosphoenolpyru | 778.7 | 4e-231 | 1 |
| gi\|227327296\|ref\|ZP_03831320.1\| | phosphoenolpyru | 778.5 | 4.6e-231 | 1 |
| gi\|163802795\|ref\|ZP_02196685.1\| | phosphoenolpyru | 778.4 | 5e-231 | 1 |
| gi\|260779573\|ref\|ZP_05888463.1\| | phosphoenolpyru | 777.9 | 6.9e-231 | 1 |
| gi\|227114312\|ref\|ZP_03827968.1\| | phosphoenolpyru | 777.8 | 7.7e-231 | 1 |
| gi\|238892353\|ref\|YP_002917087.1\| | phosphoenolpyru | 777.6 | 8.3e-231 | 1 |
| gi\|146308379\|ref\|YP_001188844.1\| | phosphoenolpyru | 777.4 | 9.7e-231 | 1 |
| gi\|120555149\|ref\|YP_959500.1\| | phosphoenolpyru | 777.2 | 1.1e-230 | 1 |
| gi\|37199939\|dbj\|BAC95768.1\| | phosphoenolpyru | 777.1 | 1.2e-230 | 1 |
| gi\|46911906\|emb\|CAG18704.1\| | putative phosph | 777.0 | 1.3e-230 | 1 |
| gi\|205359957\|ref\|ZP_02833529.2\| | phosphoenolpyru | 776.4 | 2e-230 | 1 |
| gi\|261254127\|ref\|ZP_05946700.1\| | phosphoenolpyru | 775.8 | 2.9e-230 | 1 |
| gi\|262376807\|ref\|ZP_06070034.1\| | phosphoenolpyru | 775.6 | 3.4e-230 | 1 |
| gi\|289626060\|ref\|ZP_06459014.1\| | phosphoenolpyru | 775.3 | 4.1e-230 | 1 |
| gi\|104780469\|ref\|YP_606967.1\| | phosphoenolpyru | 775.3 | 4.3e-230 | 1 |

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|---|---|---|---|---|
| gi\|66806573\|ref\|XP_637009.1\| | hypothetical pr | 775.2 | 4.6e-230 | 1 |
| gi\|197336287\|ref\|YP_002157103.1\| | phosphoenolpyru | 774.6 | 6.7e-230 | 1 |
| gi\|197300985\|ref\|ZP_02662800.2\| | phosphoenolpyru | 774.5 | 7.4e-230 | 1 |
| gi\|161936338\|ref\|YP_128506.2\| | phosphoenolpyru | 774.3 | 8.4e-230 | 1 |
| gi\|170723273\|ref\|YP_001750961.1\| | phosphoenolpyru | 774.1 | 9.4e-230 | 1 |
| gi\|153839017\|ref\|ZP_01991684.1\| | phosphoenolpyru | 774.1 | 9.9e-230 | 1 |
| gi\|268593405\|ref\|ZP_06127626.1\| | phosphoenolpyru | 773.6 | 1.4e-229 | 1 |
| gi\|209696160\|ref\|YP_002264090.1\| | phosphoenolpyru | 772.7 | 2.5e-229 | 1 |
| gi\|218551053\|ref\|YP_002384844.1\| | phosphoenolpyru | 772.0 | 4.2e-229 | 1 |
| gi\|27364763\|ref\|NP_760291.1\| | phosphoenolpyru | 771.7 | 5.3e-229 | 1 |
| gi\|194471160\|ref\|ZP_03077144.1\| | phosphoenolpyru | 771.6 | 5.6e-229 | 1 |
| gi\|26988237\|ref\|NP_743662.1\| | phosphoenolpyru | 771.4 | 6.2e-229 | 1 |
| gi\|261211215\|ref\|ZP_05925504.1\| | phosphoenolpyru | 771.3 | 6.7e-229 | 1 |
| gi\|167032123\|ref\|YP_001667354.1\| | phosphoenolpyru | 771.1 | 8e-229 | 1 |
| gi\|170769681\|ref\|ZP_02904134.1\| | phosphoenolpyru | 771.0 | 8.2e-229 | 1 |
| gi\|161486595\|ref\|NP_935797.2\| | phosphoenolpyru | 770.7 | 1e-228 | 1 |
| gi\|91213504\|ref\|YP_543490.1\| | phosphoenolpyru | 770.6 | 1.1e-228 | 1 |
| gi\|148977256\|ref\|ZP_01813883.1\| | phosphoenolpyru | 770.5 | 1.2e-228 | 1 |
| gi\|90413609\|ref\|ZP_01221599.1\| | phosphoenolpyru | 770.2 | 1.5e-228 | 1 |
| gi\|261346852\|ref\|ZP_05974496.1\| | phosphoenolpyru | 769.9 | 1.8e-228 | 1 |
| gi\|212712498\|ref\|ZP_03320626.1\| | hypothetical pr | 769.8 | 2e-228 | 1 |
| gi\|260770868\|ref\|ZP_05879797.1\| | phosphoenolpyru | 769.6 | 2.2e-228 | 1 |
| gi\|148549423\|ref\|YP_001269525.1\| | phosphoenolpyru | 769.3 | 2.7e-228 | 1 |
| gi\|269103968\|ref\|ZP_06156665.1\| | phosphoenolpyru | 769.2 | 2.9e-228 | 1 |
| gi\|206577729\|ref\|YP_002241183.1\| | phosphoenolpyru | 769.2 | 2.9e-228 | 1 |
| gi\|59712915\|ref\|YP_205691.1\| | phosphoenolpyru | 769.2 | 2.9e-228 | 1 |
| gi\|66044566\|ref\|YP_234407.1\| | phosphoenolpyru | 768.9 | 3.5e-228 | 1 |
| gi\|161505390\|ref\|YP_001572502.1\| | phosphoenolpyru | 768.2 | 5.9e-228 | 1 |
| gi\|16762323\|ref\|NP_457940.1\| | phosphoenolpyru | 768.0 | 6.5e-228 | 1 |
| gi\|194737003\|ref\|YP_002117033.1\| | phosphoenolpyru | 767.7 | 8e-228 | 1 |
| gi\|238921689\|ref\|YP_002935204.1\| | phosphoenolpyru | 767.5 | 9.1e-228 | 1 |
| gi\|269140825\|ref\|YP_003297526.1\| | phosphoenolpyru | 767.4 | 1e-227 | 1 |
| gi\|194433218\|ref\|ZP_03065499.1\| | phosphoenolpyru | 767.2 | 1.2e-227 | 1 |
| gi\|24115246\|ref\|NP_709756.1\| | phosphoenolpyru | 767.2 | 1.2e-227 | 1 |
| gi\|254032062\|gb\|ACT54615.1\| | phosphoenolpyru | 767.1 | 1.2e-227 | 1 |
| gi\|16131794\|ref\|NP_418391.1\| | phosphoenolpyru | 767.0 | 1.3e-227 | 1 |
| gi\|15834139\|ref\|NP_312912.1\| | phosphoenolpyru | 766.7 | 1.7e-227 | 1 |
| gi\|26250729\|ref\|NP_756769.1\| | phosphoenolpyru | 766.6 | 1.7e-227 | 1 |
| gi\|110807812\|ref\|YP_691332.1\| | phosphoenolpyru | 766.5 | 1.8e-227 | 1 |
| gi\|170683041\|ref\|YP_001746348.1\| | phosphoenolpyru | 766.2 | 2.3e-227 | 1 |
| gi\|218692242\|ref\|YP_002400454.1\| | phosphoenolpyru | 766.2 | 2.4e-227 | 1 |
| gi\|291092305\|gb\|EFE24866.1\| | phosphoenolpyru | 766.0 | 2.7e-227 | 1 |
| gi\|218710807\|ref\|YP_002418428.1\| | phosphoenolpyru | 766.0 | 2.7e-227 | 1 |
| gi\|15804552\|ref\|NP_290593.1\| | phosphoenolpyru | 765.9 | 2.8e-227 | 1 |
| gi\|167551379\|ref\|ZP_02345134.1\| | phosphoenolpyru | 765.9 | 2.9e-227 | 1 |
| gi\|56415957\|ref\|YP_153032.1\| | phosphoenolpyru | 765.8 | 3e-227 | 1 |
| gi\|149200328\|ref\|ZP_01877347.1\| | phosphoenolpyru | 765.7 | 3.2e-227 | 1 |
| gi\|84390835\|ref\|ZP_00991527.1\| | phosphoenolpyru | 765.6 | 3.5e-227 | 1 |
| gi\|283787363\|ref\|YP_003367228.1\| | phosphoenolpyru | 765.5 | 3.9e-227 | 1 |
| gi\|260595982\|ref\|YP_003208553.1\| | Phosphoenolpyru | 765.2 | 4.8e-227 | 1 |
| gi\|86147311\|ref\|ZP_01065625.1\| | phosphoenolpyru | 765.1 | 4.9e-227 | 1 |
| gi\|290477219\|ref\|YP_003470136.1\| | phosphoenolpyru | 765.0 | 5.2e-227 | 1 |
| gi\|16767384\|ref\|NP_462999.1\| | phosphoenolpyru | 764.9 | 5.7e-227 | 1 |
| gi\|162420514\|ref\|YP_001608201.1\| | phosphoenolpyru | 764.5 | 7.4e-227 | 1 |
| gi\|121587916\|ref\|ZP_01677671.1\| | phosphoenolpyru | 764.3 | 8.5e-227 | 1 |
| gi\|197287040\|ref\|YP_002152912.1\| | phosphoenolpyru | 764.0 | 1e-226 | 1 |
| gi\|123440516\|ref\|YP_001004510.1\| | phosphoenolpyru | 763.6 | 1.4e-226 | 1 |
| gi\|62182579\|ref\|YP_218996.1\| | phosphoenolpyru | 763.1 | 2e-226 | 1 |
| gi\|121727604\|ref\|ZP_01680712.1\| | phosphoenolpyru | 763.0 | 2.1e-226 | 1 |
| gi\|183597325\|ref\|ZP_02958818.1\| | hypothetical pr | 762.9 | 2.3e-226 | 1 |
| gi\|237800119\|ref\|ZP_04588580.1\| | phosphoenolpyru | 762.1 | 3.9e-226 | 1 |
| gi\|157373015\|ref\|YP_001481004.1\| | phosphoenolpyru | 762.1 | 3.9e-226 | 1 |
| gi\|153830201\|ref\|ZP_01982868.1\| | phosphoenolpyru | 761.8 | 4.9e-226 | 1 |
| gi\|283834724\|ref\|ZP_06354465.1\| | phosphoenolpyru | 761.4 | 6.7e-226 | 1 |
| gi\|270265165\|ref\|ZP_06193427.1\| | phosphoenolpyru | 761.3 | 6.9e-226 | 1 |
| gi\|45437741\|gb\|AAS63291.1\| | phosphoenolpyru | 761.2 | 7.5e-226 | 1 |
| gi\|82546307\|ref\|YP_410254.1\| | phosphoenolpyru | 761.0 | 8.3e-226 | 1 |
| gi\|262041721\|ref\|ZP_06014913.1\| | phosphoenolpyru | 760.8 | 1e-225 | 1 |
| gi\|193063946\|ref\|ZP_03045032.1\| | phosphoenolpyru | 760.6 | 1.1e-225 | 1 |
| gi\|254285840\|ref\|ZP_04960802.1\| | phosphoenolpyru | 760.4 | 1.3e-225 | 1 |
| gi\|82778878\|ref\|YP_405227.1\| | phosphoenolpyru | 760.3 | 1.3e-225 | 1 |

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|---|---|---|---|---|
| gi\|205354304\|ref\|YP_002228105.1\| | phosphoenolpyru | 760.3 | 1.4e-225 | 1 |
| gi\|262170418\|ref\|ZP_06038096.1\| | phosphoenolpyru | 760.3 | 1.4e-225 | 1 |
| gi\|254225390\|ref\|ZP_04919001.1\| | phosphoenolpyru | 760.3 | 1.4e-225 | 1 |
| gi\|28868714\|ref\|NP_791333.1\| | phosphoenolpyru | 760.2 | 1.5e-225 | 1 |
| gi\|91791616\|ref\|YP_561267.1\| | phosphoenolpyru | 760.1 | 1.6e-225 | 1 |
| gi\|262166662\|ref\|ZP_06034399.1\| | phosphoenolpyru | 759.9 | 1.9e-225 | 1 |
| gi\|293393511\|ref\|ZP_06637821.1\| | phosphoenolpyru | 759.4 | 2.5e-225 | 1 |
| gi\|109896934\|ref\|YP_660189.1\| | phosphoenolpyru | 759.3 | 2.8e-225 | 1 |
| gi\|225423837\|ref\|XP_002280842.1\| | PREDICTED: hypo | 759.3 | 2.8e-225 | 1 |
| gi\|126667184\|ref\|ZP_01738158.1\| | phosphoenolpyru | 759.1 | 3.1e-225 | 1 |
| gi\|258625692\|ref\|ZP_05720571.1\| | Phosphoenolpyru | 759.1 | 3.2e-225 | 1 |
| gi\|213969092\|ref\|ZP_03397231.1\| | phosphoenolpyru | 758.9 | 3.7e-225 | 1 |
| gi\|52425072\|ref\|YP_088209.1\| | phosphoenolpyru | 758.7 | 4.2e-225 | 1 |
| gi\|258620479\|ref\|ZP_05715517.1\| | Phosphoenolpyru | 758.6 | 4.4e-225 | 1 |
| gi\|157147246\|ref\|YP_001454565.1\| | phosphoenolpyru | 758.6 | 4.5e-225 | 1 |
| gi\|262373873\|ref\|ZP_06067151.1\| | phosphoenolpyru | 758.1 | 6.3e-225 | 1 |
| gi\|291619398\|ref\|YP_003522140.1\| | Ppc [Pantoea an | 757.4 | 1e-224 | 1 |
| gi\|251792638\|ref\|YP_003007364.1\| | phosphoenolpyru | 756.9 | 1.5e-224 | 1 |
| gi\|229521712\|ref\|ZP_04411130.1\| | phosphoenolpyru | 756.7 | 1.7e-224 | 1 |
| gi\|51594466\|ref\|YP_068657.1\| | phosphoenolpyru | 756.5 | 1.9e-224 | 1 |
| gi\|108806093\|ref\|YP_650009.1\| | phosphoenolpyru | 756.3 | 2.3e-224 | 1 |
| gi\|229507302\|ref\|ZP_04396807.1\| | phosphoenolpyru | 756.2 | 2.4e-224 | 1 |
| gi\|107103201\|ref\|ZP_01367119.1\| | hypothetical pr | 756.0 | 2.7e-224 | 1 |
| gi\|15598883\|ref\|NP_252377.1\| | phosphoenolpyru | 756.0 | 2.8e-224 | 1 |
| gi\|253991711\|ref\|YP_003043067.1\| | phosphoenolpyru | 756.0 | 2.8e-224 | 1 |
| gi\|160877316\|ref\|YP_001556632.1\| | phosphoenolpyru | 755.0 | 5.3e-224 | 1 |
| gi\|238750857\|ref\|ZP_04612355.1\| | Phosphoenolpyru | 755.0 | 5.6e-224 | 1 |
| gi\|229513569\|ref\|ZP_04403033.1\| | phosphoenolpyru | 754.9 | 5.8e-224 | 1 |
| gi\|218890036\|ref\|YP_002438900.1\| | phosphoenolpyru | 754.8 | 6.1e-224 | 1 |
| gi\|161581981\|ref\|NP_232274.2\| | phosphoenolpyru | 754.6 | 7.1e-224 | 1 |
| gi\|262401934\|ref\|ZP_06078499.1\| | phosphoenolpyru | 754.2 | 9.7e-224 | 1 |
| gi\|157377410\|ref\|YP_001476010.1\| | phosphoenolpyru | 754.1 | 1e-223 | 1 |
| gi\|238789607\|ref\|ZP_04633391.1\| | Phosphoenolpyru | 753.9 | 1.2e-223 | 1 |
| gi\|119773395\|ref\|YP_926135.1\| | phosphoenolpyru | 753.9 | 1.2e-223 | 1 |
| gi\|262170106\|ref\|ZP_06037795.1\| | phosphoenolpyru | 753.3 | 1.7e-223 | 1 |
| gi\|153002595\|ref\|YP_001368276.1\| | phosphoenolpyru | 753.3 | 1.8e-223 | 1 |
| gi\|161511331\|ref\|NP_994414.2\| | phosphoenolpyru | 752.9 | 2.3e-223 | 1 |
| gi\|152987651\|ref\|YP_001346835.1\| | phosphoenolpyru | 752.8 | 2.4e-223 | 1 |
| gi\|156935917\|ref\|YP_001439833.1\| | phosphoenolpyru | 752.7 | 2.7e-223 | 1 |
| gi\|292825460\|gb\|EFF84201.1\| | phosphoenolpyru | 752.6 | 2.9e-223 | 1 |
| gi\|24371872\|ref\|NP_715914.1\| | phosphoenolpyru | 752.5 | 3e-223 | 1 |
| gi\|117922338\|ref\|YP_871530.1\| | phosphoenolpyru | 752.5 | 3.1e-223 | 1 |
| gi\|170724697\|ref\|YP_001758723.1\| | phosphoenolpyru | 752.4 | 3.4e-223 | 1 |
| gi\|146313662\|ref\|YP_001178736.1\| | phosphoenolpyru | 752.1 | 4e-223 | 1 |
| gi\|226953287\|ref\|ZP_03823751.1\| | phosphoenolpyru | 752.1 | 4.1e-223 | 1 |
| gi\|116051684\|ref\|YP_789477.1\| | phosphoenolpyru | 751.8 | 5.1e-223 | 1 |
| gi\|124548514\|ref\|ZP_01707155.1\| | phosphoenolpyru | 751.6 | 5.7e-223 | 1 |
| gi\|223670909\|dbj\|BAH22704.1\| | phosphoenolpyru | 751.5 | 6.4e-223 | 1 |
| gi\|237728069\|ref\|ZP_04558550.1\| | phosphoenolpyru | 751.1 | 8.3e-223 | 1 |
| gi\|145635078\|ref\|ZP_01790784.1\| | phosphoenolpyru | 751.0 | 8.7e-223 | 1 |
| gi\|260914089\|ref\|ZP_05920562.1\| | phosphoenolpyru | 750.9 | 9.2e-223 | 1 |
| gi\|259906836\|ref\|YP_002647192.1\| | Phosphoenolpyru | 750.3 | 1.4e-222 | 1 |
| gi\|119944012\|ref\|YP_941692.1\| | phosphoenolpyru | 750.2 | 1.5e-222 | 1 |
| gi\|292486630\|ref\|YP_003529500.1\| | Phosphoenolpyru | 749.8 | 2e-222 | 1 |
| gi\|114561377\|ref\|YP_748890.1\| | phosphoenolpyru | 749.2 | 3e-222 | 1 |
| gi\|145633038\|ref\|ZP_01788770.1\| | phosphoenolpyru | 749.1 | 3.3e-222 | 1 |
| gi\|37528563\|ref\|NP_931908.1\| | phosphoenolpyru | 748.9 | 3.8e-222 | 1 |
| gi\|147809570\|emb\|CAN62388.1\| | hypothetical pr | 748.5 | 4.8e-222 | 1 |
| gi\|258637583\|ref\|ZP_05730332.1\| | Phosphoenolpyru | 748.4 | 5.3e-222 | 1 |
| gi\|15602411\|ref\|NP_245483.1\| | phosphoenolpyru | 747.9 | 7.6e-222 | 1 |
| gi\|196155561\|ref\|YP_002125050.1\| | phosphoenolpyru | 747.7 | 8.5e-222 | 1 |
| gi\|120600645\|ref\|YP_965219.1\| | phosphoenolpyru | 747.3 | 1.1e-221 | 1 |
| gi\|146294801\|ref\|YP_001185225.1\| | phosphoenolpyru | 747.2 | 1.2e-221 | 1 |
| gi\|188532292\|ref\|YP_001906089.1\| | phosphoenolpyru | 747.1 | 1.3e-221 | 1 |
| gi\|261343020\|ref\|ZP_05970878.1\| | hypothetical pr | 747.0 | 1.4e-221 | 1 |
| gi\|126176310\|ref\|YP_001052459.1\| | phosphoenolpyru | 746.7 | 1.7e-221 | 1 |
| gi\|260772057\|ref\|ZP_05880974.1\| | phosphoenolpyru | 746.0 | 2.8e-221 | 1 |
| gi\|167626000\|ref\|YP_001676294.1\| | phosphoenolpyru | 745.9 | 2.9e-221 | 1 |
| gi\|145630943\|ref\|ZP_01786719.1\| | phosphoenolpyru | 745.0 | 5.7e-221 | 1 |
| gi\|157960054\|ref\|YP_001500088.1\| | phosphoenolpyru | 745.0 | 5.7e-221 | 1 |
| gi\|148828375\|ref\|YP_001293128.1\| | phosphoenolpyru | 744.9 | 6.1e-221 | 1 |

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|---|---|---|---|---|
| gi\|229846259\|ref\|ZP_04466371.1\| | phosphoenolpyru | 744.6 | 7.4e-221 | 1 |
| gi\|113972037\|ref\|YP_735830.1\| | phosphoenolpyru | 744.6 | 7.4e-221 | 1 |
| gi\|238754721\|ref\|ZP_04616073.1\| | Phosphoenolpyru | 744.4 | 8.5e-221 | 1 |
| gi\|68249774\|ref\|YP_248886.1\| | phosphoenolpyru | 743.5 | 1.6e-220 | 1 |
| gi\|145627780\|ref\|ZP_01783581.1\| | phosphoenolpyru | 743.4 | 1.7e-220 | 1 |
| gi\|114045747\|ref\|YP_736297.1\| | phosphoenolpyru | 743.2 | 1.9e-220 | 1 |
| gi\|229844816\|ref\|ZP_04464954.1\| | phosphoenolpyru | 740.3 | 1.5e-219 | 1 |
| gi\|238764489\|ref\|ZP_04625437.1\| | Phosphoenolpyru | 740.1 | 1.7e-219 | 1 |
| gi\|212634871\|ref\|YP_002311396.1\| | Phosphoenolpyru | 739.9 | 2e-219 | 1 |
| gi\|16273525\|ref\|NP_439778.1\| | phosphoenolpyru | 739.8 | 2.1e-219 | 1 |
| gi\|163751629\|ref\|ZP_02158849.1\| | phosphoenolpyru | 739.7 | 2.2e-219 | 1 |
| gi\|145639250\|ref\|ZP_01794856.1\| | phosphoenolpyru | 739.4 | 2.7e-219 | 1 |
| gi\|170717721\|ref\|YP_001784792.1\| | phosphoenolpyru | 739.4 | 2.7e-219 | 1 |
| gi\|238786115\|ref\|ZP_04630071.1\| | Phosphoenolpyru | 739.2 | 3e-219 | 1 |
| gi\|260582158\|ref\|ZP_05849952.1\| | phosphoenolpyru | 738.9 | 3.8e-219 | 1 |
| gi\|113461137\|ref\|YP_719205.1\| | phosphoenolpyru | 738.8 | 4.2e-219 | 1 |
| gi\|238798303\|ref\|ZP_04641787.1\| | Phosphoenolpyru | 738.7 | 4.6e-219 | 1 |
| gi\|238760149\|ref\|ZP_04621297.1\| | Phosphoenolpyru | 738.6 | 4.6e-219 | 1 |
| gi\|293329260\|dbj\|BAJ03991.1\| | phosphoenolpyru | 737.3 | 1.2e-218 | 1 |
| gi\|127511134\|ref\|YP_001092331.1\| | phosphoenolpyru | 737.2 | 1.2e-218 | 1 |
| gi\|126207823\|ref\|YP_001053048.1\| | phosphoenolpyru | 737.1 | 1.4e-218 | 1 |
| gi\|146283084\|ref\|YP_001173237.1\| | phosphoenolpyru | 733.7 | 1.4e-217 | 1 |
| gi\|190149613\|ref\|YP_001968138.1\| | phosphoenolpyru | 733.3 | 1.8e-217 | 1 |
| gi\|223998678\|ref\|XP_002289012.1\| | phosphoenolpyru | 732.3 | 3.8e-217 | 1 |
| gi\|32033610\|ref\|ZP_00133921.1\| | COG2352: Phosph | 732.1 | 4.2e-217 | 1 |
| gi\|148826161\|ref\|YP_001290914.1\| | phosphoenolpyru | 731.8 | 5.2e-217 | 1 |
| gi\|92113764\|ref\|YP_573692.1\| | phosphoenolpyru | 730.3 | 1.5e-216 | 1 |
| gi\|165975797\|ref\|YP_001651390.1\| | phosphoenolpyru | 730.1 | 1.7e-216 | 1 |
| gi\|53732877\|ref\|ZP_00155206.2\| | COG2352: Phosph | 728.6 | 4.9e-216 | 1 |
| gi\|283896778\|emb\|CAX65690.1\| | phosphoenolpyru | 728.1 | 6.9e-216 | 1 |
| gi\|219870613\|ref\|YP_002474988.1\| | phosphoenolpyru | 728.0 | 7.1e-216 | 1 |
| gi\|238794908\|ref\|ZP_04638507.1\| | Phosphoenolpyru | 727.4 | 1.1e-215 | 1 |
| gi\|262363644\|gb\|ACY60365.1\| | phosphoenolpyru | 727.3 | 1.2e-215 | 1 |
| gi\|110833541\|ref\|YP_692400.1\| | phosphoenolpyru | 726.7 | 1.8e-215 | 1 |
| gi\|167855566\|ref\|ZP_02478327.1\| | phosphoenolpyru | 726.6 | 2e-215 | 1 |
| gi\|46133363\|ref\|ZP_00157068.2\| | COG2352: Phosph | 726.5 | 2e-215 | 1 |
| gi\|125524127\|gb\|EAY72241.1\| | hypothetical pr | 726.5 | 2.1e-215 | 1 |
| gi\|254481871\|ref\|ZP_05095114.1\| | phosphoenolpyru | 724.7 | 7e-215 | 1 |
| gi\|283896806\|emb\|CAX65704.1\| | phosphoenolpyru | 720.9 | 9.7e-214 | 1 |
| gi\|283896784\|emb\|CAX65693.1\| | phosphoenolpyru | 720.7 | 1.2e-213 | 1 |
| gi\|283896814\|emb\|CAX65708.1\| | phosphoenolpyru | 719.1 | 3.5e-213 | 1 |
| gi\|293336483\|ref\|NP_001170654.1\| | hypothetical pr | 716.8 | 1.7e-212 | 1 |
| gi\|254784775\|ref\|YP_003072203.1\| | phosphoenolpyru | 716.0 | 2.9e-212 | 1 |
| gi\|255566797\|ref\|XP_002524382.1\| | conserved hypot | 714.5 | 8.5e-212 | 1 |
| gi\|213616153\|ref\|ZP_03371979.1\| | phosphoenolpyru | 714.1 | 1.2e-211 | 1 |
| gi\|254360733\|ref\|ZP_04976881.1\| | phosphoenolpyru | 712.6 | 3.2e-211 | 1 |
| gi\|261496916\|ref\|ZP_05993284.1\| | phosphoenolpyru | 711.6 | 6.2e-211 | 1 |
| gi\|94500599\|ref\|ZP_01307129.1\| | Phosphoenolpyru | 710.9 | 1e-210 | 1 |
| gi\|240949435\|ref\|ZP_04753776.1\| | phosphoenolpyru | 710.8 | 1.1e-210 | 1 |
| gi\|283896780\|emb\|CAX65691.1\| | phosphoenolpyru | 710.3 | 1.6e-210 | 1 |
| gi\|257465177\|ref\|ZP_05629548.1\| | phosphoenolpyru | 710.2 | 1.6e-210 | 1 |
| gi\|283896790\|emb\|CAX65696.1\| | phosphoenolpyru | 710.2 | 1.6e-210 | 1 |
| gi\|283896810\|emb\|CAX65706.1\| | phosphoenolpyru | 710.1 | 1.7e-210 | 1 |
| gi\|261492498\|ref\|ZP_05989052.1\| | phosphoenolpyru | 710.1 | 1.8e-210 | 1 |
| gi\|283896818\|emb\|CAX65710.1\| | phosphoenolpyru | 709.6 | 2.5e-210 | 1 |
| gi\|283896796\|emb\|CAX65699.1\| | phosphoenolpyru | 709.6 | 2.6e-210 | 1 |
| gi\|283896768\|emb\|CAX65685.1\| | phosphoenolpyru | 708.8 | 4.4e-210 | 1 |
| gi\|254514836\|ref\|ZP_05126897.1\| | phosphoenolpyru | 708.3 | 6.4e-210 | 1 |
| gi\|283896770\|emb\|CAX65686.1\| | phosphoenolpyru | 706.5 | 2.1e-209 | 1 |
| gi\|283896776\|emb\|CAX65689.1\| | phosphoenolpyru | 706.4 | 2.3e-209 | 1 |
| gi\|283896804\|emb\|CAX65703.1\| | phosphoenolpyru | 706.0 | 3.1e-209 | 1 |
| gi\|283896772\|emb\|CAX65687.1\| | phosphoenolpyru | 705.5 | 4.4e-209 | 1 |
| gi\|283896782\|emb\|CAX65692.1\| | phosphoenolpyru | 705.1 | 5.6e-209 | 1 |
| gi\|283896792\|emb\|CAX65697.1\| | phosphoenolpyru | 704.7 | 7.7e-209 | 1 |
| gi\|283896808\|emb\|CAX65705.1\| | phosphoenolpyru | 704.5 | 8.5e-209 | 1 |
| gi\|283896786\|emb\|CAX65694.1\| | phosphoenolpyru | 704.5 | 8.5e-209 | 1 |
| gi\|88857492\|ref\|ZP_01132135.1\| | phosphoenolpyru | 704.5 | 8.7e-209 | 1 |
| gi\|283896800\|emb\|CAX65701.1\| | phosphoenolpyru | 701.9 | 5.3e-208 | 1 |
| gi\|283896774\|emb\|CAX65688.1\| | phosphoenolpyru | 698.0 | 8e-207 | 1 |
| gi\|283896788\|emb\|CAX65695.1\| | phosphoenolpyru | 697.8 | 8.9e-207 | 1 |
| gi\|90023020\|ref\|YP_528847.1\| | phosphoenolpyru | 697.5 | 1.1e-206 | 1 |

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|---|---|---|---|---|
| gi\|167041901\|gb\|ABZ06640.1\| | putative phosph | 697.2 | 1.4e-206 | 1 |
| gi\|283896812\|emb\|CAX65707.1\| | phosphoenolpyru | 696.1 | 3e-206 | 1 |
| gi\|283896822\|emb\|CAX65712.1\| | phosphoenolpyru | 695.4 | 4.7e-206 | 1 |
| gi\|119468657\|ref\|ZP_01611709.1\| | phosphoenolpyru | 695.2 | 5.3e-206 | 1 |
| gi\|77362226\|ref\|YP_341800.1\| | phosphoenolpyru | 694.8 | 7.2e-206 | 1 |
| gi\|219120583\|ref\|XP_002181027.1\| | predicted prote | 692.2 | 4.4e-205 | 1 |
| gi\|59936824\|gb\|AAX12115.1\| | phosphoenolpyru | 690.6 | 1.3e-204 | 1 |
| gi\|283896816\|emb\|CAX65709.1\| | phosphoenolpyru | 689.7 | 2.5e-204 | 1 |
| gi\|283896794\|emb\|CAX65698.1\| | phosphoenolpyru | 689.4 | 3.1e-204 | 1 |
| gi\|192361093\|ref\|YP_001983406.1\| | phosphoenolpyru | 688.7 | 4.8e-204 | 1 |
| gi\|88706831\|ref\|ZP_01104531.1\| | Phosphoenolpyru | 688.0 | 8.3e-204 | 1 |
| gi\|283896798\|emb\|CAX65700.1\| | phosphoenolpyru | 687.6 | 1.1e-203 | 1 |
| gi\|283896824\|emb\|CAX65713.1\| | phosphoenolpyru | 686.0 | 3.2e-203 | 1 |
| gi\|283896802\|emb\|CAX65702.1\| | phosphoenolpyru | 682.0 | 5.2e-202 | 1 |
| gi\|114772589\|ref\|ZP_01449953.1\| | phosphoenolpyru | 674.5 | 9.2e-200 | 1 |
| gi\|283896820\|emb\|CAX65711.1\| | phosphoenolpyru | 669.3 | 3.3e-198 | 1 |
| gi\|219125106\|ref\|XP_002182829.1\| | predicted prote | 667.8 | 9.9e-198 | 1 |
| gi\|254282267\|ref\|ZP_04957235.1\| | phosphoenolpyru | 660.8 | 1.2e-195 | 1 |
| gi\|40063490\|gb\|AAR38290.1\| | phosphoenolpyru | 655.4 | 5.4e-194 | 1 |
| gi\|18645092\|gb\|AAL76393.1\| | phosphoenolpyru | 655.0 | 6.8e-194 | 1 |
| gi\|71083482\|ref\|YP_266201.1\| | phosphoenolpyru | 627.8 | 1e-185 | 1 |
| gi\|221060224\|ref\|XP_002260757.1\| | phosphoenolpyru | 626.7 | 2.2e-185 | 1 |
| gi\|270239854\|emb\|CBI27087.1\| | unnamed protein | 621.5 | 8.4e-184 | 1 |
| gi\|156102026\|ref\|XP_001616706.1\| | phosphoenolpyru | 606.1 | 3.6e-179 | 1 |
| gi\|254455801\|ref\|ZP_05069230.1\| | phosphoenolpyru | 605.0 | 7.9e-179 | 1 |
| gi\|224000774\|ref\|XP_002290059.1\| | phospoenolpyruv | 602.2 | 5.5e-178 | 1 |
| gi\|124808830\|ref\|XP_001348420.1\| | phosphoenolpyru | 581.6 | 8.4e-172 | 1 |
| gi\|51701320\|sp\|Q6R2V6.1\|CAPP2_CHLRE | RecName: Full=P | 572.7 | 4.1e-169 | 1 |
| gi\|83282693\|ref\|XP_729881.1\| | phosphoenolpyru | 567.8 | 1.2e-167 | 1 |
| gi\|68071185\|ref\|XP_677506.1\| | phosphoenolpyru | 567.4 | 1.7e-167 | 1 |
| gi\|145641160\|ref\|ZP_01796740.1\| | phosphoenolpyru | 554.2 | 1.5e-163 | 1 |
| gi\|154146762\|emb\|CAM84068.1\| | phosphoenolpyru | 538.3 | 9.3e-159 | 1 |
| gi\|154146754\|emb\|CAM84064.1\| | phosphoenolpyru | 538.2 | 1e-158 | 1 |
| gi\|154146800\|emb\|CAM84087.1\| | phosphoenolpyru | 537.9 | 1.3e-158 | 1 |
| gi\|154146808\|emb\|CAM84091.1\| | phosphoenolpyru | 537.0 | 2.3e-158 | 1 |
| gi\|154146746\|emb\|CAM84060.1\| | phosphoenolpyru | 535.9 | 5e-158 | 1 |
| gi\|154146724\|emb\|CAM84049.1\| | phosphoenolpyru | 535.4 | 6.8e-158 | 1 |
| gi\|154146788\|emb\|CAM84081.1\| | phosphoenolpyru | 535.0 | 9e-158 | 1 |
| gi\|154146830\|emb\|CAM84102.1\| | phosphoenolpyru | 534.6 | 1.2e-157 | 1 |
| gi\|154146878\|emb\|CAM84126.1\| | phosphoenolpyru | 524.3 | 1.5e-154 | 1 |
| gi\|154146834\|emb\|CAM84104.1\| | phosphoenolpyru | 523.3 | 3.1e-154 | 1 |
| gi\|154146768\|emb\|CAM84071.1\| | phosphoenolpyru | 516.3 | 3.9e-152 | 1 |
| gi\|154146820\|emb\|CAM84097.1\| | phosphoenolpyru | 514.5 | 1.3e-151 | 1 |
| gi\|167470809\|ref\|ZP_02335513.1\| | phosphoenolpyru | 513.3 | 3.1e-151 | 1 |
| gi\|629595\|pir\|\|PC2167 | phosphoenolpyru | 512.9 | 4.2e-151 | 1 |
| gi\|66357588\|ref\|XP_625972.1\| | phosphoenolpyru | 507.9 | 1.4e-149 | 1 |
| gi\|67594757\|ref\|XP_665868.1\| | phosphoenolpyru | 507.0 | 2.5e-149 | 1 |
| gi\|194689768\|gb\|ACF78968.1\| | unknown [Zea ma | 505.8 | 5.7e-149 | 1 |
| gi\|154146850\|emb\|CAM84112.1\| | phosphoenolpyru | 504.3 | 1.6e-148 | 1 |
| gi\|154146844\|emb\|CAM84109.1\| | phosphoenolpyru | 504.3 | 1.7e-148 | 1 |
| gi\|154146842\|emb\|CAM84108.1\| | phosphoenolpyru | 501.7 | 9.7e-148 | 1 |
| gi\|154146896\|emb\|CAM84135.1\| | phosphoenolpyru | 499.8 | 3.5e-147 | 1 |
| gi\|154146722\|emb\|CAM84048.1\| | phosphoenolpyru | 499.8 | 3.7e-147 | 1 |
| gi\|154146786\|emb\|CAM84080.1\| | phosphoenolpyru | 499.5 | 4.4e-147 | 1 |
| gi\|154146880\|emb\|CAM84127.1\| | phosphoenolpyru | 499.4 | 4.6e-147 | 1 |
| gi\|154146910\|emb\|CAM84142.1\| | phosphoenolpyru | 499.4 | 4.9e-147 | 1 |
| gi\|154146796\|emb\|CAM84085.1\| | phosphoenolpyru | 499.2 | 5.4e-147 | 1 |
| gi\|154146752\|emb\|CAM84063.1\| | phosphoenolpyru | 498.9 | 6.9e-147 | 1 |
| gi\|154146922\|emb\|CAM84148.1\| | phosphoenolpyru | 498.7 | 7.7e-147 | 1 |
| gi\|154146854\|emb\|CAM84114.1\| | phosphoenolpyru | 497.5 | 1.8e-146 | 1 |
| gi\|154146848\|emb\|CAM84111.1\| | phosphoenolpyru | 496.8 | 2.8e-146 | 1 |
| gi\|154146718\|emb\|CAM84046.1\| | phosphoenolpyru | 495.1 | 9.7e-146 | 1 |
| gi\|154146862\|emb\|CAM84118.1\| | phosphoenolpyru | 493.8 | 2.3e-145 | 1 |
| gi\|209881885\|ref\|XP_002142380.1\| | phosphoenolpyru | 491.0 | 1.6e-144 | 1 |
| gi\|154146782\|emb\|CAM84078.1\| | phosphoenolpyru | 490.4 | 2.4e-144 | 1 |
| gi\|154146916\|emb\|CAM84145.1\| | phosphoenolpyru | 490.0 | 3.3e-144 | 1 |
| gi\|154146882\|emb\|CAM84128.1\| | phosphoenolpyru | 489.1 | 6e-144 | 1 |
| gi\|154146852\|emb\|CAM84113.1\| | phosphoenolpyru | 487.7 | 1.6e-143 | 1 |
| gi\|154146838\|emb\|CAM84106.1\| | phosphoenolpyru | 485.2 | 8.8e-143 | 1 |
| gi\|154146832\|emb\|CAM84103.1\| | phosphoenolpyru | 485.1 | 9.7e-143 | 1 |
| gi\|154146874\|emb\|CAM84124.1\| | phosphoenolpyru | 484.7 | 1.3e-142 | 1 |

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|---|---|---|---|---|
| gi\|154146904\|emb\|CAM84139.1\| | phosphoenolpyru | 484.1 | 1.9e-142 | 1 |
| gi\|154146758\|emb\|CAM84066.1\| | phosphoenolpyru | 484.1 | 1.9e-142 | 1 |
| gi\|222617602\|gb\|EEE53734.1\| | hypothetical pr | 481.5 | 1.1e-141 | 1 |
| gi\|154146756\|emb\|CAM84065.1\| | phosphoenolpyru | 480.5 | 2.3e-141 | 1 |
| gi\|154146736\|emb\|CAM84055.1\| | phosphoenolpyru | 480.4 | 2.5e-141 | 1 |
| gi\|154146770\|emb\|CAM84072.1\| | phosphoenolpyru | 477.7 | 1.6e-140 | 1 |
| gi\|154146812\|emb\|CAM84093.1\| | phosphoenolpyru | 477.7 | 1.7e-140 | 1 |
| gi\|154146902\|emb\|CAM84138.1\| | phosphoenolpyru | 477.1 | 2.5e-140 | 1 |
| gi\|154146876\|emb\|CAM84125.1\| | phosphoenolpyru | 476.7 | 3.3e-140 | 1 |
| gi\|154146846\|emb\|CAM84110.1\| | phosphoenolpyru | 476.5 | 3.8e-140 | 1 |
| gi\|154146826\|emb\|CAM84100.1\| | phosphoenolpyru | 476.0 | 5.2e-140 | 1 |
| gi\|154146908\|emb\|CAM84141.1\| | phosphoenolpyru | 475.5 | 7.5e-140 | 1 |
| gi\|154146732\|emb\|CAM84053.1\| | phosphoenolpyru | 475.1 | 1e-139 | 1 |
| gi\|154146744\|emb\|CAM84059.1\| | phosphoenolpyru | 475.1 | 1e-139 | 1 |
| gi\|154146924\|emb\|CAM84149.1\| | phosphoenolpyru | 474.4 | 1.6e-139 | 1 |
| gi\|154146858\|emb\|CAM84116.1\| | phosphoenolpyru | 473.6 | 2.7e-139 | 1 |
| gi\|154146884\|emb\|CAM84129.1\| | phosphoenolpyru | 472.7 | 5.3e-139 | 1 |
| gi\|154146860\|emb\|CAM84117.1\| | phosphoenolpyru | 472.5 | 5.8e-139 | 1 |
| gi\|154146772\|emb\|CAM84073.1\| | phosphoenolpyru | 472.5 | 6.1e-139 | 1 |
| gi\|156084500\|ref\|XP_001609733.1\| | phosphoenolpyru | 472.1 | 8e-139 | 1 |
| gi\|154146740\|emb\|CAM84057.1\| | phosphoenolpyru | 471.8 | 9.7e-139 | 1 |
| gi\|154146794\|emb\|CAM84084.1\| | phosphoenolpyru | 471.5 | 1.2e-138 | 1 |
| gi\|159900750\|ref\|YP_001546997.1\| | phosphoenolpyru | 471.2 | 1.5e-138 | 1 |
| gi\|154146720\|emb\|CAM84047.1\| | phosphoenolpyru | 470.1 | 3.1e-138 | 1 |
| gi\|154146912\|emb\|CAM84143.1\| | phosphoenolpyru | 469.1 | 6.4e-138 | 1 |
| gi\|154146816\|emb\|CAM84095.1\| | phosphoenolpyru | 468.9 | 7.4e-138 | 1 |
| gi\|154146774\|emb\|CAM84074.1\| | phosphoenolpyru | 467.9 | 1.5e-137 | 1 |
| gi\|154146798\|emb\|CAM84086.1\| | phosphoenolpyru | 467.7 | 1.7e-137 | 1 |
| gi\|154146750\|emb\|CAM84062.1\| | phosphoenolpyru | 466.5 | 3.8e-137 | 1 |
| gi\|154146824\|emb\|CAM84099.1\| | phosphoenolpyru | 464.8 | 1.3e-136 | 1 |
| gi\|154146778\|emb\|CAM84076.1\| | phosphoenolpyru | 464.7 | 1.3e-136 | 1 |
| gi\|154146734\|emb\|CAM84054.1\| | phosphoenolpyru | 464.4 | 1.6e-136 | 1 |
| gi\|154146918\|emb\|CAM84146.1\| | phosphoenolpyru | 464.0 | 2.1e-136 | 1 |
| gi\|154146906\|emb\|CAM84140.1\| | phosphoenolpyru | 463.3 | 3.6e-136 | 1 |
| gi\|154146900\|emb\|CAM84137.1\| | phosphoenolpyru | 463.2 | 3.9e-136 | 1 |
| gi\|154146828\|emb\|CAM84101.1\| | phosphoenolpyru | 462.6 | 5.9e-136 | 1 |
| gi\|154146806\|emb\|CAM84090.1\| | phosphoenolpyru | 461.6 | 1.2e-135 | 1 |
| gi\|154146890\|emb\|CAM84132.1\| | phosphoenolpyru | 461.4 | 1.3e-135 | 1 |
| gi\|269925429\|ref\|YP_003322052.1\| | Phosphoenolpyru | 461.3 | 1.4e-135 | 1 |
| gi\|154146818\|emb\|CAM84096.1\| | phosphoenolpyru | 460.9 | 1.9e-135 | 1 |
| gi\|154146914\|emb\|CAM84144.1\| | phosphoenolpyru | 460.7 | 2.2e-135 | 1 |
| gi\|154146760\|emb\|CAM84067.1\| | phosphoenolpyru | 459.7 | 4.4e-135 | 1 |
| gi\|154146814\|emb\|CAM84094.1\| | phosphoenolpyru | 459.6 | 4.5e-135 | 1 |
| gi\|154146764\|emb\|CAM84069.1\| | phosphoenolpyru | 458.5 | 9.5e-135 | 1 |
| gi\|123966995\|ref\|YP_001012076.1\| | phosphoenolpyru | 457.9 | 1.5e-134 | 1 |
| gi\|154146864\|emb\|CAM84119.1\| | phosphoenolpyru | 457.8 | 1.6e-134 | 1 |
| gi\|154146738\|emb\|CAM84056.1\| | phosphoenolpyru | 457.1 | 2.6e-134 | 1 |
| gi\|22299455\|ref\|NP_682702.1\| | phosphoenolpyru | 457.0 | 2.8e-134 | 1 |
| gi\|154146840\|emb\|CAM84107.1\| | phosphoenolpyru | 456.7 | 3.5e-134 | 1 |
| gi\|147839189\|emb\|CAN72376.1\| | hypothetical pr | 456.6 | 3.6e-134 | 1 |
| gi\|154146780\|emb\|CAM84077.1\| | phosphoenolpyru | 456.1 | 5.2e-134 | 1 |
| gi\|220907631\|ref\|YP_002482942.1\| | Phosphoenolpyru | 455.9 | 5.8e-134 | 1 |
| gi\|154146766\|emb\|CAM84070.1\| | phosphoenolpyru | 455.4 | 8.5e-134 | 1 |
| gi\|154146748\|emb\|CAM84061.1\| | phosphoenolpyru | 455.1 | 1.1e-133 | 1 |
| gi\|157414180\|ref\|YP_001485046.1\| | phosphoenolpyru | 454.6 | 1.5e-133 | 1 |
| gi\|154146894\|emb\|CAM84134.1\| | phosphoenolpyru | 451.6 | 1.1e-132 | 1 |
| gi\|159904236\|ref\|YP_001551580.1\| | phosphoenolpyru | 451.5 | 1.3e-132 | 1 |
| gi\|154146804\|emb\|CAM84089.1\| | phosphoenolpyru | 451.2 | 1.6e-132 | 1 |
| gi\|154146742\|emb\|CAM84058.1\| | phosphoenolpyru | 450.6 | 2.4e-132 | 1 |
| gi\|154146790\|emb\|CAM84082.1\| | phosphoenolpyru | 450.0 | 3.7e-132 | 1 |
| gi\|154146784\|emb\|CAM84079.1\| | phosphoenolpyru | 449.2 | 6.2e-132 | 1 |
| gi\|254526567\|ref\|ZP_05138619.1\| | phosphoenolpyru | 449.0 | 7e-132 | 1 |
| gi\|78780052\|ref\|YP_398164.1\| | phosphoenolpyru | 448.6 | 9.1e-132 | 1 |
| gi\|154146822\|emb\|CAM84098.1\| | phosphoenolpyru | 448.5 | 1e-131 | 1 |
| gi\|154146898\|emb\|CAM84136.1\| | phosphoenolpyru | 448.5 | 1e-131 | 1 |
| gi\|226326777\|ref\|ZP_03802295.1\| | hypothetical pr | 448.5 | 1e-131 | 1 |
| gi\|123969314\|ref\|YP_001010172.1\| | phosphoenolpyru | 447.4 | 2.1e-131 | 1 |
| gi\|91070220\|gb\|ABE11140.1\| | phosphoenolpyru | 447.2 | 2.5e-131 | 1 |
| gi\|154146836\|emb\|CAM84105.1\| | phosphoenolpyru | 446.1 | 5.4e-131 | 1 |
| gi\|154146726\|emb\|CAM84050.1\| | phosphoenolpyru | 445.1 | 1.1e-130 | 1 |
| gi\|33862131\|ref\|NP_893692.1\| | phosphoenolpyru | 444.8 | 1.3e-130 | 1 |

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|---|---|---|---|---|
| gi\|154146802\|emb\|CAM84088.1\| | phosphoenolpyru | 444.7 | 1.4e-130 | 1 |
| gi\|154146886\|emb\|CAM84130.1\| | phosphoenolpyru | 442.0 | 9.2e-130 | 1 |
| gi\|126697104\|ref\|YP_001091990.1\| | phosphoenolpyru | 441.1 | 1.7e-129 | 1 |
| gi\|154146728\|emb\|CAM84051.1\| | phosphoenolpyru | 440.7 | 2.3e-129 | 1 |
| gi\|154146792\|emb\|CAM84083.1\| | phosphoenolpyru | 437.3 | 2.4e-128 | 1 |
| gi\|154146856\|emb\|CAM84115.1\| | phosphoenolpyru | 437.0 | 2.9e-128 | 1 |
| gi\|154146868\|emb\|CAM84121.1\| | phosphoenolpyru | 434.7 | 1.4e-127 | 1 |
| gi\|154146872\|emb\|CAM84123.1\| | phosphoenolpyru | 432.2 | 8.1e-127 | 1 |
| gi\|86605542\|ref\|YP_474305.1\| | phosphoenolpyru | 430.7 | 2.3e-126 | 1 |
| gi\|72382985\|ref\|YP_292340.1\| | phosphoenolpyru | 430.4 | 2.9e-126 | 1 |
| gi\|124026726\|ref\|YP_001015841.1\| | phosphoenolpyru | 430.2 | 3.3e-126 | 1 |
| gi\|154146888\|emb\|CAM84131.1\| | phosphoenolpyru | 430.0 | 3.9e-126 | 1 |
| gi\|119487042\|ref\|ZP_01620914.1\| | Phosphoenolpyru | 428.1 | 1.4e-125 | 1 |
| gi\|75908353\|ref\|YP_322649.1\| | phosphoenolpyru | 428.0 | 1.5e-125 | 1 |
| gi\|161353735\|ref\|NP_488901.2\| | phosphoenolpyru | 425.8 | 6.6e-125 | 1 |
| gi\|142080\|gb\|AAA22023.1\| | phosphoenolpyru | 425.8 | 6.6e-125 | 1 |
| gi\|124023967\|ref\|YP_001018274.1\| | phosphoenolpyru | 425.7 | 7.1e-125 | 1 |
| gi\|154146892\|emb\|CAM84133.1\| | phosphoenolpyru | 425.6 | 7.7e-125 | 1 |
| gi\|261409477\|ref\|YP_003245718.1\| | Phosphoenolpyru | 425.2 | 1e-124 | 1 |
| gi\|56751855\|ref\|YP_172556.1\| | phosphoenolpyru | 425.0 | 1.2e-124 | 1 |
| gi\|81301061\|ref\|YP_401269.1\| | phosphoenolpyru | 425.0 | 1.2e-124 | 1 |
| gi\|251799599\|ref\|YP_003014330.1\| | Phosphoenolpyru | 424.4 | 1.9e-124 | 1 |
| gi\|154146810\|emb\|CAM84092.1\| | phosphoenolpyru | 423.8 | 2.7e-124 | 1 |
| gi\|253577082\|ref\|ZP_04854404.1\| | phosphoenolpyru | 422.9 | 5.2e-124 | 1 |
| gi\|254431278\|ref\|ZP_05044981.1\| | phosphoenolpyru | 422.6 | 6.3e-124 | 1 |
| gi\|154146730\|emb\|CAM84052.1\| | phosphoenolpyru | 421.0 | 1.9e-123 | 1 |
| gi\|159027003\|emb\|CAO86722.1\| | capP [Microcyst | 420.5 | 2.7e-123 | 1 |
| gi\|260436235\|ref\|ZP_05790205.1\| | phosphoenolpyru | 420.5 | 2.8e-123 | 1 |
| gi\|154146920\|emb\|CAM84147.1\| | phosphoenolpyru | 417.2 | 2.7e-122 | 1 |
| gi\|87300934\|ref\|ZP_01083776.1\| | phosphoenolpyru | 417.0 | 3.1e-122 | 1 |
| gi\|166366623\|ref\|YP_001658896.1\| | phosphoenolpyru | 416.6 | 4.1e-122 | 1 |
| gi\|154146776\|emb\|CAM84075.1\| | phosphoenolpyru | 416.4 | 4.6e-122 | 1 |
| gi\|116075789\|ref\|ZP_01473048.1\| | phosphoenolpyru | 416.0 | 6.3e-122 | 1 |
| gi\|78211948\|ref\|YP_380727.1\| | phosphoenolpyru | 415.6 | 8.2e-122 | 1 |
| gi\|282900199\|ref\|ZP_06308155.1\| | Phosphoenolpyru | 413.3 | 4e-121 | 1 |
| gi\|33241179\|ref\|NP_876121.1\| | phosphoenolpyru | 413.2 | 4.2e-121 | 1 |
| gi\|282897196\|ref\|ZP_06305198.1\| | Phosphoenolpyru | 413.2 | 4.4e-121 | 1 |
| gi\|86609298\|ref\|YP_478060.1\| | phosphoenolpyru | 412.7 | 6.2e-121 | 1 |
| gi\|87124941\|ref\|ZP_01080788.1\| | Phosphoenolpyru | 408.8 | 9e-120 | 1 |
| gi\|170078023\|ref\|YP_001734661.1\| | phosphoenolpyru | 407.0 | 3.1e-119 | 1 |
| gi\|119512252\|ref\|ZP_01631340.1\| | phosphoenolpyru | 405.8 | 7e-119 | 1 |
| gi\|148254376\|ref\|YP_001238961.1\| | phosphoenolpyru | 405.8 | 7.4e-119 | 1 |
| gi\|116072588\|ref\|ZP_01469854.1\| | phosphoenolpyru | 404.4 | 1.9e-118 | 1 |
| gi\|33863980\|ref\|NP_895540.1\| | phosphoenolpyru | 403.3 | 3.9e-118 | 1 |
| gi\|113954224\|ref\|YP_729688.1\| | phosphoenolpyru | 403.1 | 4.5e-118 | 1 |
| gi\|33866579\|ref\|NP_898138.1\| | phosphoenolpyru | 401.5 | 1.4e-117 | 1 |
| gi\|113474661\|ref\|YP_720722.1\| | phosphoenolpyru | 399.8 | 4.5e-117 | 1 |
| gi\|154146696\|emb\|CAM83983.1\| | phosphoenolpyru | 399.3 | 6.3e-117 | 1 |
| gi\|78185499\|ref\|YP_377934.1\| | phosphoenolpyru | 399.0 | 7.7e-117 | 1 |
| gi\|219847347\|ref\|YP_002461780.1\| | Phosphoenolpyru | 398.8 | 8.9e-117 | 1 |
| gi\|225517756\|ref\|ZP_03764713.1\| | Phosphoenolpyru | 397.0 | 3.1e-116 | 1 |
| gi\|269961450\|ref\|ZP_06175814.1\| | Phosphoenolpyru | 396.9 | 3.4e-116 | 1 |
| gi\|172038735\|ref\|YP_001805236.1\| | phosphoenolpyru | 396.7 | 4e-116 | 1 |
| gi\|254413284\|ref\|ZP_05027055.1\| | phosphoenolpyru | 396.6 | 4.2e-116 | 1 |
| gi\|16330985\|ref\|NP_441713.1\| | phosphoenolpyru | 395.9 | 6.8e-116 | 1 |
| gi\|218441147\|ref\|YP_002379476.1\| | phosphoenolpyru | 395.1 | 1.2e-115 | 1 |
| gi\|146339589\|ref\|YP_001204637.1\| | phosphoenolpyru | 394.6 | 1.6e-115 | 1 |
| gi\|209528283\|ref\|ZP_03276745.1\| | Phosphoenolpyru | 394.4 | 1.9e-115 | 1 |
| gi\|154146870\|emb\|CAM84122.1\| | phosphoenolpyru | 393.6 | 3.4e-115 | 1 |
| gi\|154146688\|emb\|CAM83979.1\| | phosphoenolpyru | 393.6 | 3.5e-115 | 1 |
| gi\|148238790\|ref\|YP_001224177.1\| | phosphoenolpyru | 393.2 | 4.6e-115 | 1 |
| gi\|196256031\|ref\|ZP_03154569.1\| | Phosphoenolpyru | 392.4 | 7.9e-115 | 1 |
| gi\|27378066\|ref\|NP_769595.1\| | phosphoenolpyru | 391.6 | 1.4e-114 | 1 |
| gi\|88807863\|ref\|ZP_01123374.1\| | phosphoenolpyru | 391.1 | 1.9e-114 | 1 |
| gi\|74148786\|gb\|ABA00148.1\| | phosphoenolpyru | 390.9 | 2.3e-114 | 1 |
| gi\|56417897\|gb\|AAV90837.1\| | phosphoenolpyru | 390.4 | 3.1e-114 | 1 |
| gi\|154146866\|emb\|CAM84120.1\| | phosphoenolpyru | 389.5 | 5.7e-114 | 1 |
| gi\|50251800\|dbj\|BAD27731.1\| | phosphoenolpyru | 389.1 | 7.5e-114 | 1 |
| gi\|284050999\|ref\|ZP_06381209.1\| | phosphoenolpyru | 389.0 | 8.4e-114 | 1 |
| gi\|154146684\|emb\|CAM83977.1\| | phosphoenolpyru | 388.8 | 9.4e-114 | 1 |
| gi\|154146700\|emb\|CAM83985.1\| | phosphoenolpyru | 388.0 | 1.6e-113 | 1 |

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|---|---|---|---|---|---|
| gi\|288555580\|ref\|YP_003427515.1\| | phosphoenolpyru | 387.4 | 2.5e-113 | 1 |
| gi\|158426293\|ref\|YP_001527585.1\| | phosphoenolpyru | 386.8 | 3.8e-113 | 1 |
| gi\|154146702\|emb\|CAM83986.1\| | phosphoenolpyru | 386.6 | 4.4e-113 | 1 |
| gi\|222526644\|ref\|YP_002571115.1\| | Phosphoenolpyru | 385.9 | 7.3e-113 | 1 |
| gi\|154146690\|emb\|CAM83980.1\| | phosphoenolpyru | 385.0 | 1.3e-112 | 1 |
| gi\|30248603\|ref\|NP_840673.1\| | phosphoenolpyru | 384.3 | 2.2e-112 | 1 |
| gi\|154146680\|emb\|CAM83975.1\| | phosphoenolpyru | 383.9 | 2.8e-112 | 1 |
| gi\|218288887\|ref\|ZP_03493138.1\| | Phosphoenolpyru | 383.2 | 4.4e-112 | 1 |
| gi\|154146710\|emb\|CAM83990.1\| | phosphoenolpyru | 382.8 | 6.2e-112 | 1 |
| gi\|86750702\|ref\|YP_487198.1\| | phosphoenolpyru | 382.4 | 8.2e-112 | 1 |
| gi\|291612738\|ref\|YP_003522895.1\| | Phosphoenolpyru | 382.3 | 8.6e-112 | 1 |
| gi\|154146714\|emb\|CAM83992.1\| | phosphoenolpyru | 382.0 | 1e-111 | 1 |
| gi\|254422587\|ref\|ZP_05036305.1\| | phosphoenolpyru | 381.8 | 1.2e-111 | 1 |
| gi\|154146678\|emb\|CAM83974.1\| | phosphoenolpyru | 381.3 | 1.7e-111 | 1 |
| gi\|218248219\|ref\|YP_002373590.1\| | phosphoenolpyru | 381.2 | 1.8e-111 | 1 |
| gi\|257093120\|ref\|YP_003166761.1\| | Phosphoenolpyru | 381.2 | 1.8e-111 | 1 |
| gi\|154146706\|emb\|CAM83988.1\| | phosphoenolpyru | 381.1 | 2e-111 | 1 |
| gi\|126658238\|ref\|ZP_01729388.1\| | phosphoenolpyru | 380.6 | 2.8e-111 | 1 |
| gi\|154146676\|emb\|CAM83973.1\| | phosphoenolpyru | 379.5 | 6.1e-111 | 1 |
| gi\|239993151\|ref\|ZP_04713675.1\| | phosphoenolpyru | 379.0 | 8.5e-111 | 1 |
| gi\|283848041\|ref\|ZP_06365460.1\| | Phosphoenolpyru | 378.4 | 1.3e-110 | 1 |
| gi\|114331035\|ref\|YP_747257.1\| | phosphoenolpyru | 377.4 | 2.6e-110 | 1 |
| gi\|163764698\|ref\|ZP_02171753.1\| | transposase, IS | 377.2 | 3e-110 | 1 |
| gi\|186685513\|ref\|YP_001868709.1\| | phosphoenolpyru | 376.9 | 3.7e-110 | 1 |
| gi\|154146698\|emb\|CAM83984.1\| | phosphoenolpyru | 375.8 | 7.6e-110 | 1 |
| gi\|115523808\|ref\|YP_780719.1\| | phosphoenolpyru | 375.8 | 7.9e-110 | 1 |
| gi\|20196766\|emb\|CAC86387.1\| | putative phosph | 374.9 | 1.4e-109 | 1 |
| gi\|163848702\|ref\|YP_001636746.1\| | phosphoenolpyru | 374.1 | 2.5e-109 | 1 |
| gi\|148656870\|ref\|YP_001277075.1\| | phosphoenolpyru | 374.0 | 2.7e-109 | 1 |
| gi\|209884453\|ref\|YP_002288310.1\| | phosphoenolpyru | 373.3 | 4.4e-109 | 1 |
| gi\|154146712\|emb\|CAM83991.1\| | phosphoenolpyru | 373.0 | 5.2e-109 | 1 |
| gi\|154146682\|emb\|CAM83976.1\| | phosphoenolpyru | 372.9 | 5.7e-109 | 1 |
| gi\|111024131\|ref\|YP_707103.1\| | phosphoenolpyru | 372.9 | 5.7e-109 | 1 |
| gi\|226366371\|ref\|YP_002784154.1\| | phosphoenolpyru | 371.9 | 1.2e-108 | 1 |
| gi\|258512100\|ref\|YP_003185534.1\| | Phosphoenolpyru | 371.6 | 1.5e-108 | 1 |
| gi\|251827845\|ref\|ZP_04830919.1\| | Phosphoenolpyru | 371.3 | 1.8e-108 | 1 |
| gi\|71907389\|ref\|YP_284976.1\| | phosphoenolpyru | 370.4 | 3.3e-108 | 1 |
| gi\|90423192\|ref\|YP_531562.1\| | phosphoenolpyru | 370.3 | 3.4e-108 | 1 |
| gi\|158337676\|ref\|YP_001518852.1\| | phosphoenolpyru | 370.3 | 3.6e-108 | 1 |
| gi\|37519983\|ref\|NP_923360.1\| | phosphoenolpyru | 370.1 | 3.9e-108 | 1 |
| gi\|148243189\|ref\|YP_001228346.1\| | phosphoenolpyru | 369.1 | 8.1e-108 | 1 |
| gi\|154244275\|ref\|YP_001415233.1\| | phosphoenolpyru | 368.7 | 1.1e-107 | 1 |
| gi\|154146692\|emb\|CAM83981.1\| | phosphoenolpyru | 368.0 | 1.7e-107 | 1 |
| gi\|154146704\|emb\|CAM83987.1\| | phosphoenolpyru | 366.2 | 6e-107 | 1 |
| gi\|67923850\|ref\|ZP_00517310.1\| | Phosphoenolpyru | 365.8 | 7.7e-107 | 1 |
| gi\|154146708\|emb\|CAM83989.1\| | phosphoenolpyru | 365.8 | 8e-107 | 1 |
| gi\|154146686\|emb\|CAM83978.1\| | phosphoenolpyru | 365.1 | 1.3e-106 | 1 |
| gi\|74316648\|ref\|YP_314388.1\| | phosphoenolpyru | 364.3 | 2.3e-106 | 1 |
| gi\|262202294\|ref\|YP_003273502.1\| | Phosphoenolpyru | 362.7 | 6.6e-106 | 1 |
| gi\|54023896\|ref\|YP_118138.1\| | phosphoenolpyru | 362.3 | 9e-106 | 1 |
| gi\|156742348\|ref\|YP_001432477.1\| | phosphoenolpyru | 362.0 | 1.1e-105 | 1 |
| gi\|145224288\|ref\|YP_001134966.1\| | phosphoenolpyru | 361.3 | 1.8e-105 | 1 |
| gi\|91976353\|ref\|YP_569012.1\| | phosphoenolpyru | 360.6 | 2.8e-105 | 1 |
| gi\|154146716\|emb\|CAM83993.1\| | phosphoenolpyru | 360.6 | 2.9e-105 | 1 |
| gi\|257067921\|ref\|YP_003154176.1\| | Phosphoenolpyru | 359.4 | 6.6e-105 | 1 |
| gi\|118467879\|ref\|YP_887412.1\| | phosphoenolpyru | 358.5 | 1.2e-104 | 1 |
| gi\|168700529\|ref\|ZP_02732806.1\| | Phosphoenolpyru | 358.2 | 1.5e-104 | 1 |
| gi\|289209281\|ref\|YP_003461347.1\| | Phosphoenolpyru | 357.7 | 2.2e-104 | 1 |
| gi\|226306521\|ref\|YP_002766481.1\| | phosphoenolpyru | 357.2 | 3.1e-104 | 1 |
| gi\|283779027\|ref\|YP_003369782.1\| | Phosphoenolpyru | 356.6 | 4.8e-104 | 1 |
| gi\|34495510\|ref\|NP_899725.1\| | phosphoenolpyru | 356.5 | 5.1e-104 | 1 |
| gi\|108799375\|ref\|YP_639572.1\| | phosphoenolpyru | 356.3 | 5.6e-104 | 1 |
| gi\|288793906\|ref\|ZP_06399624.1\| | Phosphoenolpyru | 355.7 | 8.6e-104 | 1 |
| gi\|75676463\|ref\|YP_318884.1\| | phosphoenolpyru | 355.2 | 1.2e-103 | 1 |
| gi\|154146694\|emb\|CAM83982.1\| | phosphoenolpyru | 355.1 | 1.3e-103 | 1 |
| gi\|77164288\|ref\|YP_342813.1\| | phosphoenolpyru | 352.7 | 7e-103 | 1 |
| gi\|254434134\|ref\|ZP_05047642.1\| | phosphoenolpyru | 352.7 | 7e-103 | 1 |
| gi\|220934054\|ref\|YP_002512953.1\| | Phosphoenolpyru | 352.5 | 8e-103 | 1 |
| gi\|20196764\|emb\|CAC86386.1\| | putative phosph | 352.1 | 1.1e-102 | 1 |
| gi\|270502847\|ref\|ZP_06219747.1\| | Phosphoenolpyru | 351.9 | 1.2e-102 | 1 |
| gi\|238062745\|ref\|ZP_04607454.1\| | phosphoenolpyru | 350.9 | 2.4e-102 | 1 |

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|---|---|---|---|---|---|
| gi\|283843167\|ref\|ZP_06360698.1\| | Phosphoenolpyru | 350.3 | 3.5e-102 | 1 |
| gi\|145593441\|ref\|YP_001157738.1\| | phosphoenolpyru | 350.2 | 3.9e-102 | 1 |
| gi\|280964818\|ref\|ZP_06239332.1\| | Phosphoenolpyru | 350.0 | 4.6e-102 | 1 |
| gi\|255062470\|ref\|ZP_05314486.1\| | Phosphoenolpyru | 349.6 | 6e-102 | 1 |
| gi\|15827227\|ref\|NP_301490.1\| | phosphoenolpyru | 349.3 | 7.6e-102 | 1 |
| gi\|78485862\|ref\|YP_391787.1\| | phosphoenolpyru | 346.8 | 4.2e-101 | 1 |
| gi\|192290365\|ref\|YP_001990970.1\| | Phosphoenolpyru | 346.7 | 4.4e-101 | 1 |
| gi\|229493485\|ref\|ZP_04387270.1\| | phosphoenolpyru | 346.0 | 7.2e-101 | 1 |
| gi\|217969857\|ref\|YP_002355091.1\| | Phosphoenolpyru | 345.8 | 8.1e-101 | 1 |
| gi\|39934841\|ref\|NP_947117.1\| | phosphoenolpyru | 345.2 | 1.3e-100 | 1 |
| gi\|85716666\|ref\|ZP_01047635.1\| | phosphoenolpyru | 345.0 | 1.4e-100 | 1 |
| gi\|2339975\|dbj\|BAA21835.1\| | phosphoenolpyru | 344.5 | 2e-100 | 1 |
| gi\|21314564\|gb\|AAM47007.1\|AF512995_1 | phosphoenolpyru | 344.0 | 2.9e-100 | 1 |
| gi\|92118201\|ref\|YP_577930.1\| | phosphoenolpyru | 342.8 | 6.4e-100 | 1 |
| gi\|111220081\|ref\|YP_710875.1\| | phosphoenolpyru | 342.2 | 1e-99 | 1 |
| gi\|229541694\|ref\|ZP_04430754.1\| | Phosphoenolpyru | 339.4 | 7e-99 | 1 |
| gi\|159036484\|ref\|YP_001535737.1\| | phosphoenolpyru | 338.9 | 9.6e-99 | 1 |
| gi\|256677249\|ref\|ZP_05487560.1\| | phosphoenolpyru | 337.7 | 2.3e-98 | 1 |
| gi\|68304977\|gb\|AAY89988.1\| | predicted PEP c | 337.5 | 2.7e-98 | 1 |
| gi\|254376064\|ref\|ZP_04991540.1\| | phosphoenolpyru | 337.1 | 3.5e-98 | 1 |
| gi\|254775781\|ref\|ZP_05217297.1\| | phosphoenolpyru | 336.9 | 4.1e-98 | 1 |
| gi\|134094240\|ref\|YP_001099315.1\| | phosphoenolpyru | 336.7 | 4.6e-98 | 1 |
| gi\|282887782\|ref\|ZP_06296361.1\| | Phosphoenolpyru | 336.2 | 6.5e-98 | 1 |
| gi\|466887\|gb\|AAA17132.1\| | ppc [Mycobacter | 335.4 | 1.1e-97 | 1 |
| gi\|2499464\|sp\|Q59757.1\|CAPP_RHOMR | RecName: Full=P | 335.2 | 1.3e-97 | 1 |
| gi\|118465776\|ref\|YP_882518.1\| | phosphoenolpyru | 334.0 | 3e-97 | 1 |
| gi\|82703804\|ref\|YP_413370.1\| | phosphoenolpyru | 333.9 | 3.2e-97 | 1 |
| gi\|289635970\|ref\|ZP_06468254.1\| | phosphoenolpyru | 333.6 | 3.9e-97 | 1 |
| gi\|152980037\|ref\|YP_001352831.1\| | phosphoenolpyru | 332.9 | 6.4e-97 | 1 |
| gi\|120403691\|ref\|YP_953520.1\| | phosphoenolpyru | 332.6 | 7.7e-97 | 1 |
| gi\|256815765\|ref\|ZP_05540780.1\| | phosphoenolpyru | 332.2 | 1.1e-96 | 1 |
| gi\|41407267\|ref\|NP_960103.1\| | phosphoenolpyru | 331.7 | 1.5e-96 | 1 |
| gi\|268317216\|ref\|YP_003290935.1\| | Phosphoenolpyru | 331.6 | 1.5e-96 | 1 |
| gi\|186476931\|ref\|YP_001858401.1\| | phosphoenolpyru | 331.6 | 1.6e-96 | 1 |
| gi\|227980965\|ref\|ZP_04028227.1\| | Phosphoenolpyru | 331.2 | 2.1e-96 | 1 |
| gi\|254818408\|ref\|ZP_05223409.1\| | phosphoenolpyru | 330.3 | 3.8e-96 | 1 |
| gi\|292492252\|ref\|YP_003527691.1\| | Phosphoenolpyru | 330.3 | 4e-96 | 1 |
| gi\|20196768\|emb\|CAC86356.1\| | putative phosph | 330.2 | 4.1e-96 | 1 |
| gi\|56476048\|ref\|YP_157637.1\| | phosphoenolpyru | 330.2 | 4.2e-96 | 1 |
| gi\|256802423\|ref\|ZP_05532047.1\| | phosphoenolpyru | 329.2 | 8.4e-96 | 1 |
| gi\|91782419\|ref\|YP_557625.1\| | phosphoenolpyru | 328.4 | 1.4e-95 | 1 |
| gi\|239930781\|ref\|ZP_04687734.1\| | phosphoenolpyru | 328.3 | 1.5e-95 | 1 |
| gi\|288962822\|ref\|YP_003453116.1\| | phosphoenolpyru | 328.1 | 1.8e-95 | 1 |
| gi\|73917654\|sp\|Q5P7H5.2\|CAPP_AZOSE | RecName: Full=P | 326.5 | 5.2e-95 | 1 |
| gi\|290580816\|ref\|YP_003485208.1\| | putative phosph | 326.3 | 6.3e-95 | 1 |
| gi\|24379180\|ref\|NP_721135.1\| | phosphoenolpyru | 325.8 | 8.5e-95 | 1 |
| gi\|25008189\|sp\|Q93MH3.1\|CAPP_CORCT | RecName: Full=P | 325.7 | 9.4e-95 | 1 |
| gi\|262039622\|ref\|ZP_06012916.1\| | phosphoenolpyru | 325.6 | 1e-94 | 1 |
| gi\|257126840\|ref\|YP_003164954.1\| | Phosphoenolpyru | 325.5 | 1e-94 | 1 |
| gi\|21221565\|ref\|NP_627344.1\| | phosphoenolpyru | 325.4 | 1.2e-94 | 1 |
| gi\|20196770\|emb\|CAC86357.1\| | putative phosph | 324.4 | 2.3e-94 | 1 |
| gi\|239981711\|ref\|ZP_04704235.1\| | phosphoenolpyru | 324.3 | 2.4e-94 | 1 |
| gi\|225165040\|ref\|ZP_03727237.1\| | Phosphoenolpyru | 323.4 | 4.7e-94 | 1 |
| gi\|19552797\|ref\|NP_600799.1\| | phosphoenolpyru | 323.1 | 5.8e-94 | 1 |
| gi\|291303250\|ref\|YP_003514528.1\| | Phosphoenolpyru | 322.8 | 6.9e-94 | 1 |
| gi\|183982260\|ref\|YP_001850551.1\| | phosphoenolpyru | 322.3 | 1e-93 | 1 |
| gi\|20196772\|emb\|CAC86358.1\| | putative phosph | 322.1 | 1.2e-93 | 1 |
| gi\|225874618\|ref\|YP_002756077.1\| | phosphoenolpyru | 322.0 | 1.2e-93 | 1 |
| gi\|145295706\|ref\|YP_001138527.1\| | phosphoenolpyru | 322.0 | 1.2e-93 | 1 |
| gi\|170691942\|ref\|ZP_02883106.1\| | Phosphoenolpyru | 321.7 | 1.5e-93 | 1 |
| gi\|290959806\|ref\|YP_003490988.1\| | phosphoenolpyru | 321.4 | 1.9e-93 | 1 |
| gi\|217977979\|ref\|YP_002362126.1\| | Phosphoenolpyru | 321.0 | 2.4e-93 | 1 |
| gi\|29830109\|ref\|NP_824743.1\| | phosphoenolpyru | 320.0 | 4.8e-93 | 1 |
| gi\|118617446\|ref\|YP_905778.1\| | phosphoenolpyru | 319.9 | 5.2e-93 | 1 |
| gi\|253755158\|ref\|YP_003028298.1\| | phosphoenolpyru | 318.1 | 1.8e-92 | 1 |
| gi\|146318181\|ref\|YP_001197893.1\| | phosphoenolpyru | 318.0 | 2e-92 | 1 |
| gi\|223933776\|ref\|ZP_03625747.1\| | Phosphoenolpyru | 317.6 | 2.5e-92 | 1 |
| gi\|158318318\|ref\|YP_001510826.1\| | phosphoenolpyru | 317.5 | 2.7e-92 | 1 |
| gi\|254407576\|ref\|ZP_05022466.1\| | phosphoenolpyru | 317.4 | 2.9e-92 | 1 |
| gi\|272527540\|ref\|ZP_06223827.1\| | phosphoenolpyru | 316.6 | 5.3e-92 | 1 |
| gi\|260891421\|ref\|ZP_05902684.1\| | phosphoenolpyru | 316.0 | 7.9e-92 | 1 |

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|---|---|---|---|---|---|
| gi\|115352520\|ref\|YP_774359.1\| | phosphoenolpyru | 315.9 | 8.1e-92 | 1 |
| gi\|187923069\|ref\|YP_001894711.1\| | phosphoenolpyru | 315.8 | 8.9e-92 | 1 |
| gi\|119962288\|ref\|YP_946565.1\| | phosphoenolpyru | 315.0 | 1.6e-91 | 1 |
| gi\|152967316\|ref\|YP_001363100.1\| | Phosphoenolpyru | 313.7 | 3.8e-91 | 1 |
| gi\|172061377\|ref\|YP_001809029.1\| | phosphoenolpyru | 313.6 | 4e-91 | 1 |
| gi\|170703457\|ref\|ZP_02894226.1\| | Phosphoenolpyru | 313.5 | 4.3e-91 | 1 |
| gi\|256776822\|ref\|ZP_05515285.1\| | putative phosph | 313.5 | 4.4e-91 | 1 |
| gi\|254396574\|ref\|ZP_05011634.1\| | phosphoenolpyru | 312.8 | 6.9e-91 | 1 |
| gi\|239941867\|ref\|ZP_04693804.1\| | putative phosph | 312.7 | 7.5e-91 | 1 |
| gi\|116669180\|ref\|YP_830113.1\| | phosphoenolpyru | 312.1 | 1.1e-90 | 1 |
| gi\|240173274\|ref\|ZP_04751932.1\| | phosphoenolpyru | 312.0 | 1.2e-90 | 1 |
| gi\|48689\|emb\|CAA32450.1\| | unnamed protein | 312.0 | 1.3e-90 | 1 |
| gi\|20196762\|emb\|CAC86385.1\| | phosphoenolpyru | 312.0 | 1.3e-90 | 1 |
| gi\|198283666\|ref\|YP_002219987.1\| | Phosphoenolpyru | 311.9 | 1.4e-90 | 1 |
| gi\|239988329\|ref\|ZP_04708993.1\| | putative phosph | 311.6 | 1.6e-90 | 1 |
| gi\|226229154\|ref\|YP_002763260.1\| | phosphoenolpyru | 311.4 | 1.9e-90 | 1 |
| gi\|260457184\|ref\|ZP_05805553.1\| | Phosphoenolpyru | 311.1 | 2.3e-90 | 1 |
| gi\|256767868\|ref\|ZP_05507042.1\| | putative phosph | 311.0 | 2.4e-90 | 1 |
| gi\|254388786\|ref\|ZP_05004018.1\| | phosphoenolpyru | 310.7 | 3e-90 | 1 |
| gi\|190891900\|ref\|YP_001978442.1\| | putative phosph | 310.7 | 3e-90 | 1 |
| gi\|227878424\|ref\|ZP_03996364.1\| | phosphoenolpyru | 310.4 | 3.8e-90 | 1 |
| gi\|238028333\|ref\|YP_002912564.1\| | Phosphoenolpyru | 310.3 | 4.1e-90 | 1 |
| gi\|209516095\|ref\|ZP_03264955.1\| | Phosphoenolpyru | 309.9 | 5.3e-90 | 1 |
| gi\|292833131\|gb\|EFF91480.1\| | phosphoenolpyru | 309.6 | 6.6e-90 | 1 |
| gi\|119897283\|ref\|YP_932496.1\| | phosphoenolpyru | 309.5 | 6.9e-90 | 1 |
| gi\|254671222\|emb\|CBA08427.1\| | Phosphoenolpyru | 309.4 | 7.3e-90 | 1 |
| gi\|254384995\|ref\|ZP_05000330.1\| | phosphoenolpyru | 309.4 | 7.4e-90 | 1 |
| gi\|221065752\|ref\|ZP_03541857.1\| | Phosphoenolpyru | 309.1 | 9.3e-90 | 1 |
| gi\|167585804\|ref\|ZP_02378192.1\| | phosphoenolpyru | 309.1 | 9.4e-90 | 1 |
| gi\|225858881\|ref\|YP_002740391.1\| | phosphoenolpyru | 308.9 | 1e-89 | 1 |
| gi\|220911519\|ref\|YP_002486828.1\| | Phosphoenolpyru | 308.6 | 1.3e-89 | 1 |
| gi\|168494501\|ref\|ZP_02718644.1\| | phosphoenolpyru | 308.6 | 1.3e-89 | 1 |
| gi\|213965583\|ref\|ZP_03393777.1\| | phosphoenolpyru | 308.5 | 1.4e-89 | 1 |
| gi\|241889879\|ref\|ZP_04777177.1\| | phosphoenolpyru | 308.5 | 1.4e-89 | 1 |
| gi\|161524047\|ref\|YP_001579059.1\| | phosphoenolpyru | 307.2 | 3.5e-89 | 1 |
| gi\|221211566\|ref\|ZP_03584545.1\| | phosphoenolpyru | 307.1 | 3.8e-89 | 1 |
| gi\|254491458\|ref\|ZP_05104637.1\| | phosphoenolpyru | 306.9 | 4.2e-89 | 1 |
| gi\|15903018\|ref\|NP_358568.1\| | phosphoenolpyru | 306.8 | 4.4e-89 | 1 |
| gi\|282865456\|ref\|ZP_06274507.1\| | Phosphoenolpyru | 306.6 | 5.2e-89 | 1 |
| gi\|76787926\|ref\|YP_329507.1\| | phosphoenolpyru | 306.2 | 6.9e-89 | 1 |
| gi\|148989111\|ref\|ZP_01820501.1\| | phosphoenolpyru | 306.1 | 7.5e-89 | 1 |
| gi\|262046224\|ref\|ZP_06019187.1\| | phosphoenolpyru | 305.9 | 8.7e-89 | 1 |
| gi\|225861034\|ref\|YP_002742543.1\| | phosphoenolpyru | 305.6 | 1.1e-88 | 1 |
| gi\|149006260\|ref\|ZP_01829972.1\| | phosphoenolpyru | 305.5 | 1.1e-88 | 1 |
| gi\|269214612\|ref\|ZP_06158686.1\| | phosphoenolpyru | 305.3 | 1.3e-88 | 1 |
| gi\|15900937\|ref\|NP_345541.1\| | phosphoenolpyru | 305.3 | 1.3e-88 | 1 |
| gi\|149003977\|ref\|ZP_01828785.1\| | phosphoenolpyru | 305.3 | 1.3e-88 | 1 |
| gi\|148994184\|ref\|ZP_01823499.1\| | phosphoenolpyru | 305.2 | 1.3e-88 | 1 |
| gi\|264679666\|ref\|YP_003279573.1\| | phosphoenolpyru | 305.2 | 1.4e-88 | 1 |
| gi\|284044871\|ref\|YP_003395211.1\| | Phosphoenolpyru | 305.2 | 1.4e-88 | 1 |
| gi\|293381352\|ref\|ZP_06627354.1\| | phosphoenolpyru | 305.1 | 1.5e-88 | 1 |
| gi\|168487465\|ref\|ZP_02711973.1\| | phosphoenolpyru | 305.0 | 1.6e-88 | 1 |
| gi\|221199352\|ref\|ZP_03572396.1\| | phosphoenolpyru | 304.9 | 1.7e-88 | 1 |
| gi\|256843881\|ref\|ZP_05549368.1\| | phosphoenolpyru | 304.8 | 1.8e-88 | 1 |
| gi\|22536923\|ref\|NP_687774.1\| | phosphoenolpyru | 304.8 | 1.8e-88 | 1 |
| gi\|148985039\|ref\|ZP_01818282.1\| | phosphoenolpyru | 304.8 | 1.9e-88 | 1 |
| gi\|168576207\|ref\|ZP_02722101.1\| | phosphoenolpyru | 304.4 | 2.4e-88 | 1 |
| gi\|169833797\|ref\|YP_001694494.1\| | phosphoenolpyru | 303.9 | 3.4e-88 | 1 |
| gi\|206560970\|ref\|YP_002231735.1\| | phosphoenolpyru | 303.7 | 3.9e-88 | 1 |
| gi\|149925330\|ref\|ZP_01913594.1\| | phosphoenolpyru | 303.4 | 4.7e-88 | 1 |
| gi\|258654566\|ref\|YP_003203722.1\| | Phosphoenolpyru | 303.4 | 4.8e-88 | 1 |
| gi\|78067222\|ref\|YP_369991.1\| | phosphoenolpyru | 302.4 | 9.8e-88 | 1 |
| gi\|116690446\|ref\|YP_836069.1\| | phosphoenolpyru | 302.2 | 1.1e-87 | 1 |
| gi\|107023363\|ref\|YP_621690.1\| | phosphoenolpyru | 302.2 | 1.1e-87 | 1 |
| gi\|237745485\|ref\|ZP_04575965.1\| | phosphoenolpyru | 302.0 | 1.3e-87 | 1 |
| gi\|144899948\|emb\|CAM76812.1\| | Phosphoenolpyru | 302.0 | 1.3e-87 | 1 |
| gi\|225856712\|ref\|YP_002738223.1\| | phosphoenolpyru | 301.7 | 1.6e-87 | 1 |
| gi\|222152768\|ref\|YP_002561945.1\| | phosphoenolpyru | 301.6 | 1.7e-87 | 1 |
| gi\|25028259\|ref\|NP_738313.1\| | phosphoenolpyru | 301.5 | 1.8e-87 | 1 |
| gi\|195977846\|ref\|YP_002123090.1\| | phosphoenolpyru | 301.2 | 2.2e-87 | 1 |
| gi\|189219750\|ref\|YP_001940391.1\| | Phosphoenolpyru | 301.1 | 2.3e-87 | 1 |

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|---|---|---|---|---|
| gi\|293365250\|ref\|ZP_06611967.1\| | phosphoenolpyru | 301.1 | 2.3e-87 | 1 |
| gi\|77409086\|ref\|ZP_00785802.1\| | phosphoenolpyru | 300.9 | 2.7e-87 | 1 |
| gi\|194397283\|ref\|YP_002037699.1\| | phosphoenolpyru | 300.4 | 3.8e-87 | 1 |
| gi\|224826000\|ref\|ZP_03699103.1\| | Phosphoenolpyru | 300.2 | 4.5e-87 | 1 |
| gi\|76810271\|ref\|YP_332639.1\| | phosphoenolpyru | 300.1 | 4.8e-87 | 1 |
| gi\|254261244\|ref\|ZP_04952298.1\| | phosphoenolpyru | 300.1 | 4.8e-87 | 1 |
| gi\|53718655\|ref\|YP_107641.1\| | phosphoenolpyru | 300.0 | 5.2e-87 | 1 |
| gi\|126440608\|ref\|YP_001058119.1\| | phosphoenolpyru | 300.0 | 5.2e-87 | 1 |
| gi\|126451534\|ref\|YP_001065355.1\| | phosphoenolpyru | 300.0 | 5.2e-87 | 1 |
| gi\|167003501\|ref\|ZP_02269287.1\| | phosphoenolpyru | 299.9 | 5.6e-87 | 1 |
| gi\|260101538\|ref\|ZP_05751775.1\| | phosphoenolpyru | 299.9 | 5.6e-87 | 1 |
| gi\|160897676\|ref\|YP_001563258.1\| | phosphoenolpyru | 299.8 | 5.7e-87 | 1 |
| gi\|89143166\|emb\|CAJ44471.1\| | phosphoenolpyru | 299.8 | 5.9e-87 | 1 |
| gi\|218767367\|ref\|YP_002341879.1\| | phosphoenolpyru | 299.7 | 6.4e-87 | 1 |
| gi\|11267798\|pir\|\|D81953 | phosphoenolpyru | 299.7 | 6.4e-87 | 1 |
| gi\|222111549\|ref\|YP_002553813.1\| | Phosphoenolpyru | 299.6 | 6.6e-87 | 1 |
| gi\|170733766\|ref\|YP_001765713.1\| | phosphoenolpyru | 299.5 | 7.2e-87 | 1 |
| gi\|77413069\|ref\|ZP_00789270.1\| | phosphoenolpyru | 299.4 | 7.8e-87 | 1 |
| gi\|254247510\|ref\|ZP_04940831.1\| | Phosphoenolpyru | 299.3 | 8e-87 | 1 |
| gi\|282873614\|ref\|ZP_06282580.1\| | Phosphoenolpyru | 299.1 | 9.7e-87 | 1 |
| gi\|182438172\|ref\|YP_001825891.1\| | putative phosph | 299.0 | 1e-86 | 1 |
| gi\|258594352\|ref\|ZP_05709164.1\| | Phosphoenolpyru | 298.8 | 1.2e-86 | 1 |
| gi\|167561969\|ref\|ZP_02354885.1\| | phosphoenolpyru | 298.7 | 1.3e-86 | 1 |
| gi\|167618301\|ref\|ZP_02386932.1\| | phosphoenolpyru | 298.6 | 1.3e-86 | 1 |
| gi\|167580195\|ref\|ZP_02373069.1\| | phosphoenolpyru | 298.5 | 1.4e-86 | 1 |
| gi\|225870168\|ref\|YP_002746115.1\| | phosphoenolpyru | 298.4 | 1.6e-86 | 1 |
| gi\|15677883\|ref\|NP_275051.1\| | phosphoenolpyru | 298.2 | 1.7e-86 | 1 |
| gi\|254251704\|ref\|ZP_04945022.1\| | Phosphoenolpyru | 298.2 | 1.8e-86 | 1 |
| gi\|121595210\|ref\|YP_987106.1\| | phosphoenolpyru | 298.0 | 2e-86 | 1 |
| gi\|134296608\|ref\|YP_001120343.1\| | phosphoenolpyru | 298.0 | 2.1e-86 | 1 |
| gi\|251782035\|ref\|YP_002996337.1\| | phosphoenolpyru | 297.9 | 2.2e-86 | 1 |
| gi\|161507563\|ref\|YP_001577517.1\| | phosphoenolpyru | 297.6 | 2.7e-86 | 1 |
| gi\|254181387\|ref\|ZP_04887984.1\| | phosphoenolpyru | 297.1 | 3.8e-86 | 1 |
| gi\|167918035\|ref\|ZP_02505126.1\| | phosphoenolpyru | 297.1 | 3.8e-86 | 1 |
| gi\|241759416\|ref\|ZP_04757520.1\| | phosphoenolpyru | 296.9 | 4.4e-86 | 1 |
| gi\|225868820\|ref\|YP_002744768.1\| | phosphoenolpyru | 296.6 | 5.4e-86 | 1 |
| gi\|83719610\|ref\|YP_441427.1\| | phosphoenolpyru | 296.1 | 7.5e-86 | 1 |
| gi\|116627590\|ref\|YP_820209.1\| | phosphoenolpyru | 296.1 | 7.8e-86 | 1 |
| gi\|261379952\|ref\|ZP_05984525.1\| | phosphoenolpyru | 295.4 | 1.2e-85 | 1 |
| gi\|239814380\|ref\|YP_002943290.1\| | Phosphoenolpyru | 295.3 | 1.3e-85 | 1 |
| gi\|254190787\|ref\|ZP_04897294.1\| | phosphoenolpyru | 294.5 | 2.3e-85 | 1 |
| gi\|226194359\|ref\|ZP_03789957.1\| | phosphoenolpyru | 294.5 | 2.3e-85 | 1 |
| gi\|55820784\|ref\|YP_139226.1\| | phosphoenolpyru | 294.5 | 2.3e-85 | 1 |
| gi\|288905708\|ref\|YP_003430930.1\| | putative phosph | 294.4 | 2.5e-85 | 1 |
| gi\|237747682\|ref\|ZP_04578162.1\| | phosphoenolpyru | 294.0 | 3.3e-85 | 1 |
| gi\|284989422\|ref\|YP_003407976.1\| | Phosphoenolpyru | 293.2 | 5.8e-85 | 1 |
| gi\|288942679\|ref\|YP_003444919.1\| | Phosphoenolpyru | 293.1 | 5.9e-85 | 1 |
| gi\|240114073\|ref\|ZP_04728563.1\| | phosphoenolpyru | 293.0 | 6.5e-85 | 1 |
| gi\|268600141\|ref\|ZP_06134308.1\| | phosphoenolpyru | 293.0 | 6.5e-85 | 1 |
| gi\|161869130\|ref\|YP_001598297.1\| | phosphoenolpyru | 292.9 | 7e-85 | 1 |
| gi\|261393385\|emb\|CAX51021.1\| | phosphoenolpyru | 292.6 | 8.5e-85 | 1 |
| gi\|288918904\|ref\|ZP_06413247.1\| | Phosphoenolpyru | 292.5 | 9.3e-85 | 1 |
| gi\|240122526\|ref\|ZP_04735482.1\| | phosphoenolpyru | 292.3 | 1e-84 | 1 |
| gi\|268681114\|ref\|ZP_06147976.1\| | phosphoenolpyru | 292.3 | 1e-84 | 1 |
| gi\|240081793\|ref\|ZP_04726336.1\| | phosphoenolpyru | 292.3 | 1e-84 | 1 |
| gi\|268597893\|ref\|ZP_06132060.1\| | phosphoenolpyru | 292.3 | 1e-84 | 1 |
| gi\|291044869\|ref\|ZP_06570578.1\| | phosphoenolpyru | 292.3 | 1e-84 | 1 |
| gi\|121635719\|ref\|YP_975964.1\| | phosphoenolpyru | 292.3 | 1.1e-84 | 1 |
| gi\|289167828\|ref\|YP_003446097.1\| | phosphoenolpyru | 292.1 | 1.2e-84 | 1 |
| gi\|167569217\|ref\|ZP_02362091.1\| | phosphoenolpyru | 291.1 | 2.5e-84 | 1 |
| gi\|171780080\|ref\|ZP_02920984.1\| | hypothetical pr | 290.9 | 2.9e-84 | 1 |
| gi\|121605982\|ref\|YP_983311.1\| | phosphoenolpyru | 290.8 | 2.9e-84 | 1 |
| gi\|270292890\|ref\|ZP_06199101.1\| | phosphoenolpyru | 290.7 | 3.1e-84 | 1 |
| gi\|197104620\|ref\|YP_002129997.1\| | phosphoenolpyru | 290.7 | 3.1e-84 | 1 |
| gi\|55822687\|ref\|YP_141128.1\| | phosphoenolpyru | 290.7 | 3.2e-84 | 1 |
| gi\|116513617\|ref\|YP_812523.1\| | phosphoenolpyru | 290.4 | 4e-84 | 1 |
| gi\|194690202\|gb\|ACF79185.1\| | unknown [Zea ma | 289.5 | 7.4e-84 | 1 |
| gi\|83814357\|ref\|YP_444246.1\| | phosphoenolpyru | 289.4 | 7.8e-84 | 1 |
| gi\|161572971\|ref\|YP_209040.2\| | phosphoenolpyru | 289.3 | 8.5e-84 | 1 |
| gi\|268602565\|ref\|ZP_06136732.1\| | phosphoenolpyru | 289.3 | 8.5e-84 | 1 |
| gi\|194099706\|ref\|YP_002002841.1\| | phosphoenolpyru | 289.3 | 8.5e-84 | 1 |

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|---|---|---|---|---|
| gi\|293397945\|ref\|ZP_06642151.1\| | phosphoenolpyru | 289.3 | 8.5e-84 | 1 |
| gi\|254492745\|ref\|ZP_05105916.1\| | phosphoenolpyru | 289.1 | 9.5e-84 | 1 |
| gi\|239999896\|ref\|ZP_04719820.1\| | phosphoenolpyru | 289.1 | 9.5e-84 | 1 |
| gi\|94265456\|ref\|ZP_01289207.1\| | Phosphoenolpyru | 288.8 | 1.2e-83 | 1 |
| gi\|225021380\|ref\|ZP_03710572.1\| | hypothetical pr | 288.3 | 1.7e-83 | 1 |
| gi\|269213946\|ref\|ZP_05983221.2\| | phosphoenolpyru | 287.7 | 2.6e-83 | 1 |
| gi\|254804129\|ref\|YP_003082350.1\| | Phosphoenolpyru | 286.8 | 4.8e-83 | 1 |
| gi\|240015599\|ref\|ZP_04722139.1\| | phosphoenolpyru | 286.3 | 6.7e-83 | 1 |
| gi\|20196784\|emb\|CAC86364.1\| | putative phosph | 285.2 | 1.5e-82 | 1 |
| gi\|241766972\|ref\|ZP_04764768.1\| | Phosphoenolpyru | 284.6 | 2.2e-82 | 1 |
| gi\|270494458\|ref\|ZP_06211504.1\| | phosphoenolpyru | 283.2 | 5.6e-82 | 1 |
| gi\|252126365\|ref\|ZP_04836407.1\| | phosphoenolpyru | 283.1 | 6.3e-82 | 1 |
| gi\|262196990\|ref\|YP_003268199.1\| | Phosphoenolpyru | 282.9 | 7.2e-82 | 1 |
| gi\|104773626\|ref\|YP_618606.1\| | phosphoenolpyru | 280.8 | 3.1e-81 | 1 |
| gi\|20196776\|emb\|CAC86360.1\| | putative phosph | 280.1 | 5e-81 | 1 |
| gi\|227881566\|ref\|ZP_03999428.1\| | Phosphoenolpyru | 280.0 | 5.3e-81 | 1 |
| gi\|256389410\|ref\|YP_003110974.1\| | Phosphoenolpyru | 279.7 | 6.6e-81 | 1 |
| gi\|94264993\|ref\|ZP_01288763.1\| | Phosphoenolpyru | 278.9 | 1.1e-80 | 1 |
| gi\|56807908\|ref\|ZP_00365735.1\| | COG2352: Phosph | 277.9 | 2.2e-80 | 1 |
| gi\|94990008\|ref\|YP_598108.1\| | phosphoenolpyru | 277.7 | 2.6e-80 | 1 |
| gi\|94988126\|ref\|YP_596227.1\| | phosphoenolpyru | 277.7 | 2.6e-80 | 1 |
| gi\|71903150\|ref\|YP_279953.1\| | phosphoenolpyru | 277.6 | 2.8e-80 | 1 |
| gi\|197103239\|ref\|YP_002128617.1\| | phosphoenolpyru | 277.0 | 4.2e-80 | 1 |
| gi\|209559064\|ref\|YP_002285536.1\| | Phosphoenolpyru | 276.8 | 4.9e-80 | 1 |
| gi\|293168120\|ref\|ZP_06606869.1\| | phosphoenolpyru | 276.2 | 7.5e-80 | 1 |
| gi\|21909966\|ref\|NP_664234.1\| | phosphoenolpyru | 276.1 | 8.1e-80 | 1 |
| gi\|50913872\|ref\|YP_059844.1\| | phosphoenolpyru | 275.9 | 9.3e-80 | 1 |
| gi\|120610680\|ref\|YP_970358.1\| | phosphoenolpyru | 275.8 | 9.7e-80 | 1 |
| gi\|261365408\|ref\|ZP_05978291.1\| | phosphoenolpyru | 275.6 | 1.1e-79 | 1 |
| gi\|16588669\|gb\|AAL26863.1\|AF314923_1 | phosphoenolpyru | 275.1 | 1.6e-79 | 1 |
| gi\|221633046\|ref\|YP_002522271.1\| | phosphoenolpyru | 275.0 | 1.7e-79 | 1 |
| gi\|94993920\|ref\|YP_602018.1\| | phosphoenolpyru | 274.6 | 2.3e-79 | 1 |
| gi\|94970716\|ref\|YP_592764.1\| | phosphoenolpyru | 274.4 | 2.5e-79 | 1 |
| gi\|68536075\|ref\|YP_250780.1\| | phosphoenolpyru | 274.0 | 3.5e-79 | 1 |
| gi\|73540405\|ref\|YP_294925.1\| | phosphoenolpyru | 273.9 | 3.7e-79 | 1 |
| gi\|91789513\|ref\|YP_550465.1\| | phosphoenolpyru | 273.8 | 3.8e-79 | 1 |
| gi\|73920189\|sp\|Q8K873.2\|CAPP_STRP3 | RecName: Full=P | 273.8 | 4e-79 | 1 |
| gi\|260578770\|ref\|ZP_05846677.1\| | phosphoenolpyru | 273.6 | 4.5e-79 | 1 |
| gi\|139474183\|ref\|YP_001128899.1\| | phosphoenolpyru | 273.6 | 4.5e-79 | 1 |
| gi\|255067797\|ref\|ZP_05319652.1\| | phosphoenolpyru | 272.7 | 8.2e-79 | 1 |
| gi\|229824131\|ref\|ZP_04450200.1\| | hypothetical pr | 272.2 | 1.2e-78 | 1 |
| gi\|257455375\|ref\|ZP_05620610.1\| | phosphoenolpyru | 271.0 | 2.7e-78 | 1 |
| gi\|19745716\|ref\|NP_606852.1\| | phosphoenolpyru | 270.6 | 3.7e-78 | 1 |
| gi\|71910318\|ref\|YP_281868.1\| | phosphoenolpyru | 269.7 | 6.7e-78 | 1 |
| gi\|241663753\|ref\|YP_002982113.1\| | Phosphoenolpyru | 269.5 | 7.8e-78 | 1 |
| gi\|15674689\|ref\|NP_268863.1\| | phosphoenolpyru | 269.4 | 8.2e-78 | 1 |
| gi\|225024256\|ref\|ZP_03713448.1\| | hypothetical pr | 269.4 | 8.3e-78 | 1 |
| gi\|121608028\|ref\|YP_995835.1\| | phosphoenolpyru | 269.2 | 9.4e-78 | 1 |
| gi\|171057452\|ref\|YP_001789801.1\| | phosphoenolpyru | 269.1 | 9.9e-78 | 1 |
| gi\|113868876\|ref\|YP_727365.1\| | phosphoenolpyru | 268.7 | 1.3e-77 | 1 |
| gi\|283821743\|ref\|ZP_06348554.1\| | Phosphoenolpyru | 267.9 | 2.3e-77 | 1 |
| gi\|228476844\|ref\|ZP_04061489.1\| | phosphoenolpyru | 267.8 | 2.5e-77 | 1 |
| gi\|227890073\|ref\|ZP_04007878.1\| | phosphoenolpyru | 267.3 | 3.7e-77 | 1 |
| gi\|227832350\|ref\|YP_002834057.1\| | Phosphoenolpyru | 266.8 | 4.9e-77 | 1 |
| gi\|261855598\|ref\|YP_003262881.1\| | Phosphoenolpyru | 266.4 | 6.7e-77 | 1 |
| gi\|194290491\|ref\|YP_002006398.1\| | phosphoenolpyru | 265.6 | 1.1e-76 | 1 |
| gi\|255021660\|ref\|ZP_05293702.1\| | Phosphoenolpyru | 265.4 | 1.3e-76 | 1 |
| gi\|125718332\|ref\|YP_001035465.1\| | phosphoenolpyru | 265.4 | 1.3e-76 | 1 |
| gi\|227904011\|ref\|ZP_04021816.1\| | phosphoenolpyru | 265.3 | 1.4e-76 | 1 |
| gi\|20196778\|emb\|CAC86361.1\| | putative phosph | 265.0 | 1.8e-76 | 1 |
| gi\|187929645\|ref\|YP_001900132.1\| | Phosphoenolpyru | 263.6 | 4.6e-76 | 1 |
| gi\|83749206\|ref\|ZP_00946208.1\| | Phosphoenolpyru | 263.2 | 5.9e-76 | 1 |
| gi\|256759173\|ref\|ZP_05499837.1\| | Phosphoenolpyru | 262.7 | 8.5e-76 | 1 |
| gi\|116629723\|ref\|YP_814895.1\| | phosphoenolpyru | 262.4 | 1.1e-75 | 1 |
| gi\|268319407\|ref\|YP_003293063.1\| | hypothetical pr | 262.0 | 1.4e-75 | 1 |
| gi\|227505333\|ref\|ZP_03935382.1\| | phosphoenolpyru | 261.7 | 1.7e-75 | 1 |
| gi\|269123480\|ref\|YP_003306057.1\| | Phosphoenolpyru | 261.5 | 1.9e-75 | 1 |
| gi\|58337382\|ref\|YP_193967.1\| | phosphoenolpyru | 261.5 | 2e-75 | 1 |
| gi\|78221527\|ref\|YP_383274.1\| | phosphoenolpyru | 261.2 | 2.4e-75 | 1 |
| gi\|238020526\|ref\|ZP_04600952.1\| | hypothetical pr | 261.1 | 2.6e-75 | 1 |
| gi\|148652373\|ref\|YP_001279466.1\| | phosphoenolpyru | 260.8 | 3.3e-75 | 1 |

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|---|---|---|---|---|
| gi\|226819197\|ref\|ZP_03808316.1\| | phosphoenolpyru | 259.5 | 7.9e-75 | 1 |
| gi\|222055605\|ref\|YP_002537967.1\| | Phosphoenolpyru | 258.8 | 1.3e-74 | 1 |
| gi\|17547077\|ref\|NP_520479.1\| | phosphoenolpyru | 258.3 | 1.8e-74 | 1 |
| gi\|157149951\|ref\|YP_001450059.1\| | phosphoenolpyru | 257.5 | 3.3e-74 | 1 |
| gi\|94311682\|ref\|YP_584892.1\| | phosphoenolpyru | 256.3 | 7.4e-74 | 1 |
| gi\|93006646\|ref\|YP_581083.1\| | phosphoenolpyru | 256.2 | 7.9e-74 | 1 |
| gi\|227521038\|ref\|ZP_03951087.1\| | phosphoenolpyru | 255.6 | 1.1e-73 | 1 |
| gi\|238853373\|ref\|ZP_04643752.1\| | phosphoenolpyru | 255.6 | 1.2e-73 | 1 |
| gi\|292656740\|ref\|YP_003536637.1\| | phosphoenolpyru | 255.0 | 1.7e-73 | 1 |
| gi\|227893638\|ref\|ZP_04011443.1\| | phosphoenolpyru | 254.8 | 2e-73 | 1 |
| gi\|292492516\|ref\|YP_003527955.1\| | Phosphoenolpyru | 254.7 | 2.3e-73 | 1 |
| gi\|182677139\|ref\|YP_001831285.1\| | phosphoenolpyru | 254.5 | 2.6e-73 | 1 |
| gi\|262282657\|ref\|ZP_06060425.1\| | phosphoenolpyru | 254.4 | 2.8e-73 | 1 |
| gi\|229538486\|ref\|ZP_04427622.1\| | phosphoenolpyru | 253.9 | 3.7e-73 | 1 |
| gi\|226355772\|ref\|YP_002785512.1\| | putative Phosph | 253.3 | 5.9e-73 | 1 |
| gi\|271962867\|ref\|YP_003337063.1\| | Phosphoenolpyru | 252.6 | 9.4e-73 | 1 |
| gi\|291295381\|ref\|YP_003506779.1\| | Phosphoenolpyru | 252.0 | 1.4e-72 | 1 |
| gi\|227506616\|ref\|ZP_03936665.1\| | possible phosph | 251.4 | 2.2e-72 | 1 |
| gi\|71065696\|ref\|YP_264423.1\| | phosphoenolpyru | 249.6 | 7.6e-72 | 1 |
| gi\|258545813\|ref\|ZP_05706047.1\| | transposition p | 249.5 | 8.2e-72 | 1 |
| gi\|20196788\|emb\|CAC86366.1\| | putative phosph | 249.0 | 1.1e-71 | 1 |
| gi\|283782535\|ref\|YP_003373289.1\| | phosphoenolpyru | 248.0 | 2.4e-71 | 1 |
| gi\|38233712\|ref\|NP_939479.1\| | phosphoenolpyru | 247.7 | 2.9e-71 | 1 |
| gi\|269921664\|ref\|ZP_06170573.1\| | Phosphoenolpyru | 246.8 | 5.3e-71 | 1 |
| gi\|226942050\|ref\|YP_002797124.1\| | CapP [Laribacte | 244.6 | 2.4e-70 | 1 |
| gi\|1213341\|dbj\|BAA05398.1\| | phosphoenolpyru | 244.2 | 3.1e-70 | 1 |
| gi\|1213343\|dbj\|BAA05396.1\| | phosphoenolpyru | 243.7 | 4.6e-70 | 1 |
| gi\|253999144\|ref\|YP_003051207.1\| | Phosphoenolpyru | 242.6 | 9.5e-70 | 1 |
| gi\|110669081\|ref\|YP_658892.1\| | phosphoenolpyru | 242.5 | 1e-69 | 1 |
| gi\|269128325\|ref\|YP_003301695.1\| | Phosphoenolpyru | 241.4 | 2.2e-69 | 1 |
| gi\|284167583\|ref\|YP_003405861.1\| | Phosphoenolpyru | 238.3 | 1.9e-68 | 1 |
| gi\|46198568\|ref\|YP_004235.1\| | phosphoenolpyru | 238.0 | 2.3e-68 | 1 |
| gi\|20196774\|emb\|CAC86359.1\| | putative phosph | 237.0 | 4.8e-68 | 1 |
| gi\|222480720\|ref\|YP_002566957.1\| | phosphoenolpyru | 235.5 | 1.4e-67 | 1 |
| gi\|284165765\|ref\|YP_003404044.1\| | Phosphoenolpyru | 234.3 | 3e-67 | 1 |
| gi\|89900503\|ref\|YP_522974.1\| | phosphoenolpyru | 232.4 | 1.2e-66 | 1 |
| gi\|108759396\|ref\|YP_632739.1\| | phosphoenolpyru | 232.0 | 1.5e-66 | 1 |
| gi\|269958054\|ref\|YP_003327843.1\| | Phosphoenolpyru | 231.3 | 2.4e-66 | 1 |
| gi\|148556039\|ref\|YP_001263621.1\| | phosphoenolpyru | 231.2 | 2.6e-66 | 1 |
| gi\|187476834\|ref\|YP_784858.1\| | phosphoenolpyru | 230.5 | 4.2e-66 | 1 |
| gi\|124268187\|ref\|YP_001022191.1\| | phosphoenolpyru | 230.2 | 5.2e-66 | 1 |
| gi\|284172789\|ref\|YP_003406171.1\| | Phosphoenolpyru | 229.9 | 6.3e-66 | 1 |
| gi\|254525149\|ref\|ZP_05137204.1\| | phosphoenolpyru | 229.8 | 6.7e-66 | 1 |
| gi\|269796282\|ref\|YP_003315737.1\| | Phosphoenolpyru | 229.8 | 6.8e-66 | 1 |
| gi\|291455731\|ref\|ZP_06595121.1\| | phosphoenolpyru | 229.5 | 8.5e-66 | 1 |
| gi\|194364406\|ref\|YP_002027016.1\| | Phosphoenolpyru | 228.9 | 1.3e-65 | 1 |
| gi\|94496216\|ref\|ZP_01302794.1\| | phosphoenolpyru | 228.8 | 1.3e-65 | 1 |
| gi\|103488557\|ref\|YP_618118.1\| | phosphoenolpyru | 228.7 | 1.5e-65 | 1 |
| gi\|213690981\|ref\|YP_002321567.1\| | Phosphoenolpyru | 227.2 | 4.1e-65 | 1 |
| gi\|23465189\|ref\|NP_695792.1\| | phosphoenolpyru | 226.9 | 5.1e-65 | 1 |
| gi\|292676674\|dbj\|BAI98192.1\| | phosphoenolpyru | 225.9 | 1e-64 | 1 |
| gi\|171741712\|ref\|ZP_02917519.1\| | hypothetical pr | 224.8 | 2.2e-64 | 1 |
| gi\|46190357\|ref\|ZP_00121597.2\| | COG2352: Phosph | 224.2 | 3.3e-64 | 1 |
| gi\|72162953\|ref\|YP_290610.1\| | phosphoenolpyru | 224.1 | 3.7e-64 | 1 |
| gi\|33599409\|ref\|NP_886969.1\| | phosphoenolpyru | 223.9 | 4.2e-64 | 1 |
| gi\|291517702\|emb\|CBK71318.1\| | Phosphoenolpyru | 221.5 | 2.1e-63 | 1 |
| gi\|227547454\|ref\|ZP_03977503.1\| | possible phosph | 221.3 | 2.4e-63 | 1 |
| gi\|20196786\|emb\|CAC86365.1\| | putative phosph | 221.2 | 2.7e-63 | 1 |
| gi\|163858843\|ref\|YP_001633141.1\| | phosphoenolpyru | 221.0 | 3.2e-63 | 1 |
| gi\|227988853\|ref\|ZP_04035945.1\| | Phosphoenolpyru | 220.4 | 4.5e-63 | 1 |
| gi\|183602906\|ref\|ZP_02964265.1\| | hypothetical pr | 220.3 | 5e-63 | 1 |
| gi\|289177836\|gb\|ADC85082.1\| | Phosphoenolpyru | 220.3 | 5e-63 | 1 |
| gi\|94984768\|ref\|YP_604132.1\| | phosphoenolpyru | 219.6 | 7.9e-63 | 1 |
| gi\|257052544\|ref\|YP_003130377.1\| | Phosphoenolpyru | 219.2 | 1e-62 | 1 |
| gi\|254419270\|ref\|ZP_05032994.1\| | phosphoenolpyru | 219.1 | 1.1e-62 | 1 |
| gi\|33595127\|ref\|NP_882770.1\| | phosphoenolpyru | 219.0 | 1.2e-62 | 1 |
| gi\|241761565\|ref\|ZP_04759652.1\| | Phosphoenolpyru | 218.2 | 2.1e-62 | 1 |
| gi\|260753930\|ref\|YP_003226823.1\| | Phosphoenolpyru | 217.3 | 3.9e-62 | 1 |
| gi\|56552392\|ref\|YP_163231.1\| | Phosphoenolpyru | 217.3 | 4e-62 | 1 |
| gi\|190572823\|ref\|YP_001970668.1\| | putative phosph | 216.9 | 5.4e-62 | 1 |
| gi\|117927606\|ref\|YP_872157.1\| | phosphoenolpyru | 216.2 | 8.5e-62 | 1 |

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|---|---|---|---|---|
| gi\|229821216\|ref\|YP_002882742.1\| | Phosphoenolpyru | 215.7 | 1.2e-61 | 1 |
| gi\|289580156\|ref\|YP_003478622.1\| | Phosphoenolpyru | 215.6 | 1.3e-61 | 1 |
| gi\|270284604\|ref\|ZP_05966403.2\| | phosphoenolpyru | 214.9 | 2.1e-61 | 1 |
| gi\|229816951\|ref\|ZP_04447233.1\| | hypothetical pr | 213.6 | 5.3e-61 | 1 |
| gi\|78046414\|ref\|YP_362589.1\| | phosphoenolpyru | 213.2 | 6.8e-61 | 1 |
| gi\|163797958\|ref\|ZP_02191900.1\| | phosphoenolpyru | 213.1 | 7.4e-61 | 1 |
| gi\|33591459\|ref\|NP_879103.1\| | phosphoenolpyru | 212.4 | 1.2e-60 | 1 |
| gi\|289670989\|ref\|ZP_06492064.1\| | phosphoenolpyru | 212.1 | 1.4e-60 | 1 |
| gi\|289663604\|ref\|ZP_06485185.1\| | phosphoenolpyru | 212.0 | 1.5e-60 | 1 |
| gi\|224283986\|ref\|ZP_03647308.1\| | Phosphoenolpyru | 211.5 | 2.2e-60 | 1 |
| gi\|209965727\|ref\|YP_002298642.1\| | phosphoenolpyru | 210.3 | 5.1e-60 | 1 |
| gi\|15806301\|ref\|NP_295007.1\| | phosphoenolpyru | 208.7 | 1.5e-59 | 1 |
| gi\|212715167\|ref\|ZP_03323295.1\| | hypothetical pr | 208.1 | 2.4e-59 | 1 |
| gi\|16125740\|ref\|NP_420304.1\| | phosphoenolpyru | 208.0 | 2.5e-59 | 1 |
| gi\|167645723\|ref\|YP_001683386.1\| | phosphoenolpyru | 207.3 | 4.1e-59 | 1 |
| gi\|254671854\|emb\|CBA04047.1\| | Phosphoenolpyru | 207.3 | 4.2e-59 | 1 |
| gi\|55377433\|ref\|YP_135283.1\| | phosphoenolpyru | 206.8 | 5.8e-59 | 1 |
| gi\|148271562\|ref\|YP_001221123.1\| | hypothetical pr | 206.8 | 5.9e-59 | 1 |
| gi\|166710682\|ref\|ZP_02241889.1\| | phosphoenolpyru | 206.2 | 8.7e-59 | 1 |
| gi\|154486362\|ref\|ZP_02027769.1\| | hypothetical pr | 205.6 | 1.3e-58 | 1 |
| gi\|66769781\|ref\|YP_244543.1\| | phosphoenolpyru | 205.6 | 1.3e-58 | 1 |
| gi\|1705591\|sp\|P51060.1\|CAPP_THES7 | RecName: Full=P | 205.4 | 1.5e-58 | 1 |
| gi\|58583419\|ref\|YP_202435.1\| | phosphoenolpyru | 205.2 | 1.8e-58 | 1 |
| gi\|73920190\|sp\|Q8PP82.2\|CAPP_XANAC | RecName: Full=P | 204.9 | 2.2e-58 | 1 |
| gi\|1581933\|prf\|\|2117330A | phosphoenolpyru | 204.4 | 2.9e-58 | 1 |
| gi\|21230228\|ref\|NP_636145.1\| | phosphoenolpyru | 203.7 | 4.8e-58 | 1 |
| gi\|188575328\|ref\|YP_001912257.1\| | phosphoenolpyru | 203.3 | 6.4e-58 | 1 |
| gi\|225352396\|ref\|ZP_03743419.1\| | hypothetical pr | 203.2 | 7.2e-58 | 1 |
| gi\|170782299\|ref\|YP_001710632.1\| | phosphoenolpyru | 202.1 | 1.5e-57 | 1 |
| gi\|218295525\|ref\|ZP_03496338.1\| | Phosphoenolpyru | 201.9 | 1.7e-57 | 1 |
| gi\|119025042\|ref\|YP_908887.1\| | hypothetical pr | 201.7 | 2e-57 | 1 |
| gi\|292606014\|gb\|EFF49287.1\| | phosphoenolpyru | 199.8 | 7.5e-57 | 1 |
| gi\|162451699\|ref\|YP_001614066.1\| | hypothetical pr | 199.6 | 8.4e-57 | 1 |
| gi\|21241576\|ref\|NP_641158.1\| | phosphoenolpyru | 199.6 | 8.8e-57 | 1 |
| gi\|292601213\|gb\|EFF45267.1\| | phosphoenolpyru | 199.1 | 1.2e-56 | 1 |
| gi\|20196792\|emb\|CAC86368.1\| | putative phosph | 198.9 | 1.4e-56 | 1 |
| gi\|20196794\|emb\|CAC86369.1\| | putative phosph | 198.0 | 2.7e-56 | 1 |
| gi\|266627058\|ref\|ZP_06119989.1\| | Phosphoenolpyru | 196.6 | 6.6e-56 | 1 |
| gi\|285019549\|ref\|YP_003377260.1\| | probable phosph | 196.3 | 8.3e-56 | 1 |
| gi\|229243257\|ref\|ZP_04367569.1\| | Phosphoenolpyru | 192.1 | 1.5e-54 | 1 |
| gi\|229206299\|ref\|ZP_04332755.1\| | Phosphoenolpyru | 191.8 | 1.9e-54 | 1 |
| gi\|20196796\|emb\|CAC86370.1\| | putative phosph | 189.7 | 8.3e-54 | 1 |
| gi\|262189851\|ref\|ZP_06048182.1\| | phosphoenolpyru | 188.4 | 2.1e-53 | 1 |
| gi\|15022444\|dbj\|BAB62259.1\| | phosphoenolpyru | 186.0 | 1e-52 | 1 |
| gi\|227516707\|ref\|ZP_03946756.1\| | possible phosph | 184.8 | 2.4e-52 | 1 |
| gi\|257388564\|ref\|YP_003178337.1\| | Phosphoenolpyru | 184.5 | 3.1e-52 | 1 |
| gi\|114706303\|ref\|ZP_01439205.1\| | phosphoenolpyru | 184.0 | 4.4e-52 | 1 |
| gi\|10241562\|emb\|CAC09415.1\| | putative C4 Pho | 183.4 | 6.3e-52 | 1 |
| gi\|119964668\|gb\|ABM17097.1\| | phosphoenolpyru | 181.5 | 2.3e-51 | 1 |
| gi\|229815948\|ref\|ZP_04446271.1\| | hypothetical pr | 178.7 | 1.7e-50 | 1 |
| gi\|20196798\|emb\|CAC86371.1\| | putative phosph | 178.4 | 2e-50 | 1 |
| gi\|157273487\|gb\|ABV27386.1\| | phosphoenolpyru | 177.3 | 4.5e-50 | 1 |
| gi\|241771836\|ref\|ZP_04769202.1\| | Phosphoenolpyru | 177.2 | 4.6e-50 | 1 |
| gi\|196228554\|ref\|ZP_03127421.1\| | Phosphoenolpyru | 174.8 | 2.5e-49 | 1 |
| gi\|18076761\|emb\|CAC84924.1\| | phosphoenolpyru | 172.2 | 1.5e-48 | 1 |
| gi\|7768121\|emb\|CAB90621.1\| | phosphoenolpyru | 170.3 | 5.7e-48 | 1 |
| gi\|7768376\|emb\|CAB90716.1\| | phosphoenolpyru | 169.4 | 1e-47 | 1 |
| gi\|7768374\|emb\|CAB90715.1\| | phosphoenolpyru | 168.8 | 1.6e-47 | 1 |
| gi\|217977880\|ref\|YP_002362027.1\| | Phosphoenolpyru | 168.8 | 1.6e-47 | 1 |
| gi\|119356395\|ref\|YP_911039.1\| | phosphoenolpyru | 168.5 | 1.9e-47 | 1 |
| gi\|194335801\|ref\|YP_002017595.1\| | Phosphoenolpyru | 168.3 | 2.3e-47 | 1 |
| gi\|18073888\|emb\|CAC84967.1\| | phosphoenolpyru | 167.9 | 3e-47 | 1 |
| gi\|32473418\|ref\|NP_866412.1\| | phosphoenolpyru | 167.8 | 3.2e-47 | 1 |
| gi\|7768132\|emb\|CAB90627.1\| | phosphoenolpyru | 167.7 | 3.3e-47 | 1 |
| gi\|7768364\|emb\|CAB90712.1\| | phosphoenolpyru | 167.5 | 3.9e-47 | 1 |
| gi\|189499547\|ref\|YP_001959017.1\| | Phosphoenolpyru | 165.7 | 1.3e-46 | 1 |
| gi\|8247239\|emb\|CAB92916.1\| | phosphoenolpyru | 165.4 | 1.7e-46 | 1 |
| gi\|18073874\|emb\|CAC84957.1\| | phosphoenolpyru | 165.0 | 2.3e-46 | 1 |
| gi\|257784777\|ref\|YP_003179994.1\| | Phosphoenolpyru | 164.7 | 2.8e-46 | 1 |
| gi\|145637525\|ref\|ZP_01793183.1\| | phosphoenolpyru | 163.6 | 5.8e-46 | 1 |
| gi\|193214511\|ref\|YP_001995710.1\| | Phosphoenolpyru | 163.1 | 8.4e-46 | 1 |

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|---|---|---|---|---|
| gi\|7768372\|emb\|CAB90714.1\| | phosphoenolpyru | 163.1 | 8.4e-46 | 1 |
| gi\|18073872\|emb\|CAC84956.1\| | phosphoenolpyru | 162.6 | 1.2e-45 | 1 |
| gi\|171911854\|ref\|ZP_02927324.1\| | Phosphoenolpyru | 162.2 | 1.5e-45 | 1 |
| gi\|193212217\|ref\|YP_001998170.1\| | Phosphoenolpyru | 162.0 | 1.7e-45 | 1 |
| gi\|18076765\|emb\|CAC84926.1\| | phosphoenolpyru | 161.9 | 1.9e-45 | 1 |
| gi\|18073868\|emb\|CAC84951.1\| | phosphoenolpyru | 161.9 | 1.9e-45 | 1 |
| gi\|197116626\|ref\|YP_002137053.1\| | phosphoenolpyru | 161.5 | 2.5e-45 | 1 |
| gi\|18073870\|emb\|CAC84955.1\| | phosphoenolpyru | 161.5 | 2.5e-45 | 1 |
| gi\|21674458\|ref\|NP_662523.1\| | phosphoenolpyru | 161.3 | 2.8e-45 | 1 |
| gi\|284029411\|ref\|YP_003379342.1\| | Phosphoenolpyru | 161.3 | 2.9e-45 | 1 |
| gi\|20196790\|emb\|CAC86367.1\| | putative phosph | 160.8 | 4e-45 | 1 |
| gi\|18073864\|emb\|CAC84949.1\| | phosphoenolpyru | 160.6 | 4.6e-45 | 1 |
| gi\|253698863\|ref\|YP_003020052.1\| | Phosphoenolpyru | 160.5 | 5.1e-45 | 1 |
| gi\|83779598\|gb\|ABC47615.1\| | phosphoenolpyru | 160.2 | 6e-45 | 1 |
| gi\|210632317\|ref\|ZP_03297284.1\| | hypothetical pr | 159.5 | 9.7e-45 | 1 |
| gi\|18072430\|emb\|CAC84922.1\| | phosphoenolpyru | 159.3 | 1.1e-44 | 1 |
| gi\|70950271\|ref\|XP_744473.1\| | phosphoenolpyru | 157.9 | 3.1e-44 | 1 |
| gi\|170750063\|ref\|YP_001756323.1\| | phosphoenolpyru | 157.7 | 3.4e-44 | 1 |
| gi\|18073866\|emb\|CAC84950.1\| | phosphoenolpyru | 157.6 | 3.7e-44 | 1 |
| gi\|7768244\|emb\|CAB90659.1\| | phosphoenolpyru | 157.3 | 4.6e-44 | 1 |
| gi\|18073652\|emb\|CAC83643.1\| | phosphoenolpyru | 156.6 | 7.7e-44 | 1 |
| gi\|83779594\|gb\|ABC47613.1\| | phosphoenolpyru | 155.9 | 1.2e-43 | 1 |
| gi\|18073860\|emb\|CAC84947.1\| | phosphoenolpyru | 153.6 | 5.8e-43 | 1 |
| gi\|83779602\|gb\|ABC47617.1\| | phosphoenolpyru | 153.3 | 7.4e-43 | 1 |
| gi\|18073830\|emb\|CAC84932.1\| | phosphoenolpyru | 152.7 | 1.1e-42 | 1 |
| gi\|18073828\|emb\|CAC84931.1\| | phosphoenolpyru | 152.2 | 1.5e-42 | 1 |
| gi\|220926859\|ref\|YP_002502161.1\| | phosphoenolpyru | 152.2 | 1.6e-42 | 1 |
| gi\|18076769\|emb\|CAC84952.1\| | phosphoenolpyru | 151.6 | 2.4e-42 | 1 |
| gi\|10303369\|emb\|CAA65116.1\| | phosphoenolpyru | 151.4 | 2.7e-42 | 1 |
| gi\|83779596\|gb\|ABC47614.1\| | phosphoenolpyru | 150.5 | 5.3e-42 | 1 |
| gi\|18073838\|emb\|CAC84936.1\| | phosphoenolpyru | 150.2 | 6.5e-42 | 1 |
| gi\|18073844\|emb\|CAC84939.1\| | phosphoenolpyru | 149.9 | 7.6e-42 | 1 |
| gi\|221195730\|ref\|ZP_03568784.1\| | phosphoenolpyru | 149.9 | 8e-42 | 1 |
| gi\|78187483\|ref\|YP_375526.1\| | phosphoenolpyru | 149.5 | 1e-41 | 1 |
| gi\|124268439\|ref\|YP_001022443.1\| | phosphoenolpyru | 149.4 | 1.1e-41 | 1 |
| gi\|18076771\|emb\|CAC84953.1\| | phosphoenolpyru | 149.3 | 1.2e-41 | 1 |
| gi\|18072424\|emb\|CAC84919.1\| | phosphoenolpyru | 149.1 | 1.3e-41 | 1 |
| gi\|83779600\|gb\|ABC47616.1\| | phosphoenolpyru | 148.8 | 1.6e-41 | 1 |
| gi\|18073858\|emb\|CAC84946.1\| | phosphoenolpyru | 148.2 | 2.6e-41 | 1 |
| gi\|18076774\|emb\|CAC84954.1\| | phosphoenolpyru | 148.2 | 2.6e-41 | 1 |
| gi\|18073834\|emb\|CAC84934.1\| | phosphoenolpyru | 148.1 | 2.7e-41 | 1 |
| gi\|18073822\|emb\|CAC84916.1\| | phosphoenolpyru | 148.0 | 2.9e-41 | 1 |
| gi\|18073846\|emb\|CAC84940.1\| | phosphoenolpyru | 147.2 | 5.1e-41 | 1 |
| gi\|114326718\|ref\|YP_743875.1\| | phosphoenolpyru | 147.2 | 5.2e-41 | 1 |
| gi\|163851228\|ref\|YP_001639271.1\| | phosphoenolpyru | 146.2 | 9.9e-41 | 1 |
| gi\|1166442\|emb\|CAA61086.1\| | phosphoenolpyru | 146.1 | 1.1e-40 | 1 |
| gi\|18076757\|emb\|CAC84915.1\| | phosphoenolpyru | 146.0 | 1.1e-40 | 1 |
| gi\|18073842\|emb\|CAC84938.1\| | phosphoenolpyru | 145.7 | 1.4e-40 | 1 |
| gi\|7320917\|emb\|CAB81955.1\| | phosphoenolpyru | 145.7 | 1.5e-40 | 1 |
| gi\|18073836\|emb\|CAC84935.1\| | phosphoenolpyru | 145.5 | 1.6e-40 | 1 |
| gi\|254467180\|ref\|ZP_05080591.1\| | phosphoenolpyru | 144.5 | 3.3e-40 | 1 |
| gi\|1166448\|emb\|CAA61085.1\| | phosphoenolpyru | 143.8 | 5.2e-40 | 1 |
| gi\|18073904\|emb\|CAC84980.1\| | phosphoenolpyru | 143.6 | 6.1e-40 | 1 |
| gi\|18073878\|emb\|CAC84958.1\| | phosphoenolpyru | 143.2 | 8e-40 | 1 |
| gi\|1552964\|gb\|AAB08697.1\| | phosphoenolpyru | 142.2 | 1.6e-39 | 1 |
| gi\|7768123\|emb\|CAB90622.1\| | phosphoenolpyru | 142.2 | 1.6e-39 | 1 |
| gi\|218530096\|ref\|YP_002420912.1\| | Phosphoenolpyru | 141.9 | 2e-39 | 1 |
| gi\|7768238\|emb\|CAB90653.1\| | phosphoenolpyru | 141.5 | 2.7e-39 | 1 |
| gi\|18072436\|emb\|CAC84929.1\| | phosphoenolpyru | 141.0 | 3.7e-39 | 1 |
| gi\|188581006\|ref\|YP_001924451.1\| | Phosphoenolpyru | 139.9 | 8.1e-39 | 1 |
| gi\|254560927\|ref\|YP_003068022.1\| | phosphoenolpyru | 139.8 | 8.6e-39 | 1 |
| gi\|26554388\|ref\|NP_758322.1\| | phosphoenolpyru | 139.4 | 1.2e-38 | 1 |
| gi\|18072432\|emb\|CAC84383.1\| | phosphoenolpyru | 138.7 | 1.8e-38 | 1 |
| gi\|28572162\|gb\|AAB58883.2\| | methylotrophic | 138.7 | 1.9e-38 | 1 |
| gi\|7768144\|emb\|CAB90626.1\| | phosphoenolpyru | 138.6 | 2e-38 | 1 |
| gi\|194703414\|gb\|ACF85791.1\| | unknown [Zea ma | 138.5 | 2.1e-38 | 1 |
| gi\|170744593\|ref\|YP_001773248.1\| | phosphoenolpyru | 137.2 | 5.3e-38 | 1 |
| gi\|18072428\|emb\|CAC84921.1\| | phosphoenolpyru | 136.9 | 6.1e-38 | 1 |
| gi\|18076763\|emb\|CAC84925.1\| | phosphoenolpyru | 136.0 | 1.2e-37 | 1 |
| gi\|189346143\|ref\|YP_001942672.1\| | Phosphoenolpyru | 135.6 | 1.5e-37 | 1 |
| gi\|257792699\|ref\|YP_003183305.1\| | Phosphoenolpyru | 135.5 | 1.7e-37 | 1 |

| | | | | |
|---|---|---|---|---|
| gi\|18073880\|emb\|CAC84959.1\| | phosphoenolpyru | 134.8 | 2.7e-37 | 1 |
| gi\|18076753\|emb\|CAC81349.1\| | phosphoenolpyru | 133.8 | 5.6e-37 | 1 |
| gi\|7768119\|emb\|CAB90620.1\| | phosphoenolpyru | 132.4 | 1.4e-36 | 1 |
| gi\|34558172\|ref\|NP_907987.1\| | phosphoenolpyru | 132.4 | 1.4e-36 | 1 |
| gi\|18073882\|emb\|CAC84960.1\| | phosphoenolpyru | 132.4 | 1.5e-36 | 1 |
| gi\|224437040\|ref\|ZP_03658021.1\| | phosphoenolpyru | 131.7 | 2.4e-36 | 1 |
| gi\|110597068\|ref\|ZP_01385357.1\| | Phosphoenolpyru | 131.5 | 2.6e-36 | 1 |
| gi\|7768200\|emb\|CAB90643.1\| | phosphoenolpyru | 128.6 | 2e-35 | 1 |
| gi\|18072442\|emb\|CAC84971.1\| | phosphoenolpyru | 128.3 | 2.5e-35 | 1 |
| gi\|159897337\|ref\|YP_001543584.1\| | phosphoenolpyru | 128.1 | 2.7e-35 | 1 |
| gi\|18073820\|emb\|CAC84914.1\| | phosphoenolpyru | 127.4 | 4.5e-35 | 1 |
| gi\|7768220\|emb\|CAB90656.1\| | phosphoenolpyru | 127.4 | 4.5e-35 | 1 |
| gi\|7768117\|emb\|CAB90619.1\| | phosphoenolpyru | 126.2 | 1e-34 | 1 |
| gi\|1362025\|pir\|\|PC2168 | phosphoenolpyru | 124.6 | 3.3e-34 | 1 |
| gi\|18072438\|emb\|CAC84930.1\| | phosphoenolpyru | 123.7 | 6.1e-34 | 1 |
| gi\|7768218\|emb\|CAB90649.1\| | phosphoenolpyru | 121.3 | 3.1e-33 | 1 |
| gi\|18073648\|emb\|CAC83651.1\| | phosphoenolpyru | 120.1 | 7e-33 | 1 |
| gi\|118581379\|ref\|YP_902629.1\| | phosphoenolpyru | 120.0 | 7.9e-33 | 1 |
| gi\|18072426\|emb\|CAC84920.1\| | phosphoenolpyru | 119.3 | 1.2e-32 | 1 |
| gi\|7768125\|emb\|CAB90618.1\| | phosphoenolpyru | 117.9 | 3.3e-32 | 1 |
| gi\|260220723\|emb\|CBA28569.1\| | Phosphoenolpyru | 117.8 | 3.5e-32 | 1 |
| gi\|7768140\|emb\|CAB90630.1\| | phosphoenolpyru | 117.7 | 3.9e-32 | 1 |
| gi\|110681362\|ref\|YP_684369.1\| | phosphoenolpyru | 117.6 | 4.1e-32 | 1 |
| gi\|212275001\|ref\|NP_001130365.1\| | hypothetical pr | 117.4 | 4.8e-32 | 1 |
| gi\|18073892\|emb\|CAC84969.1\| | phosphoenolpyru | 117.3 | 5.1e-32 | 1 |
| gi\|18073840\|emb\|CAC84937.1\| | phosphoenolpyru | 115.8 | 1.4e-31 | 1 |
| gi\|18073890\|emb\|CAC84968.1\| | phosphoenolpyru | 115.6 | 1.7e-31 | 1 |
| gi\|186470717\|ref\|YP_001862035.1\| | phosphoenolpyru | 114.8 | 2.8e-31 | 1 |
| gi\|110639236\|ref\|YP_679445.1\| | phosphoenolpyru | 112.8 | 1.2e-30 | 1 |
| gi\|224417773\|ref\|ZP_03655779.1\| | phosphoenolpyru | 112.6 | 1.3e-30 | 1 |
| gi\|7768115\|emb\|CAB90617.1\| | phosphoenolpyru | 112.1 | 1.8e-30 | 1 |
| gi\|7768138\|emb\|CAB90629.1\| | phosphoenolpyru | 111.1 | 3.8e-30 | 1 |
| gi\|156742915\|ref\|YP_001433044.1\| | phosphoenolpyru | 110.3 | 6.4e-30 | 1 |
| gi\|18073850\|emb\|CAC84942.1\| | phosphoenolpyru | 109.6 | 1.1e-29 | 1 |
| gi\|32266702\|ref\|NP_860734.1\| | phosphoenolpyru | 109.2 | 1.4e-29 | 1 |
| gi\|18073848\|emb\|CAC84941.1\| | phosphoenolpyru | 108.5 | 2.3e-29 | 1 |
| gi\|7768136\|emb\|CAB90625.1\| | phosphoenolpyru | 107.8 | 3.6e-29 | 1 |
| gi\|164415616\|gb\|ABY53227.1\| | phosphoenolpyru | 106.9 | 6.7e-29 | 1 |
| gi\|18076755\|emb\|CAC84274.1\| | phosphoenolpyru | 106.4 | 9.4e-29 | 1 |
| gi\|7768113\|emb\|CAB90624.1\| | phosphoenolpyru | 102.9 | 1.1e-27 | 1 |
| gi\|219847014\|ref\|YP_002461447.1\| | Phosphoenolpyru | 102.8 | 1.2e-27 | 1 |
| gi\|254459897\|ref\|ZP_05073313.1\| | phosphoenolpyru | 101.6 | 2.7e-27 | 1 |
| gi\|18073876\|emb\|CAC84395.1\| | phosphoenolpyru | 100.8 | 4.8e-27 | 1 |
| gi\|10303403\|emb\|CAA65117.1\| | phosphoenolpyru | 100.3 | 6.7e-27 | 1 |
| gi\|18073862\|emb\|CAC84948.1\| | phosphoenolpyru | 100.1 | 7.4e-27 | 1 |
| gi\|148657218\|ref\|YP_001277423.1\| | phosphoenolpyru | 98.7 | 2e-26 | 1 |
| gi\|163849410\|ref\|YP_001637454.1\| | phosphoenolpyru | 96.2 | 1.1e-25 | 1 |
| gi\|7768226\|emb\|CAB90660.1\| | phosphoenolpyru | 95.4 | 1.9e-25 | 1 |
| gi\|18073902\|emb\|CAC84979.1\| | phosphoenolpyru | 95.4 | 2e-25 | 1 |
| gi\|18073832\|emb\|CAC84933.1\| | phosphoenolpyru | 94.9 | 2.7e-25 | 1 |
| gi\|7768228\|emb\|CAB90661.1\| | phosphoenolpyru | 93.8 | 6.1e-25 | 1 |
| gi\|7768246\|emb\|CAB90654.1\| | phosphoenolpyru | 93.8 | 6.1e-25 | 1 |
| gi\|254445406\|ref\|ZP_05058882.1\| | phosphoenolpyru | 93.4 | 8e-25 | 1 |
| gi\|7768236\|emb\|CAB90652.1\| | phosphoenolpyru | 92.2 | 1.8e-24 | 1 |
| gi\|7768242\|emb\|CAB90658.1\| | phosphoenolpyru | 91.4 | 3.1e-24 | 1 |
| gi\|7768230\|emb\|CAB90644.1\| | phosphoenolpyru | 91.3 | 3.3e-24 | 1 |
| gi\|114769507\|ref\|ZP_01447133.1\| | phosphoenolpyru | 91.2 | 3.8e-24 | 1 |
| gi\|242309960\|ref\|ZP_04809115.1\| | phosphoenolpyru | 90.4 | 6.2e-24 | 1 |
| gi\|18073898\|emb\|CAC84977.1\| | phosphoenolpyru | 90.3 | 6.7e-24 | 1 |
| gi\|7768378\|emb\|CAB90717.1\| | phosphoenolpyru | 90.1 | 7.6e-24 | 1 |
| gi\|291277543\|ref\|YP_003517315.1\| | putative phosph | 89.6 | 1.1e-23 | 1 |
| gi\|255264237\|ref\|ZP_05343579.1\| | phosphoenolpyru | 89.2 | 1.5e-23 | 1 |
| gi\|7768224\|emb\|CAB90648.1\| | phosphoenolpyru | 86.7 | 8e-23 | 1 |
| gi\|10303367\|emb\|CAA65112.1\| | phosphoenolpyru | 84.9 | 2.8e-22 | 1 |
| gi\|7768232\|emb\|CAB90650.1\| | phosphoenolpyru | 84.9 | 3e-22 | 1 |
| gi\|7768222\|emb\|CAB90647.1\| | phosphoenolpyru | 84.6 | 3.4e-22 | 1 |
| gi\|2145451\|emb\|CAA62829.1\| | phosphoenolpyru | 83.9 | 5.5e-22 | 1 |
| gi\|18073856\|emb\|CAC84945.1\| | phosphoenolpyru | 81.8 | 2.5e-21 | 1 |
| gi\|7739277\|emb\|CAB90713.1\| | phosphoenolpyru | 81.2 | 3.7e-21 | 1 |
| gi\|56696455\|ref\|YP_166812.1\| | phosphoenolpyru | 78.4 | 2.6e-20 | 1 |
| gi\|18073852\|emb\|CAC84943.1\| | phosphoenolpyru | 77.8 | 3.9e-20 | 1 |

| | | | | |
|---|---|---|---|---|
| gi\|7768248\|emb\|CAB90645.1\| | phosphoenolpyru | 75.3 | 2.2e-19 | 1 |
| gi\|7768366\|emb\|CAB90709.1\| | phosphoenolpyru | 74.4 | 4.2e-19 | 1 |
| gi\|18076776\|emb\|CAC84961.1\| | phosphoenolpyru | 74.2 | 4.9e-19 | 1 |
| gi\|1166446\|emb\|CAA61084.1\| | phosphoenolpyru | 74.0 | 5.6e-19 | 1 |
| gi\|7768234\|emb\|CAB90651.1\| | phosphoenolpyru | 71.7 | 2.8e-18 | 1 |
| gi\|237752184\|ref\|ZP_04582664.1\| | phosphoenolpyru | 71.4 | 3.4e-18 | 1 |
| gi\|2145471\|emb\|CAA62826.1\| | phosphoenolpyru | 70.6 | 5.8e-18 | 1 |
| gi\|2145354\|emb\|CAA62825.1\| | phosphoenolpyru | 70.3 | 7.1e-18 | 1 |
| gi\|7768306\|emb\|CAB90681.1\| | phosphoenolpyru | 66.5 | 9.7e-17 | 1 |
| gi\|10303371\|emb\|CAA65108.1\| | phosphoenolpyru | 64.0 | 5.5e-16 | 1 |
| gi\|1166444\|emb\|CAA61083.1\| | phosphoenolpyru | 62.9 | 1.2e-15 | 1 |
| gi\|2145426\|emb\|CAA62827.1\| | phosphoenolpyru | 62.2 | 1.9e-15 | 1 |
| gi\|7768368\|emb\|CAB90710.1\| | phosphoenolpyru | 61.5 | 3.1e-15 | 1 |
| gi\|7768216\|emb\|CAB90662.1\| | phosphoenolpyru | 61.5 | 3.2e-15 | 1 |
| gi\|7768093\|emb\|CAB90612.1\| | phosphoenolpyru | 59.3 | 1.4e-14 | 1 |
| gi\|7768259\|emb\|CAB90665.1\| | phosphoenolpyru | 59.0 | 1.8e-14 | 1 |
| gi\|18073824\|emb\|CAC84917.1\| | phosphoenolpyru | 56.6 | 9.6e-14 | 1 |
| gi\|7768091\|emb\|CAB90611.1\| | phosphoenolpyru | 55.2 | 2.4e-13 | 1 |
| gi\|2145479\|emb\|CAA62828.1\| | phosphoenolpyru | 53.8 | 6.5e-13 | 1 |
| gi\|7768148\|emb\|CAB90635.1\| | phosphoenolpyru | 52.0 | 2.3e-12 | 1 |
| gi\|7768308\|emb\|CAB90705.1\| | phosphoenolpyru | 51.5 | 3.2e-12 | 1 |
| gi\|7768302\|emb\|CAB90679.1\| | phosphoenolpyru | 51.0 | 4.5e-12 | 1 |
| gi\|10303358\|emb\|CAA65114.1\| | phosphoenolpyru | 50.3 | 7.3e-12 | 1 |
| gi\|7768304\|emb\|CAB90680.1\| | phosphoenolpyru | 47.9 | 3.8e-11 | 1 |
| gi\|7768310\|emb\|CAB90706.1\| | phosphoenolpyru | 47.6 | 4.9e-11 | 1 |
| gi\|7768370\|emb\|CAB90711.1\| | phosphoenolpyru | 47.2 | 6.5e-11 | 1 |
| gi\|7768146\|emb\|CAB90632.1\| | phosphoenolpyru | 44.9 | 3.2e-10 | 1 |
| gi\|7768257\|emb\|CAB90664.1\| | phosphoenolpyru | 44.9 | 3.2e-10 | 1 |
| gi\|7768095\|emb\|CAB90613.1\| | phosphoenolpyru | 43.8 | 6.9e-10 | 1 |
| gi\|7768382\|emb\|CAB90719.1\| | phosphoenolpyru | 43.5 | 8e-10 | 1 |
| gi\|139438299\|ref\|ZP_01771852.1\| | Hypothetical pr | 43.4 | 9.1e-10 | 1 |
| gi\|7768134\|emb\|CAB90628.1\| | phosphoenolpyru | 42.5 | 1.7e-09 | 1 |
| gi\|2145352\|emb\|CAA62830.1\| | phosphoenolpyru | 40.2 | 8.1e-09 | 1 |
| gi\|7768198\|emb\|CAB90642.1\| | phosphoenolpyru | 39.8 | 1e-08 | 1 |
| gi\|88799804\|ref\|ZP_01115377.1\| | Phosphoenolpyru | 39.1 | 1.8e-08 | 1 |
| gi\|7768097\|emb\|CAB90616.1\| | phosphoenolpyru | 35.5 | 2.2e-07 | 1 |
| gi\|237750822\|ref\|ZP_04581302.1\| | phosphoenolpyru | 35.1 | 2.8e-07 | 1 |
| gi\|255588103\|ref\|XP_002534501.1\| | Phosphoenolpyru | 34.3 | 5e-07 | 1 |
| gi\|18073654\|emb\|CAC81270.1\| | phosphoenolpyru | 31.0 | 4.8e-06 | 1 |
| gi\|119504081\|ref\|ZP_01626162.1\| | phosphoenolpyru | 25.8 | 0.00017 | 1 |
| gi\|149019670\|ref\|ZP_01834989.1\| | phosphoenolpyru | 19.6 | 0.013 | 1 |
| gi\|19070128\|gb\|AAL83719.1\|AF236126_1 | PEP carboxylase | 18.9 | 0.022 | 1 |
| gi\|10303354\|emb\|CAA65110.1\| | phosphoenolpyru | 16.1 | 0.15 | 1 |
| gi\|18072440\|emb\|CAC84970.1\| | phosphoenolpyru | 14.2 | 0.53 | 1 |
| gi\|256370921\|ref\|YP_003108745.1\| | Phosphoenolpyru | 12.3 | 2 | 1 |
| gi\|6119717\|emb\|CAB59571.1\| | phosphoenolpyru | 10.9 | 3 | 1 |
| gi\|7768255\|emb\|CAB90663.1\| | phosphoenolpyru | 2.4 | 3.3 | 1 |
| gi\|18073660\|emb\|CAC81273.1\| | phosphoenolpyru | -2.8 | 3.4 | 1 |
| gi\|255037677\|ref\|YP_003088298.1\| | Phosphoenolpyru | -6.1 | 3.5 | 1 |
| gi\|18073658\|emb\|CAC81272.1\| | phosphoenolpyru | -9.9 | 3.7 | 1 |
| gi\|18073656\|emb\|CAC81271.1\| | phosphoenolpyru | -10.6 | 3.7 | 1 |
| gi\|18076788\|emb\|CAC84974.1\| | phosphoenolpyru | -11.7 | 3.7 | 1 |
| gi\|213580501\|ref\|ZP_03362327.1\| | phosphoenolpyru | -15.8 | 3.9 | 1 |
| gi\|10303360\|emb\|CAA65115.1\| | phosphoenolpyru | -15.8 | 3.9 | 1 |
| gi\|120435841\|ref\|YP_861527.1\| | phosphoenolpyru | -16.8 | 3.9 | 1 |
| gi\|18076784\|emb\|CAC84972.1\| | phosphoenolpyru | -20.9 | 4 | 1 |
| gi\|18076786\|emb\|CAC84973.1\| | phosphoenolpyru | -22.0 | 4.1 | 1 |
| gi\|7768111\|emb\|CAB90623.1\| | phosphoenolpyru | -24.0 | 4.1 | 1 |
| gi\|86135028\|ref\|ZP_01053610.1\| | Phosphoenolpyru | -24.4 | 4.2 | 1 |
| gi\|149278227\|ref\|ZP_01884365.1\| | phosphoenolpyru | -24.8 | 4.2 | 1 |
| gi\|88801380\|ref\|ZP_01116908.1\| | phosphoenolpyru | -28.4 | 4.3 | 1 |
| gi\|118377471\|ref\|XP_001021914.1\| | Phosphoenolpyru | -32.0 | 4.4 | 1 |
| gi\|7768261\|emb\|CAB90666.1\| | phosphoenolpyru | -33.5 | 4.5 | 1 |
| gi\|146300556\|ref\|YP_001195147.1\| | phosphoenolpyru | -33.6 | 4.5 | 1 |
| gi\|2695868\|emb\|CAA75817.1\| | phosphoenolpyru | -40.5 | 4.8 | 1 |
| gi\|163787422\|ref\|ZP_02181869.1\| | Phosphoenolpyru | -42.2 | 4.8 | 1 |
| gi\|126648531\|ref\|ZP_01721018.1\| | phosphoenolpyru | -43.4 | 4.9 | 1 |
| gi\|227366515\|ref\|ZP_03850064.1\| | phosphoenolpyru | -45.8 | 5 | 1 |
| gi\|11596397\|gb\|AAG38601.1\|AF317284_1 | PEP carboxylase | -45.8 | 5 | 1 |
| gi\|260063588\|ref\|YP_003196668.1\| | phosphoenolpyru | -46.9 | 5.1 | 1 |
| gi\|255534738\|ref\|YP_003095109.1\| | Phosphoenolpyru | -47.4 | 5.1 | 1 |

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gi|629594|pir||PC2170                phosphoenolpyru   -47.5        5.1   1
gi|255534144|ref|YP_003094516.1|     Phosphoenolpyru   -48.3        5.1   1
gi|126662794|ref|ZP_01733793.1|      phosphoenolpyru   -51.3        5.3   1
gi|149926183|ref|ZP_01914445.1|      phosphoenolpyru   -51.7        5.3   1
gi|88713052|ref|ZP_01107136.1|       phosphoenolpyru   -54.7        5.4   1
gi|256420516|ref|YP_003121169.1|     Phosphoenolpyru   -54.7        5.4   1
gi|163755567|ref|ZP_02162686.1|      phosphoenolpyru   -55.0        5.4   1
gi|86143373|ref|ZP_01061775.1|       Phosphoenolpyru   -55.8        5.5   1
gi|89890758|ref|ZP_01202267.1|       phosphoenolpyru   -59.0        5.6   1
gi|86130467|ref|ZP_01049067.1|       phosphoenolpyru   -59.7        5.7   1
gi|225011063|ref|ZP_03701527.1|      Phosphoenolpyru   -60.9        5.7   1
gi|224368853|ref|YP_002603015.1|     Ppc [Desulfobac   -62.5        5.8   1
gi|227540600|ref|ZP_03970649.1|      phosphoenolpyru   -66.7          6   1
gi|1552966|gb|AAB08698.1|            phosphoenolpyru   -69.5        6.2   1
gi|241892653|ref|ZP_04779949.1|      phosphoenolpyru   -70.3        6.2   1
gi|225012795|ref|ZP_03703229.1|      Phosphoenolpyru   -70.6        6.2   1
gi|207723607|ref|YP_002254005.1|     phosphoenolpyru   -78.7        6.7   1
gi|268685594|ref|ZP_06152456.1|      phosphoenolpyru   -84.4          7   1
gi|257139898|ref|ZP_05588160.1|      phosphoenolpyru   -98.7        7.9   1
gi|241667414|ref|ZP_04754992.1|      phosphoenolpyru  -101.3        8.1   1
gi|254875963|ref|ZP_05248673.1|      predicted prote  -101.3        8.1   1
gi|167626833|ref|YP_001677333.1|     phosphoenolpyru  -103.1        8.3   1
gi|89892437|gb|ABD79011.1|           HI1636-like pro  -109.6        8.7   1
gi|159475421|ref|XP_001695817.1|     phosphoenolpyru  -117.0        9.3   1
gi|224101659|ref|XP_002312371.1|     predicted prote  -121.8        9.7   1

Parsed for domains:
Sequence                             Domain  seq-f seq-t    hmm-f hmm-t      score  E-value
--------                             ------- ----- -----    ----- -----      -----  -------
gi|231684|sp|Q01647.1|CAPP1_FLAPR      1/1      11   967 .]     1   960 []  2796.7        0
gi|763097|emb|CAA88829.1|              1/1      11   966 .]     1   960 []  2791.9        0
gi|20162467|gb|AAM14597.1|AF494192_1   1/1      11   966 .]     1   960 []  2780.8        0
gi|242096062|ref|XP_002438521.1|       1/1       8   961 .]     1   960 []  2766.5        0
gi|115578|sp|P15804.2|CAPP3_SORBI      1/1       8   960 .]     1   960 []  2765.2        0
gi|20162465|gb|AAM14596.1|AF494191_1   1/1      11   966 .]     1   960 []  2757.4        0
gi|10443870|gb|AAG17618.1|AF248079_1   1/1      11   965 .]     1   960 []  2725.0        0
gi|10185175|emb|CAC08829.1|            1/1       8   961 .]     1   960 []  2715.2        0
gi|21464596|emb|CAC85930.1|            1/1       8   961 .]     1   960 []  2711.4        0
gi|23306662|gb|AAN15222.1|             1/1       8   961 .]     1   960 []  2704.1        0
gi|231685|sp|Q01648.1|CAPP1_FLATR      1/1      11   967 .]     1   960 []  2693.2        0
gi|1345665|sp|P30694.2|CAPP2_FLATR     1/1      11   966 .]     1   960 []  2683.7        0
gi|2499466|sp|Q42730.1|CAPP_FLAAU      1/1      11   966 .]     1   960 []  2681.7        0
gi|10443872|gb|AAG17619.1|AF248080_1   1/1      11   967 .]     1   960 []  2674.9        0
gi|228246|prf||1801241A                1/1      11   966 .]     1   960 []  2674.3        0
gi|27764449|emb|CAD60555.1|            1/1      15   970 .]     1   960 []  2649.3        0
gi|238624101|ref|NP_001154820.1|       1/1      15   970 .]     1   960 []  2646.7        0
gi|162461756|ref|NP_001105418.1|       1/1      15   970 .]     1   960 []  2642.2        0
gi|212898592|gb|ACJ38542.1|            1/1      15   970 .]     1   960 []  2640.0        0
gi|295855|emb|CAA33663.1|              1/1      15   970 .]     1   960 []  2637.5        0
gi|224121514|ref|XP_002330719.1|       1/1       3   957 .]     1   960 []  2623.3        0
gi|224114804|ref|XP_002316861.1|       1/1      12   966 .]     1   960 []  2618.6        0
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gi|255553993|ref|XP_002518037.1|       1/1      11   965 .]     1   960 []  2604.3        0
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gi|972511|emb|CAA62469.1|              1/1      11   965 .]     1   960 []  2602.4        0
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gi|157812633|gb|ABV80356.1|            1/1      17   971 .]     1   960 []  2594.7        0
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gi|115610|sp|P27154.1|CAPP_TOBAC       1/1      11   964 .]     1   960 []  2580.8        0
gi|223976187|gb|ACN32213.1|            1/1      10   966 .]     1   960 []  2578.6        0
gi|166714353|gb|ABY87944.1|            1/1      13   968 .]     1   960 []  2573.1        0
gi|399182|sp|Q02909.1|CAPP1_SOYBN      1/1      11   967 .]     1   960 []  2571.3        0
gi|225446609|ref|XP_002280569.1|       1/1      11   965 .]     1   960 []  2565.8        0
gi|242061132|ref|XP_002451855.1|       1/1       7   960 .]     1   960 []  2565.3        0
gi|184097733|gb|ACC66283.1|            1/1      10   966 .]     1   960 []  2564.1        0
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| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| gi\|115587\|sp\|P29195.1\|CAPP1_SORBI | 1/1 | 7 | 960 .] | 1 | 960 [] | 2562.2 | 0 |
| gi\|162458095\|ref\|NP_001105503.1\| | 1/1 | 7 | 960 .] | 1 | 960 [] | 2561.5 | 0 |
| gi\|6688531\|emb\|CAB65170.1\| | 1/1 | 11 | 964 .] | 1 | 960 [] | 2560.4 | 0 |
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| gi\|23503558\|dbj\|BAC20365.1\| | 1/1 | 11 | 967 .] | 1 | 960 [] | 2554.8 | 0 |
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| gi\|4033351\|emb\|CAA11415.1\| | 1/1 | 11 | 964 .] | 1 | 960 [] | 2545.2 | 0 |
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| gi\|14279572\|gb\|AAK58636.1\|AF271162_1 | 1/1 | 14 | 968 .] | 1 | 960 [] | 2530.3 | 0 |
| gi\|162458345\|ref\|NP_001105438.1\| | 1/1 | 13 | 967 .] | 1 | 960 [] | 2529.8 | 0 |
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| gi\|30088841\|gb\|AAP06951.1\| | 1/1 | 8 | 961 .] | 1 | 960 [] | 2527.6 | 0 |
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| gi\|23503556\|dbj\|BAC20364.1\| | 1/1 | 11 | 961 .] | 1 | 960 [] | 2520.1 | 0 |
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| gi\|5616255\|gb\|AAD45696.1\|AF159051_1 | 1/1 | 3 | 955 .] | 1 | 960 [] | 2515.3 | 0 |
| gi\|148908467\|gb\|ABR17346.1\| | 1/1 | 11 | 963 .] | 1 | 960 [] | 2515.3 | 0 |
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| gi\|222619275\|gb\|EEE55407.1\| | 1/1 | 11 | 966 .] | 1 | 960 [] | 2512.3 | 0 |
| gi\|3649776\|emb\|CAA09588.1\| | 1/1 | 10 | 966 .] | 1 | 960 [] | 2512.2 | 0 |
| gi\|51091643\|dbj\|BAD36412.1\| | 1/1 | 18 | 972 .] | 1 | 960 [] | 2511.8 | 0 |
| gi\|115478504\|ref\|NP_001062847.1\| | 1/1 | 21 | 975 .] | 1 | 960 [] | 2511.8 | 0 |
| gi\|157279525\|dbj\|BAF80187.1\| | 1/1 | 10 | 964 .] | 1 | 960 [] | 2511.5 | 0 |
| gi\|1705590\|sp\|P51063.1\|CAPP_PICAB | 1/1 | 11 | 963 .] | 1 | 960 [] | 2511.4 | 0 |
| gi\|63053872\|gb\|AAY28731.1\| | 1/1 | 11 | 966 .] | 1 | 960 [] | 2510.9 | 0 |
| gi\|63053870\|gb\|AAY28730.1\| | 1/1 | 11 | 966 .] | 1 | 960 [] | 2510.6 | 0 |
| gi\|1705589\|sp\|P51062.1\|CAPP_PEA | 1/1 | 10 | 967 .] | 1 | 960 [] | 2509.4 | 0 |
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| gi\|51574147\|gb\|AAU07997.1\| | 1/1 | 11 | 967 .] | 1 | 960 [] | 2504.3 | 0 |
| gi\|242058751\|ref\|XP_002458521.1\| | 1/1 | 11 | 966 .] | 1 | 960 [] | 2502.5 | 0 |
| gi\|270232663\|emb\|CBI21984.1\| | 1/1 | 11 | 944 .] | 1 | 960 [] | 2495.8 | 0 |
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| gi\|20257597\|gb\|AAM15963.1\|AF495586_1 | 1/1 | 11 | 964 .] | 1 | 960 [] | 2489.3 | 0 |
| gi\|108742705\|gb\|ABG01962.1\| | 1/1 | 11 | 966 .] | 1 | 960 [] | 2480.0 | 0 |
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| gi\|6688533\|emb\|CAB65171.1\| | 1/1 | 11 | 964 .] | 1 | 960 [] | 2466.8 | 0 |
| gi\|27462753\|gb\|AAO15570.1\|AF459644_1 | 1/1 | 11 | 967 .] | 1 | 960 [] | 2466.2 | 0 |
| gi\|90652448\|emb\|CAJ86550.1\| | 1/1 | 12 | 968 .] | 1 | 960 [] | 2464.6 | 0 |
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| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| gi\|23491823\|dbj\|BAC19851.1\| | 1/1 | 11 | 968 | .] | 1 | 960 | [] | 2433.1 | 0 |
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| gi\|4877832\|gb\|AAD31452.1\|AF135371_1 | 1/1 | 11 | 957 | .] | 1 | 960 | [] | 2430.1 | 0 |
| gi\|11991545\|gb\|AAG42288.1\| | 1/1 | 10 | 955 | .] | 1 | 960 | [] | 2427.4 | 0 |
| gi\|219944332\|gb\|AAX98688.3\| | 1/1 | 8 | 964 | .] | 1 | 960 | [] | 2427.2 | 0 |
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| gi\|1870188\|emb\|CAA60627.1\| | 1/1 | 4 | 956 | .] | 1 | 960 | [] | 2416.6 | 0 |
| gi\|164449187\|gb\|ABY56044.1\| | 1/1 | 11 | 965 | .] | 1 | 960 | [] | 2414.4 | 0 |
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| gi\|2499465\|sp\|Q43299.1\|CAPP_AMAHP | 1/1 | 11 | 964 | .] | 1 | 960 | [] | 2408.9 | 0 |
| gi\|22347639\|gb\|AAM95946.1\| | 1/1 | 11 | 954 | .] | 1 | 960 | [] | 2399.6 | 0 |
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| gi\|222622510\|gb\|EEE56642.1\| | 1/1 | 15 | 937 | .] | 1 | 960 | [] | 2384.8 | 0 |
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| gi\|1870190\|emb\|CAA60626.1\| | 1/1 | 4 | 958 | .] | 1 | 960 | [] | 2377.7 | 0 |
| gi\|4559332\|gb\|AAD22994.1\| | 1/1 | 11 | 941 | .] | 1 | 960 | [] | 2371.1 | 0 |
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| gi\|115435200\|ref\|NP_001042358.1\| | 1/1 | 56 | 1014 | .] | 1 | 960 | [] | 2286.8 | 0 |
| gi\|168027443\|ref\|XP_001766239.1\| | 1/1 | 8 | 969 | .] | 1 | 960 | [] | 2225.4 | 0 |
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| gi\|168016115\|ref\|XP_001760595.1\| | 1/1 | 6 | 965 | .] | 1 | 960 | [] | 2182.3 | 0 |
| gi\|168042979\|ref\|XP_001773964.1\| | 1/1 | 9 | 958 | .] | 1 | 960 | [] | 2153.6 | 0 |
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| gi\|108782496\|gb\|ABG20460.1\| | 1/1 | 1 | 851 | [] | 1 | 960 | [] | 2073.5 | 0 |
| gi\|290350842\|dbj\|BAI78342.1\| | 1/1 | 11 | 969 | .. | 1 | 960 | [] | 1988.5 | 0 |
| gi\|20152211\|dbj\|BAB89367.1\| | 1/1 | 1 | 820 | [] | 1 | 960 | [] | 1987.4 | 0 |
| gi\|108782498\|gb\|ABG20461.1\| | 1/1 | 1 | 830 | [] | 1 | 960 | [] | 1987.3 | 0 |
| gi\|20152209\|dbj\|BAB89366.1\| | 1/1 | 1 | 750 | [] | 1 | 960 | [] | 1782.0 | 0 |
| gi\|125527770\|gb\|EAY75884.1\| | 1/1 | 11 | 748 | .] | 1 | 960 | [] | 1605.5 | 0 |
| gi\|3649778\|emb\|CAA09589.1\| | 1/1 | 1 | 704 | [] | 1 | 960 | [] | 1566.1 | 0 |
| gi\|219884355\|gb\|ACL52552.1\| | 1/1 | 1 | 658 | [] | 1 | 960 | [] | 1415.5 | 0 |
| gi\|38044102\|dbj\|BAB89368.2\| | 1/1 | 1 | 657 | [] | 1 | 960 | [] | 1363.6 | 0 |
| gi\|2145477\|emb\|CAA62749.1\| | 1/1 | 1 | 676 | [] | 1 | 960 | [] | 1342.0 | 0 |
| gi\|108782500\|gb\|ABG20462.1\| | 1/1 | 1 | 671 | [] | 1 | 960 | [] | 1341.1 | 0 |
| gi\|283896826\|emb\|CAX65714.1\| | 1/1 | 1 | 658 | [] | 1 | 960 | [] | 1305.7 | 0 |
| gi\|254587351\|emb\|CAR63824.1\| | 1/1 | 1 | 650 | [] | 1 | 960 | [] | 1298.7 | 0 |
| gi\|283898028\|emb\|CAX65715.1\| | 1/1 | 1 | 641 | [] | 1 | 960 | [] | 1277.0 | 0 |
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| gi\|254587353\|emb\|CAR63825.1\| | 1/1 | 1 | 640 | [] | 1 | 960 | [] | 1255.8 | 0 |
| gi\|154146668\|emb\|CAM83969.1\| | 1/1 | 1 | 628 | [] | 1 | 960 | [] | 1241.8 | 0 |
| gi\|154146674\|emb\|CAM83972.1\| | 1/1 | 1 | 628 | [] | 1 | 960 | [] | 1240.3 | 0 |
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| gi\|51701301\|sp\|P81831.2\|CAPP1_CHLRE | 1/1 | 13 | 974 | .] | 1 | 960 | [] | 1170.8 | 0 |
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| gi\|154146670\|emb\|CAM83970.1\| | 1/1 | 1 | 630 | [] | 1 | 960 | [] | 1051.9 | 0 |
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| gi\|281207688\|gb\|EFA81868.1\| | 1/1 | 3 | 917 | .. | 1 | 960 | [] | 888.9 | 2.7e-264 |
| gi\|114319423\|ref\|YP_741106.1\| | 1/1 | 2 | 882 | .] | 1 | 960 | [] | 857.8 | 6e-255 |
| gi\|255561196\|ref\|XP_002521610.1\| | 1/1 | 1 | 607 | [] | 1 | 960 | [] | 846.2 | 1.9e-251 |
| gi\|70671531\|gb\|AAZ06136.1\| | 1/1 | 1 | 526 | [] | 1 | 960 | [] | 825.6 | 3e-245 |
| gi\|152995284\|ref\|YP_001340119.1\| | 1/1 | 1 | 876 | [] | 1 | 960 | [] | 817.4 | 9.2e-243 |
| gi\|226320262\|gb\|ACO48252.1\| | 1/1 | 16 | 1036 | .] | 1 | 960 | [] | 811.9 | 4e-241 |
| gi\|83644641\|ref\|YP_433076.1\| | 1/1 | 1 | 881 | [] | 1 | 960 | [] | 808.3 | 4.9e-240 |
| gi\|12324139\|gb\|AAG52040.1\|AC011914_10 | 1/1 | 2 | 981 | .] | 1 | 960 | [] | 807.9 | 6.5e-240 |
| gi\|87118647\|ref\|ZP_01074546.1\| | 1/1 | 1 | 854 | [] | 1 | 960 | [] | 807.1 | 1.1e-239 |
| gi\|89094559\|ref\|ZP_01167497.1\| | 1/1 | 1 | 869 | [] | 1 | 960 | [] | 806.6 | 1.6e-239 |
| gi\|115434082\|ref\|NP_001041799.1\| | 1/1 | 16 | 1035 | .] | 1 | 960 | [] | 804.7 | 6e-239 |
| gi\|30697740\|ref\|NP_177043.2\| | 1/1 | 2 | 1032 | .] | 1 | 960 | [] | 804.2 | 8.2e-239 |
| gi\|119476550\|ref\|ZP_01616901.1\| | 1/1 | 1 | 884 | [] | 1 | 960 | [] | 801.7 | 4.9e-238 |
| gi\|149911768\|ref\|ZP_01900373.1\| | 1/1 | 6 | 876 | .] | 1 | 960 | [] | 798.3 | 4.9e-237 |
| gi\|149789412\|gb\|ABR29877.1\| | 1/1 | 2 | 1052 | .] | 1 | 960 | [] | 798.2 | 5.4e-237 |
| gi\|224284385\|gb\|ACN39927.1\| | 1/1 | 2 | 1073 | .] | 1 | 960 | [] | 795.9 | 2.6e-236 |
| gi\|237806868\|ref\|YP_002891308.1\| | 1/1 | 3 | 877 | .] | 1 | 960 | [] | 795.8 | 2.9e-236 |
| gi\|254508198\|ref\|ZP_05120323.1\| | 1/1 | 1 | 880 | [] | 1 | 960 | [] | 794.3 | 8.3e-236 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| gi\|262370772\|ref\|ZP_06064096.1\| | 1/1 | 4 | 894 | .] | 1 | 960 | [] | 793.1 | 1.8e-235 |
| gi\|242052357\|ref\|XP_002455324.1\| | 1/1 | 16 | 1038 | .] | 1 | 960 | [] | 790.8 | 9.1e-235 |
| gi\|156972425\|ref\|YP_001443332.1\| | 1/1 | 3 | 888 | .] | 1 | 960 | [] | 790.7 | 9.7e-235 |
| gi\|5734703\|gb\|AAD49968.1\|AC008075_1 | 1/1 | 2 | 980 | .] | 1 | 960 | [] | 790.4 | 1.2e-234 |
| gi\|90407116\|ref\|ZP_01215305.1\| | 1/1 | 6 | 877 | .] | 1 | 960 | [] | 789.9 | 1.6e-234 |
| gi\|50086573\|ref\|YP_048083.1\| | 1/1 | 4 | 894 | .] | 1 | 960 | [] | 789.6 | 2.1e-234 |
| gi\|254229794\|ref\|ZP_04923201.1\| | 1/1 | 3 | 888 | .] | 1 | 960 | [] | 788.8 | 3.7e-234 |
| gi\|145297649\|ref\|YP_001140490.1\| | 1/1 | 6 | 877 | .] | 1 | 960 | [] | 787.7 | 7.7e-234 |
| gi\|149189173\|ref\|ZP_01867460.1\| | 1/1 | 3 | 888 | .] | 1 | 960 | [] | 787.6 | 8.5e-234 |
| gi\|262280608\|ref\|ZP_06058392.1\| | 1/1 | 4 | 894 | .] | 1 | 960 | [] | 787.3 | 1e-233 |
| gi\|45505267\|gb\|AAS67005.1\| | 1/1 | 2 | 1032 | .] | 1 | 960 | [] | 787.1 | 1.2e-233 |
| gi\|255318037\|ref\|ZP_05359282.1\| | 1/1 | 4 | 894 | .] | 1 | 960 | [] | 787.0 | 1.3e-233 |
| gi\|90580872\|ref\|ZP_01236674.1\| | 1/1 | 1 | 876 | [] | 1 | 960 | [] | 786.9 | 1.3e-233 |
| gi\|262380617\|ref\|ZP_06073771.1\| | 1/1 | 4 | 894 | .] | 1 | 960 | [] | 786.7 | 1.5e-233 |
| gi\|271498759\|ref\|YP_003331784.1\| | 1/1 | 1 | 879 | [] | 1 | 960 | [] | 786.0 | 2.5e-233 |
| gi\|292826793\|gb\|EFF85158.1\| | 1/1 | 4 | 894 | .] | 1 | 960 | [] | 785.9 | 2.6e-233 |
| gi\|149374698\|ref\|ZP_01892472.1\| | 1/1 | 1 | 868 | [] | 1 | 960 | [] | 785.8 | 2.9e-233 |
| gi\|239502757\|ref\|ZP_04662067.1\| | 1/1 | 4 | 894 | .] | 1 | 960 | [] | 785.7 | 3e-233 |
| gi\|152972745\|ref\|YP_001337891.1\| | 1/1 | 1 | 891 | [] | 1 | 960 | [] | 785.3 | 4e-233 |
| gi\|121999069\|ref\|YP_001003856.1\| | 1/1 | 1 | 883 | [] | 1 | 960 | [] | 784.9 | 5.6e-233 |
| gi\|126643456\|ref\|YP_001086440.1\| | 1/1 | 4 | 894 | .] | 1 | 960 | [] | 784.8 | 5.8e-233 |
| gi\|169634906\|ref\|YP_001708642.1\| | 1/1 | 4 | 894 | .] | 1 | 960 | [] | 784.8 | 6e-233 |
| gi\|50119147\|ref\|YP_048314.1\| | 1/1 | 1 | 879 | [] | 1 | 960 | [] | 784.5 | 7e-233 |
| gi\|226945972\|ref\|YP_002801045.1\| | 1/1 | 3 | 878 | .] | 1 | 960 | [] | 784.1 | 9.5e-233 |
| gi\|260553863\|ref\|ZP_05826131.1\| | 1/1 | 4 | 894 | .] | 1 | 960 | [] | 784.0 | 1e-232 |
| gi\|229588773\|ref\|YP_002870892.1\| | 1/1 | 3 | 875 | .] | 1 | 960 | [] | 783.6 | 1.3e-232 |
| gi\|169794232\|ref\|YP_001712025.1\| | 1/1 | 4 | 894 | .] | 1 | 960 | [] | 782.9 | 2.2e-232 |
| gi\|213158772\|ref\|YP_002321193.1\| | 1/1 | 4 | 894 | .] | 1 | 960 | [] | 782.8 | 2.3e-232 |
| gi\|251791486\|ref\|YP_003006207.1\| | 1/1 | 1 | 879 | [] | 1 | 960 | [] | 782.7 | 2.5e-232 |
| gi\|262393083\|ref\|YP_003284937.1\| | 1/1 | 1 | 877 | [] | 1 | 960 | [] | 782.3 | 3.3e-232 |
| gi\|261823543\|ref\|YP_003261649.1\| | 1/1 | 1 | 879 | [] | 1 | 960 | [] | 782.0 | 4e-232 |
| gi\|117621332\|ref\|YP_855124.1\| | 1/1 | 6 | 877 | .] | 1 | 960 | [] | 781.7 | 4.9e-232 |
| gi\|262273438\|ref\|ZP_06051252.1\| | 1/1 | 1 | 876 | [] | 1 | 960 | [] | 781.7 | 5.1e-232 |
| gi\|77457296\|ref\|YP_346801.1\| | 1/1 | 3 | 876 | .] | 1 | 960 | [] | 781.6 | 5.3e-232 |
| gi\|91227300\|ref\|ZP_01261725.1\| | 1/1 | 1 | 877 | [] | 1 | 960 | [] | 781.4 | 6.3e-232 |
| gi\|71735722\|ref\|YP_276003.1\| | 1/1 | 3 | 878 | .] | 1 | 960 | [] | 781.2 | 7.2e-232 |
| gi\|89075195\|ref\|ZP_01161626.1\| | 1/1 | 1 | 876 | [] | 1 | 960 | [] | 780.8 | 9.1e-232 |
| gi\|253690426\|ref\|YP_003019616.1\| | 1/1 | 1 | 879 | [] | 1 | 960 | [] | 780.7 | 1e-231 |
| gi\|28807771\|dbj\|BAC61024.1\| | 1/1 | 3 | 888 | .] | 1 | 960 | [] | 780.4 | 1.2e-231 |
| gi\|70728529\|ref\|YP_258278.1\| | 1/1 | 3 | 876 | .] | 1 | 960 | [] | 779.7 | 2e-231 |
| gi\|242237649\|ref\|YP_002985830.1\| | 1/1 | 1 | 880 | [] | 1 | 960 | [] | 778.7 | 4e-231 |
| gi\|227327296\|ref\|ZP_03831320.1\| | 1/1 | 1 | 879 | [] | 1 | 960 | [] | 778.5 | 4.6e-231 |
| gi\|163802795\|ref\|ZP_02196685.1\| | 1/1 | 1 | 877 | [] | 1 | 960 | [] | 778.4 | 5e-231 |
| gi\|260779573\|ref\|ZP_05888463.1\| | 1/1 | 1 | 877 | [] | 1 | 960 | [] | 777.9 | 6.9e-231 |
| gi\|227114312\|ref\|ZP_03827968.1\| | 1/1 | 1 | 879 | [] | 1 | 960 | [] | 777.8 | 7.7e-231 |
| gi\|238892353\|ref\|YP_002917087.1\| | 1/1 | 1 | 883 | [] | 1 | 960 | [] | 777.6 | 8.3e-231 |
| gi\|146308379\|ref\|YP_001188844.1\| | 1/1 | 3 | 878 | .] | 1 | 960 | [] | 777.4 | 9.7e-231 |
| gi\|120555149\|ref\|YP_959500.1\| | 1/1 | 1 | 881 | [] | 1 | 960 | [] | 777.2 | 1.1e-230 |
| gi\|37199939\|dbj\|BAC95768.1\| | 1/1 | 3 | 888 | .] | 1 | 960 | [] | 777.1 | 1.2e-230 |
| gi\|46911906\|emb\|CAG18704.1\| | 1/1 | 9 | 892 | .] | 1 | 960 | [] | 777.0 | 1.3e-230 |
| gi\|205359957\|ref\|ZP_02833529.2\| | 1/1 | 17 | 912 | .] | 1 | 960 | [] | 776.4 | 2e-230 |
| gi\|261254127\|ref\|ZP_05946700.1\| | 1/1 | 1 | 877 | [] | 1 | 960 | [] | 775.8 | 2.9e-230 |
| gi\|262376807\|ref\|ZP_06070034.1\| | 1/1 | 4 | 894 | .] | 1 | 960 | [] | 775.6 | 3.4e-230 |
| gi\|289626060\|ref\|ZP_06459014.1\| | 1/1 | 3 | 878 | .] | 1 | 960 | [] | 775.3 | 4.1e-230 |
| gi\|104780469\|ref\|YP_606967.1\| | 1/1 | 3 | 875 | .] | 1 | 960 | [] | 775.3 | 4.3e-230 |
| gi\|66806573\|ref\|XP_637009.1\| | 1/1 | 10 | 931 | .] | 1 | 960 | [] | 775.2 | 4.6e-230 |
| gi\|197336287\|ref\|YP_002157103.1\| | 1/1 | 1 | 876 | [] | 1 | 960 | [] | 774.6 | 6.7e-230 |
| gi\|197300985\|ref\|ZP_02662800.2\| | 1/1 | 17 | 912 | .] | 1 | 960 | [] | 774.5 | 7.4e-230 |
| gi\|161936338\|ref\|YP_128506.2\| | 1/1 | 1 | 876 | [] | 1 | 960 | [] | 774.3 | 8.4e-230 |
| gi\|170723273\|ref\|YP_001750961.1\| | 1/1 | 3 | 875 | .] | 1 | 960 | [] | 774.1 | 9.4e-230 |
| gi\|153839017\|ref\|ZP_01991684.1\| | 1/1 | 1 | 877 | [] | 1 | 960 | [] | 774.1 | 9.9e-230 |
| gi\|268593405\|ref\|ZP_06127626.1\| | 1/1 | 1 | 879 | [] | 1 | 960 | [] | 773.6 | 1.4e-229 |
| gi\|209696160\|ref\|YP_002264090.1\| | 1/1 | 1 | 876 | [] | 1 | 960 | [] | 772.7 | 2.5e-229 |
| gi\|218551053\|ref\|YP_002384844.1\| | 1/1 | 1 | 883 | [] | 1 | 960 | [] | 772.0 | 4.2e-229 |
| gi\|27364763\|ref\|NP_760291.1\| | 1/1 | 1 | 877 | [] | 1 | 960 | [] | 771.7 | 5.3e-229 |
| gi\|194471160\|ref\|ZP_03077144.1\| | 1/1 | 17 | 912 | .] | 1 | 960 | [] | 771.6 | 5.6e-229 |
| gi\|26988237\|ref\|NP_743662.1\| | 1/1 | 3 | 875 | .] | 1 | 960 | [] | 771.4 | 6.2e-229 |
| gi\|261211215\|ref\|ZP_05925504.1\| | 1/1 | 1 | 876 | [] | 1 | 960 | [] | 771.3 | 6.7e-229 |
| gi\|167032123\|ref\|YP_001667354.1\| | 1/1 | 3 | 875 | .] | 1 | 960 | [] | 771.1 | 8e-229 |
| gi\|170769681\|ref\|ZP_02904134.1\| | 1/1 | 1 | 883 | [] | 1 | 960 | [] | 771.0 | 8.2e-229 |
| gi\|161486595\|ref\|NP_935797.2\| | 1/1 | 1 | 877 | [] | 1 | 960 | [] | 770.7 | 1e-228 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| gi\|91213504\|ref\|YP_543490.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 770.6 | 1.1e-228 |
| gi\|148977256\|ref\|ZP_01813883.1\| | 1/1 | 1 | 876 [] | 1 | 960 [] | 770.5 | 1.2e-228 |
| gi\|90413609\|ref\|ZP_01221599.1\| | 1/1 | 1 | 876 [] | 1 | 960 [] | 770.2 | 1.5e-228 |
| gi\|261346852\|ref\|ZP_05974496.1\| | 1/1 | 1 | 879 [] | 1 | 960 [] | 769.9 | 1.8e-228 |
| gi\|212712498\|ref\|ZP_03320626.1\| | 1/1 | 1 | 879 [] | 1 | 960 [] | 769.8 | 2e-228 |
| gi\|260770868\|ref\|ZP_05879797.1\| | 1/1 | 1 | 877 [] | 1 | 960 [] | 769.6 | 2.2e-228 |
| gi\|148549423\|ref\|YP_001269525.1\| | 1/1 | 3 | 875 .] | 1 | 960 [] | 769.3 | 2.7e-228 |
| gi\|269103968\|ref\|ZP_06156665.1\| | 1/1 | 1 | 876 [] | 1 | 960 [] | 769.2 | 2.9e-228 |
| gi\|206577729\|ref\|YP_002241183.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 769.2 | 2.9e-228 |
| gi\|59712915\|ref\|YP_205691.1\| | 1/1 | 1 | 876 [] | 1 | 960 [] | 769.2 | 2.9e-228 |
| gi\|66044566\|ref\|YP_234407.1\| | 1/1 | 3 | 878 .] | 1 | 960 [] | 768.9 | 3.5e-228 |
| gi\|161505390\|ref\|YP_001572502.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 768.2 | 5.9e-228 |
| gi\|16762323\|ref\|NP_457940.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 768.0 | 6.5e-228 |
| gi\|194737003\|ref\|YP_002117033.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 767.7 | 8e-228 |
| gi\|238921689\|ref\|YP_002935204.1\| | 1/1 | 1 | 877 [] | 1 | 960 [] | 767.5 | 9.1e-228 |
| gi\|269140825\|ref\|YP_003297526.1\| | 1/1 | 1 | 877 [] | 1 | 960 [] | 767.4 | 1e-227 |
| gi\|194433218\|ref\|ZP_03065499.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 767.2 | 1.2e-227 |
| gi\|24115246\|ref\|NP_709756.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 767.2 | 1.2e-227 |
| gi\|254032062\|gb\|ACT54615.1\| | 1/1 | 2 | 1051 .] | 1 | 960 [] | 767.1 | 1.2e-227 |
| gi\|16131794\|ref\|NP_418391.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 767.0 | 1.3e-227 |
| gi\|15834139\|ref\|NP_312912.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 766.7 | 1.7e-227 |
| gi\|26250729\|ref\|NP_756769.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 766.6 | 1.7e-227 |
| gi\|110807812\|ref\|YP_691332.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 766.5 | 1.8e-227 |
| gi\|170683041\|ref\|YP_001746348.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 766.2 | 2.3e-227 |
| gi\|218692242\|ref\|YP_002400454.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 766.2 | 2.4e-227 |
| gi\|291092305\|gb\|EFE24866.1\| | 1/1 | 1 | 877 [] | 1 | 960 [] | 766.0 | 2.7e-227 |
| gi\|218710807\|ref\|YP_002418428.1\| | 1/1 | 1 | 876 [] | 1 | 960 [] | 766.0 | 2.7e-227 |
| gi\|15804552\|ref\|NP_290593.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 765.9 | 2.8e-227 |
| gi\|167551379\|ref\|ZP_02345134.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 765.9 | 2.9e-227 |
| gi\|56415957\|ref\|YP_153032.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 765.8 | 3e-227 |
| gi\|149200328\|ref\|ZP_01877347.1\| | 1/1 | 1 | 882 [] | 1 | 960 [] | 765.7 | 3.2e-227 |
| gi\|84390835\|ref\|ZP_00991527.1\| | 1/1 | 1 | 876 [] | 1 | 960 [] | 765.6 | 3.5e-227 |
| gi\|283787363\|ref\|YP_003367228.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 765.5 | 3.9e-227 |
| gi\|260595982\|ref\|YP_003208553.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 765.2 | 4.8e-227 |
| gi\|86147311\|ref\|ZP_01065625.1\| | 1/1 | 1 | 876 [] | 1 | 960 [] | 765.1 | 4.9e-227 |
| gi\|290477219\|ref\|YP_003470136.1\| | 1/1 | 1 | 878 [] | 1 | 960 [] | 765.0 | 5.2e-227 |
| gi\|16767384\|ref\|NP_462999.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 764.9 | 5.7e-227 |
| gi\|162420514\|ref\|YP_001608201.1\| | 1/1 | 8 | 898 .] | 1 | 960 [] | 764.5 | 7.4e-227 |
| gi\|121587916\|ref\|ZP_01677671.1\| | 1/1 | 3 | 887 .] | 1 | 960 [] | 764.3 | 8.5e-227 |
| gi\|197287040\|ref\|YP_002152912.1\| | 1/1 | 1 | 878 [] | 1 | 960 [] | 764.0 | 1e-226 |
| gi\|123440516\|ref\|YP_001004510.1\| | 1/1 | 1 | 879 [] | 1 | 960 [] | 763.6 | 1.4e-226 |
| gi\|62182579\|ref\|YP_218996.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 763.1 | 2e-226 |
| gi\|121727604\|ref\|ZP_01680712.1\| | 1/1 | 3 | 887 .] | 1 | 960 [] | 763.0 | 2.1e-226 |
| gi\|183597325\|ref\|ZP_02958818.1\| | 1/1 | 1 | 879 [] | 1 | 960 [] | 762.9 | 2.3e-226 |
| gi\|237800119\|ref\|ZP_04588580.1\| | 1/1 | 3 | 878 .] | 1 | 960 [] | 762.1 | 3.9e-226 |
| gi\|157373015\|ref\|YP_001481004.1\| | 1/1 | 1 | 878 [] | 1 | 960 [] | 762.1 | 3.9e-226 |
| gi\|153830201\|ref\|ZP_01982868.1\| | 1/1 | 3 | 887 .] | 1 | 960 [] | 761.8 | 4.9e-226 |
| gi\|283834724\|ref\|ZP_06354465.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 761.4 | 6.7e-226 |
| gi\|270265165\|ref\|ZP_06193427.1\| | 1/1 | 1 | 878 [] | 1 | 960 [] | 761.3 | 6.9e-226 |
| gi\|45437741\|gb\|AAS63291.1\| | 1/1 | 8 | 898 .] | 1 | 960 [] | 761.2 | 7.5e-226 |
| gi\|82546307\|ref\|YP_410254.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 761.0 | 8.3e-226 |
| gi\|262041721\|ref\|ZP_06014913.1\| | 1/1 | 1 | 870 [] | 1 | 960 [] | 760.8 | 1e-225 |
| gi\|193063946\|ref\|ZP_03045032.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 760.6 | 1.1e-225 |
| gi\|254285840\|ref\|ZP_04960802.1\| | 1/1 | 3 | 887 .] | 1 | 960 [] | 760.4 | 1.3e-225 |
| gi\|82778878\|ref\|YP_405227.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 760.3 | 1.3e-225 |
| gi\|205354304\|ref\|YP_002228105.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 760.3 | 1.4e-225 |
| gi\|262170418\|ref\|ZP_06038096.1\| | 1/1 | 1 | 876 [] | 1 | 960 [] | 760.3 | 1.4e-225 |
| gi\|254225390\|ref\|ZP_04919001.1\| | 1/1 | 3 | 887 .] | 1 | 960 [] | 760.3 | 1.4e-225 |
| gi\|28868714\|ref\|NP_791333.1\| | 1/1 | 3 | 878 .] | 1 | 960 [] | 760.2 | 1.5e-225 |
| gi\|91791616\|ref\|YP_561267.1\| | 1/1 | 1 | 887 [] | 1 | 960 [] | 760.1 | 1.6e-225 |
| gi\|262166662\|ref\|ZP_06034399.1\| | 1/1 | 1 | 876 [] | 1 | 960 [] | 759.9 | 1.9e-225 |
| gi\|293393511\|ref\|ZP_06637821.1\| | 1/1 | 19 | 907 .] | 1 | 960 [] | 759.4 | 2.5e-225 |
| gi\|109896934\|ref\|YP_660189.1\| | 1/1 | 4 | 872 .] | 1 | 960 [] | 759.3 | 2.8e-225 |
| gi\|225423837\|ref\|XP_002280842.1\| | 1/1 | 16 | 1061 .] | 1 | 960 [] | 759.3 | 2.8e-225 |
| gi\|126667184\|ref\|ZP_01738158.1\| | 1/1 | 1 | 876 [] | 1 | 960 [] | 759.1 | 3.1e-225 |
| gi\|258625692\|ref\|ZP_05720571.1\| | 1/1 | 1 | 876 [] | 1 | 960 [] | 759.1 | 3.2e-225 |
| gi\|213969092\|ref\|ZP_03397231.1\| | 1/1 | 3 | 878 .] | 1 | 960 [] | 758.9 | 3.7e-225 |
| gi\|52425072\|ref\|YP_088209.1\| | 1/1 | 1 | 880 [] | 1 | 960 [] | 758.7 | 4.2e-225 |
| gi\|258620479\|ref\|ZP_05715517.1\| | 1/1 | 2 | 878 .] | 1 | 960 [] | 758.6 | 4.4e-225 |
| gi\|157147246\|ref\|YP_001454565.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 758.6 | 4.5e-225 |
| gi\|262373873\|ref\|ZP_06067151.1\| | 1/1 | 4 | 893 .] | 1 | 960 [] | 758.1 | 6.3e-225 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| gi\|291619398\|ref\|YP_003522140.1\| | 1/1 | 1 | 882 [] | 1 | 960 [] | 757.4 | 1e-224 |
| gi\|251792638\|ref\|YP_003007364.1\| | 1/1 | 6 | 879 .] | 1 | 960 [] | 756.9 | 1.5e-224 |
| gi\|229521712\|ref\|ZP_04411130.1\| | 1/1 | 2 | 878 .] | 1 | 960 [] | 756.7 | 1.7e-224 |
| gi\|51594466\|ref\|YP_068657.1\| | 1/1 | 1 | 878 [] | 1 | 960 [] | 756.5 | 1.9e-224 |
| gi\|108806093\|ref\|YP_650009.1\| | 1/1 | 1 | 878 [] | 1 | 960 [] | 756.3 | 2.3e-224 |
| gi\|229507302\|ref\|ZP_04396807.1\| | 1/1 | 2 | 878 .] | 1 | 960 [] | 756.2 | 2.4e-224 |
| gi\|107103201\|ref\|ZP_01367119.1\| | 1/1 | 3 | 878 .] | 1 | 960 [] | 756.0 | 2.7e-224 |
| gi\|15598883\|ref\|NP_252377.1\| | 1/1 | 3 | 878 .] | 1 | 960 [] | 756.0 | 2.8e-224 |
| gi\|253991711\|ref\|YP_003043067.1\| | 1/1 | 1 | 878 [] | 1 | 960 [] | 756.0 | 2.8e-224 |
| gi\|160877316\|ref\|YP_001556632.1\| | 1/1 | 11 | 889 .] | 1 | 960 [] | 755.0 | 5.3e-224 |
| gi\|238750857\|ref\|ZP_04612355.1\| | 1/1 | 1 | 878 [] | 1 | 960 [] | 755.0 | 5.6e-224 |
| gi\|229513569\|ref\|ZP_04403033.1\| | 1/1 | 2 | 878 .] | 1 | 960 [] | 754.9 | 5.8e-224 |
| gi\|218890036\|ref\|YP_002438900.1\| | 1/1 | 3 | 878 .] | 1 | 960 [] | 754.8 | 6.1e-224 |
| gi\|161581981\|ref\|NP_232274.2\| | 1/1 | 1 | 876 [] | 1 | 960 [] | 754.6 | 7.1e-224 |
| gi\|262401934\|ref\|ZP_06078499.1\| | 1/1 | 1 | 876 [] | 1 | 960 [] | 754.2 | 9.7e-224 |
| gi\|157377410\|ref\|YP_001476010.1\| | 1/1 | 3 | 878 .] | 1 | 960 [] | 754.1 | 1e-223 |
| gi\|238789607\|ref\|ZP_04633391.1\| | 1/1 | 1 | 878 [] | 1 | 960 [] | 753.9 | 1.2e-223 |
| gi\|119773395\|ref\|YP_926135.1\| | 1/1 | 12 | 887 .] | 1 | 960 [] | 753.9 | 1.2e-223 |
| gi\|262170106\|ref\|ZP_06037795.1\| | 1/1 | 1 | 876 [] | 1 | 960 [] | 753.3 | 1.7e-223 |
| gi\|153002595\|ref\|YP_001368276.1\| | 1/1 | 11 | 889 .] | 1 | 960 [] | 753.3 | 1.8e-223 |
| gi\|161511331\|ref\|NP_994414.2\| | 1/1 | 1 | 878 [] | 1 | 960 [] | 752.9 | 2.3e-223 |
| gi\|152987651\|ref\|YP_001346835.1\| | 1/1 | 3 | 878 .] | 1 | 960 [] | 752.8 | 2.4e-223 |
| gi\|156935917\|ref\|YP_001439833.1\| | 1/1 | 1 | 870 [] | 1 | 960 [] | 752.7 | 2.7e-223 |
| gi\|292825460\|gb\|EFF84201.1\| | 1/1 | 4 | 893 .] | 1 | 960 [] | 752.6 | 2.9e-223 |
| gi\|24371872\|ref\|NP_715914.1\| | 1/1 | 3 | 881 .] | 1 | 960 [] | 752.5 | 3e-223 |
| gi\|117922338\|ref\|YP_871530.1\| | 1/1 | 11 | 889 .] | 1 | 960 [] | 752.5 | 3.1e-223 |
| gi\|170724697\|ref\|YP_001758723.1\| | 1/1 | 3 | 878 .] | 1 | 960 [] | 752.4 | 3.4e-223 |
| gi\|146313662\|ref\|YP_001178736.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 752.1 | 4e-223 |
| gi\|226953287\|ref\|ZP_03823751.1\| | 1/1 | 4 | 893 .] | 1 | 960 [] | 752.1 | 4.1e-223 |
| gi\|116051684\|ref\|YP_789477.1\| | 1/1 | 3 | 878 .] | 1 | 960 [] | 751.8 | 5.1e-223 |
| gi\|124548514\|ref\|ZP_01707155.1\| | 1/1 | 11 | 889 .] | 1 | 960 [] | 751.6 | 5.7e-223 |
| gi\|223670909\|dbj\|BAH22704.1\| | 1/1 | 73 | 1011 .] | 1 | 960 [] | 751.5 | 6.4e-223 |
| gi\|237728069\|ref\|ZP_04558550.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 751.1 | 8.3e-223 |
| gi\|145635078\|ref\|ZP_01790784.1\| | 1/1 | 2 | 879 .] | 1 | 960 [] | 751.0 | 8.7e-223 |
| gi\|260914089\|ref\|ZP_05920562.1\| | 1/1 | 2 | 879 .] | 1 | 960 [] | 750.9 | 9.2e-223 |
| gi\|259906836\|ref\|YP_002647192.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 750.3 | 1.4e-222 |
| gi\|119944012\|ref\|YP_941692.1\| | 1/1 | 6 | 878 .] | 1 | 960 [] | 750.2 | 1.5e-222 |
| gi\|292486630\|ref\|YP_003529500.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 749.8 | 2e-222 |
| gi\|114561377\|ref\|YP_748890.1\| | 1/1 | 7 | 882 .] | 1 | 960 [] | 749.2 | 3e-222 |
| gi\|145633038\|ref\|ZP_01788770.1\| | 1/1 | 2 | 879 .] | 1 | 960 [] | 749.1 | 3.3e-222 |
| gi\|37528563\|ref\|NP_931908.1\| | 1/1 | 1 | 878 [] | 1 | 960 [] | 748.9 | 3.8e-222 |
| gi\|147809570\|emb\|CAN62388.1\| | 1/1 | 16 | 1069 .] | 1 | 960 [] | 748.5 | 4.8e-222 |
| gi\|258637583\|ref\|ZP_05730332.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 748.4 | 5.3e-222 |
| gi\|15602411\|ref\|NP_245483.1\| | 1/1 | 2 | 879 .] | 1 | 960 [] | 747.9 | 7.6e-222 |
| gi\|196155561\|ref\|YP_002125050.1\| | 1/1 | 4 | 873 .] | 1 | 960 [] | 747.7 | 8.5e-222 |
| gi\|120600645\|ref\|YP_965219.1\| | 1/1 | 11 | 889 .] | 1 | 960 [] | 747.3 | 1.1e-221 |
| gi\|146294801\|ref\|YP_001185225.1\| | 1/1 | 11 | 889 .] | 1 | 960 [] | 747.2 | 1.2e-221 |
| gi\|188532292\|ref\|YP_001906089.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 747.1 | 1.3e-221 |
| gi\|261343020\|ref\|ZP_05970878.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 747.0 | 1.4e-221 |
| gi\|126176310\|ref\|YP_001052459.1\| | 1/1 | 11 | 889 .] | 1 | 960 [] | 746.7 | 1.7e-221 |
| gi\|260772057\|ref\|ZP_05880974.1\| | 1/1 | 1 | 877 [] | 1 | 960 [] | 746.0 | 2.8e-221 |
| gi\|167626000\|ref\|YP_001676294.1\| | 1/1 | 3 | 878 .] | 1 | 960 [] | 745.9 | 2.9e-221 |
| gi\|145630943\|ref\|ZP_01786719.1\| | 1/1 | 2 | 879 .] | 1 | 960 [] | 745.0 | 5.7e-221 |
| gi\|157960054\|ref\|YP_001500088.1\| | 1/1 | 3 | 878 .] | 1 | 960 [] | 745.0 | 5.7e-221 |
| gi\|148828375\|ref\|YP_001293128.1\| | 1/1 | 2 | 879 .] | 1 | 960 [] | 744.9 | 6.1e-221 |
| gi\|229846259\|ref\|ZP_04466371.1\| | 1/1 | 2 | 879 .] | 1 | 960 [] | 744.6 | 7.4e-221 |
| gi\|113972037\|ref\|YP_735830.1\| | 1/1 | 11 | 889 .] | 1 | 960 [] | 744.6 | 7.4e-221 |
| gi\|238754721\|ref\|ZP_04616073.1\| | 1/1 | 1 | 878 [] | 1 | 960 [] | 744.4 | 8.5e-221 |
| gi\|68249774\|ref\|YP_248886.1\| | 1/1 | 2 | 879 .] | 1 | 960 [] | 743.5 | 1.6e-220 |
| gi\|145627780\|ref\|ZP_01783581.1\| | 1/1 | 2 | 879 .] | 1 | 960 [] | 743.4 | 1.7e-220 |
| gi\|114045747\|ref\|YP_736297.1\| | 1/1 | 11 | 889 .] | 1 | 960 [] | 743.2 | 1.9e-220 |
| gi\|229844816\|ref\|ZP_04464954.1\| | 1/1 | 2 | 879 .] | 1 | 960 [] | 740.3 | 1.5e-219 |
| gi\|238764489\|ref\|ZP_04625437.1\| | 1/1 | 1 | 865 [] | 1 | 960 [] | 740.1 | 1.7e-219 |
| gi\|212634871\|ref\|YP_002311396.1\| | 1/1 | 3 | 878 .] | 1 | 960 [] | 739.9 | 2e-219 |
| gi\|16273525\|ref\|NP_439778.1\| | 1/1 | 2 | 879 .] | 1 | 960 [] | 739.8 | 2.1e-219 |
| gi\|163751629\|ref\|ZP_02158849.1\| | 1/1 | 3 | 877 .] | 1 | 960 [] | 739.7 | 2.2e-219 |
| gi\|145639250\|ref\|ZP_01794856.1\| | 1/1 | 2 | 879 .] | 1 | 960 [] | 739.4 | 2.7e-219 |
| gi\|170717721\|ref\|YP_001784792.1\| | 1/1 | 1 | 879 [] | 1 | 960 [] | 739.4 | 2.7e-219 |
| gi\|238786115\|ref\|ZP_04630071.1\| | 1/1 | 1 | 865 [] | 1 | 960 [] | 739.2 | 3e-219 |
| gi\|260582158\|ref\|ZP_05849952.1\| | 1/1 | 2 | 879 .] | 1 | 960 [] | 738.9 | 3.8e-219 |
| gi\|113461137\|ref\|YP_719205.1\| | 1/1 | 1 | 879 [] | 1 | 960 [] | 738.8 | 4.2e-219 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| gi\|238798303\|ref\|ZP_04641787.1\| | 1/1 | 1 | 865 | [] | 1 | 960 | [] | 738.7 | 4.6e-219 |
| gi\|238760149\|ref\|ZP_04621297.1\| | 1/1 | 1 | 865 | [] | 1 | 960 | [] | 738.6 | 4.6e-219 |
| gi\|293329260\|dbj\|BAJ03991.1\| | 1/1 | 3 | 877 | .] | 1 | 960 | [] | 737.3 | 1.2e-218 |
| gi\|127511134\|ref\|YP_001092331.1\| | 1/1 | 3 | 878 | .] | 1 | 960 | [] | 737.2 | 1.2e-218 |
| gi\|126207823\|ref\|YP_001053048.1\| | 1/1 | 2 | 879 | .] | 1 | 960 | [] | 737.1 | 1.4e-218 |
| gi\|146283084\|ref\|YP_001173237.1\| | 1/1 | 4 | 879 | .] | 1 | 960 | [] | 733.7 | 1.4e-217 |
| gi\|190149613\|ref\|YP_001968138.1\| | 1/1 | 2 | 879 | .] | 1 | 960 | [] | 733.3 | 1.8e-217 |
| gi\|223998678\|ref\|XP_002289012.1\| | 1/1 | 1 | 883 | [] | 1 | 960 | [] | 732.3 | 3.8e-217 |
| gi\|32033610\|ref\|ZP_00133921.1\| | 1/1 | 1 | 872 | [] | 1 | 960 | [] | 732.1 | 4.2e-217 |
| gi\|148826161\|ref\|YP_001290914.1\| | 1/1 | 2 | 879 | .] | 1 | 960 | [] | 731.8 | 5.2e-217 |
| gi\|92113764\|ref\|YP_573692.1\| | 1/1 | 8 | 883 | .] | 1 | 960 | [] | 730.3 | 1.5e-216 |
| gi\|165975797\|ref\|YP_001651390.1\| | 1/1 | 2 | 879 | .] | 1 | 960 | [] | 730.1 | 1.7e-216 |
| gi\|53732877\|ref\|ZP_00155206.2\| | 1/1 | 1 | 866 | [] | 1 | 960 | [] | 728.6 | 4.9e-216 |
| gi\|283896778\|emb\|CAX65690.1\| | 1/1 | 1 | 502 | [] | 1 | 960 | [] | 728.1 | 6.9e-216 |
| gi\|219870613\|ref\|YP_002474988.1\| | 1/1 | 1 | 879 | [] | 1 | 960 | [] | 728.0 | 7.1e-216 |
| gi\|238794908\|ref\|ZP_04638507.1\| | 1/1 | 1 | 865 | [] | 1 | 960 | [] | 727.4 | 1.1e-215 |
| gi\|262363644\|gb\|ACY60365.1\| | 1/1 | 2 | 852 | .] | 1 | 960 | [] | 727.3 | 1.2e-215 |
| gi\|110833541\|ref\|YP_692400.1\| | 1/1 | 1 | 888 | [] | 1 | 960 | [] | 726.7 | 1.8e-215 |
| gi\|167855566\|ref\|ZP_02478327.1\| | 1/1 | 1 | 879 | [] | 1 | 960 | [] | 726.6 | 2e-215 |
| gi\|46133363\|ref\|ZP_00157068.2\| | 1/1 | 1 | 866 | [] | 1 | 960 | [] | 726.5 | 2e-215 |
| gi\|125524127\|gb\|EAY72241.1\| | 1/1 | 16 | 1009 | .] | 1 | 960 | [] | 726.5 | 2.1e-215 |
| gi\|254481871\|ref\|ZP_05095114.1\| | 1/1 | 15 | 879 | .] | 1 | 960 | [] | 724.7 | 7e-215 |
| gi\|283896806\|emb\|CAX65704.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 720.9 | 9.7e-214 |
| gi\|283896784\|emb\|CAX65693.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 720.7 | 1.2e-213 |
| gi\|283896814\|emb\|CAX65708.1\| | 1/1 | 1 | 502 | [] | 1 | 960 | [] | 719.1 | 3.5e-213 |
| gi\|293336483\|ref\|NP_001170654.1\| | 1/1 | 1 | 506 | [] | 1 | 960 | [] | 716.8 | 1.7e-212 |
| gi\|254784775\|ref\|YP_003072203.1\| | 1/1 | 3 | 878 | .] | 1 | 960 | [] | 716.0 | 2.9e-212 |
| gi\|255566797\|ref\|XP_002524382.1\| | 1/1 | 1 | 986 | [] | 1 | 960 | [] | 714.5 | 8.5e-212 |
| gi\|213616153\|ref\|ZP_03371979.1\| | 1/1 | 2 | 840 | .] | 1 | 960 | [] | 714.1 | 1.2e-211 |
| gi\|254360733\|ref\|ZP_04976881.1\| | 1/1 | 1 | 879 | [] | 1 | 960 | [] | 712.6 | 3.2e-211 |
| gi\|261496916\|ref\|ZP_05993284.1\| | 1/1 | 1 | 879 | [] | 1 | 960 | [] | 711.6 | 6.2e-211 |
| gi\|94500599\|ref\|ZP_01307129.1\| | 1/1 | 1 | 877 | [] | 1 | 960 | [] | 710.9 | 1e-210 |
| gi\|240949435\|ref\|ZP_04753776.1\| | 1/1 | 1 | 879 | [] | 1 | 960 | [] | 710.8 | 1.1e-210 |
| gi\|283896780\|emb\|CAX65691.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 710.3 | 1.6e-210 |
| gi\|257465177\|ref\|ZP_05629548.1\| | 1/1 | 1 | 879 | [] | 1 | 960 | [] | 710.2 | 1.6e-210 |
| gi\|283896790\|emb\|CAX65696.1\| | 1/1 | 1 | 502 | [] | 1 | 960 | [] | 710.2 | 1.6e-210 |
| gi\|283896810\|emb\|CAX65706.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 710.1 | 1.7e-210 |
| gi\|261492498\|ref\|ZP_05989052.1\| | 1/1 | 1 | 879 | [] | 1 | 960 | [] | 710.1 | 1.8e-210 |
| gi\|283896818\|emb\|CAX65710.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 709.6 | 2.5e-210 |
| gi\|283896796\|emb\|CAX65699.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 709.6 | 2.6e-210 |
| gi\|283896768\|emb\|CAX65685.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 708.8 | 4.4e-210 |
| gi\|254514836\|ref\|ZP_05126897.1\| | 1/1 | 2 | 885 | .] | 1 | 960 | [] | 708.3 | 6.4e-210 |
| gi\|283896770\|emb\|CAX65686.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 706.5 | 2.1e-209 |
| gi\|283896776\|emb\|CAX65689.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 706.4 | 2.3e-209 |
| gi\|283896804\|emb\|CAX65703.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 706.0 | 3.1e-209 |
| gi\|283896772\|emb\|CAX65687.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 705.5 | 4.4e-209 |
| gi\|283896782\|emb\|CAX65692.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 705.1 | 5.6e-209 |
| gi\|283896792\|emb\|CAX65697.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 704.7 | 7.7e-209 |
| gi\|283896808\|emb\|CAX65705.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 704.5 | 8.5e-209 |
| gi\|283896786\|emb\|CAX65694.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 704.5 | 8.5e-209 |
| gi\|88857492\|ref\|ZP_01132135.1\| | 1/1 | 1 | 873 | [] | 1 | 960 | [] | 704.5 | 8.7e-209 |
| gi\|283896800\|emb\|CAX65701.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 701.9 | 5.3e-208 |
| gi\|283896774\|emb\|CAX65688.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 698.0 | 8e-207 |
| gi\|283896788\|emb\|CAX65695.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 697.8 | 8.9e-207 |
| gi\|90023020\|ref\|YP_528847.1\| | 1/1 | 2 | 873 | .] | 1 | 960 | [] | 697.5 | 1.1e-206 |
| gi\|167041901\|gb\|ABZ06640.1\| | 1/1 | 4 | 906 | .] | 1 | 960 | [] | 697.2 | 1.4e-206 |
| gi\|283896812\|emb\|CAX65707.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 696.1 | 3e-206 |
| gi\|283896822\|emb\|CAX65712.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 695.4 | 4.7e-206 |
| gi\|119468657\|ref\|ZP_01611709.1\| | 1/1 | 1 | 881 | [] | 1 | 960 | [] | 695.2 | 5.3e-206 |
| gi\|77362226\|ref\|YP_341800.1\| | 1/1 | 1 | 881 | [] | 1 | 960 | [] | 694.8 | 7.2e-206 |
| gi\|219120583\|ref\|XP_002181027.1\| | 1/1 | 72 | 1009 | .] | 1 | 960 | [] | 692.2 | 4.4e-205 |
| gi\|59936824\|gb\|AAX12115.1\| | 1/1 | 1 | 492 | [] | 1 | 960 | [] | 690.6 | 1.3e-204 |
| gi\|283896816\|emb\|CAX65709.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 689.7 | 2.5e-204 |
| gi\|283896794\|emb\|CAX65698.1\| | 1/1 | 1 | 504 | [] | 1 | 960 | [] | 689.4 | 3.1e-204 |
| gi\|192361093\|ref\|YP_001983406.1\| | 1/1 | 3 | 871 | .] | 1 | 960 | [] | 688.7 | 4.8e-204 |
| gi\|88706831\|ref\|ZP_01104531.1\| | 1/1 | 11 | 885 | .] | 1 | 960 | [] | 688.0 | 8.3e-204 |
| gi\|283896798\|emb\|CAX65700.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 687.6 | 1.1e-203 |
| gi\|283896824\|emb\|CAX65713.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 686.0 | 3.2e-203 |
| gi\|283896802\|emb\|CAX65702.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 682.0 | 5.2e-202 |
| gi\|114772589\|ref\|ZP_01449953.1\| | 1/1 | 6 | 878 | .] | 1 | 960 | [] | 674.5 | 9.2e-200 |
| gi\|283896820\|emb\|CAX65711.1\| | 1/1 | 1 | 503 | [] | 1 | 960 | [] | 669.3 | 3.3e-198 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| gi\|219125106\|ref\|XP_002182829.1\| | 1/1 | 1 | 877 | [] | 1 | 960 | [] | 667.8 | 9.9e-198 |
| gi\|254282267\|ref\|ZP_04957235.1\| | 1/1 | 4 | 870 | .] | 1 | 960 | [] | 660.8 | 1.2e-195 |
| gi\|40063490\|gb\|AAR38290.1\| | 1/1 | 1 | 873 | [] | 1 | 960 | [] | 655.4 | 5.4e-194 |
| gi\|18645092\|gb\|AAL76393.1\| | 1/1 | 1 | 873 | [] | 1 | 960 | [] | 655.0 | 6.8e-194 |
| gi\|71083482\|ref\|YP_266201.1\| | 1/1 | 1 | 895 | [] | 1 | 960 | [] | 627.8 | 1e-185 |
| gi\|221060224\|ref\|XP_002260757.1\| | 1/1 | 61 | 1044 | .. | 1 | 960 | [] | 626.7 | 2.2e-185 |
| gi\|270239854\|emb\|CBI27087.1\| | 1/1 | 16 | 987 | .] | 1 | 960 | [] | 621.5 | 8.4e-184 |
| gi\|156102026\|ref\|XP_001616706.1\| | 1/1 | 58 | 1050 | .. | 1 | 960 | [] | 606.1 | 3.6e-179 |
| gi\|254455801\|ref\|ZP_05069230.1\| | 1/1 | 1 | 895 | [] | 1 | 960 | [] | 605.0 | 7.9e-179 |
| gi\|224000774\|ref\|XP_002290059.1\| | 1/1 | 1 | 843 | [] | 1 | 960 | [] | 602.2 | 5.5e-178 |
| gi\|124808830\|ref\|XP_001348420.1\| | 1/1 | 29 | 1008 | .. | 1 | 960 | [] | 581.6 | 8.4e-172 |
| gi\|51701320\|sp\|Q6R2V6.1\|CAPP2_CHLRE | 1/1 | 1 | 1221 | [] | 1 | 960 | [] | 572.7 | 4.1e-169 |
| gi\|83282693\|ref\|XP_729881.1\| | 1/1 | 15 | 987 | .. | 1 | 960 | [] | 567.8 | 1.2e-167 |
| gi\|68071185\|ref\|XP_677506.1\| | 1/1 | 15 | 993 | .. | 1 | 960 | [] | 567.4 | 1.7e-167 |
| gi\|145641160\|ref\|ZP_01796740.1\| | 1/1 | 1 | 758 | [] | 1 | 960 | [] | 554.2 | 1.5e-163 |
| gi\|154146762\|emb\|CAM84068.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 538.3 | 9.3e-159 |
| gi\|154146754\|emb\|CAM84064.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 538.2 | 1e-158 |
| gi\|154146800\|emb\|CAM84087.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 537.9 | 1.3e-158 |
| gi\|154146808\|emb\|CAM84091.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 537.0 | 2.3e-158 |
| gi\|154146746\|emb\|CAM84060.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 535.9 | 5e-158 |
| gi\|154146724\|emb\|CAM84049.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 535.4 | 6.8e-158 |
| gi\|154146788\|emb\|CAM84081.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 535.0 | 9e-158 |
| gi\|154146830\|emb\|CAM84102.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 534.6 | 1.2e-157 |
| gi\|154146878\|emb\|CAM84126.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 524.3 | 1.5e-154 |
| gi\|154146834\|emb\|CAM84104.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 523.3 | 3.1e-154 |
| gi\|154146768\|emb\|CAM84071.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 516.3 | 3.9e-152 |
| gi\|154146820\|emb\|CAM84097.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 514.5 | 1.3e-151 |
| gi\|167470809\|ref\|ZP_02335513.1\| | 1/1 | 1 | 773 | [. | 1 | 960 | [] | 513.3 | 3.1e-151 |
| gi\|629595\|pir\|\|PC2167 | 1/1 | 1 | 453 | [] | 1 | 960 | [] | 512.9 | 4.2e-151 |
| gi\|66357588\|ref\|XP_625972.1\| | 1/1 | 55 | 1148 | .] | 1 | 960 | [] | 507.9 | 1.4e-149 |
| gi\|67594757\|ref\|XP_665868.1\| | 1/1 | 55 | 1148 | .] | 1 | 960 | [] | 507.0 | 2.5e-149 |
| gi\|194689768\|gb\|ACF78968.1\| | 1/1 | 1 | 435 | [] | 1 | 960 | [] | 505.8 | 5.7e-149 |
| gi\|154146850\|emb\|CAM84112.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 504.3 | 1.6e-148 |
| gi\|154146844\|emb\|CAM84109.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 504.3 | 1.7e-148 |
| gi\|154146842\|emb\|CAM84108.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 501.7 | 9.7e-148 |
| gi\|154146896\|emb\|CAM84135.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 499.8 | 3.5e-147 |
| gi\|154146722\|emb\|CAM84048.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 499.8 | 3.7e-147 |
| gi\|154146786\|emb\|CAM84080.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 499.5 | 4.4e-147 |
| gi\|154146880\|emb\|CAM84127.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 499.4 | 4.6e-147 |
| gi\|154146910\|emb\|CAM84142.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 499.4 | 4.9e-147 |
| gi\|154146796\|emb\|CAM84085.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 499.2 | 5.4e-147 |
| gi\|154146752\|emb\|CAM84063.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 498.9 | 6.9e-147 |
| gi\|154146922\|emb\|CAM84148.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 498.7 | 7.7e-147 |
| gi\|154146854\|emb\|CAM84114.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 497.5 | 1.8e-146 |
| gi\|154146848\|emb\|CAM84111.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 496.8 | 2.8e-146 |
| gi\|154146718\|emb\|CAM84046.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 495.1 | 9.7e-146 |
| gi\|154146862\|emb\|CAM84118.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 493.8 | 2.3e-145 |
| gi\|209881885\|ref\|XP_002142380.1\| | 1/1 | 76 | 1164 | .] | 1 | 960 | [] | 491.0 | 1.6e-144 |
| gi\|154146782\|emb\|CAM84078.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 490.4 | 2.4e-144 |
| gi\|154146916\|emb\|CAM84145.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 490.0 | 3.3e-144 |
| gi\|154146882\|emb\|CAM84128.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 489.1 | 6e-144 |
| gi\|154146852\|emb\|CAM84113.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 487.7 | 1.6e-143 |
| gi\|154146838\|emb\|CAM84106.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 485.2 | 8.8e-143 |
| gi\|154146832\|emb\|CAM84103.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 485.1 | 9.7e-143 |
| gi\|154146874\|emb\|CAM84124.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 484.7 | 1.3e-142 |
| gi\|154146904\|emb\|CAM84139.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 484.1 | 1.9e-142 |
| gi\|154146758\|emb\|CAM84066.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 484.1 | 1.9e-142 |
| gi\|222617602\|gb\|EEE53734.1\| | 1/1 | 16 | 946 | .] | 1 | 960 | [] | 481.5 | 1.1e-141 |
| gi\|154146756\|emb\|CAM84065.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 480.5 | 2.3e-141 |
| gi\|154146736\|emb\|CAM84055.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 480.4 | 2.5e-141 |
| gi\|154146770\|emb\|CAM84072.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 477.7 | 1.6e-140 |
| gi\|154146812\|emb\|CAM84093.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 477.7 | 1.7e-140 |
| gi\|154146902\|emb\|CAM84138.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 477.1 | 2.5e-140 |
| gi\|154146876\|emb\|CAM84125.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 476.7 | 3.3e-140 |
| gi\|154146846\|emb\|CAM84110.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 476.5 | 3.8e-140 |
| gi\|154146826\|emb\|CAM84100.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 476.0 | 5.2e-140 |
| gi\|154146908\|emb\|CAM84141.1\| | 1/1 | 1 | 438 | [] | 1 | 960 | [] | 475.5 | 7.5e-140 |
| gi\|154146732\|emb\|CAM84053.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 475.1 | 1e-139 |
| gi\|154146744\|emb\|CAM84059.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 475.1 | 1e-139 |
| gi\|154146924\|emb\|CAM84149.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 474.4 | 1.6e-139 |
| gi\|154146858\|emb\|CAM84116.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 473.6 | 2.7e-139 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| gi\|154146884\|emb\|CAM84129.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 472.7 | 5.3e-139 |
| gi\|154146860\|emb\|CAM84117.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 472.5 | 5.8e-139 |
| gi\|154146772\|emb\|CAM84073.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 472.5 | 6.1e-139 |
| gi\|156084500\|ref\|XP_001609733.1\| | 1/1 | 5 | 954 | .] | 1 | 960 | [] | 472.1 | 8e-139 |
| gi\|154146740\|emb\|CAM84057.1\| | 1/1 | 1 | 438 | [] | 1 | 960 | [] | 471.8 | 9.7e-139 |
| gi\|154146794\|emb\|CAM84084.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 471.5 | 1.2e-138 |
| gi\|159900750\|ref\|YP_001546997.1\| | 1/1 | 6 | 929 | .] | 1 | 960 | [] | 471.2 | 1.5e-138 |
| gi\|154146720\|emb\|CAM84047.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 470.1 | 3.1e-138 |
| gi\|154146912\|emb\|CAM84143.1\| | 1/1 | 1 | 438 | [] | 1 | 960 | [] | 469.1 | 6.4e-138 |
| gi\|154146816\|emb\|CAM84095.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 468.9 | 7.4e-138 |
| gi\|154146774\|emb\|CAM84074.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 467.9 | 1.5e-137 |
| gi\|154146798\|emb\|CAM84086.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 467.7 | 1.7e-137 |
| gi\|154146750\|emb\|CAM84062.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 466.5 | 3.8e-137 |
| gi\|154146824\|emb\|CAM84099.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 464.8 | 1.3e-136 |
| gi\|154146778\|emb\|CAM84076.1\| | 1/1 | 1 | 441 | [] | 1 | 960 | [] | 464.7 | 1.3e-136 |
| gi\|154146734\|emb\|CAM84054.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 464.4 | 1.6e-136 |
| gi\|154146918\|emb\|CAM84146.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 464.0 | 2.1e-136 |
| gi\|154146906\|emb\|CAM84140.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 463.3 | 3.6e-136 |
| gi\|154146900\|emb\|CAM84137.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 463.2 | 3.9e-136 |
| gi\|154146828\|emb\|CAM84101.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 462.6 | 5.9e-136 |
| gi\|154146806\|emb\|CAM84090.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 461.6 | 1.2e-135 |
| gi\|154146890\|emb\|CAM84132.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 461.4 | 1.3e-135 |
| gi\|269925429\|ref\|YP_003322052.1\| | 1/1 | 2 | 931 | .] | 1 | 960 | [] | 461.3 | 1.4e-135 |
| gi\|154146818\|emb\|CAM84096.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 460.9 | 1.9e-135 |
| gi\|154146914\|emb\|CAM84144.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 460.7 | 2.2e-135 |
| gi\|154146760\|emb\|CAM84067.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 459.7 | 4.4e-135 |
| gi\|154146814\|emb\|CAM84094.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 459.6 | 4.5e-135 |
| gi\|154146764\|emb\|CAM84069.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 458.5 | 9.5e-135 |
| gi\|123966995\|ref\|YP_001012076.1\| | 1/1 | 3 | 989 | .] | 1 | 960 | [] | 457.9 | 1.5e-134 |
| gi\|154146864\|emb\|CAM84119.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 457.8 | 1.6e-134 |
| gi\|154146738\|emb\|CAM84056.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 457.1 | 2.6e-134 |
| gi\|22299455\|ref\|NP_682702.1\| | 1/1 | 6 | 1011 | .] | 1 | 960 | [] | 457.0 | 2.8e-134 |
| gi\|154146840\|emb\|CAM84107.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 456.7 | 3.5e-134 |
| gi\|147839189\|emb\|CAN72376.1\| | 1/1 | 1 | 434 | [] | 1 | 960 | [] | 456.6 | 3.6e-134 |
| gi\|154146780\|emb\|CAM84077.1\| | 1/1 | 1 | 442 | [] | 1 | 960 | [] | 456.1 | 5.2e-134 |
| gi\|220907631\|ref\|YP_002482942.1\| | 1/1 | 47 | 1018 | .] | 1 | 960 | [] | 455.9 | 5.8e-134 |
| gi\|154146766\|emb\|CAM84070.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 455.4 | 8.5e-134 |
| gi\|154146748\|emb\|CAM84061.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 455.1 | 1.1e-133 |
| gi\|157414180\|ref\|YP_001485046.1\| | 1/1 | 5 | 989 | .] | 1 | 960 | [] | 454.6 | 1.5e-133 |
| gi\|154146894\|emb\|CAM84134.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 451.6 | 1.1e-132 |
| gi\|159904236\|ref\|YP_001551580.1\| | 1/1 | 18 | 1007 | .] | 1 | 960 | [] | 451.5 | 1.3e-132 |
| gi\|154146804\|emb\|CAM84089.1\| | 1/1 | 1 | 442 | [] | 1 | 960 | [] | 451.2 | 1.6e-132 |
| gi\|154146742\|emb\|CAM84058.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 450.6 | 2.4e-132 |
| gi\|154146790\|emb\|CAM84082.1\| | 1/1 | 1 | 438 | [] | 1 | 960 | [] | 450.0 | 3.7e-132 |
| gi\|154146784\|emb\|CAM84079.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 449.2 | 6.2e-132 |
| gi\|254526567\|ref\|ZP_05138619.1\| | 1/1 | 5 | 989 | .] | 1 | 960 | [] | 449.0 | 7e-132 |
| gi\|78780052\|ref\|YP_398164.1\| | 1/1 | 5 | 989 | .] | 1 | 960 | [] | 448.6 | 9.1e-132 |
| gi\|154146822\|emb\|CAM84098.1\| | 1/1 | 1 | 440 | [] | 1 | 960 | [] | 448.5 | 1e-131 |
| gi\|154146898\|emb\|CAM84136.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 448.5 | 1e-131 |
| gi\|226326777\|ref\|ZP_03802295.1\| | 1/1 | 1 | 691 | [] | 1 | 960 | [] | 448.5 | 1e-131 |
| gi\|123969314\|ref\|YP_001010172.1\| | 1/1 | 5 | 989 | .] | 1 | 960 | [] | 447.4 | 2.1e-131 |
| gi\|91070220\|gb\|ABE11140.1\| | 1/1 | 5 | 989 | .] | 1 | 960 | [] | 447.2 | 2.5e-131 |
| gi\|154146836\|emb\|CAM84105.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 446.1 | 5.4e-131 |
| gi\|154146726\|emb\|CAM84050.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 445.1 | 1.1e-130 |
| gi\|33862131\|ref\|NP_893692.1\| | 1/1 | 3 | 989 | .] | 1 | 960 | [] | 444.8 | 1.3e-130 |
| gi\|154146802\|emb\|CAM84088.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 444.7 | 1.4e-130 |
| gi\|154146886\|emb\|CAM84130.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 442.0 | 9.2e-130 |
| gi\|126697104\|ref\|YP_001091990.1\| | 1/1 | 5 | 989 | .] | 1 | 960 | [] | 441.1 | 1.7e-129 |
| gi\|154146728\|emb\|CAM84051.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 440.7 | 2.3e-129 |
| gi\|154146792\|emb\|CAM84083.1\| | 1/1 | 1 | 438 | [] | 1 | 960 | [] | 437.3 | 2.4e-128 |
| gi\|154146856\|emb\|CAM84115.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 437.0 | 2.9e-128 |
| gi\|154146868\|emb\|CAM84121.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 434.7 | 1.4e-127 |
| gi\|154146872\|emb\|CAM84123.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 432.2 | 8.1e-127 |
| gi\|86605542\|ref\|YP_474305.1\| | 1/1 | 28 | 978 | .] | 1 | 960 | [] | 430.7 | 2.3e-126 |
| gi\|72382985\|ref\|YP_292340.1\| | 1/1 | 9 | 994 | .] | 1 | 960 | [] | 430.4 | 2.9e-126 |
| gi\|124026726\|ref\|YP_001015841.1\| | 1/1 | 9 | 994 | .] | 1 | 960 | [] | 430.2 | 3.3e-126 |
| gi\|154146888\|emb\|CAM84131.1\| | 1/1 | 1 | 439 | [] | 1 | 960 | [] | 430.0 | 3.9e-126 |
| gi\|119487042\|ref\|ZP_01620914.1\| | 1/1 | 3 | 1038 | .] | 1 | 960 | [] | 428.1 | 1.4e-125 |
| gi\|75908353\|ref\|YP_322649.1\| | 1/1 | 47 | 1023 | .] | 1 | 960 | [] | 428.0 | 1.5e-125 |
| gi\|161353735\|ref\|NP_488901.2\| | 1/1 | 47 | 1026 | .] | 1 | 960 | [] | 425.8 | 6.6e-125 |
| gi\|142080\|gb\|AAA22023.1\| | 1/1 | 3 | 982 | .] | 1 | 960 | [] | 425.8 | 6.6e-125 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| gi\|124023967\|ref\|YP_001018274.1\| | 1/1 | 22 | 1002 .] | 1 | 960 [] | 425.7 | 7.1e-125 |
| gi\|154146892\|emb\|CAM84133.1\| | 1/1 | 1 | 439 [] | 1 | 960 [] | 425.6 | 7.7e-125 |
| gi\|261409477\|ref\|YP_003245718.1\| | 1/1 | 1 | 928 [] | 1 | 960 [] | 425.2 | 1e-124 |
| gi\|56751855\|ref\|YP_172556.1\| | 1/1 | 53 | 1053 .] | 1 | 960 [] | 425.0 | 1.2e-124 |
| gi\|81301061\|ref\|YP_401269.1\| | 1/1 | 17 | 1017 .] | 1 | 960 [] | 425.0 | 1.2e-124 |
| gi\|251799599\|ref\|YP_003014330.1\| | 1/1 | 8 | 936 .] | 1 | 960 [] | 424.4 | 1.9e-124 |
| gi\|154146810\|emb\|CAM84092.1\| | 1/1 | 1 | 439 [] | 1 | 960 [] | 423.8 | 2.7e-124 |
| gi\|253577082\|ref\|ZP_04854404.1\| | 1/1 | 2 | 933 .] | 1 | 960 [] | 422.9 | 5.2e-124 |
| gi\|254431278\|ref\|ZP_05044981.1\| | 1/1 | 6 | 1000 .] | 1 | 960 [] | 422.6 | 6.3e-124 |
| gi\|154146730\|emb\|CAM84052.1\| | 1/1 | 1 | 439 [] | 1 | 960 [] | 421.0 | 1.9e-123 |
| gi\|159027003\|emb\|CAO86722.1\| | 1/1 | 1 | 1018 [] | 1 | 960 [] | 420.5 | 2.7e-123 |
| gi\|260436235\|ref\|ZP_05790205.1\| | 1/1 | 19 | 1009 .] | 1 | 960 [] | 420.5 | 2.8e-123 |
| gi\|154146920\|emb\|CAM84147.1\| | 1/1 | 1 | 439 [] | 1 | 960 [] | 417.2 | 2.7e-122 |
| gi\|87300934\|ref\|ZP_01083776.1\| | 1/1 | 13 | 1002 .] | 1 | 960 [] | 417.0 | 3.1e-122 |
| gi\|166366623\|ref\|YP_001658896.1\| | 1/1 | 7 | 1018 .] | 1 | 960 [] | 416.6 | 4.1e-122 |
| gi\|154146776\|emb\|CAM84075.1\| | 1/1 | 1 | 439 [] | 1 | 960 [] | 416.4 | 4.6e-122 |
| gi\|116075789\|ref\|ZP_01473048.1\| | 1/1 | 15 | 1003 .] | 1 | 960 [] | 416.0 | 6.3e-122 |
| gi\|78211948\|ref\|YP_380727.1\| | 1/1 | 7 | 997 .] | 1 | 960 [] | 415.6 | 8.2e-122 |
| gi\|282900199\|ref\|ZP_06308155.1\| | 1/1 | 2 | 985 .] | 1 | 960 [] | 413.3 | 4e-121 |
| gi\|33241179\|ref\|NP_876121.1\| | 1/1 | 3 | 1001 .] | 1 | 960 [] | 413.2 | 4.2e-121 |
| gi\|282897196\|ref\|ZP_06305198.1\| | 1/1 | 31 | 984 .] | 1 | 960 [] | 413.2 | 4.4e-121 |
| gi\|86609298\|ref\|YP_478060.1\| | 1/1 | 28 | 978 .] | 1 | 960 [] | 412.7 | 6.2e-121 |
| gi\|87124941\|ref\|ZP_01080788.1\| | 1/1 | 1 | 979 [] | 1 | 960 [] | 408.8 | 9e-120 |
| gi\|170078023\|ref\|YP_001734661.1\| | 1/1 | 9 | 995 .] | 1 | 960 [] | 407.0 | 3.1e-119 |
| gi\|119512252\|ref\|ZP_01631340.1\| | 1/1 | 57 | 1034 .] | 1 | 960 [] | 405.8 | 7e-119 |
| gi\|148254376\|ref\|YP_001238961.1\| | 1/1 | 8 | 928 .] | 1 | 960 [] | 405.8 | 7.4e-119 |
| gi\|116072588\|ref\|ZP_01469854.1\| | 1/1 | 4 | 995 .] | 1 | 960 [] | 404.4 | 1.9e-118 |
| gi\|33863980\|ref\|NP_895540.1\| | 1/1 | 24 | 1004 .] | 1 | 960 [] | 403.3 | 3.9e-118 |
| gi\|113954224\|ref\|YP_729688.1\| | 1/1 | 18 | 1001 .] | 1 | 960 [] | 403.1 | 4.5e-118 |
| gi\|33866579\|ref\|NP_898138.1\| | 1/1 | 23 | 1010 .] | 1 | 960 [] | 401.5 | 1.4e-117 |
| gi\|113474661\|ref\|YP_720722.1\| | 1/1 | 5 | 1038 .] | 1 | 960 [] | 399.8 | 4.5e-117 |
| gi\|154146696\|emb\|CAM83983.1\| | 1/1 | 1 | 439 [] | 1 | 960 [] | 399.3 | 6.3e-117 |
| gi\|78185499\|ref\|YP_377934.1\| | 1/1 | 4 | 995 .] | 1 | 960 [] | 399.0 | 7.7e-117 |
| gi\|219847347\|ref\|YP_002461780.1\| | 1/1 | 1 | 933 [] | 1 | 960 [] | 398.8 | 8.9e-117 |
| gi\|225517756\|ref\|ZP_03764713.1\| | 1/1 | 46 | 1017 .] | 1 | 960 [] | 397.0 | 3.1e-116 |
| gi\|269961450\|ref\|ZP_06175814.1\| | 1/1 | 1 | 654 [] | 1 | 960 [] | 396.9 | 3.4e-116 |
| gi\|172038735\|ref\|YP_001805236.1\| | 1/1 | 9 | 1020 .] | 1 | 960 [] | 396.7 | 4e-116 |
| gi\|254413284\|ref\|ZP_05027055.1\| | 1/1 | 49 | 1034 .] | 1 | 960 [] | 396.6 | 4.2e-116 |
| gi\|16330985\|ref\|NP_441713.1\| | 1/1 | 9 | 1034 .] | 1 | 960 [] | 395.9 | 6.8e-116 |
| gi\|218441147\|ref\|YP_002379476.1\| | 1/1 | 2 | 1021 .] | 1 | 960 [] | 395.1 | 1.2e-115 |
| gi\|146339589\|ref\|YP_001204637.1\| | 1/1 | 11 | 933 .] | 1 | 960 [] | 394.6 | 1.6e-115 |
| gi\|209528283\|ref\|ZP_03276745.1\| | 1/1 | 2 | 1035 .] | 1 | 960 [] | 394.4 | 1.9e-115 |
| gi\|154146870\|emb\|CAM84122.1\| | 1/1 | 1 | 439 [] | 1 | 960 [] | 393.6 | 3.4e-115 |
| gi\|154146688\|emb\|CAM83979.1\| | 1/1 | 1 | 441 [] | 1 | 960 [] | 393.6 | 3.5e-115 |
| gi\|148238790\|ref\|YP_001224177.1\| | 1/1 | 22 | 1003 .] | 1 | 960 [] | 393.2 | 4.6e-115 |
| gi\|196256031\|ref\|ZP_03154569.1\| | 1/1 | 47 | 1020 .] | 1 | 960 [] | 392.4 | 7.9e-115 |
| gi\|27378066\|ref\|NP_769595.1\| | 1/1 | 8 | 932 .] | 1 | 960 [] | 391.6 | 1.4e-114 |
| gi\|88807863\|ref\|ZP_01123374.1\| | 1/1 | 11 | 991 .] | 1 | 960 [] | 391.1 | 1.9e-114 |
| gi\|74148786\|gb\|ABA00148.1\| | 1/1 | 1 | 414 [] | 1 | 960 [] | 390.9 | 2.3e-114 |
| gi\|56417897\|gb\|AAV90837.1\| | 1/1 | 9 | 995 .] | 1 | 960 [] | 390.4 | 3.1e-114 |
| gi\|154146866\|emb\|CAM84120.1\| | 1/1 | 1 | 439 [] | 1 | 960 [] | 389.5 | 5.7e-114 |
| gi\|50251800\|dbj\|BAD27731.1\| | 1/1 | 15 | 452 .] | 1 | 960 [] | 389.1 | 7.5e-114 |
| gi\|284050999\|ref\|ZP_06381209.1\| | 1/1 | 2 | 1035 .] | 1 | 960 [] | 389.0 | 8.4e-114 |
| gi\|154146684\|emb\|CAM83977.1\| | 1/1 | 1 | 439 [] | 1 | 960 [] | 388.8 | 9.4e-114 |
| gi\|154146700\|emb\|CAM83985.1\| | 1/1 | 1 | 438 [] | 1 | 960 [] | 388.0 | 1.6e-113 |
| gi\|288555580\|ref\|YP_003427515.1\| | 1/1 | 3 | 918 .] | 1 | 960 [] | 387.4 | 2.5e-113 |
| gi\|158426293\|ref\|YP_001527585.1\| | 1/1 | 4 | 931 .] | 1 | 960 [] | 386.8 | 3.8e-113 |
| gi\|154146702\|emb\|CAM83986.1\| | 1/1 | 1 | 438 [] | 1 | 960 [] | 386.6 | 4.4e-113 |
| gi\|222526644\|ref\|YP_002571115.1\| | 1/1 | 13 | 933 .] | 1 | 960 [] | 385.9 | 7.3e-113 |
| gi\|154146690\|emb\|CAM83980.1\| | 1/1 | 1 | 438 [] | 1 | 960 [] | 385.0 | 1.3e-112 |
| gi\|30248603\|ref\|NP_840673.1\| | 1/1 | 2 | 933 .] | 1 | 960 [] | 384.3 | 2.2e-112 |
| gi\|154146680\|emb\|CAM83975.1\| | 1/1 | 1 | 439 [] | 1 | 960 [] | 383.9 | 2.8e-112 |
| gi\|218288887\|ref\|ZP_03493138.1\| | 1/1 | 1 | 906 [] | 1 | 960 [] | 383.2 | 4.4e-112 |
| gi\|154146710\|emb\|CAM83990.1\| | 1/1 | 1 | 438 [] | 1 | 960 [] | 382.8 | 6.2e-112 |
| gi\|86750702\|ref\|YP_487198.1\| | 1/1 | 11 | 933 .] | 1 | 960 [] | 382.4 | 8.2e-112 |
| gi\|291612738\|ref\|YP_003522895.1\| | 1/1 | 4 | 922 .] | 1 | 960 [] | 382.3 | 8.6e-112 |
| gi\|154146714\|emb\|CAM83992.1\| | 1/1 | 1 | 438 [] | 1 | 960 [] | 382.0 | 1e-111 |
| gi\|254422587\|ref\|ZP_05036305.1\| | 1/1 | 8 | 1032 .] | 1 | 960 [] | 381.8 | 1.2e-111 |
| gi\|154146678\|emb\|CAM83974.1\| | 1/1 | 1 | 438 [] | 1 | 960 [] | 381.3 | 1.7e-111 |
| gi\|218248219\|ref\|YP_002373590.1\| | 1/1 | 10 | 1024 .] | 1 | 960 [] | 381.2 | 1.8e-111 |
| gi\|257093120\|ref\|YP_003166761.1\| | 1/1 | 1 | 918 [] | 1 | 960 [] | 381.2 | 1.8e-111 |

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|---|---|---|---|---|---|---|---|---|---|
| gi\|154146706\|emb\|CAM83988.1\| | 1/1 | 1 | 438 [] | 1 | 960 [] | 381.1 | 2e-111 |
| gi\|126658238\|ref\|ZP_01729388.1\| | 1/1 | 5 | 1016 .] | 1 | 960 [] | 380.6 | 2.8e-111 |
| gi\|154146676\|emb\|CAM83973.1\| | 1/1 | 1 | 438 [] | 1 | 960 [] | 379.5 | 6.1e-111 |
| gi\|239993151\|ref\|ZP_04713675.1\| | 1/1 | 1 | 662 [] | 1 | 960 [] | 379.0 | 8.5e-111 |
| gi\|283848041\|ref\|ZP_06365460.1\| | 1/1 | 1 | 921 [] | 1 | 960 [] | 378.4 | 1.3e-110 |
| gi\|114331035\|ref\|YP_747257.1\| | 1/1 | 2 | 933 .] | 1 | 960 [] | 377.4 | 2.6e-110 |
| gi\|163764698\|ref\|ZP_02171753.1\| | 1/1 | 1 | 922 [] | 1 | 960 [] | 377.2 | 3e-110 |
| gi\|186685513\|ref\|YP_001868709.1\| | 1/1 | 47 | 1037 .] | 1 | 960 [] | 376.9 | 3.7e-110 |
| gi\|154146698\|emb\|CAM83984.1\| | 1/1 | 1 | 440 [] | 1 | 960 [] | 375.8 | 7.6e-110 |
| gi\|115523808\|ref\|YP_780719.1\| | 1/1 | 11 | 927 .] | 1 | 960 [] | 375.8 | 7.9e-110 |
| gi\|20196766\|emb\|CAC86387.1\| | 1/1 | 1 | 398 [] | 1 | 960 [] | 374.9 | 1.4e-109 |
| gi\|163848702\|ref\|YP_001636746.1\| | 1/1 | 13 | 939 .] | 1 | 960 [] | 374.1 | 2.5e-109 |
| gi\|148656870\|ref\|YP_001277075.1\| | 1/1 | 11 | 952 .] | 1 | 960 [] | 374.0 | 2.7e-109 |
| gi\|209884453\|ref\|YP_002288310.1\| | 1/1 | 9 | 916 .] | 1 | 960 [] | 373.3 | 4.4e-109 |
| gi\|154146712\|emb\|CAM83991.1\| | 1/1 | 1 | 438 [] | 1 | 960 [] | 373.0 | 5.2e-109 |
| gi\|154146682\|emb\|CAM83976.1\| | 1/1 | 1 | 436 [] | 1 | 960 [] | 372.9 | 5.7e-109 |
| gi\|111024131\|ref\|YP_707103.1\| | 1/1 | 1 | 918 [] | 1 | 960 [] | 372.9 | 5.7e-109 |
| gi\|226366371\|ref\|YP_002784154.1\| | 1/1 | 1 | 918 [] | 1 | 960 [] | 371.9 | 1.2e-108 |
| gi\|258512100\|ref\|YP_003185534.1\| | 1/1 | 1 | 906 [] | 1 | 960 [] | 371.6 | 1.5e-108 |
| gi\|251827845\|ref\|ZP_04830919.1\| | 1/1 | 4 | 922 .] | 1 | 960 [] | 371.3 | 1.8e-108 |
| gi\|71907389\|ref\|YP_284976.1\| | 1/1 | 1 | 918 [] | 1 | 960 [] | 370.4 | 3.3e-108 |
| gi\|90423192\|ref\|YP_531562.1\| | 1/1 | 7 | 929 .] | 1 | 960 [] | 370.3 | 3.4e-108 |
| gi\|158337676\|ref\|YP_001518852.1\| | 1/1 | 4 | 1012 .] | 1 | 960 [] | 370.3 | 3.6e-108 |
| gi\|37519983\|ref\|NP_923360.1\| | 1/1 | 2 | 939 .] | 1 | 960 [] | 370.1 | 3.9e-108 |
| gi\|148243189\|ref\|YP_001228346.1\| | 1/1 | 6 | 992 .] | 1 | 960 [] | 369.1 | 8.1e-108 |
| gi\|154244275\|ref\|YP_001415233.1\| | 1/1 | 1 | 926 [] | 1 | 960 [] | 368.7 | 1.1e-107 |
| gi\|154146692\|emb\|CAM83981.1\| | 1/1 | 1 | 438 [] | 1 | 960 [] | 368.0 | 1.7e-107 |
| gi\|154146704\|emb\|CAM83987.1\| | 1/1 | 1 | 438 [] | 1 | 960 [] | 366.2 | 6e-107 |
| gi\|67923850\|ref\|ZP_00517310.1\| | 1/1 | 5 | 1016 .] | 1 | 960 [] | 365.8 | 7.7e-107 |
| gi\|154146708\|emb\|CAM83989.1\| | 1/1 | 1 | 439 [] | 1 | 960 [] | 365.8 | 8e-107 |
| gi\|154146686\|emb\|CAM83978.1\| | 1/1 | 1 | 438 [] | 1 | 960 [] | 365.1 | 1.3e-106 |
| gi\|74316648\|ref\|YP_314388.1\| | 1/1 | 1 | 939 [] | 1 | 960 [] | 364.3 | 2.3e-106 |
| gi\|262202294\|ref\|YP_003273502.1\| | 1/1 | 18 | 945 .] | 1 | 960 [] | 362.7 | 6.6e-106 |
| gi\|54023896\|ref\|YP_118138.1\| | 1/1 | 5 | 923 .] | 1 | 960 [] | 362.3 | 9e-106 |
| gi\|156742348\|ref\|YP_001432477.1\| | 1/1 | 2 | 938 .] | 1 | 960 [] | 362.0 | 1.1e-105 |
| gi\|145224288\|ref\|YP_001134966.1\| | 1/1 | 14 | 937 .] | 1 | 960 [] | 361.3 | 1.8e-105 |
| gi\|91976353\|ref\|YP_569012.1\| | 1/1 | 16 | 933 .] | 1 | 960 [] | 360.6 | 2.8e-105 |
| gi\|154146716\|emb\|CAM83993.1\| | 1/1 | 1 | 438 [] | 1 | 960 [] | 360.6 | 2.9e-105 |
| gi\|257067921\|ref\|YP_003154176.1\| | 1/1 | 24 | 942 .] | 1 | 960 [] | 359.4 | 6.6e-105 |
| gi\|118467879\|ref\|YP_887412.1\| | 1/1 | 1 | 933 [] | 1 | 960 [] | 358.5 | 1.2e-104 |
| gi\|168700529\|ref\|ZP_02732806.1\| | 1/1 | 2 | 920 .] | 1 | 960 [] | 358.2 | 1.5e-104 |
| gi\|289209281\|ref\|YP_003461347.1\| | 1/1 | 3 | 946 .] | 1 | 960 [] | 357.7 | 2.2e-104 |
| gi\|226306521\|ref\|YP_002766481.1\| | 1/1 | 3 | 925 .] | 1 | 960 [] | 357.2 | 3.1e-104 |
| gi\|283779027\|ref\|YP_003369782.1\| | 1/1 | 15 | 942 .] | 1 | 960 [] | 356.6 | 4.8e-104 |
| gi\|34495510\|ref\|NP_899725.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 356.5 | 5.1e-104 |
| gi\|108799375\|ref\|YP_639572.1\| | 1/1 | 22 | 946 .] | 1 | 960 [] | 356.3 | 5.6e-104 |
| gi\|288793906\|ref\|ZP_06399624.1\| | 1/1 | 11 | 928 .] | 1 | 960 [] | 355.7 | 8.6e-104 |
| gi\|75676463\|ref\|YP_318884.1\| | 1/1 | 3 | 928 .] | 1 | 960 [] | 355.2 | 1.2e-103 |
| gi\|154146694\|emb\|CAM83982.1\| | 1/1 | 1 | 438 [] | 1 | 960 [] | 355.1 | 1.3e-103 |
| gi\|77164288\|ref\|YP_342813.1\| | 1/1 | 14 | 957 .] | 1 | 960 [] | 352.7 | 7e-103 |
| gi\|254434134\|ref\|ZP_05047642.1\| | 1/1 | 11 | 954 .] | 1 | 960 [] | 352.7 | 7e-103 |
| gi\|220934054\|ref\|YP_002512953.1\| | 1/1 | 1 | 947 [] | 1 | 960 [] | 352.5 | 8e-103 |
| gi\|20196764\|emb\|CAC86386.1\| | 1/1 | 1 | 398 [] | 1 | 960 [] | 352.1 | 1.1e-102 |
| gi\|270502847\|ref\|ZP_06219747.1\| | 1/1 | 11 | 928 .] | 1 | 960 [] | 351.9 | 1.2e-102 |
| gi\|238062745\|ref\|ZP_04607454.1\| | 1/1 | 11 | 928 .] | 1 | 960 [] | 350.9 | 2.4e-102 |
| gi\|283843167\|ref\|ZP_06360698.1\| | 1/1 | 7 | 936 .] | 1 | 960 [] | 350.3 | 3.5e-102 |
| gi\|145593441\|ref\|YP_001157738.1\| | 1/1 | 37 | 972 .] | 1 | 960 [] | 350.2 | 3.9e-102 |
| gi\|280964818\|ref\|ZP_06239332.1\| | 1/1 | 38 | 968 .] | 1 | 960 [] | 350.0 | 4.6e-102 |
| gi\|255062470\|ref\|ZP_05314486.1\| | 1/1 | 3 | 933 .] | 1 | 960 [] | 349.6 | 6e-102 |
| gi\|15827227\|ref\|NP_301490.1\| | 1/1 | 11 | 934 .] | 1 | 960 [] | 349.3 | 7.6e-102 |
| gi\|78485862\|ref\|YP_391787.1\| | 1/1 | 7 | 929 .] | 1 | 960 [] | 346.8 | 4.2e-101 |
| gi\|192290365\|ref\|YP_001990970.1\| | 1/1 | 22 | 936 .] | 1 | 960 [] | 346.7 | 4.4e-101 |
| gi\|229493485\|ref\|ZP_04387270.1\| | 1/1 | 3 | 925 .] | 1 | 960 [] | 346.0 | 7.2e-101 |
| gi\|217969857\|ref\|YP_002355091.1\| | 1/1 | 4 | 920 .] | 1 | 960 [] | 345.8 | 8.1e-101 |
| gi\|39934841\|ref\|NP_947117.1\| | 1/1 | 22 | 936 .] | 1 | 960 [] | 345.2 | 1.3e-100 |
| gi\|85716666\|ref\|ZP_01047635.1\| | 1/1 | 45 | 973 .] | 1 | 960 [] | 345.0 | 1.4e-100 |
| gi\|2339975\|dbj\|BAA21835.1\| | 1/1 | 22 | 936 .] | 1 | 960 [] | 344.5 | 2e-100 |
| gi\|21314564\|gb\|AAM47007.1\|AF512995_1 | 1/1 | 1 | 410 [] | 1 | 960 [] | 344.0 | 2.9e-100 |
| gi\|92118201\|ref\|YP_577930.1\| | 1/1 | 20 | 929 .] | 1 | 960 [] | 342.8 | 6.4e-100 |
| gi\|111220081\|ref\|YP_710875.1\| | 1/1 | 43 | 978 .] | 1 | 960 [] | 342.2 | 1e-99 |
| gi\|229541694\|ref\|ZP_04430754.1\| | 1/1 | 3 | 919 .] | 1 | 960 [] | 339.4 | 7e-99 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| gi\|159036484\|ref\|YP_001535737.1\| | 1/1 | 11 | 928 .] | 1 | 960 [] | 338.9 | 9.6e-99 |
| gi\|256677249\|ref\|ZP_05487560.1\| | 1/1 | 2 | 913 .] | 1 | 960 [] | 337.7 | 2.3e-98 |
| gi\|68304977\|gb\|AAY89988.1\| | 1/1 | 13 | 933 .] | 1 | 960 [] | 337.5 | 2.7e-98 |
| gi\|254376064\|ref\|ZP_04991540.1\| | 1/1 | 2 | 913 .] | 1 | 960 [] | 337.1 | 3.5e-98 |
| gi\|254775781\|ref\|ZP_05217297.1\| | 1/1 | 11 | 935 .] | 1 | 960 [] | 336.9 | 4.1e-98 |
| gi\|134094240\|ref\|YP_001099315.1\| | 1/1 | 4 | 944 .] | 1 | 960 [] | 336.7 | 4.6e-98 |
| gi\|282887782\|ref\|ZP_06296361.1\| | 1/1 | 107 | 1055 .] | 1 | 960 [] | 336.2 | 6.5e-98 |
| gi\|466887\|gb\|AAA17132.1\| | 1/1 | 1 | 907 [] | 1 | 960 [] | 335.4 | 1.1e-97 |
| gi\|2499464\|sp\|Q59757.1\|CAPP_RHOMR | 1/1 | 6 | 936 .] | 1 | 960 [] | 335.2 | 1.3e-97 |
| gi\|118465776\|ref\|YP_882518.1\| | 1/1 | 11 | 935 .] | 1 | 960 [] | 334.0 | 3e-97 |
| gi\|82703804\|ref\|YP_413370.1\| | 1/1 | 10 | 937 .] | 1 | 960 [] | 333.9 | 3.2e-97 |
| gi\|289635970\|ref\|ZP_06468254.1\| | 1/1 | 142 | 1090 .] | 1 | 960 [] | 333.6 | 3.9e-97 |
| gi\|152980037\|ref\|YP_001352831.1\| | 1/1 | 16 | 959 .] | 1 | 960 [] | 332.9 | 6.4e-97 |
| gi\|120403691\|ref\|YP_953520.1\| | 1/1 | 14 | 936 .] | 1 | 960 [] | 332.6 | 7.7e-97 |
| gi\|256815765\|ref\|ZP_05540780.1\| | 1/1 | 3 | 913 .] | 1 | 960 [] | 332.2 | 1.1e-96 |
| gi\|41407267\|ref\|NP_960103.1\| | 1/1 | 11 | 935 .] | 1 | 960 [] | 331.7 | 1.5e-96 |
| gi\|268317216\|ref\|YP_003290935.1\| | 1/1 | 2 | 938 .] | 1 | 960 [] | 331.6 | 1.5e-96 |
| gi\|186476931\|ref\|YP_001858401.1\| | 1/1 | 81 | 1030 .] | 1 | 960 [] | 331.6 | 1.6e-96 |
| gi\|227980965\|ref\|ZP_04028227.1\| | 1/1 | 1 | 921 [] | 1 | 960 [] | 331.2 | 2.1e-96 |
| gi\|254818408\|ref\|ZP_05223409.1\| | 1/1 | 14 | 938 .] | 1 | 960 [] | 330.3 | 3.8e-96 |
| gi\|292492252\|ref\|YP_003527691.1\| | 1/1 | 20 | 962 .] | 1 | 960 [] | 330.3 | 4e-96 |
| gi\|20196768\|emb\|CAC86356.1\| | 1/1 | 1 | 398 [] | 1 | 960 [] | 330.2 | 4.1e-96 |
| gi\|56476048\|ref\|YP_157637.1\| | 1/1 | 65 | 990 .] | 1 | 960 [] | 330.2 | 4.2e-96 |
| gi\|256802423\|ref\|ZP_05532047.1\| | 1/1 | 3 | 910 .] | 1 | 960 [] | 329.2 | 8.4e-96 |
| gi\|91782419\|ref\|YP_557625.1\| | 1/1 | 46 | 994 .] | 1 | 960 [] | 328.4 | 1.4e-95 |
| gi\|239930781\|ref\|ZP_04687734.1\| | 1/1 | 3 | 910 .] | 1 | 960 [] | 328.3 | 1.5e-95 |
| gi\|288962822\|ref\|YP_003453116.1\| | 1/1 | 1 | 923 [] | 1 | 960 [] | 328.1 | 1.8e-95 |
| gi\|73917654\|sp\|Q5P7H5.2\|CAPP_AZOSE | 1/1 | 4 | 916 .] | 1 | 960 [] | 326.5 | 5.2e-95 |
| gi\|290580816\|ref\|YP_003485208.1\| | 1/1 | 1 | 907 [] | 1 | 960 [] | 326.3 | 6.3e-95 |
| gi\|24379180\|ref\|NP_721135.1\| | 1/1 | 1 | 907 [] | 1 | 960 [] | 325.8 | 8.5e-95 |
| gi\|25008189\|sp\|Q93MH3.1\|CAPP_CORCT | 1/1 | 1 | 919 [] | 1 | 960 [] | 325.7 | 9.4e-95 |
| gi\|262039622\|ref\|ZP_06012916.1\| | 1/1 | 7 | 929 .] | 1 | 960 [] | 325.6 | 1e-94 |
| gi\|257126840\|ref\|YP_003164954.1\| | 1/1 | 5 | 933 .] | 1 | 960 [] | 325.5 | 1e-94 |
| gi\|21221565\|ref\|NP_627344.1\| | 1/1 | 3 | 911 .] | 1 | 960 [] | 325.4 | 1.2e-94 |
| gi\|20196770\|emb\|CAC86357.1\| | 1/1 | 1 | 398 [] | 1 | 960 [] | 324.4 | 2.3e-94 |
| gi\|239981711\|ref\|ZP_04704235.1\| | 1/1 | 3 | 928 .] | 1 | 960 [] | 324.3 | 2.4e-94 |
| gi\|225165040\|ref\|ZP_03727237.1\| | 1/1 | 24 | 966 .] | 1 | 960 [] | 323.4 | 4.7e-94 |
| gi\|19552797\|ref\|NP_600799.1\| | 1/1 | 1 | 919 [] | 1 | 960 [] | 323.1 | 5.8e-94 |
| gi\|291303250\|ref\|YP_003514528.1\| | 1/1 | 1 | 914 [] | 1 | 960 [] | 322.8 | 6.9e-94 |
| gi\|183982260\|ref\|YP_001850551.1\| | 1/1 | 11 | 935 .] | 1 | 960 [] | 322.3 | 1e-93 |
| gi\|20196772\|emb\|CAC86358.1\| | 1/1 | 1 | 398 [] | 1 | 960 [] | 322.1 | 1.2e-93 |
| gi\|225874618\|ref\|YP_002756077.1\| | 1/1 | 26 | 947 .] | 1 | 960 [] | 322.0 | 1.2e-93 |
| gi\|145295706\|ref\|YP_001138527.1\| | 1/1 | 1 | 920 [] | 1 | 960 [] | 322.0 | 1.2e-93 |
| gi\|170691942\|ref\|ZP_02883106.1\| | 1/1 | 136 | 1081 .] | 1 | 960 [] | 321.7 | 1.5e-93 |
| gi\|290959806\|ref\|YP_003490988.1\| | 1/1 | 3 | 910 .] | 1 | 960 [] | 321.4 | 1.9e-93 |
| gi\|217977979\|ref\|YP_002362126.1\| | 1/1 | 1 | 923 [] | 1 | 960 [] | 321.0 | 2.4e-93 |
| gi\|29830109\|ref\|NP_824743.1\| | 1/1 | 3 | 910 .] | 1 | 960 [] | 320.0 | 4.8e-93 |
| gi\|118617446\|ref\|YP_905778.1\| | 1/1 | 11 | 935 .] | 1 | 960 [] | 319.9 | 5.2e-93 |
| gi\|253755158\|ref\|YP_003028298.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 318.1 | 1.8e-92 |
| gi\|146318181\|ref\|YP_001197893.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 318.0 | 2e-92 |
| gi\|223933776\|ref\|ZP_03625747.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 317.6 | 2.5e-92 |
| gi\|158318318\|ref\|YP_001510826.1\| | 1/1 | 34 | 981 .] | 1 | 960 [] | 317.5 | 2.7e-92 |
| gi\|254407576\|ref\|ZP_05022466.1\| | 1/1 | 3 | 913 .] | 1 | 960 [] | 317.4 | 2.9e-92 |
| gi\|272527540\|ref\|ZP_06223827.1\| | 1/1 | 125 | 1072 .] | 1 | 960 [] | 316.6 | 5.3e-92 |
| gi\|260891421\|ref\|ZP_05902684.1\| | 1/1 | 9 | 933 .] | 1 | 960 [] | 316.0 | 7.9e-92 |
| gi\|115352520\|ref\|YP_774359.1\| | 1/1 | 50 | 998 .] | 1 | 960 [] | 315.9 | 8.1e-92 |
| gi\|187923069\|ref\|YP_001894711.1\| | 1/1 | 125 | 1075 .] | 1 | 960 [] | 315.8 | 8.9e-92 |
| gi\|119962288\|ref\|YP_946565.1\| | 1/1 | 10 | 932 .] | 1 | 960 [] | 315.0 | 1.6e-91 |
| gi\|152967316\|ref\|YP_001363100.1\| | 1/1 | 28 | 954 .] | 1 | 960 [] | 313.7 | 3.8e-91 |
| gi\|172061377\|ref\|YP_001809029.1\| | 1/1 | 53 | 998 .] | 1 | 960 [] | 313.6 | 4e-91 |
| gi\|170703457\|ref\|ZP_02894226.1\| | 1/1 | 53 | 998 .] | 1 | 960 [] | 313.5 | 4.3e-91 |
| gi\|256776822\|ref\|ZP_05515285.1\| | 1/1 | 3 | 906 .] | 1 | 960 [] | 313.5 | 4.4e-91 |
| gi\|254396574\|ref\|ZP_05011634.1\| | 1/1 | 3 | 909 .] | 1 | 960 [] | 312.8 | 6.9e-91 |
| gi\|239941867\|ref\|ZP_04693804.1\| | 1/1 | 2 | 909 .] | 1 | 960 [] | 312.7 | 7.5e-91 |
| gi\|116669180\|ref\|YP_830113.1\| | 1/1 | 26 | 954 .] | 1 | 960 [] | 312.1 | 1.1e-90 |
| gi\|240173274\|ref\|ZP_04751932.1\| | 1/1 | 15 | 939 .] | 1 | 960 [] | 312.0 | 1.2e-90 |
| gi\|48689\|emb\|CAA32450.1\| | 1/1 | 1 | 919 [] | 1 | 960 [] | 312.0 | 1.3e-90 |
| gi\|20196762\|emb\|CAC86385.1\| | 1/1 | 1 | 398 [] | 1 | 960 [] | 312.0 | 1.3e-90 |
| gi\|198283666\|ref\|YP_002219987.1\| | 1/1 | 1 | 929 [] | 1 | 960 [] | 311.9 | 1.4e-90 |
| gi\|239988329\|ref\|ZP_04708993.1\| | 1/1 | 2 | 909 .] | 1 | 960 [] | 311.6 | 1.6e-90 |
| gi\|226229154\|ref\|YP_002763260.1\| | 1/1 | 5 | 933 .] | 1 | 960 [] | 311.4 | 1.9e-90 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| gi\|260457184\|ref\|ZP_05805553.1\| | 1/1 | 3 | 909 .] | 1 | 960 [] | 311.1 | 2.3e-90 |
| gi\|256767868\|ref\|ZP_05507042.1\| | 1/1 | 3 | 928 .] | 1 | 960 [] | 311.0 | 2.4e-90 |
| gi\|254388786\|ref\|ZP_05004018.1\| | 1/1 | 3 | 909 .] | 1 | 960 [] | 310.7 | 3e-90 |
| gi\|190891900\|ref\|YP_001978442.1\| | 1/1 | 1 | 926 [] | 1 | 960 [] | 310.7 | 3e-90 |
| gi\|227878424\|ref\|ZP_03996364.1\| | 1/1 | 1 | 912 [] | 1 | 960 [] | 310.4 | 3.8e-90 |
| gi\|238028333\|ref\|YP_002912564.1\| | 1/1 | 84 | 1031 .] | 1 | 960 [] | 310.3 | 4.1e-90 |
| gi\|209516095\|ref\|ZP_03264955.1\| | 1/1 | 67 | 1014 .] | 1 | 960 [] | 309.9 | 5.3e-90 |
| gi\|292833131\|gb\|EFF91480.1\| | 1/1 | 3 | 909 .] | 1 | 960 [] | 309.6 | 6.6e-90 |
| gi\|119897283\|ref\|YP_932496.1\| | 1/1 | 1 | 917 [] | 1 | 960 [] | 309.5 | 6.9e-90 |
| gi\|254671222\|emb\|CBA08427.1\| | 1/1 | 18 | 917 .] | 1 | 960 [] | 309.4 | 7.3e-90 |
| gi\|254384995\|ref\|ZP_05000330.1\| | 1/1 | 3 | 920 .] | 1 | 960 [] | 309.4 | 7.4e-90 |
| gi\|221065752\|ref\|ZP_03541857.1\| | 1/1 | 9 | 949 .] | 1 | 960 [] | 309.1 | 9.3e-90 |
| gi\|167585804\|ref\|ZP_02378192.1\| | 1/1 | 59 | 1007 .] | 1 | 960 [] | 309.1 | 9.4e-90 |
| gi\|225858881\|ref\|YP_002740391.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 308.9 | 1e-89 |
| gi\|220911519\|ref\|YP_002486828.1\| | 1/1 | 11 | 937 .] | 1 | 960 [] | 308.6 | 1.3e-89 |
| gi\|168494501\|ref\|ZP_02718644.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 308.6 | 1.3e-89 |
| gi\|213965583\|ref\|ZP_03393777.1\| | 1/1 | 14 | 942 .] | 1 | 960 [] | 308.5 | 1.4e-89 |
| gi\|241889879\|ref\|ZP_04777177.1\| | 1/1 | 3 | 896 .] | 1 | 960 [] | 308.5 | 1.4e-89 |
| gi\|161524047\|ref\|YP_001579059.1\| | 1/1 | 57 | 1004 .] | 1 | 960 [] | 307.2 | 3.5e-89 |
| gi\|221211566\|ref\|ZP_03584545.1\| | 1/1 | 57 | 1004 .] | 1 | 960 [] | 307.1 | 3.8e-89 |
| gi\|254491458\|ref\|ZP_05104637.1\| | 1/1 | 1 | 947 [] | 1 | 960 [] | 306.9 | 4.2e-89 |
| gi\|15903018\|ref\|NP_358568.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 306.8 | 4.4e-89 |
| gi\|282865456\|ref\|ZP_06274507.1\| | 1/1 | 3 | 909 .] | 1 | 960 [] | 306.6 | 5.2e-89 |
| gi\|76787926\|ref\|YP_329507.1\| | 1/1 | 3 | 931 .] | 1 | 960 [] | 306.2 | 6.9e-89 |
| gi\|148989111\|ref\|ZP_01820501.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 306.1 | 7.5e-89 |
| gi\|262046224\|ref\|ZP_06019187.1\| | 1/1 | 1 | 912 [] | 1 | 960 [] | 305.9 | 8.7e-89 |
| gi\|225861034\|ref\|YP_002742543.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 305.6 | 1.1e-88 |
| gi\|149006260\|ref\|ZP_01829972.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 305.5 | 1.1e-88 |
| gi\|269214612\|ref\|ZP_06158686.1\| | 1/1 | 19 | 918 .] | 1 | 960 [] | 305.3 | 1.3e-88 |
| gi\|15900937\|ref\|NP_345541.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 305.3 | 1.3e-88 |
| gi\|149003977\|ref\|ZP_01828785.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 305.3 | 1.3e-88 |
| gi\|148994184\|ref\|ZP_01823499.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 305.2 | 1.3e-88 |
| gi\|264679666\|ref\|YP_003279573.1\| | 1/1 | 17 | 949 .] | 1 | 960 [] | 305.2 | 1.4e-88 |
| gi\|284044871\|ref\|YP_003395211.1\| | 1/1 | 5 | 881 .] | 1 | 960 [] | 305.2 | 1.4e-88 |
| gi\|293381352\|ref\|ZP_06627354.1\| | 1/1 | 1 | 912 [] | 1 | 960 [] | 305.1 | 1.5e-88 |
| gi\|168487465\|ref\|ZP_02711973.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 305.0 | 1.6e-88 |
| gi\|221199352\|ref\|ZP_03572396.1\| | 1/1 | 57 | 1004 .] | 1 | 960 [] | 304.9 | 1.7e-88 |
| gi\|256843881\|ref\|ZP_05549368.1\| | 1/1 | 1 | 912 [] | 1 | 960 [] | 304.8 | 1.8e-88 |
| gi\|22536923\|ref\|NP_687774.1\| | 1/1 | 3 | 931 .] | 1 | 960 [] | 304.8 | 1.8e-88 |
| gi\|148985039\|ref\|ZP_01818282.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 304.8 | 1.9e-88 |
| gi\|168576207\|ref\|ZP_02722101.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 304.4 | 2.4e-88 |
| gi\|169833797\|ref\|YP_001694494.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 303.9 | 3.4e-88 |
| gi\|206560970\|ref\|YP_002231735.1\| | 1/1 | 38 | 989 .] | 1 | 960 [] | 303.7 | 3.9e-88 |
| gi\|149925330\|ref\|ZP_01913594.1\| | 1/1 | 1 | 919 [] | 1 | 960 [] | 303.4 | 4.7e-88 |
| gi\|258654566\|ref\|YP_003203722.1\| | 1/1 | 25 | 945 .] | 1 | 960 [] | 303.4 | 4.8e-88 |
| gi\|78067222\|ref\|YP_369991.1\| | 1/1 | 58 | 1008 .] | 1 | 960 [] | 302.4 | 9.8e-88 |
| gi\|116690446\|ref\|YP_836069.1\| | 1/1 | 59 | 1009 .] | 1 | 960 [] | 302.2 | 1.1e-87 |
| gi\|107023363\|ref\|YP_621690.1\| | 1/1 | 44 | 994 .] | 1 | 960 [] | 302.2 | 1.1e-87 |
| gi\|237745485\|ref\|ZP_04575965.1\| | 1/1 | 9 | 957 .] | 1 | 960 [] | 302.0 | 1.3e-87 |
| gi\|144899948\|emb\|CAM76812.1\| | 1/1 | 6 | 933 .] | 1 | 960 [] | 302.0 | 1.3e-87 |
| gi\|225856712\|ref\|YP_002738223.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 301.7 | 1.6e-87 |
| gi\|222152768\|ref\|YP_002561945.1\| | 1/1 | 1 | 902 [] | 1 | 960 [] | 301.6 | 1.7e-87 |
| gi\|25028259\|ref\|NP_738313.1\| | 1/1 | 2 | 919 .] | 1 | 960 [] | 301.5 | 1.8e-87 |
| gi\|195977846\|ref\|YP_002123090.1\| | 1/1 | 1 | 927 [] | 1 | 960 [] | 301.2 | 2.2e-87 |
| gi\|189219750\|ref\|YP_001940391.1\| | 1/1 | 2 | 931 .] | 1 | 960 [] | 301.1 | 2.3e-87 |
| gi\|293365250\|ref\|ZP_06611967.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 301.1 | 2.3e-87 |
| gi\|77409086\|ref\|ZP_00785802.1\| | 1/1 | 3 | 931 .] | 1 | 960 [] | 300.9 | 2.7e-87 |
| gi\|194397283\|ref\|YP_002037699.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 300.4 | 3.8e-87 |
| gi\|224826000\|ref\|ZP_03699103.1\| | 1/1 | 1 | 901 [] | 1 | 960 [] | 300.2 | 4.5e-87 |
| gi\|76810271\|ref\|YP_332639.1\| | 1/1 | 128 | 1085 .] | 1 | 960 [] | 300.1 | 4.8e-87 |
| gi\|254261244\|ref\|ZP_04952298.1\| | 1/1 | 37 | 994 .] | 1 | 960 [] | 300.1 | 4.8e-87 |
| gi\|53718655\|ref\|YP_107641.1\| | 1/1 | 37 | 994 .] | 1 | 960 [] | 300.0 | 5.2e-87 |
| gi\|126440608\|ref\|YP_001058119.1\| | 1/1 | 37 | 994 .] | 1 | 960 [] | 300.0 | 5.2e-87 |
| gi\|126451534\|ref\|YP_001065355.1\| | 1/1 | 67 | 1024 .] | 1 | 960 [] | 300.0 | 5.2e-87 |
| gi\|167003501\|ref\|ZP_02269287.1\| | 1/1 | 37 | 994 .] | 1 | 960 [] | 299.9 | 5.6e-87 |
| gi\|260101538\|ref\|ZP_05751775.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 299.9 | 5.6e-87 |
| gi\|160897676\|ref\|YP_001563258.1\| | 1/1 | 10 | 949 .] | 1 | 960 [] | 299.8 | 5.7e-87 |
| gi\|89143166\|emb\|CAJ44471.1\| | 1/1 | 1 | 940 [] | 1 | 960 [] | 299.8 | 5.9e-87 |
| gi\|218767367\|ref\|YP_002341879.1\| | 1/1 | 1 | 900 [] | 1 | 960 [] | 299.7 | 6.4e-87 |
| gi\|11267798\|pir\|\|D81953 | 1/1 | 18 | 917 .] | 1 | 960 [] | 299.7 | 6.4e-87 |
| gi\|222111549\|ref\|YP_002553813.1\| | 1/1 | 7 | 949 .] | 1 | 960 [] | 299.6 | 6.6e-87 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| gi\|170733766\|ref\|YP_001765713.1\| | 1/1 | 59 | 1009 .] | 1 | 960 [] | 299.5 | 7.2e-87 |
| gi\|77413069\|ref\|ZP_00789270.1\| | 1/1 | 3 | 931 .] | 1 | 960 [] | 299.4 | 7.8e-87 |
| gi\|254247510\|ref\|ZP_04940831.1\| | 1/1 | 59 | 1009 .] | 1 | 960 [] | 299.3 | 8e-87 |
| gi\|282873614\|ref\|ZP_06282580.1\| | 1/1 | 2 | 909 .] | 1 | 960 [] | 299.1 | 9.7e-87 |
| gi\|182438172\|ref\|YP_001825891.1\| | 1/1 | 2 | 909 .] | 1 | 960 [] | 299.0 | 1e-86 |
| gi\|258594352\|ref\|ZP_05709164.1\| | 1/1 | 4 | 971 .] | 1 | 960 [] | 298.8 | 1.2e-86 |
| gi\|167561969\|ref\|ZP_02354885.1\| | 1/1 | 4 | 952 .] | 1 | 960 [] | 298.7 | 1.3e-86 |
| gi\|167618301\|ref\|ZP_02386932.1\| | 1/1 | 40 | 994 .] | 1 | 960 [] | 298.6 | 1.3e-86 |
| gi\|167580195\|ref\|ZP_02373069.1\| | 1/1 | 40 | 994 .] | 1 | 960 [] | 298.5 | 1.4e-86 |
| gi\|225870168\|ref\|YP_002746115.1\| | 1/1 | 1 | 927 [] | 1 | 960 [] | 298.4 | 1.6e-86 |
| gi\|15677883\|ref\|NP_275051.1\| | 1/1 | 1 | 900 [] | 1 | 960 [] | 298.2 | 1.7e-86 |
| gi\|254251704\|ref\|ZP_04945022.1\| | 1/1 | 61 | 1012 .] | 1 | 960 [] | 298.2 | 1.8e-86 |
| gi\|121595210\|ref\|YP_987106.1\| | 1/1 | 7 | 949 .] | 1 | 960 [] | 298.0 | 2e-86 |
| gi\|134296608\|ref\|YP_001120343.1\| | 1/1 | 52 | 997 .] | 1 | 960 [] | 298.0 | 2.1e-86 |
| gi\|251782035\|ref\|YP_002996337.1\| | 1/1 | 22 | 943 .] | 1 | 960 [] | 297.9 | 2.2e-86 |
| gi\|161507563\|ref\|YP_001577517.1\| | 1/1 | 1 | 912 [] | 1 | 960 [] | 297.6 | 2.7e-86 |
| gi\|254181387\|ref\|ZP_04887984.1\| | 1/1 | 53 | 994 .] | 1 | 960 [] | 297.1 | 3.8e-86 |
| gi\|167918035\|ref\|ZP_02505126.1\| | 1/1 | 53 | 994 .] | 1 | 960 [] | 297.1 | 3.8e-86 |
| gi\|241759416\|ref\|ZP_04757520.1\| | 1/1 | 1 | 900 [] | 1 | 960 [] | 296.9 | 4.4e-86 |
| gi\|225868820\|ref\|YP_002744768.1\| | 1/1 | 1 | 927 [] | 1 | 960 [] | 296.6 | 5.4e-86 |
| gi\|83719610\|ref\|YP_441427.1\| | 1/1 | 134 | 1088 .] | 1 | 960 [] | 296.1 | 7.5e-86 |
| gi\|116627590\|ref\|YP_820209.1\| | 1/1 | 1 | 940 [] | 1 | 960 [] | 296.1 | 7.8e-86 |
| gi\|261379952\|ref\|ZP_05984525.1\| | 1/1 | 1 | 900 [] | 1 | 960 [] | 295.4 | 1.2e-85 |
| gi\|239814380\|ref\|YP_002943290.1\| | 1/1 | 1 | 947 [] | 1 | 960 [] | 295.3 | 1.3e-85 |
| gi\|254190787\|ref\|ZP_04897294.1\| | 1/1 | 37 | 994 .] | 1 | 960 [] | 294.5 | 2.3e-85 |
| gi\|226194359\|ref\|ZP_03789957.1\| | 1/1 | 67 | 1024 .] | 1 | 960 [] | 294.5 | 2.3e-85 |
| gi\|55820784\|ref\|YP_139226.1\| | 1/1 | 1 | 940 [] | 1 | 960 [] | 294.5 | 2.3e-85 |
| gi\|288905708\|ref\|YP_003430930.1\| | 1/1 | 1 | 941 [] | 1 | 960 [] | 294.4 | 2.5e-85 |
| gi\|237747682\|ref\|ZP_04578162.1\| | 1/1 | 16 | 970 .] | 1 | 960 [] | 294.0 | 3.3e-85 |
| gi\|284989422\|ref\|YP_003407976.1\| | 1/1 | 5 | 939 .] | 1 | 960 [] | 293.2 | 5.8e-85 |
| gi\|288942679\|ref\|YP_003444919.1\| | 1/1 | 11 | 930 .] | 1 | 960 [] | 293.1 | 5.9e-85 |
| gi\|240114073\|ref\|ZP_04728563.1\| | 1/1 | 1 | 900 [] | 1 | 960 [] | 293.0 | 6.5e-85 |
| gi\|268600141\|ref\|ZP_06134308.1\| | 1/1 | 15 | 914 .] | 1 | 960 [] | 293.0 | 6.5e-85 |
| gi\|161869130\|ref\|YP_001598297.1\| | 1/1 | 18 | 917 .] | 1 | 960 [] | 292.9 | 7e-85 |
| gi\|261393385\|emb\|CAX51021.1\| | 1/1 | 1 | 900 [] | 1 | 960 [] | 292.6 | 8.5e-85 |
| gi\|288918904\|ref\|ZP_06413247.1\| | 1/1 | 1 | 944 [] | 1 | 960 [] | 292.5 | 9.3e-85 |
| gi\|240122526\|ref\|ZP_04735482.1\| | 1/1 | 1 | 900 [] | 1 | 960 [] | 292.3 | 1e-84 |
| gi\|268681114\|ref\|ZP_06147976.1\| | 1/1 | 18 | 917 .] | 1 | 960 [] | 292.3 | 1e-84 |
| gi\|240081793\|ref\|ZP_04726336.1\| | 1/1 | 1 | 900 [] | 1 | 960 [] | 292.3 | 1e-84 |
| gi\|268597893\|ref\|ZP_06132060.1\| | 1/1 | 18 | 917 .] | 1 | 960 [] | 292.3 | 1e-84 |
| gi\|291044869\|ref\|ZP_06570578.1\| | 1/1 | 21 | 920 .] | 1 | 960 [] | 292.3 | 1e-84 |
| gi\|121635719\|ref\|YP_975964.1\| | 1/1 | 1 | 900 [] | 1 | 960 [] | 292.3 | 1.1e-84 |
| gi\|289167828\|ref\|YP_003446097.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 292.1 | 1.2e-84 |
| gi\|167569217\|ref\|ZP_02362091.1\| | 1/1 | 4 | 952 .] | 1 | 960 [] | 291.1 | 2.5e-84 |
| gi\|171780080\|ref\|ZP_02920984.1\| | 1/1 | 3 | 943 .] | 1 | 960 [] | 290.9 | 2.9e-84 |
| gi\|121605982\|ref\|YP_983311.1\| | 1/1 | 38 | 982 .] | 1 | 960 [] | 290.8 | 2.9e-84 |
| gi\|270292890\|ref\|ZP_06199101.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 290.7 | 3.1e-84 |
| gi\|197104620\|ref\|YP_002129997.1\| | 1/1 | 4 | 898 .] | 1 | 960 [] | 290.7 | 3.1e-84 |
| gi\|55822687\|ref\|YP_141128.1\| | 1/1 | 1 | 940 [] | 1 | 960 [] | 290.7 | 3.2e-84 |
| gi\|116513617\|ref\|YP_812523.1\| | 1/1 | 50 | 967 .] | 1 | 960 [] | 290.4 | 4e-84 |
| gi\|194690202\|gb\|ACF79185.1\| | 1/1 | 1 | 383 [] | 1 | 960 [] | 289.5 | 7.4e-84 |
| gi\|83814357\|ref\|YP_444246.1\| | 1/1 | 6 | 957 .] | 1 | 960 [] | 289.4 | 7.8e-84 |
| gi\|161572971\|ref\|YP_209040.2\| | 1/1 | 1 | 900 [] | 1 | 960 [] | 289.3 | 8.5e-84 |
| gi\|268602565\|ref\|ZP_06136732.1\| | 1/1 | 18 | 917 .] | 1 | 960 [] | 289.3 | 8.5e-84 |
| gi\|194099706\|ref\|YP_002002841.1\| | 1/1 | 24 | 923 .] | 1 | 960 [] | 289.3 | 8.5e-84 |
| gi\|293397945\|ref\|ZP_06642151.1\| | 1/1 | 21 | 920 .] | 1 | 960 [] | 289.3 | 8.5e-84 |
| gi\|254492745\|ref\|ZP_05105916.1\| | 1/1 | 18 | 917 .] | 1 | 960 [] | 289.1 | 9.5e-84 |
| gi\|239999896\|ref\|ZP_04719820.1\| | 1/1 | 1 | 900 [] | 1 | 960 [] | 289.1 | 9.5e-84 |
| gi\|94265456\|ref\|ZP_01289207.1\| | 1/1 | 12 | 947 .] | 1 | 960 [] | 288.8 | 1.2e-83 |
| gi\|225021380\|ref\|ZP_03710572.1\| | 1/1 | 1 | 922 [] | 1 | 960 [] | 288.3 | 1.7e-83 |
| gi\|269213946\|ref\|ZP_05983221.2\| | 1/1 | 19 | 918 .] | 1 | 960 [] | 287.7 | 2.6e-83 |
| gi\|254804129\|ref\|YP_003082350.1\| | 1/1 | 18 | 917 .] | 1 | 960 [] | 286.8 | 4.8e-83 |
| gi\|240015599\|ref\|ZP_04722139.1\| | 1/1 | 1 | 904 [] | 1 | 960 [] | 286.3 | 6.7e-83 |
| gi\|20196784\|emb\|CAC86364.1\| | 1/1 | 1 | 396 [] | 1 | 960 [] | 285.2 | 1.5e-82 |
| gi\|241766972\|ref\|ZP_04764768.1\| | 1/1 | 2 | 929 .] | 1 | 960 [] | 284.6 | 2.2e-82 |
| gi\|270494458\|ref\|ZP_06211504.1\| | 1/1 | 11 | 951 .] | 1 | 960 [] | 283.2 | 5.6e-82 |
| gi\|252126365\|ref\|ZP_04836407.1\| | 1/1 | 1 | 922 [] | 1 | 960 [] | 283.1 | 6.3e-82 |
| gi\|262196990\|ref\|YP_003268199.1\| | 1/1 | 1 | 907 [] | 1 | 960 [] | 282.9 | 7.2e-82 |
| gi\|104773626\|ref\|YP_618606.1\| | 1/1 | 1 | 909 [] | 1 | 960 [] | 280.8 | 3.1e-81 |
| gi\|20196776\|emb\|CAC86360.1\| | 1/1 | 1 | 387 [] | 1 | 960 [] | 280.1 | 5e-81 |
| gi\|227881566\|ref\|ZP_03999428.1\| | 1/1 | 1 | 897 [] | 1 | 960 [] | 280.0 | 5.3e-81 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| gi\|256389410\|ref\|YP_003110974.1\| | 1/1 | 20 | 940 | .] | 1 | 960 | [] | 279.7 | 6.6e-81 |
| gi\|94264993\|ref\|ZP_01288763.1\| | 1/1 | 18 | 947 | .] | 1 | 960 | [] | 278.9 | 1.1e-80 |
| gi\|56807908\|ref\|ZP_00365735.1\| | 1/1 | 10 | 932 | .] | 1 | 960 | [] | 277.9 | 2.2e-80 |
| gi\|94990008\|ref\|YP_598108.1\| | 1/1 | 15 | 937 | .] | 1 | 960 | [] | 277.7 | 2.6e-80 |
| gi\|94988126\|ref\|YP_596227.1\| | 1/1 | 15 | 937 | .] | 1 | 960 | [] | 277.7 | 2.6e-80 |
| gi\|71903150\|ref\|YP_279953.1\| | 1/1 | 15 | 937 | .] | 1 | 960 | [] | 277.6 | 2.8e-80 |
| gi\|197103239\|ref\|YP_002128617.1\| | 1/1 | 1 | 888 | [] | 1 | 960 | [] | 277.0 | 4.2e-80 |
| gi\|209559064\|ref\|YP_002285536.1\| | 1/1 | 10 | 932 | .] | 1 | 960 | [] | 276.8 | 4.9e-80 |
| gi\|293168120\|ref\|ZP_06606869.1\| | 1/1 | 7 | 930 | .] | 1 | 960 | [] | 276.2 | 7.5e-80 |
| gi\|21909966\|ref\|NP_664234.1\| | 1/1 | 10 | 932 | .] | 1 | 960 | [] | 276.1 | 8.1e-80 |
| gi\|50913872\|ref\|YP_059844.1\| | 1/1 | 15 | 937 | .] | 1 | 960 | [] | 275.9 | 9.3e-80 |
| gi\|120610680\|ref\|YP_970358.1\| | 1/1 | 11 | 951 | .] | 1 | 960 | [] | 275.8 | 9.7e-80 |
| gi\|261365408\|ref\|ZP_05978291.1\| | 1/1 | 1 | 900 | [] | 1 | 960 | [] | 275.6 | 1.1e-79 |
| gi\|16588669\|gb\|AAL26863.1\|AF314923_1 | 1/1 | 1 | 391 | [] | 1 | 960 | [] | 275.1 | 1.6e-79 |
| gi\|221633046\|ref\|YP_002522271.1\| | 1/1 | 6 | 928 | .] | 1 | 960 | [] | 275.0 | 1.7e-79 |
| gi\|94993920\|ref\|YP_602018.1\| | 1/1 | 15 | 937 | .] | 1 | 960 | [] | 274.6 | 2.3e-79 |
| gi\|94970716\|ref\|YP_592764.1\| | 1/1 | 13 | 900 | .] | 1 | 960 | [] | 274.4 | 2.5e-79 |
| gi\|68536075\|ref\|YP_250780.1\| | 1/1 | 10 | 948 | .] | 1 | 960 | [] | 274.0 | 3.5e-79 |
| gi\|73540405\|ref\|YP_294925.1\| | 1/1 | 52 | 1006 | .] | 1 | 960 | [] | 273.9 | 3.7e-79 |
| gi\|91789513\|ref\|YP_550465.1\| | 1/1 | 18 | 970 | .] | 1 | 960 | [] | 273.8 | 3.8e-79 |
| gi\|73920189\|sp\|Q8K873.2\|CAPP_STRP3 | 1/1 | 1 | 920 | [] | 1 | 960 | [] | 273.8 | 4e-79 |
| gi\|260578770\|ref\|ZP_05846677.1\| | 1/1 | 10 | 948 | .] | 1 | 960 | [] | 273.6 | 4.5e-79 |
| gi\|139474183\|ref\|YP_001128899.1\| | 1/1 | 1 | 920 | [] | 1 | 960 | [] | 273.6 | 4.5e-79 |
| gi\|255067797\|ref\|ZP_05319652.1\| | 1/1 | 1 | 900 | [] | 1 | 960 | [] | 272.7 | 8.2e-79 |
| gi\|229824131\|ref\|ZP_04450200.1\| | 1/1 | 2 | 895 | .] | 1 | 960 | [] | 272.2 | 1.2e-78 |
| gi\|257455375\|ref\|ZP_05620610.1\| | 1/1 | 31 | 956 | .] | 1 | 960 | [] | 271.0 | 2.7e-78 |
| gi\|19745716\|ref\|NP_606852.1\| | 1/1 | 1 | 920 | [] | 1 | 960 | [] | 270.6 | 3.7e-78 |
| gi\|71910318\|ref\|YP_281868.1\| | 1/1 | 15 | 937 | .] | 1 | 960 | [] | 269.7 | 6.7e-78 |
| gi\|241663753\|ref\|YP_002982113.1\| | 1/1 | 56 | 1002 | .] | 1 | 960 | [] | 269.5 | 7.8e-78 |
| gi\|15674689\|ref\|NP_268863.1\| | 1/1 | 1 | 920 | [] | 1 | 960 | [] | 269.4 | 8.2e-78 |
| gi\|225024256\|ref\|ZP_03713448.1\| | 1/1 | 1 | 902 | [] | 1 | 960 | [] | 269.4 | 8.3e-78 |
| gi\|121608028\|ref\|YP_995835.1\| | 1/1 | 1 | 930 | [] | 1 | 960 | [] | 269.2 | 9.4e-78 |
| gi\|171057452\|ref\|YP_001789801.1\| | 1/1 | 15 | 950 | .] | 1 | 960 | [] | 269.1 | 9.9e-78 |
| gi\|113868876\|ref\|YP_727365.1\| | 1/1 | 65 | 1012 | .] | 1 | 960 | [] | 268.7 | 1.3e-77 |
| gi\|283821743\|ref\|ZP_06348554.1\| | 1/1 | 1 | 919 | [] | 1 | 960 | [] | 267.9 | 2.3e-77 |
| gi\|228476844\|ref\|ZP_04061489.1\| | 1/1 | 1 | 940 | [] | 1 | 960 | [] | 267.8 | 2.5e-77 |
| gi\|227890073\|ref\|ZP_04007878.1\| | 1/1 | 2 | 912 | .] | 1 | 960 | [] | 267.3 | 3.7e-77 |
| gi\|227832350\|ref\|YP_002834057.1\| | 1/1 | 1 | 884 | [] | 1 | 960 | [] | 266.8 | 4.9e-77 |
| gi\|261855598\|ref\|YP_003262881.1\| | 1/1 | 3 | 938 | .] | 1 | 960 | [] | 266.4 | 6.7e-77 |
| gi\|194290491\|ref\|YP_002006398.1\| | 1/1 | 55 | 1009 | .] | 1 | 960 | [] | 265.6 | 1.1e-76 |
| gi\|255021660\|ref\|ZP_05293702.1\| | 1/1 | 1 | 930 | [] | 1 | 960 | [] | 265.4 | 1.3e-76 |
| gi\|125718332\|ref\|YP_001035465.1\| | 1/1 | 1 | 948 | [] | 1 | 960 | [] | 265.4 | 1.3e-76 |
| gi\|227904011\|ref\|ZP_04021816.1\| | 1/1 | 1 | 912 | [] | 1 | 960 | [] | 265.3 | 1.4e-76 |
| gi\|20196778\|emb\|CAC86361.1\| | 1/1 | 1 | 383 | [] | 1 | 960 | [] | 265.0 | 1.8e-76 |
| gi\|187929645\|ref\|YP_001900132.1\| | 1/1 | 56 | 1001 | .] | 1 | 960 | [] | 263.6 | 4.6e-76 |
| gi\|83749206\|ref\|ZP_00946208.1\| | 1/1 | 67 | 1020 | .] | 1 | 960 | [] | 263.2 | 5.9e-76 |
| gi\|256759173\|ref\|ZP_05499837.1\| | 1/1 | 1 | 936 | [] | 1 | 960 | [] | 262.7 | 8.5e-76 |
| gi\|116629723\|ref\|YP_814895.1\| | 1/1 | 14 | 929 | .] | 1 | 960 | [] | 262.4 | 1.1e-75 |
| gi\|268319407\|ref\|YP_003293063.1\| | 1/1 | 2 | 912 | .] | 1 | 960 | [] | 262.0 | 1.4e-75 |
| gi\|227505333\|ref\|ZP_03935382.1\| | 1/1 | 1 | 892 | [] | 1 | 960 | [] | 261.7 | 1.7e-75 |
| gi\|269123480\|ref\|YP_003306057.1\| | 1/1 | 1 | 884 | [] | 1 | 960 | [] | 261.5 | 1.9e-75 |
| gi\|58337382\|ref\|YP_193967.1\| | 1/1 | 1 | 912 | [] | 1 | 960 | [] | 261.5 | 2e-75 |
| gi\|78221527\|ref\|YP_383274.1\| | 1/1 | 10 | 931 | .] | 1 | 960 | [] | 261.2 | 2.4e-75 |
| gi\|238020526\|ref\|ZP_04600952.1\| | 1/1 | 1 | 900 | [] | 1 | 960 | [] | 261.1 | 2.6e-75 |
| gi\|148652373\|ref\|YP_001279466.1\| | 1/1 | 3 | 932 | .] | 1 | 960 | [] | 260.8 | 3.3e-75 |
| gi\|226819197\|ref\|ZP_03808316.1\| | 1/1 | 2 | 912 | .] | 1 | 960 | [] | 259.5 | 7.9e-75 |
| gi\|222055605\|ref\|YP_002537967.1\| | 1/1 | 35 | 931 | .] | 1 | 960 | [] | 258.8 | 1.3e-74 |
| gi\|17547077\|ref\|NP_520479.1\| | 1/1 | 39 | 985 | .] | 1 | 960 | [] | 258.3 | 1.8e-74 |
| gi\|157149951\|ref\|YP_001450059.1\| | 1/1 | 4 | 948 | .] | 1 | 960 | [] | 257.5 | 3.3e-74 |
| gi\|94311682\|ref\|YP_584892.1\| | 1/1 | 60 | 1009 | .] | 1 | 960 | [] | 256.3 | 7.4e-74 |
| gi\|93006646\|ref\|YP_581083.1\| | 1/1 | 2 | 926 | .] | 1 | 960 | [] | 256.2 | 7.9e-74 |
| gi\|227521038\|ref\|ZP_03951087.1\| | 1/1 | 9 | 924 | .] | 1 | 960 | [] | 255.6 | 1.1e-73 |
| gi\|238853373\|ref\|ZP_04643752.1\| | 1/1 | 2 | 912 | .] | 1 | 960 | [] | 255.6 | 1.2e-73 |
| gi\|292656740\|ref\|YP_003536637.1\| | 1/1 | 1 | 897 | [] | 1 | 960 | [] | 255.0 | 1.7e-73 |
| gi\|227893638\|ref\|ZP_04011443.1\| | 1/1 | 1 | 906 | [] | 1 | 960 | [] | 254.8 | 2e-73 |
| gi\|292492516\|ref\|YP_003527955.1\| | 1/1 | 8 | 932 | .] | 1 | 960 | [] | 254.7 | 2.3e-73 |
| gi\|182677139\|ref\|YP_001831285.1\| | 1/1 | 3 | 932 | .] | 1 | 960 | [] | 254.5 | 2.6e-73 |
| gi\|262282657\|ref\|ZP_06060425.1\| | 1/1 | 1 | 948 | [] | 1 | 960 | [] | 254.4 | 2.8e-73 |
| gi\|229538486\|ref\|ZP_04427622.1\| | 1/1 | 3 | 931 | .] | 1 | 960 | [] | 253.9 | 3.7e-73 |
| gi\|226355772\|ref\|YP_002785512.1\| | 1/1 | 2 | 828 | .] | 1 | 960 | [] | 253.3 | 5.9e-73 |
| gi\|271962867\|ref\|YP_003337063.1\| | 1/1 | 2 | 879 | .] | 1 | 960 | [] | 252.6 | 9.4e-73 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| gi\|291295381\|ref\|YP_003506779.1\| | 1/1 | 13 | 892 .] | 1 | 960 [] | 252.0 | 1.4e-72 |
| gi\|227506616\|ref\|ZP_03936665.1\| | 1/1 | 37 | 918 .] | 1 | 960 [] | 251.4 | 2.2e-72 |
| gi\|71065696\|ref\|YP_264423.1\| | 1/1 | 2 | 926 .] | 1 | 960 [] | 249.6 | 7.6e-72 |
| gi\|258545813\|ref\|ZP_05706047.1\| | 1/1 | 11 | 924 .] | 1 | 960 [] | 249.5 | 8.2e-72 |
| gi\|20196788\|emb\|CAC86366.1\| | 1/1 | 1 | 396 [] | 1 | 960 [] | 249.0 | 1.1e-71 |
| gi\|283782535\|ref\|YP_003373289.1\| | 1/1 | 37 | 918 .] | 1 | 960 [] | 248.0 | 2.4e-71 |
| gi\|38233712\|ref\|NP_939479.1\| | 1/1 | 1 | 902 [] | 1 | 960 [] | 247.7 | 2.9e-71 |
| gi\|269921664\|ref\|ZP_06170573.1\| | 1/1 | 1 | 902 [] | 1 | 960 [] | 246.8 | 5.3e-71 |
| gi\|226942050\|ref\|YP_002797124.1\| | 1/1 | 4 | 907 .] | 1 | 960 [] | 244.6 | 2.4e-70 |
| gi\|1213341\|dbj\|BAA05398.1\| | 1/1 | 1 | 384 [] | 1 | 960 [] | 244.2 | 3.1e-70 |
| gi\|1213343\|dbj\|BAA05396.1\| | 1/1 | 1 | 384 [] | 1 | 960 [] | 243.7 | 4.6e-70 |
| gi\|253999144\|ref\|YP_003051207.1\| | 1/1 | 20 | 952 .] | 1 | 960 [] | 242.6 | 9.5e-70 |
| gi\|110669081\|ref\|YP_658892.1\| | 1/1 | 1 | 897 [] | 1 | 960 [] | 242.5 | 1e-69 |
| gi\|269128325\|ref\|YP_003301695.1\| | 1/1 | 8 | 892 .] | 1 | 960 [] | 241.4 | 2.2e-69 |
| gi\|284167583\|ref\|YP_003405861.1\| | 1/1 | 1 | 896 [] | 1 | 960 [] | 238.3 | 1.9e-68 |
| gi\|46198568\|ref\|YP_004235.1\| | 1/1 | 2 | 858 .] | 1 | 960 [] | 238.0 | 2.3e-68 |
| gi\|20196774\|emb\|CAC86359.1\| | 1/1 | 1 | 375 [] | 1 | 960 [] | 237.0 | 4.8e-68 |
| gi\|222480720\|ref\|YP_002566957.1\| | 1/1 | 1 | 900 [] | 1 | 960 [] | 235.5 | 1.4e-67 |
| gi\|284165765\|ref\|YP_003404044.1\| | 1/1 | 1 | 897 [] | 1 | 960 [] | 234.3 | 3e-67 |
| gi\|89900503\|ref\|YP_522974.1\| | 1/1 | 1 | 957 [] | 1 | 960 [] | 232.4 | 1.2e-66 |
| gi\|108759396\|ref\|YP_632739.1\| | 1/1 | 2 | 889 .] | 1 | 960 [] | 232.0 | 1.5e-66 |
| gi\|269958054\|ref\|YP_003327843.1\| | 1/1 | 20 | 913 .] | 1 | 960 [] | 231.3 | 2.4e-66 |
| gi\|148556039\|ref\|YP_001263621.1\| | 1/1 | 24 | 929 .] | 1 | 960 [] | 231.2 | 2.6e-66 |
| gi\|187476834\|ref\|YP_784858.1\| | 1/1 | 1 | 936 [] | 1 | 960 [] | 230.5 | 4.2e-66 |
| gi\|124268187\|ref\|YP_001022191.1\| | 1/1 | 1 | 934 [] | 1 | 960 [] | 230.2 | 5.2e-66 |
| gi\|284172789\|ref\|YP_003406171.1\| | 1/1 | 1 | 896 [] | 1 | 960 [] | 229.9 | 6.3e-66 |
| gi\|254525149\|ref\|ZP_05137204.1\| | 1/1 | 12 | 903 .] | 1 | 960 [] | 229.8 | 6.7e-66 |
| gi\|269796282\|ref\|YP_003315737.1\| | 1/1 | 14 | 900 .] | 1 | 960 [] | 229.8 | 6.8e-66 |
| gi\|291455731\|ref\|ZP_06595121.1\| | 1/1 | 10 | 917 .] | 1 | 960 [] | 229.5 | 8.5e-66 |
| gi\|194364406\|ref\|YP_002027016.1\| | 1/1 | 12 | 903 .] | 1 | 960 [] | 228.9 | 1.3e-65 |
| gi\|94496216\|ref\|ZP_01302794.1\| | 1/1 | 1 | 899 [] | 1 | 960 [] | 228.8 | 1.3e-65 |
| gi\|103488557\|ref\|YP_618118.1\| | 1/1 | 1 | 889 [] | 1 | 960 [] | 228.7 | 1.5e-65 |
| gi\|213690981\|ref\|YP_002321567.1\| | 1/1 | 10 | 917 .] | 1 | 960 [] | 227.2 | 4.1e-65 |
| gi\|23465189\|ref\|NP_695792.1\| | 1/1 | 10 | 917 .] | 1 | 960 [] | 226.9 | 5.1e-65 |
| gi\|292676674\|dbj\|BAI98192.1\| | 1/1 | 5 | 905 .] | 1 | 960 [] | 225.9 | 1e-64 |
| gi\|171741712\|ref\|ZP_02917519.1\| | 1/1 | 37 | 918 .] | 1 | 960 [] | 224.8 | 2.2e-64 |
| gi\|46190357\|ref\|ZP_00121597.2\| | 1/1 | 10 | 917 .] | 1 | 960 [] | 224.2 | 3.3e-64 |
| gi\|72162953\|ref\|YP_290610.1\| | 1/1 | 1 | 875 [] | 1 | 960 [] | 224.1 | 3.7e-64 |
| gi\|33599409\|ref\|NP_886969.1\| | 1/1 | 33 | 982 .] | 1 | 960 [] | 223.9 | 4.2e-64 |
| gi\|291517702\|emb\|CBK71318.1\| | 1/1 | 10 | 917 .] | 1 | 960 [] | 221.5 | 2.1e-63 |
| gi\|227547454\|ref\|ZP_03977503.1\| | 1/1 | 10 | 917 .] | 1 | 960 [] | 221.3 | 2.4e-63 |
| gi\|20196786\|emb\|CAC86365.1\| | 1/1 | 1 | 396 [] | 1 | 960 [] | 221.2 | 2.7e-63 |
| gi\|163858843\|ref\|YP_001633141.1\| | 1/1 | 1 | 951 [] | 1 | 960 [] | 221.0 | 3.2e-63 |
| gi\|227988853\|ref\|ZP_04035945.1\| | 1/1 | 1 | 892 [] | 1 | 960 [] | 220.4 | 4.5e-63 |
| gi\|183602906\|ref\|ZP_02964265.1\| | 1/1 | 37 | 918 .] | 1 | 960 [] | 220.3 | 5e-63 |
| gi\|289177836\|gb\|ADC85082.1\| | 1/1 | 67 | 948 .] | 1 | 960 [] | 220.3 | 5e-63 |
| gi\|94984768\|ref\|YP_604132.1\| | 1/1 | 3 | 831 .] | 1 | 960 [] | 219.6 | 7.9e-63 |
| gi\|257052544\|ref\|YP_003130377.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 219.2 | 1e-62 |
| gi\|254419270\|ref\|ZP_05032994.1\| | 1/1 | 1 | 901 [] | 1 | 960 [] | 219.1 | 1.1e-62 |
| gi\|33595127\|ref\|NP_882770.1\| | 1/1 | 33 | 982 .] | 1 | 960 [] | 219.0 | 1.2e-62 |
| gi\|241761565\|ref\|ZP_04759652.1\| | 1/1 | 1 | 885 [] | 1 | 960 [] | 218.2 | 2.1e-62 |
| gi\|260753930\|ref\|YP_003226823.1\| | 1/1 | 1 | 885 [] | 1 | 960 [] | 217.3 | 3.9e-62 |
| gi\|56552392\|ref\|YP_163231.1\| | 1/1 | 1 | 885 [] | 1 | 960 [] | 217.3 | 4e-62 |
| gi\|190572823\|ref\|YP_001970668.1\| | 1/1 | 12 | 903 .] | 1 | 960 [] | 216.9 | 5.4e-62 |
| gi\|117927606\|ref\|YP_872157.1\| | 1/1 | 47 | 915 .] | 1 | 960 [] | 216.2 | 8.5e-62 |
| gi\|229821216\|ref\|YP_002882742.1\| | 1/1 | 4 | 888 .] | 1 | 960 [] | 215.7 | 1.2e-61 |
| gi\|289580156\|ref\|YP_003478622.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 215.6 | 1.3e-61 |
| gi\|270284604\|ref\|ZP_05966403.2\| | 1/1 | 12 | 918 .] | 1 | 960 [] | 214.9 | 2.1e-61 |
| gi\|229816951\|ref\|ZP_04447233.1\| | 1/1 | 10 | 915 .] | 1 | 960 [] | 213.6 | 5.3e-61 |
| gi\|78046414\|ref\|YP_362589.1\| | 1/1 | 3 | 904 .] | 1 | 960 [] | 213.2 | 6.8e-61 |
| gi\|163797958\|ref\|ZP_02191900.1\| | 1/1 | 1 | 876 [] | 1 | 960 [] | 213.1 | 7.4e-61 |
| gi\|33591459\|ref\|NP_879103.1\| | 1/1 | 33 | 980 .] | 1 | 960 [] | 212.4 | 1.2e-60 |
| gi\|289670989\|ref\|ZP_06492064.1\| | 1/1 | 3 | 904 .] | 1 | 960 [] | 212.1 | 1.4e-60 |
| gi\|289663604\|ref\|ZP_06485185.1\| | 1/1 | 3 | 904 .] | 1 | 960 [] | 212.0 | 1.5e-60 |
| gi\|224283986\|ref\|ZP_03647308.1\| | 1/1 | 35 | 918 .] | 1 | 960 [] | 211.5 | 2.2e-60 |
| gi\|209965727\|ref\|YP_002298642.1\| | 1/1 | 1 | 902 [] | 1 | 960 [] | 210.3 | 5.1e-60 |
| gi\|15806301\|ref\|NP_295007.1\| | 1/1 | 1 | 829 [] | 1 | 960 [] | 208.7 | 1.5e-59 |
| gi\|212715167\|ref\|ZP_03323295.1\| | 1/1 | 37 | 918 .] | 1 | 960 [] | 208.1 | 2.4e-59 |
| gi\|16125740\|ref\|NP_420304.1\| | 1/1 | 7 | 909 .] | 1 | 960 [] | 208.0 | 2.5e-59 |
| gi\|167645723\|ref\|YP_001683386.1\| | 1/1 | 4 | 905 .] | 1 | 960 [] | 207.3 | 4.1e-59 |
| gi\|254671854\|emb\|CBA04047.1\| | 1/1 | 1 | 821 [] | 1 | 960 [] | 207.3 | 4.2e-59 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| gi\|55377433\|ref\|YP_135283.1\| | 1/1 | 1 | 898 [] | 1 | 960 [] | 206.8 | 5.8e-59 |
| gi\|148271562\|ref\|YP_001221123.1\| | 1/1 | 16 | 910 .] | 1 | 960 [] | 206.8 | 5.9e-59 |
| gi\|166710682\|ref\|ZP_02241889.1\| | 1/1 | 3 | 904 .] | 1 | 960 [] | 206.2 | 8.7e-59 |
| gi\|154486362\|ref\|ZP_02027769.1\| | 1/1 | 37 | 918 .] | 1 | 960 [] | 205.6 | 1.3e-58 |
| gi\|66769781\|ref\|YP_244543.1\| | 1/1 | 3 | 904 .] | 1 | 960 [] | 205.6 | 1.3e-58 |
| gi\|1705591\|sp\|P51060.1\|CAPP_THES7 | 1/1 | 1 | 857 [] | 1 | 960 [] | 205.4 | 1.5e-58 |
| gi\|58583419\|ref\|YP_202435.1\| | 1/1 | 3 | 904 .] | 1 | 960 [] | 205.2 | 1.8e-58 |
| gi\|73920190\|sp\|Q8PP82.2\|CAPP_XANAC | 1/1 | 3 | 904 .] | 1 | 960 [] | 204.9 | 2.2e-58 |
| gi\|1581933\|prf\|\|2117330A | 1/1 | 1 | 857 [] | 1 | 960 [] | 204.4 | 2.9e-58 |
| gi\|21230228\|ref\|NP_636145.1\| | 1/1 | 3 | 904 .] | 1 | 960 [] | 203.7 | 4.8e-58 |
| gi\|188575328\|ref\|YP_001912257.1\| | 1/1 | 4 | 896 .] | 1 | 960 [] | 203.3 | 6.4e-58 |
| gi\|225352396\|ref\|ZP_03743419.1\| | 1/1 | 37 | 918 .] | 1 | 960 [] | 203.2 | 7.2e-58 |
| gi\|170782299\|ref\|YP_001710632.1\| | 1/1 | 16 | 910 .] | 1 | 960 [] | 202.1 | 1.5e-57 |
| gi\|218295525\|ref\|ZP_03496338.1\| | 1/1 | 1 | 857 [] | 1 | 960 [] | 201.9 | 1.7e-57 |
| gi\|119025042\|ref\|YP_908887.1\| | 1/1 | 37 | 918 .] | 1 | 960 [] | 201.7 | 2e-57 |
| gi\|292606014\|gb\|EFF49287.1\| | 1/1 | 3 | 904 .] | 1 | 960 [] | 199.8 | 7.5e-57 |
| gi\|162451699\|ref\|YP_001614066.1\| | 1/1 | 1 | 913 [] | 1 | 960 [] | 199.6 | 8.4e-57 |
| gi\|21241576\|ref\|NP_641158.1\| | 1/1 | 7 | 888 .] | 1 | 960 [] | 199.6 | 8.8e-57 |
| gi\|292601213\|gb\|EFF45267.1\| | 1/1 | 3 | 904 .] | 1 | 960 [] | 199.1 | 1.2e-56 |
| gi\|20196792\|emb\|CAC86368.1\| | 1/1 | 1 | 381 [] | 1 | 960 [] | 198.9 | 1.4e-56 |
| gi\|20196794\|emb\|CAC86369.1\| | 1/1 | 1 | 395 [] | 1 | 960 [] | 198.0 | 2.7e-56 |
| gi\|266627058\|ref\|ZP_06119989.1\| | 1/1 | 3 | 909 .] | 1 | 960 [] | 196.6 | 6.6e-56 |
| gi\|285019549\|ref\|YP_003377260.1\| | 1/1 | 12 | 904 .] | 1 | 960 [] | 196.3 | 8.3e-56 |
| gi\|229243257\|ref\|ZP_04367569.1\| | 1/1 | 3 | 891 .] | 1 | 960 [] | 192.1 | 1.5e-54 |
| gi\|229206299\|ref\|ZP_04332755.1\| | 1/1 | 4 | 853 .] | 1 | 960 [] | 191.8 | 1.9e-54 |
| gi\|20196796\|emb\|CAC86370.1\| | 1/1 | 1 | 396 [] | 1 | 960 [] | 189.7 | 8.3e-54 |
| gi\|262189851\|ref\|ZP_06048182.1\| | 1/1 | 1 | 585 [] | 1 | 960 [] | 188.4 | 2.1e-53 |
| gi\|15022444\|dbj\|BAB62259.1\| | 1/1 | 1 | 368 [] | 1 | 960 [] | 186.0 | 1e-52 |
| gi\|227516707\|ref\|ZP_03946756.1\| | 1/1 | 66 | 949 .] | 1 | 960 [] | 184.8 | 2.4e-52 |
| gi\|257388564\|ref\|YP_003178337.1\| | 1/1 | 7 | 898 .] | 1 | 960 [] | 184.5 | 3.1e-52 |
| gi\|114706303\|ref\|ZP_01439205.1\| | 1/1 | 15 | 930 .] | 1 | 960 [] | 184.0 | 4.4e-52 |
| gi\|10241562\|emb\|CAC09415.1\| | 1/1 | 1 | 389 [. | 1 | 960 [] | 183.4 | 6.3e-52 |
| gi\|119964668\|gb\|ABM17097.1\| | 1/1 | 1 | 878 [] | 1 | 960 [] | 181.5 | 2.3e-51 |
| gi\|229815948\|ref\|ZP_04446271.1\| | 1/1 | 46 | 941 .] | 1 | 960 [] | 178.7 | 1.7e-50 |
| gi\|20196798\|emb\|CAC86371.1\| | 1/1 | 1 | 386 [] | 1 | 960 [] | 178.4 | 2e-50 |
| gi\|157273487\|gb\|ABV27386.1\| | 1/1 | 1 | 915 [] | 1 | 960 [] | 177.3 | 4.5e-50 |
| gi\|241771836\|ref\|ZP_04769202.1\| | 1/1 | 1 | 890 [] | 1 | 960 [] | 177.2 | 4.6e-50 |
| gi\|196228554\|ref\|ZP_03127421.1\| | 1/1 | 1 | 926 [] | 1 | 960 [] | 174.8 | 2.5e-49 |
| gi\|18076761\|emb\|CAC84924.1\| | 1/1 | 1 | 364 [] | 1 | 960 [] | 172.2 | 1.5e-48 |
| gi\|7768121\|emb\|CAB90621.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 170.3 | 5.7e-48 |
| gi\|7768376\|emb\|CAB90716.1\| | 1/1 | 1 | 364 [] | 1 | 960 [] | 169.4 | 1e-47 |
| gi\|7768374\|emb\|CAB90715.1\| | 1/1 | 1 | 364 [] | 1 | 960 [] | 168.8 | 1.6e-47 |
| gi\|217977880\|ref\|YP_002362027.1\| | 1/1 | 3 | 919 .] | 1 | 960 [] | 168.8 | 1.6e-47 |
| gi\|119356395\|ref\|YP_911039.1\| | 1/1 | 1 | 922 [] | 1 | 960 [] | 168.5 | 1.9e-47 |
| gi\|194335801\|ref\|YP_002017595.1\| | 1/1 | 1 | 922 [] | 1 | 960 [] | 168.3 | 2.3e-47 |
| gi\|18073888\|emb\|CAC84967.1\| | 1/1 | 1 | 364 [] | 1 | 960 [] | 167.9 | 3e-47 |
| gi\|32473418\|ref\|NP_866412.1\| | 1/1 | 1 | 937 [] | 1 | 960 [] | 167.8 | 3.2e-47 |
| gi\|7768132\|emb\|CAB90627.1\| | 1/1 | 1 | 370 [] | 1 | 960 [] | 167.7 | 3.3e-47 |
| gi\|7768364\|emb\|CAB90712.1\| | 1/1 | 1 | 370 [] | 1 | 960 [] | 167.5 | 3.9e-47 |
| gi\|189499547\|ref\|YP_001959017.1\| | 1/1 | 1 | 922 [] | 1 | 960 [] | 165.7 | 1.3e-46 |
| gi\|8247239\|emb\|CAB92916.1\| | 1/1 | 1 | 370 [] | 1 | 960 [] | 165.4 | 1.7e-46 |
| gi\|18073874\|emb\|CAC84957.1\| | 1/1 | 1 | 364 [] | 1 | 960 [] | 165.0 | 2.3e-46 |
| gi\|257784777\|ref\|YP_003179994.1\| | 1/1 | 61 | 955 .] | 1 | 960 [] | 164.7 | 2.8e-46 |
| gi\|145637525\|ref\|ZP_01793183.1\| | 1/1 | 3 | 588 .] | 1 | 960 [] | 163.6 | 5.8e-46 |
| gi\|193214511\|ref\|YP_001995710.1\| | 1/1 | 2 | 922 .] | 1 | 960 [] | 163.1 | 8.4e-46 |
| gi\|7768372\|emb\|CAB90714.1\| | 1/1 | 1 | 364 [] | 1 | 960 [] | 163.1 | 8.4e-46 |
| gi\|18073872\|emb\|CAC84956.1\| | 1/1 | 1 | 364 [] | 1 | 960 [] | 162.6 | 1.2e-45 |
| gi\|171911854\|ref\|ZP_02927324.1\| | 1/1 | 4 | 929 .] | 1 | 960 [] | 162.2 | 1.5e-45 |
| gi\|193212217\|ref\|YP_001998170.1\| | 1/1 | 1 | 919 [] | 1 | 960 [] | 162.0 | 1.7e-45 |
| gi\|18076765\|emb\|CAC84926.1\| | 1/1 | 1 | 364 [] | 1 | 960 [] | 161.9 | 1.9e-45 |
| gi\|18073868\|emb\|CAC84951.1\| | 1/1 | 1 | 373 [] | 1 | 960 [] | 161.9 | 1.9e-45 |
| gi\|197116626\|ref\|YP_002137053.1\| | 1/1 | 1 | 911 [] | 1 | 960 [] | 161.5 | 2.5e-45 |
| gi\|18073870\|emb\|CAC84955.1\| | 1/1 | 1 | 364 [] | 1 | 960 [] | 161.5 | 2.5e-45 |
| gi\|21674458\|ref\|NP_662523.1\| | 1/1 | 1 | 914 [] | 1 | 960 [] | 161.3 | 2.8e-45 |
| gi\|284029411\|ref\|YP_003379342.1\| | 1/1 | 7 | 879 .] | 1 | 960 [] | 161.3 | 2.9e-45 |
| gi\|20196790\|emb\|CAC86367.1\| | 1/1 | 1 | 382 [] | 1 | 960 [] | 160.8 | 4e-45 |
| gi\|18073864\|emb\|CAC84949.1\| | 1/1 | 1 | 373 [] | 1 | 960 [] | 160.6 | 4.6e-45 |
| gi\|253698863\|ref\|YP_003020052.1\| | 1/1 | 2 | 912 .] | 1 | 960 [] | 160.5 | 5.1e-45 |
| gi\|83779598\|gb\|ABC47615.1\| | 1/1 | 1 | 364 [] | 1 | 960 [] | 160.2 | 6e-45 |
| gi\|210632317\|ref\|ZP_03297284.1\| | 1/1 | 46 | 941 .] | 1 | 960 [] | 159.5 | 9.7e-45 |
| gi\|18072430\|emb\|CAC84922.1\| | 1/1 | 1 | 362 [] | 1 | 960 [] | 159.3 | 1.1e-44 |

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|---|---|---|---|---|---|---|---|---|---|
| gi\|70950271\|ref\|XP_744473.1\| | 1/1 | 1 | 726 | [. | 1 | 960 | [] | 157.9 | 3.1e-44 |
| gi\|170750063\|ref\|YP_001756323.1\| | 1/1 | 12 | 916 | .] | 1 | 960 | [] | 157.7 | 3.4e-44 |
| gi\|18073866\|emb\|CAC84950.1\| | 1/1 | 1 | 373 | [] | 1 | 960 | [] | 157.6 | 3.7e-44 |
| gi\|7768244\|emb\|CAB90659.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 157.3 | 4.6e-44 |
| gi\|18073652\|emb\|CAC83643.1\| | 1/1 | 1 | 362 | [] | 1 | 960 | [] | 156.6 | 7.7e-44 |
| gi\|83779594\|gb\|ABC47613.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 155.9 | 1.2e-43 |
| gi\|18073860\|emb\|CAC84947.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 153.6 | 5.8e-43 |
| gi\|83779602\|gb\|ABC47617.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 153.3 | 7.4e-43 |
| gi\|18073830\|emb\|CAC84932.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 152.7 | 1.1e-42 |
| gi\|18073828\|emb\|CAC84931.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 152.2 | 1.5e-42 |
| gi\|220926859\|ref\|YP_002502161.1\| | 1/1 | 1 | 920 | [] | 1 | 960 | [] | 152.2 | 1.6e-42 |
| gi\|18076769\|emb\|CAC84952.1\| | 1/1 | 1 | 363 | [] | 1 | 960 | [] | 151.6 | 2.4e-42 |
| gi\|10303369\|emb\|CAA65116.1\| | 1/1 | 1 | 369 | [] | 1 | 960 | [] | 151.4 | 2.7e-42 |
| gi\|83779596\|gb\|ABC47614.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 150.5 | 5.3e-42 |
| gi\|18073838\|emb\|CAC84936.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 150.2 | 6.5e-42 |
| gi\|18073844\|emb\|CAC84939.1\| | 1/1 | 1 | 363 | [] | 1 | 960 | [] | 149.9 | 7.6e-42 |
| gi\|221195730\|ref\|ZP_03568784.1\| | 1/1 | 63 | 970 | .] | 1 | 960 | [] | 149.9 | 8e-42 |
| gi\|78187483\|ref\|YP_375526.1\| | 1/1 | 1 | 923 | [] | 1 | 960 | [] | 149.5 | 1e-41 |
| gi\|124268439\|ref\|YP_001022443.1\| | 1/1 | 5 | 920 | .] | 1 | 960 | [] | 149.4 | 1.1e-41 |
| gi\|18076771\|emb\|CAC84953.1\| | 1/1 | 1 | 363 | [] | 1 | 960 | [] | 149.3 | 1.2e-41 |
| gi\|18072424\|emb\|CAC84919.1\| | 1/1 | 1 | 362 | [] | 1 | 960 | [] | 149.1 | 1.3e-41 |
| gi\|83779600\|gb\|ABC47616.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 148.8 | 1.6e-41 |
| gi\|18073858\|emb\|CAC84946.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 148.2 | 2.6e-41 |
| gi\|18076774\|emb\|CAC84954.1\| | 1/1 | 1 | 363 | [] | 1 | 960 | [] | 148.2 | 2.6e-41 |
| gi\|18073834\|emb\|CAC84934.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 148.1 | 2.7e-41 |
| gi\|18073822\|emb\|CAC84916.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 148.0 | 2.9e-41 |
| gi\|18073846\|emb\|CAC84940.1\| | 1/1 | 1 | 366 | [] | 1 | 960 | [] | 147.2 | 5.1e-41 |
| gi\|114326718\|ref\|YP_743875.1\| | 1/1 | 1 | 926 | [] | 1 | 960 | [] | 147.2 | 5.2e-41 |
| gi\|163851228\|ref\|YP_001639271.1\| | 1/1 | 12 | 922 | .] | 1 | 960 | [] | 146.2 | 9.9e-41 |
| gi\|1166442\|emb\|CAA61086.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 146.1 | 1.1e-40 |
| gi\|18076757\|emb\|CAC84915.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 146.0 | 1.1e-40 |
| gi\|18073842\|emb\|CAC84938.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 145.7 | 1.4e-40 |
| gi\|7320917\|emb\|CAB81955.1\| | 1/1 | 1 | 372 | [] | 1 | 960 | [] | 145.7 | 1.5e-40 |
| gi\|18073836\|emb\|CAC84935.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 145.5 | 1.6e-40 |
| gi\|254467180\|ref\|ZP_05080591.1\| | 1/1 | 1 | 886 | [] | 1 | 960 | [] | 144.5 | 3.3e-40 |
| gi\|1166448\|emb\|CAA61085.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 143.8 | 5.2e-40 |
| gi\|18073904\|emb\|CAC84980.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 143.6 | 6.1e-40 |
| gi\|18073878\|emb\|CAC84958.1\| | 1/1 | 1 | 365 | [] | 1 | 960 | [] | 143.2 | 8e-40 |
| gi\|1552964\|gb\|AAB08697.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 142.2 | 1.6e-39 |
| gi\|7768123\|emb\|CAB90622.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 142.2 | 1.6e-39 |
| gi\|218530096\|ref\|YP_002420912.1\| | 1/1 | 12 | 922 | .] | 1 | 960 | [] | 141.9 | 2e-39 |
| gi\|7768238\|emb\|CAB90653.1\| | 1/1 | 1 | 365 | [] | 1 | 960 | [] | 141.5 | 2.7e-39 |
| gi\|18072436\|emb\|CAC84929.1\| | 1/1 | 1 | 363 | [] | 1 | 960 | [] | 141.0 | 3.7e-39 |
| gi\|188581006\|ref\|YP_001924451.1\| | 1/1 | 12 | 922 | .] | 1 | 960 | [] | 139.9 | 8.1e-39 |
| gi\|254560927\|ref\|YP_003068022.1\| | 1/1 | 12 | 922 | .] | 1 | 960 | [] | 139.8 | 8.6e-39 |
| gi\|26554388\|ref\|NP_758322.1\| | 1/1 | 6 | 911 | .] | 1 | 960 | [] | 139.4 | 1.2e-38 |
| gi\|18072432\|emb\|CAC84383.1\| | 1/1 | 1 | 363 | [] | 1 | 960 | [] | 138.7 | 1.8e-38 |
| gi\|28572162\|gb\|AAB58883.2\| | 1/1 | 12 | 922 | .] | 1 | 960 | [] | 138.7 | 1.9e-38 |
| gi\|7768144\|emb\|CAB90626.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 138.6 | 2e-38 |
| gi\|194703414\|gb\|ACF85791.1\| | 1/1 | 1 | 347 | [] | 1 | 960 | [] | 138.5 | 2.1e-38 |
| gi\|170744593\|ref\|YP_001773248.1\| | 1/1 | 1 | 920 | [] | 1 | 960 | [] | 137.2 | 5.3e-38 |
| gi\|18072428\|emb\|CAC84921.1\| | 1/1 | 1 | 362 | [] | 1 | 960 | [] | 136.9 | 6.1e-38 |
| gi\|18076763\|emb\|CAC84925.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 136.0 | 1.2e-37 |
| gi\|189346143\|ref\|YP_001942672.1\| | 1/1 | 1 | 922 | [] | 1 | 960 | [] | 135.6 | 1.5e-37 |
| gi\|257792699\|ref\|YP_003183305.1\| | 1/1 | 32 | 927 | .] | 1 | 960 | [] | 135.5 | 1.7e-37 |
| gi\|18073880\|emb\|CAC84959.1\| | 1/1 | 1 | 365 | [] | 1 | 960 | [] | 134.8 | 2.7e-37 |
| gi\|18076753\|emb\|CAC81349.1\| | 1/1 | 1 | 362 | [] | 1 | 960 | [] | 133.8 | 5.6e-37 |
| gi\|7768119\|emb\|CAB90620.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 132.4 | 1.4e-36 |
| gi\|34558172\|ref\|NP_907987.1\| | 1/1 | 1 | 885 | [] | 1 | 960 | [] | 132.4 | 1.4e-36 |
| gi\|18073882\|emb\|CAC84960.1\| | 1/1 | 1 | 365 | [] | 1 | 960 | [] | 132.4 | 1.5e-36 |
| gi\|224437040\|ref\|ZP_03658021.1\| | 1/1 | 17 | 905 | .] | 1 | 960 | [] | 131.7 | 2.4e-36 |
| gi\|110597068\|ref\|ZP_01385357.1\| | 1/1 | 1 | 918 | [] | 1 | 960 | [] | 131.5 | 2.6e-36 |
| gi\|7768200\|emb\|CAB90643.1\| | 1/1 | 1 | 371 | [] | 1 | 960 | [] | 128.6 | 2e-35 |
| gi\|18072442\|emb\|CAC84971.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 128.3 | 2.5e-35 |
| gi\|159897337\|ref\|YP_001543584.1\| | 1/1 | 1 | 908 | [] | 1 | 960 | [] | 128.1 | 2.7e-35 |
| gi\|18073820\|emb\|CAC84914.1\| | 1/1 | 1 | 363 | [] | 1 | 960 | [] | 127.4 | 4.5e-35 |
| gi\|7768220\|emb\|CAB90656.1\| | 1/1 | 1 | 371 | [] | 1 | 960 | [] | 127.4 | 4.5e-35 |
| gi\|7768117\|emb\|CAB90619.1\| | 1/1 | 1 | 364 | [] | 1 | 960 | [] | 126.2 | 1e-34 |
| gi\|1362025\|pir\|\|PC2168 | 1/1 | 1 | 411 | [] | 1 | 960 | [] | 124.6 | 3.3e-34 |
| gi\|18072438\|emb\|CAC84930.1\| | 1/1 | 1 | 363 | [] | 1 | 960 | [] | 123.7 | 6.1e-34 |
| gi\|7768218\|emb\|CAB90649.1\| | 1/1 | 1 | 371 | [] | 1 | 960 | [] | 121.3 | 3.1e-33 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| gi\|18073648\|emb\|CAC83651.1\| | 1/1 | 1 | 362 [] | 1 | 960 [] | 120.1 | 7e-33 |
| gi\|118581379\|ref\|YP_902629.1\| | 1/1 | 1 | 914 [] | 1 | 960 [] | 120.0 | 7.9e-33 |
| gi\|18072426\|emb\|CAC84920.1\| | 1/1 | 1 | 362 [] | 1 | 960 [] | 119.3 | 1.2e-32 |
| gi\|7768125\|emb\|CAB90618.1\| | 1/1 | 1 | 364 [] | 1 | 960 [] | 117.9 | 3.3e-32 |
| gi\|260220723\|emb\|CBA28569.1\| | 1/1 | 11 | 893 .] | 1 | 960 [] | 117.8 | 3.5e-32 |
| gi\|7768140\|emb\|CAB90630.1\| | 1/1 | 1 | 364 [] | 1 | 960 [] | 117.7 | 3.9e-32 |
| gi\|110681362\|ref\|YP_684369.1\| | 1/1 | 4 | 871 .] | 1 | 960 [] | 117.6 | 4.1e-32 |
| gi\|212275001\|ref\|NP_001130365.1\| | 1/1 | 1 | 354 [] | 1 | 960 [] | 117.4 | 4.8e-32 |
| gi\|18073892\|emb\|CAC84969.1\| | 1/1 | 1 | 362 [] | 1 | 960 [] | 117.3 | 5.1e-32 |
| gi\|18073840\|emb\|CAC84937.1\| | 1/1 | 1 | 364 [] | 1 | 960 [] | 115.8 | 1.4e-31 |
| gi\|18073890\|emb\|CAC84968.1\| | 1/1 | 1 | 362 [] | 1 | 960 [] | 115.6 | 1.7e-31 |
| gi\|186470717\|ref\|YP_001862035.1\| | 1/1 | 11 | 946 .] | 1 | 960 [] | 114.8 | 2.8e-31 |
| gi\|110639236\|ref\|YP_679445.1\| | 1/1 | 1 | 922 [] | 1 | 960 [] | 112.8 | 1.2e-30 |
| gi\|224417773\|ref\|ZP_03655779.1\| | 1/1 | 3 | 883 .] | 1 | 960 [] | 112.6 | 1.3e-30 |
| gi\|7768115\|emb\|CAB90617.1\| | 1/1 | 1 | 363 [] | 1 | 960 [] | 112.1 | 1.8e-30 |
| gi\|7768138\|emb\|CAB90629.1\| | 1/1 | 1 | 364 [] | 1 | 960 [] | 111.1 | 3.8e-30 |
| gi\|156742915\|ref\|YP_001433044.1\| | 1/1 | 7 | 910 .] | 1 | 960 [] | 110.3 | 6.4e-30 |
| gi\|18073850\|emb\|CAC84942.1\| | 1/1 | 1 | 364 [] | 1 | 960 [] | 109.6 | 1.1e-29 |
| gi\|32266702\|ref\|NP_860734.1\| | 1/1 | 12 | 899 .] | 1 | 960 [] | 109.2 | 1.4e-29 |
| gi\|18073848\|emb\|CAC84941.1\| | 1/1 | 1 | 364 [] | 1 | 960 [] | 108.5 | 2.3e-29 |
| gi\|7768136\|emb\|CAB90625.1\| | 1/1 | 1 | 364 [] | 1 | 960 [] | 107.8 | 3.6e-29 |
| gi\|164415616\|gb\|ABY53227.1\| | 1/1 | 2 | 558 .] | 1 | 960 [] | 106.9 | 6.7e-29 |
| gi\|18076755\|emb\|CAC84274.1\| | 1/1 | 1 | 362 [] | 1 | 960 [] | 106.4 | 9.4e-29 |
| gi\|7768113\|emb\|CAB90624.1\| | 1/1 | 1 | 364 [] | 1 | 960 [] | 102.9 | 1.1e-27 |
| gi\|219847014\|ref\|YP_002461447.1\| | 1/1 | 1 | 910 [] | 1 | 960 [] | 102.8 | 1.2e-27 |
| gi\|254459897\|ref\|ZP_05073313.1\| | 1/1 | 1 | 879 [] | 1 | 960 [] | 101.6 | 2.7e-27 |
| gi\|18073876\|emb\|CAC84395.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 100.8 | 4.8e-27 |
| gi\|10303403\|emb\|CAA65117.1\| | 1/1 | 1 | 363 [] | 1 | 960 [] | 100.3 | 6.7e-27 |
| gi\|18073862\|emb\|CAC84948.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 100.1 | 7.4e-27 |
| gi\|148657218\|ref\|YP_001277423.1\| | 1/1 | 1 | 908 [] | 1 | 960 [] | 98.7 | 2e-26 |
| gi\|163849410\|ref\|YP_001637454.1\| | 1/1 | 1 | 910 [] | 1 | 960 [] | 96.2 | 1.1e-25 |
| gi\|7768226\|emb\|CAB90660.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 95.4 | 1.9e-25 |
| gi\|18073902\|emb\|CAC84979.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 95.4 | 2e-25 |
| gi\|18073832\|emb\|CAC84933.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 94.9 | 2.7e-25 |
| gi\|7768228\|emb\|CAB90661.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 93.8 | 6.1e-25 |
| gi\|7768246\|emb\|CAB90654.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 93.8 | 6.1e-25 |
| gi\|254445406\|ref\|ZP_05058882.1\| | 1/1 | 9 | 933 .] | 1 | 960 [] | 93.4 | 8e-25 |
| gi\|7768236\|emb\|CAB90652.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 92.2 | 1.8e-24 |
| gi\|7768242\|emb\|CAB90658.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 91.4 | 3.1e-24 |
| gi\|7768230\|emb\|CAB90644.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 91.3 | 3.3e-24 |
| gi\|114769507\|ref\|ZP_01447133.1\| | 1/1 | 9 | 907 .] | 1 | 960 [] | 91.2 | 3.8e-24 |
| gi\|242309960\|ref\|ZP_04809115.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 90.4 | 6.2e-24 |
| gi\|18073898\|emb\|CAC84977.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 90.3 | 6.7e-24 |
| gi\|7768378\|emb\|CAB90717.1\| | 1/1 | 1 | 363 [] | 1 | 960 [] | 90.1 | 7.6e-24 |
| gi\|291277543\|ref\|YP_003517315.1\| | 1/1 | 1 | 883 [] | 1 | 960 [] | 89.6 | 1.1e-23 |
| gi\|255264237\|ref\|ZP_05343579.1\| | 1/1 | 1 | 872 [] | 1 | 960 [] | 89.2 | 1.5e-23 |
| gi\|7768224\|emb\|CAB90648.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 86.7 | 8e-23 |
| gi\|10303367\|emb\|CAA65112.1\| | 1/1 | 1 | 367 [] | 1 | 960 [] | 84.9 | 2.8e-22 |
| gi\|7768232\|emb\|CAB90650.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 84.9 | 3e-22 |
| gi\|7768222\|emb\|CAB90647.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 84.6 | 3.4e-22 |
| gi\|2145451\|emb\|CAA62829.1\| | 1/1 | 1 | 363 [] | 1 | 960 [] | 83.9 | 5.5e-22 |
| gi\|18073856\|emb\|CAC84945.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 81.8 | 2.5e-21 |
| gi\|7739277\|emb\|CAB90713.1\| | 1/1 | 1 | 362 [] | 1 | 960 [] | 81.2 | 3.7e-21 |
| gi\|56696455\|ref\|YP_166812.1\| | 1/1 | 10 | 879 .] | 1 | 960 [] | 78.4 | 2.6e-20 |
| gi\|18073852\|emb\|CAC84943.1\| | 1/1 | 1 | 366 [] | 1 | 960 [] | 77.8 | 3.9e-20 |
| gi\|7768248\|emb\|CAB90645.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 75.3 | 2.2e-19 |
| gi\|7768366\|emb\|CAB90709.1\| | 1/1 | 1 | 369 [] | 1 | 960 [] | 74.4 | 4.2e-19 |
| gi\|18076776\|emb\|CAC84961.1\| | 1/1 | 1 | 357 [] | 1 | 960 [] | 74.2 | 4.9e-19 |
| gi\|1166446\|emb\|CAA61084.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 74.0 | 5.6e-19 |
| gi\|7768234\|emb\|CAB90651.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 71.7 | 2.8e-18 |
| gi\|237752184\|ref\|ZP_04582664.1\| | 1/1 | 1 | 880 [] | 1 | 960 [] | 71.4 | 3.4e-18 |
| gi\|2145471\|emb\|CAA62826.1\| | 1/1 | 1 | 357 [] | 1 | 960 [] | 70.6 | 5.8e-18 |
| gi\|2145354\|emb\|CAA62825.1\| | 1/1 | 1 | 356 [] | 1 | 960 [] | 70.3 | 7.1e-18 |
| gi\|7768306\|emb\|CAB90681.1\| | 1/1 | 1 | 367 [] | 1 | 960 [] | 66.5 | 9.7e-17 |
| gi\|10303371\|emb\|CAA65108.1\| | 1/1 | 1 | 368 [] | 1 | 960 [] | 64.0 | 5.5e-16 |
| gi\|1166444\|emb\|CAA61083.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 62.9 | 1.2e-15 |
| gi\|2145426\|emb\|CAA62827.1\| | 1/1 | 1 | 361 [] | 1 | 960 [] | 62.2 | 1.9e-15 |
| gi\|7768368\|emb\|CAB90710.1\| | 1/1 | 1 | 368 [] | 1 | 960 [] | 61.5 | 3.1e-15 |
| gi\|7768216\|emb\|CAB90662.1\| | 1/1 | 1 | 368 [] | 1 | 960 [] | 61.5 | 3.2e-15 |
| gi\|7768093\|emb\|CAB90612.1\| | 1/1 | 1 | 367 [] | 1 | 960 [] | 59.3 | 1.4e-14 |
| gi\|7768259\|emb\|CAB90665.1\| | 1/1 | 1 | 368 [] | 1 | 960 [] | 59.0 | 1.8e-14 |

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|---|---|---|---|---|---|---|---|---|---|
| gi\|18073824\|emb\|CAC84917.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 56.6 | 9.6e-14 | | |
| gi\|7768091\|emb\|CAB90611.1\| | 1/1 | 1 | 371 [] | 1 | 960 [] | 55.2 | 2.4e-13 | | |
| gi\|2145479\|emb\|CAA62828.1\| | 1/1 | 1 | 362 [] | 1 | 960 [] | 53.8 | 6.5e-13 | | |
| gi\|7768148\|emb\|CAB90635.1\| | 1/1 | 1 | 371 [] | 1 | 960 [] | 52.0 | 2.3e-12 | | |
| gi\|7768308\|emb\|CAB90705.1\| | 1/1 | 1 | 371 [] | 1 | 960 [] | 51.5 | 3.2e-12 | | |
| gi\|7768302\|emb\|CAB90679.1\| | 1/1 | 1 | 369 [] | 1 | 960 [] | 51.0 | 4.5e-12 | | |
| gi\|10303358\|emb\|CAA65114.1\| | 1/1 | 1 | 365 [] | 1 | 960 [] | 50.3 | 7.3e-12 | | |
| gi\|7768304\|emb\|CAB90680.1\| | 1/1 | 1 | 369 [] | 1 | 960 [] | 47.9 | 3.8e-11 | | |
| gi\|7768310\|emb\|CAB90706.1\| | 1/1 | 1 | 375 [] | 1 | 960 [] | 47.6 | 4.9e-11 | | |
| gi\|7768370\|emb\|CAB90711.1\| | 1/1 | 1 | 371 [] | 1 | 960 [] | 47.2 | 6.5e-11 | | |
| gi\|7768146\|emb\|CAB90632.1\| | 1/1 | 1 | 375 [] | 1 | 960 [] | 44.9 | 3.2e-10 | | |
| gi\|7768257\|emb\|CAB90664.1\| | 1/1 | 1 | 366 [] | 1 | 960 [] | 44.9 | 3.2e-10 | | |
| gi\|7768095\|emb\|CAB90613.1\| | 1/1 | 1 | 371 [] | 1 | 960 [] | 43.8 | 6.9e-10 | | |
| gi\|7768382\|emb\|CAB90719.1\| | 1/1 | 1 | 363 [] | 1 | 960 [] | 43.5 | 8e-10 | | |
| gi\|139438299\|ref\|ZP_01771852.1\| | 1/1 | 46 | 889 .] | 1 | 960 [] | 43.4 | 9.1e-10 | | |
| gi\|7768134\|emb\|CAB90628.1\| | 1/1 | 1 | 368 [] | 1 | 960 [] | 42.5 | 1.7e-09 | | |
| gi\|2145352\|emb\|CAA62830.1\| | 1/1 | 1 | 355 [] | 1 | 960 [] | 40.2 | 8.1e-09 | | |
| gi\|7768198\|emb\|CAB90642.1\| | 1/1 | 1 | 379 [] | 1 | 960 [] | 39.8 | 1e-08 | | |
| gi\|88799804\|ref\|ZP_01115377.1\| | 1/1 | 1 | 517 [] | 1 | 960 [] | 39.1 | 1.8e-08 | | |
| gi\|7768097\|emb\|CAB90616.1\| | 1/1 | 1 | 369 [] | 1 | 960 [] | 35.5 | 2.2e-07 | | |
| gi\|237750822\|ref\|ZP_04581302.1\| | 1/1 | 1 | 931 [] | 1 | 960 [] | 35.1 | 2.8e-07 | | |
| gi\|255588103\|ref\|XP_002534501.1\| | 1/1 | 6 | 852 .] | 1 | 960 [] | 34.3 | 5e-07 | | |
| gi\|18073654\|emb\|CAC81270.1\| | 1/1 | 1 | 358 [] | 1 | 960 [] | 31.0 | 4.8e-06 | | |
| gi\|119504081\|ref\|ZP_01626162.1\| | 1/1 | 1 | 626 [] | 1 | 960 [] | 25.8 | 0.00017 | | |
| gi\|149019670\|ref\|ZP_01834989.1\| | 1/1 | 1 | 709 [] | 1 | 960 [] | 19.6 | 0.013 | | |
| gi\|19070128\|gb\|AAL83719.1\|AF236126_1 | 1/1 | 1 | 339 [] | 1 | 960 [] | 18.9 | 0.022 | | |
| gi\|10303354\|emb\|CAA65110.1\| | 1/1 | 1 | 371 [] | 1 | 960 [] | 16.1 | 0.15 | | |
| gi\|18072440\|emb\|CAC84970.1\| | 1/1 | 1 | 339 [] | 1 | 960 [] | 14.2 | 0.53 | | |
| gi\|256370921\|ref\|YP_003108745.1\| | 1/1 | 1 | 772 [] | 1 | 960 [] | 12.3 | 2 | | |
| gi\|6119717\|emb\|CAB59571.1\| | 1/1 | 1 | 335 [] | 1 | 960 [] | 10.9 | 3 | | |
| gi\|7768255\|emb\|CAB90663.1\| | 1/1 | 1 | 372 [] | 1 | 960 [] | 2.4 | 3.3 | | |
| gi\|18073660\|emb\|CAC81273.1\| | 1/1 | 1 | 358 [] | 1 | 960 [] | -2.8 | 3.4 | | |
| gi\|255037677\|ref\|YP_003088298.1\| | 1/1 | 1 | 860 [] | 1 | 960 [] | -6.1 | 3.5 | | |
| gi\|18073658\|emb\|CAC81272.1\| | 1/1 | 1 | 360 [] | 1 | 960 [] | -9.9 | 3.7 | | |
| gi\|18073656\|emb\|CAC81271.1\| | 1/1 | 1 | 360 [] | 1 | 960 [] | -10.6 | 3.7 | | |
| gi\|18076788\|emb\|CAC84974.1\| | 1/1 | 1 | 357 [] | 1 | 960 [] | -11.7 | 3.7 | | |
| gi\|213580501\|ref\|ZP_03362327.1\| | 1/1 | 1 | 584 [] | 1 | 960 [] | -15.8 | 3.9 | | |
| gi\|10303360\|emb\|CAA65115.1\| | 1/1 | 1 | 371 [] | 1 | 960 [] | -15.8 | 3.9 | | |
| gi\|120435841\|ref\|YP_861527.1\| | 1/1 | 2 | 857 .] | 1 | 960 [] | -16.8 | 3.9 | | |
| gi\|18076784\|emb\|CAC84972.1\| | 1/1 | 1 | 357 [] | 1 | 960 [] | -20.9 | 4 | | |
| gi\|18076786\|emb\|CAC84973.1\| | 1/1 | 1 | 357 [] | 1 | 960 [] | -22.0 | 4.1 | | |
| gi\|7768111\|emb\|CAB90623.1\| | 1/1 | 1 | 401 [] | 1 | 960 [] | -24.0 | 4.1 | | |
| gi\|86135028\|ref\|ZP_01053610.1\| | 1/1 | 2 | 859 .] | 1 | 960 [] | -24.4 | 4.2 | | |
| gi\|149278227\|ref\|ZP_01884365.1\| | 1/1 | 6 | 862 .] | 1 | 960 [] | -24.8 | 4.2 | | |
| gi\|88801380\|ref\|ZP_01116908.1\| | 1/1 | 2 | 859 .] | 1 | 960 [] | -28.4 | 4.3 | | |
| gi\|118377471\|ref\|XP_001021914.1\| | 1/1 | 58 | 926 .] | 1 | 960 [] | -32.0 | 4.4 | | |
| gi\|7768261\|emb\|CAB90666.1\| | 1/1 | 1 | 371 [] | 1 | 960 [] | -33.5 | 4.5 | | |
| gi\|146300556\|ref\|YP_001195147.1\| | 1/1 | 6 | 861 .] | 1 | 960 [] | -33.6 | 4.5 | | |
| gi\|2695868\|emb\|CAA75817.1\| | 1/1 | 1 | 328 [] | 1 | 960 [] | -40.5 | 4.8 | | |
| gi\|163787422\|ref\|ZP_02181869.1\| | 1/1 | 1 | 835 [] | 1 | 960 [] | -42.2 | 4.8 | | |
| gi\|126648531\|ref\|ZP_01721018.1\| | 1/1 | 1 | 844 [] | 1 | 960 [] | -43.4 | 4.9 | | |
| gi\|227366515\|ref\|ZP_03850064.1\| | 1/1 | 1 | 844 [] | 1 | 960 [] | -45.8 | 5 | | |
| gi\|11596397\|gb\|AAG38601.1\|AF317284_1 | 1/1 | 37 | 811 .] | 1 | 960 [] | -45.8 | 5 | | |
| gi\|260063588\|ref\|YP_003196668.1\| | 1/1 | 2 | 848 .] | 1 | 960 [] | -46.9 | 5.1 | | |
| gi\|255534738\|ref\|YP_003095109.1\| | 1/1 | 1 | 846 [] | 1 | 960 [] | -47.4 | 5.1 | | |
| gi\|629594\|pir\|\|PC2170 | 1/1 | 1 | 368 [. | 1 | 960 [] | -47.5 | 5.1 | | |
| gi\|255534144\|ref\|YP_003094516.1\| | 1/1 | 6 | 862 .] | 1 | 960 [] | -48.3 | 5.1 | | |
| gi\|126662794\|ref\|ZP_01733793.1\| | 1/1 | 6 | 857 .] | 1 | 960 [] | -51.3 | 5.3 | | |
| gi\|149926183\|ref\|ZP_01914445.1\| | 1/1 | 1 | 849 [] | 1 | 960 [] | -51.7 | 5.3 | | |
| gi\|88713052\|ref\|ZP_01107136.1\| | 1/1 | 2 | 847 .] | 1 | 960 [] | -54.7 | 5.4 | | |
| gi\|256420516\|ref\|YP_003121169.1\| | 1/1 | 6 | 855 .. | 1 | 960 [] | -54.7 | 5.4 | | |
| gi\|163755567\|ref\|ZP_02162686.1\| | 1/1 | 15 | 862 .] | 1 | 960 [] | -55.0 | 5.4 | | |
| gi\|86143373\|ref\|ZP_01061775.1\| | 1/1 | 2 | 861 .] | 1 | 960 [] | -55.8 | 5.5 | | |
| gi\|89890758\|ref\|ZP_01202267.1\| | 1/1 | 1 | 848 [] | 1 | 960 [] | -59.0 | 5.6 | | |
| gi\|86130467\|ref\|ZP_01049067.1\| | 1/1 | 2 | 859 .] | 1 | 960 [] | -59.7 | 5.7 | | |
| gi\|225011063\|ref\|ZP_03701527.1\| | 1/1 | 2 | 847 .] | 1 | 960 [] | -60.9 | 5.7 | | |
| gi\|224368853\|ref\|YP_002603015.1\| | 1/1 | 2 | 850 .] | 1 | 960 [] | -62.5 | 5.8 | | |
| gi\|227540600\|ref\|ZP_03970649.1\| | 1/1 | 2 | 858 .] | 1 | 960 [] | -66.7 | 6 | | |
| gi\|1552966\|gb\|AAB08698.1\| | 1/1 | 1 | 305 [] | 1 | 960 [] | -69.5 | 6.2 | | |
| gi\|241892653\|ref\|ZP_04779949.1\| | 1/1 | 2 | 858 .] | 1 | 960 [] | -70.3 | 6.2 | | |
| gi\|225012795\|ref\|ZP_03703229.1\| | 1/1 | 2 | 862 .] | 1 | 960 [] | -70.6 | 6.2 | | |

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gi|207723607|ref|YP_002254005.1|        1/1       1   682 []     1   960 []   -78.7      6.7
gi|268685594|ref|ZP_06152456.1|         1/1       1   653 []     1   960 []   -84.4        7
gi|257139898|ref|ZP_05588160.1|         1/1       1   671 []     1   960 []   -98.7      7.9
gi|241667414|ref|ZP_04754992.1|         1/1       5   844 .]     1   960 []  -101.3      8.1
gi|254875963|ref|ZP_05248673.1|         1/1       7   846 .]     1   960 []  -101.3      8.1
gi|167626833|ref|YP_001677333.1|        1/1       5   844 .]     1   960 []  -103.1      8.3
gi|89892437|gb|ABD79011.1|              1/1       1   472 []     1   960 []  -109.6      8.7
gi|159475421|ref|XP_001695817.1|        1/1       1   447 [.     1   960 []  -117.0      9.3
gi|224101659|ref|XP_002312371.1|        1/1       1   466 []     1   960 []  -121.8      9.7

Alignments of top-scoring domains:
gi|231684|sp|Q01647.1|CAPP1_FLAPR: domain 1 of 1, from 11 to 967: score 2796.7, E = 0
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                     siDAqLRlLvPGKvsed+kLieYDALLlDkFLDiLqDLHGedLkEav
  gi|231684|    11    SIDAQLRLLVPGKVSEDDKLIEYDALLLDKFLDILQDLHGEDLKEAV 57

                     qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     qECYElsAeYEGK+D+kKLeELG++LtsLdP+D+i++Aka++HmLnLAnL
  gi|231684|    58 QECYELSAEYEGKHDPKKLEELGSVLTSLDPGDSIVIAKAFSHMLNLANL 107

                     AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     AEEv++AyRRRik+k+ GDFaDEa+AttEsDiEEt+KkLvlklnKsPeEv
  gi|231684|   108 AEEVQIAYRRRIKLKR-GDFADEANATTESDIEETFKKLVLKLNKSPEEV 156

                     FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     F+ALKnq+vDLvltAHPtqsvRRsLLqK++RiRnCLaqL+AKD+t++DK+
  gi|231684|   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLAQLYAKDITPDDKQ 206

                     ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     ELDEALHREiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|231684|   207 ELDEALHREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

                     RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     RvDtALKniGinER+PY++PLi+FssWmGGDRDGk+PRvtPEvtRDvCLL
  gi|231684|   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDGKHPRVTPEVTRDVCLL 306

                     aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                     aRmmA+n+Y+sq+EDLmFE+smWRCn+ELRvRAEElyrta+rd  vK+Yi
  gi|231684|   307 ARMMASNMYFSQIEDLMFEMSMWRCNSELRVRAEELYRTARRD--VKHYI 354

                     EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
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  gi|231684|   355 EFWKQVPPTEPYRVILGDVRDKLYNTRERSRHLLAHGISDIPEEAVYTNV 404

                     EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                     E+FLEPLELCY+sLC+CGD+viADGsLLD+LRqvstFGLsLvKLDiRqEs
  gi|231684|   405 EQFLEPLELCYRSLCDCGDRVIADGSLLDFLRQVSTFGLSLVKLDIRQES 454

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  gi|231684|   455 DRHTDVLDAITQHLEIGSYREWSEEKRQEWLLAELSGKRPLFGSDLPKTE 504

                     EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
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  gi|231684|   505 EVKDVLDTFNVLAELPSDCFGAYIISMATSPSDVLAVELLQRECHVKHPL 554

                     rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                     rvvPLFEkLADLeAAPAa+++LFsiDWY+nridGKqevm+GYsDsGKDAG
  gi|231684|   555 RVVPLFEKLADLEAAPAAMARLFSIDWYRNRIDGKQEVMIGYSDSGKDAG 604

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                     R+sAAWqLYkAqEEiiKvAK++GvKLv+FHGRGGtvGRGGGPtHLAiLsq
  gi|231684|   605 RFSAAWQLYKAQEEIIKVAKEFGVKLVIFHGRGGTVGRGGGPTHLAILSQ 654

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  gi|231684|   655 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFCAATLEHGMNPPISP 704

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  gi|231684|   705 RPEWRELMDQMAVVATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 754
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  gi|231684|   755 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAIKKDSKNL 804

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  gi|231684|   805 QMLQEMYKTWPFFRVTIDLVEMVFAKGDPGIAALNDKLLVSEDLWPFGES 854

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  gi|231684|   855 LRANYEETKDYLLKIAGHRDLLEGDPYLKQRIRLRDSYITTLNVCQAYTL 904

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  gi|231684|   955 TMKGIAAGMQNTG    967

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  gi|763097|   108 AEEVQIAYRRRIKLKR-GDFADEANATTESDIEETFKKLVLKLNKSPEEV 156

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  gi|763097|   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLAQLYAKDITPDDKQ 206

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  gi|763097|   207 ELDEALHREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

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  gi|763097|   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

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  gi|763097|   654 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFCAATLEHGMNPPISP 703

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  gi|763097|   754 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAIKKDSKNL 803

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  gi|763097|   804 QMLQEMYKTWPFFRVTIDLVEMVFAKGDPGIAALNDKLLVSEDLWPFGES 853

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  gi|763097|   854 LRANYEETKDYLLKIAGHRDLLEGDPYLKQRIRLRDSYITTLNVCQAYTL 903

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  gi|763097|   904 KRIRDPNYHVTLRPHISKEYAAEPSKPADELIHLNPTSEYAPGLEDTLIL 953

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  gi|763097|   954 TMKGIAAGMQNTG    966

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  gi|2016246    11    SIDAQLRLLVPGKVSEDDKLIEYDALLLDKFLDILQDLHGEDLKEAV 57

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  gi|2016246    58 QECYELSAEYEGKHDPKKLEELGSVLTSLDPGDSIVIAKAFSHMLNLANL 107

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  gi|2016246   108 AEEVQIAYRRRIKLKR-GDFADEANATTESDIEETFKRLVHKLNKSPEEV 156

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  gi|2016246   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLAQLYAKDITPDDKQ 206

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  gi|2016246   306 ARMMASNMYFSQIEDLMFEMSMWRCNSELRVRAEELYRTARRD--VKHYI 353

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  gi|2016246   354 EFWKQVPPTEPYRVILGDVRDKLYNTRERSRHLLAHGMSDIPDEAVYTNV 403

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  gi|2016246   404 EQFLEPLELCYRSLCDCGDRVIADGSLLDFLRQVSTFGLSLVKLDIRQES 453

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  gi|2016246   554 RVVPLFEKLADLEAAPAAMARLFSIDWYRNRIDGKQEVMIGYSDSGKDAG 603

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  gi|2016246   604 RFSAAWQLYKAQEEIIKVAKEFGVKLVIFHGRGGTVGRGGGPTHLALLSQ 653

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  gi|2016246   654 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFCAATLEHGMNPPISP 703

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  gi|2016246   704 RPEWRELMDQMAVVATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 753

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  gi|2016246   754 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGTAFKHAIKKDSKNL 803

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+L+EmYk+WPFFRvt+DL+EmvFAKGDPGiAaL+DkLLv+E+L+PFG+s
  gi|2016246   804 QMLQEMYKTWPFFRVTIDLVEMVFAKGDPGIAALNDKLLVSEDLWPFGES 853

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  gi|2016246   854 LRANYEETKDYLLKIAGHKDLLEGDPYLKQRIRLRDSYITTLNVCQAYTL 903

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  gi|2016246   904 KRIRDPNYHVTLRPHISKEYAAEPSKPADELIHLNPTSEYAPGLEDTLIL 953

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  gi|2420960     8    SIDAQLRALAPGKVS--EELIQYDALLVDRFLDILQDLHGPSLREFV 52

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE+sA+YEGKkDt+KL+ELGakLt+L+PaDailvA++ilHmLnLAnL
  gi|2420960    53 QECYEVSADYEGKKDTSKLGELGAKLTGLAPADAILVASSILHMLNLANL 102

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  gi|2420960   103 AEEVELAHRRRNSKLKHGDFSDEGSATTESDIEETLKRLVSLG-KTPAEV 151

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  gi|2420960   152 FEALKNQSVDLVFTAHPTQSARRSLLQKNARIRNCLTQLSAKDVTVEDKK 201

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|2420960   202 ELDEALHREIQAAFRTDEIRRAQPTPQDEMRYGMSYIHETVWNGVPKFLR 251

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  gi|2420960   252 RVDTALKNIGINERLPYDVPLIKFCSWMGGDRDG-NPRVTPEVTRDVCLL 300

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|2420960   301 SRMMAANLYINQVEDLMFELSMWRCNDELRARAEEVQSTPASKKVTKYYI 350

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  gi|2420960   401 EEFLEPLELCYKSLCECGDKAIADGSLLDLLRQVFAFGLSLVKLDIRQES 450

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  gi|2420960   451 ERHTDVIDAITTHLGIGSYRSWPEDKRMEWLVSELKGKRPLLPPDLPMTE 500

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  gi|2420960   501 EIADVIGAMRVLAELPIDSFGPYIISMCTAPSDVLAVELLQRECGIRQTL 550

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  gi|2420960   551 PVVPLFERLADLQAAPASVEKLFSTDWYINHINGKQQVMVGYSDSGKDAG 600

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  gi|2420960   601 RLSAAWQLYVAQEEMAKVAKKYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 650

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  gi|2420960   701 KPEWRKLMEEMAVVATEEYRSVVVKEPRFVEYFRSATPETEYGKMNIGSR 750

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  gi|2420960   751 PAKRKPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKWAIDKDIKNF 800

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  gi|2420960   801 QKLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVAEELKPFGKQ 850

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRdkYvEt++lLL+iAGHkD+LEGDPYLKq+lRLR++YittLnvfqAYtL
  gi|2420960   851 LRDKYVETQQLLLQIAGHKDILEGDPYLKQGLRLRNPYITTLNVFQAYTL 900

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
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  gi|2420960   901 KRIRDPSFKVTPQPPLSKEFADEN--KPAGLVKLNPASEYPPGLEDTLIL 948

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                    tmKGiAAGmqntG
  gi|2420960   949 TMKGIAAGMQNTG    961

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  gi|115578|     8    SIDAQLRALAPGKVS--EELIQYDALLVDRFLDILQDLHGPSLREFV 52

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE+sA+YEGKkDt+KL+ELGakLt+L+PaDailvA++ilHmLnLAnL
  gi|115578|    53 QECYEVSADYEGKKDTSKLGELGAKLTGLAPADAILVASSILHMLNLANL 102

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEvelA+RRR++k+khGDF+DE+sAttEsDiEEtlK+Lv+++ K+P+Ev
  gi|115578|   103 AEEVELAHRRRRNSKLKHGDFSDEGSATTESDIEETLKRLVSLG-KTPAEV 151

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  gi|115578|   152 FEALKNQSVDLVFTAHPTQSARRSLLQKNARIRNCLTQLSAKDVTVEDKK 201

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  gi|115578|   202 ELDEALHREIQAAFRTDEIRRAQPTPQDEMRYGMSYIHETVWNGVPKFLR 251
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  gi|115578|   252 RVDTALKNIGINERLPYDVPLIKFCSWMGGDRDG-NPRVTPEVTRDVCLL 300

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  gi|115578|   301 SRMMAANLYINQVEDLMFELSMWRCNDELRARAEEVQSTPASKKVTKYYI 350

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  gi|115578|   351 EFWKQIPPNEPYRVILGAVRDKLYNTRERARHLLATGFSEISEDAVFTKI 400

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  gi|115578|   401 EEFLEPLELCYKSLCECGDKAIADGSLLDLLRQVFTFGLSLVKLDIRQES 450

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  gi|115578|   451 ERQTDVIDAITTHLGIGSYRSWPEDKRMEWLVSELKGKRPLLPPDLPMTE 500

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  gi|115578|   501 EIADVIGAMRVLAELPIDSFGPYIISMCTAPSDVLAVELLQRECGIRQTL 550

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  gi|115578|   551 PVVPLFERLADLQAAPASVEKLFSTDWYINHINGKQQVMVGYSDSGKDAG 600

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  gi|115578|   601 RLSAAWQLYVAQEEMAKVAKKYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 650

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  gi|115578|   651 PPDTINGSIRVTVQGEVIEFMFGEENLCFQSLQRFTAATLEHGMHPPVSP 700

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  gi|115578|   751 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKWAIDKDIKNF 800

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  gi|115578|   801 QKLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVAEELKPFGKQ 850

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                    LRdkYvEt++lLL+iAGHkD+LEGDPYLKq+lRLR++YittLnvfqAYtL
  gi|115578|   851 LRDKYVETQQLLLQIAGHKDILEGDPYLKQGLRLRNPYITTLNVFQAYTL 900

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                    KRiRDPs+kvt++P+lsKE+AdEn  k+++LvkLn +erv+PGLEDtLiL
  gi|115578|   901 KRIRDPSFKVTPQPPLSKEFADEN--KPAGLVKLN-GERVPPGLEDTLIL 947

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  gi|115578|   948 TMKGIAAGMQNTG    960

gi|20162465|gb|AAM14596.1|AF494191_1: domain 1 of 1, from 11 to 966: score 2757.4, E = 0
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  gi|2016246    11    SIDAQLRLLVPGKVSEDDKLIEYDALLLDKFLDILQDLHGEDLKEAV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYElsAeYEGK+D+kKLeELG++LtsLdP+D+i++Aka++HmLnLAnL
  gi|2016246    58 QECYELSAEYEGKHDPKKLEELGSVLTSLDPGDSIVIAKAFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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gi|2016246   108 AEEVQIAYRRRIKLKR-GDFADEANATTESDIEETFKRLVHKLNKSPEEV 156

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gi|2016246   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLAQLYAKDITPDDKQ 206

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                ELDEALHREiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
gi|2016246   207 ELDEALHREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

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gi|2016246   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

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gi|2016246   306 ARMMASNMYFSQIEDLMFEMSMWRCNSEVRVRAEELYRTARKD--VKHYI 353

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gi|2016246   354 EFWKQVPPTEPYRVILGDVRDKLYNTIERSRHLLAHGMSDIPDEAVYTNV 403

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gi|2016246   404 EQFLEPLELCYRSLCDSGDRVIADGSLLDFLRQVSTFGLSLVKLDIRQES 453

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gi|2016246   454 DRHTDVLDAITQHLKIGSYREWSEEKRQEWLLAELSGKRPLFGSDLPKTE 503

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gi|2016246   504 EVKDVLDTFNVIAELPSDCFGAYIISMATSPSDVLAVELLQRECHVKHPL 553

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gi|2016246   554 RVVPLFEKLADLEAAPASMARLFSIDWYRNRIDGKQEVMIGYSDSGKDAG 603

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gi|2016246   604 RFSAAWQLYKAQEEIIKVAKEFGVKLVIFHGRGGTVGRGGGPTHLALLSQ 653

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                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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gi|2016246   804 QMLQEMYKTWPFFRVTIDLVEMVFAKGDPGIAALNDKLLVSEDLWPFGES 853

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gi|2016246   854 LRANYEETKDYLLKIAGHKDLLEGDPYLKQRIRLRDAYITTLNVCQAYTL 903

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gi|2016246   904 KRIRDPNYHVTLRPHISKEYAAEPSKPADELIHLNPTSEYAPGLEDTLIL 953

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gi|2016246   954 TMKGIAAGMQNTG    966
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  gi|1044387    11    SIDAHLRLLVPGKVSEDDKLIEYDALLLDKFLDILQDLHGEDLKETV 57

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  gi|1044387   108 AEEVQIAYRRRIKLKK-GDFADEAHATTESDMEETLKKLVYKLNKSPEEV 156

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  gi|1044387   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLAQLYAKDITPDDKQ 206

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  gi|1018517   801 QKLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDLLLVADDLKPFGKQ 850

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  gi|1018517   851 LRDKYVETEKLLLQIAGHKDILEGDPYLKQGLRLRNPYITTLNVLQAYTL 900

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  gi|1018517   949 TMKGIAAGMQNTG    961

gi|21464596|emb|CAC85930.1|: domain 1 of 1, from 8 to 961: score 2711.4, E = 0
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gi|23306662|gb|AAN15222.1|: domain 1 of 1, from 8 to 961: score 2704.1, E = 0
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                    KRiRDPs+kvt++P+lsKE+AdEn  k+++LvkLnp+++++PGLEDtLiL
  gi|2330666   901 KRIRDPSFKVTPQPPLSKEFADEN--KPAGLVKLNPASEYPPGLEDTLIL 948

                    tmKGiAAGmqntG<-*
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  gi|2330666   949 TMKGIAAGMQNTG    961

gi|231685|sp|Q01648.1|CAPP1_FLATR: domain 1 of 1, from 11 to 967: score 2693.2, E = 0
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  gi|231685|    11    SIDAQLRLLVPGKVSEDDKLVEYDALLLDKFLDILQDLHGEDLKEAV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    q CYElsAeYEGK+D+kKL+ELG+ LtsLdP+D+i++Aka++HmLnLAnL
  gi|231685|    58 QQCYELSAEYEGKHDPKKLDELGSLLTSLDPGDSIVIAKAFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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  gi|231685|   108 AEEVQIAYRRRIKLKS-GDFADEANATTESDIEETFKRLVHKLNKSPEEV 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+v+LvltAHPtqs+RRsLLqK++RiRnCLaqL+AKD+t++DK+
  gi|231685|   157 FDALKNQTVELVLTAHPTQSIRRSLLQKHGRIRNCLAQLYAKDITPDDKQ 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEALHREiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|231685|   207 ELDEALHREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinER PY++PLi+FssWmGGDRDGk+PRvtPEvtRDvCLL
  gi|231685|   257 RVDTALKNIGINERFPYNAPLIQFSSWMGGDRDGKHPRVTPEVTRDVCLL 306

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmm +n+Y+sq+EDLm E+smWRCn+ELRvRAEElyrta++d  vK+Yi
  gi|231685|   307 ARMMTSNMYFSQIEDLMIEMSMWRCNSELRVRAEELYRTARKD--VKHYI 354

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP+ PYRviLGdvRDKLYntRER+RHLL  G s+i++eAvyt+v
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  gi|231685|   355 EFWKQIPPNQPYRVILGDVRDKLYNTRERSRHLLVDGKSDIPDEAVYTNV 404

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                   E+ LEPLELCY+sLC+ GD+viADGsLLD+LRqvstFGLsLvKLDiRqEs
  gi|231685|   405 EQLLEPLELCYRSLCDSGDHVIADGSLLDFLRQVSTFGLSLVKLDIRQES 454

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|231685|   455 DRHTEVLDAITQHLGIGSYREWSEEKRQEWLLAELSGKRPLIGPDLPKTE 504

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   EvkD ld+f+vLAELP+D+FGaYiismat+ sDvLAvELLqRE ++k++L
  gi|231685|   505 EVKDCLDTFNVLAELPSDCFGAYIISMATSTSDVLAVELLQREYHIKHPL 554

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAa+ +LFs+DWY+nridGKqevm+GYsDsGKDAG
  gi|231685|   555 RVVPLFEKLADLEAAPAAMTRLFSMDWYRNRIDGKQEVMIGYSDSGKDAG 604

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   R+sAAWqLYk qE i+K+AK++GvKLv+FHGRGGtvGRGGGPtHLA+Lsq
  gi|231685|   605 RFSAAWQLYKTQEQIVKIAKEFGVKLVIFHGRGGTVGRGGGPTHLALLSQ 654

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvtvqGEviE+sFGEE+LCFr+LqRF+AAtLEHGmnPP+sP
  gi|231685|   655 PPDTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFCAATLEHGMNPPISP 704

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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  gi|231685|   705 RPEWRELMDQMAVVATEEYRSVVFKEPRFVEYFRLATPELEFGRMNIGSR 754

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiF+WtqtRFHLPvWLG+GAAFKhAi+KD+Knl
  gi|231685|   755 PSKRKPSGGIESLRAIPWIFSWTQTRFHLPVWLGFGAAFKHAIQKDSKNL 804

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q+L+EmYk+WPFFRvt+DL+EmvFAKG PGiAaL+DkLLv+E+L+PFG+s
  gi|231685|   805 QMLQEMYKTWPFFRVTIDLVEMVFAKGNPGIAALNDKLLVSEDLRPFGES 854

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Etk++LLkiAGHkDlLEGDPYLKq++RLRd+YittLnv+qAYtL
  gi|231685|   855 LRANYEETKNYLLKIAGHKDLLEGDPYLKQGIRLRDPYITTLNVCQAYTL 904

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y+vtlrPh+sKEyA+E+sk+adeL++Lnpt+++aPGLEDtLiL
  gi|231685|   905 KRIRDPNYHVTLRPHISKEYAAEPSKPADELIHLNPTSEYAPGLEDTLIL 954

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  gi|231685|   955 TMKGIAAGMQNTG    967

gi|1345665|sp|P30694.2|CAPP2_FLATR: domain 1 of 1, from 11 to 966: score 2683.7, E = 0
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  gi|1345665    11    SIDAQLRLLVPGKVSEDDKLVEYDALLLDKFLDILQDLHGEDLKEAV 57

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   q CYElsAeYEGK+D+kKLeELG+ LtsLd +D+i++Aka++HmLnLAnL
  gi|1345665    58 QQCYELSAEYEGKHDPKKLEELGSLLTSLDTGDSIVIAKAFSHMLNLANL 107

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEE ++AyRRRik+k  GDFaDEa+AttEsDiEEt+K+Lv klnKsPeEv
  gi|1345665   108 AEELQIAYRRRIKLKS-GDFADEANATTESDIEETFKRLVHKLNKSPEEV 156

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  gi|1345665   157 FDALKNQTVELVLTAHPTQSVRRSLLQKHGRIRNCLAQLYAKDITPDDKQ 206

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                   ELDEALHREiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|1345665   207 ELDEALHREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256
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                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinER PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1345665   257 RVDTALKNIGINERFPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmm +n+Y+sq+EDLm E+smWRCn+ELRvRAEElyrta++d  vK+Yi
  gi|1345665   306 ARMMTSNMYFSQIEDLMIEMSMWRCNSELRVRAEELYRTARKD--VKHYI 353

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK +PP+ PYRviLGdvRDKLYntRER+RHLL  G s+i++eAvyt+v
  gi|1345665   354 EFWKRIPPNQPYRVILGDVRDKLYNTRERSRHLLVDGKSDIPDEAVYTNV 403

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+ LEPLELCY+sLC+CGD+viADGsLLD+LRqvstFGLsLvKLDiRqEs
  gi|1345665   404 EQLLEPLELCYRSLCDCGDHVIADGSLLDFLRQVSTFGLSLVKLDIRQES 453

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|1345665   454 DRHTEVLDAITQHLGIGSYREWSEEKRQEWLLAELSGKRPLIGPDLPKTE 503

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  gi|1345665   504 EVKDCLDTFKVLAELPSDCFGAYIISMATSTSDVLAVELLQREYHIKHPL 553

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  gi|1345665   554 RVVPLFEKLADLEAAPAAMTRLFSMDWYRNRIDGKQEVMIGYSDSGKDAG 603

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                    R+sAAWqLYk qE i+K+AK++GvKLv+FHGRGGtvGRGGGPtHLA+Lsq
  gi|1345665   604 RFSAAWQLYKTQEQIVKIAKEFGVKLVIFHGRGGTVGRGGGPTHLALLSQ 653

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  gi|1345665   704 RPEWRELMDQMAVVATEEYRSVVFKEPRFVEYFRLATPELEFGRMNIGSR 753

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  gi|1345665   754 PSKRKPSGGIESLRAIPWIFSWTQTRFHLPVWLGFGAAFKHAIQKDSKNL 803

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  gi|1345665   804 QMLQEMYKTWPFFRVTIDLVEMVFAKGNPGIAALNDKLLVSEDLRPFGES 853

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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  gi|1345665   854 LRANYEETKNYLLKIAGHKDLLEGDPYLKQGIRLRDPYITTLNVCQAYTL 903

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                    KRiRDP+y+vtlrPh+sKEyA+E+sk+adeL++Lnpt+++aPGLEDtLiL
  gi|1345665   904 KRIRDPNYHVTLRPHISKEYAAEPSKPADELIHLNPTSEYAPGLEDTLIL 953

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                    tmKGiAAGmqntG
  gi|1345665   954 TMKGIAAGMQNTG    966

gi|2499466|sp|Q42730.1|CAPP_FLAAU: domain 1 of 1, from 11 to 966: score 2681.7, E = 0
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  gi|2499466    11    SIDAQLRLLVPGKVSEDDKLVEYDALLLDKFLDILQDLHGEDLKEAV 57

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                    q CYElsAeYEGK+D+kKLeELG+ LtsLd +D+i++Aka++HmLnLAnL
  gi|2499466    58 QQCYELSAEYEGKHDPKKLEELGSLLTSLDTGDSIVIAKAFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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  gi|2499466   157 FDALKNQTVELVLTAHPTQSVRRSLLQKHGRIRNCLAQLYAKDITPDDKQ 206

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  gi|2499466   207 ELDEALHREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

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  gi|2499466   257 RVDTALKNIGINERFPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

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  gi|2499466   306 ARMMTSNMYFSQIEDLMIEMSMWRCNSELRVRAEELYRTARKD--VKHYI 353

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  gi|2499466   354 EFWKRIPPNQPYRVILGDVRDKLYNTRERSRHLLVDGKSDIPDKAVYTNV 403

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+ LEPLELCY+sLC+CGD+viADGsLLD+LRqvstFGLsLvKLDiRqEs
  gi|2499466   404 EQLLEPLELCYRSLCDCGDHVIADGSLLDFLRQVSTFGLSLVKLDIRQES 453

                    eRqtDvlDAitthLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|2499466   454 DRHTEVLDAITQHLGIGSYREWSEEKRQEWLLAELSGKRPLIGPDLPKTE 503

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
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  gi|2499466   504 EVKDCLDTFKVLAELPSDCFGAYIISMATSTSDVLAVELLQREYHIKHPL 553

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  gi|2499466   554 RVVPLFEKLADLEAAPAAMTRLFSMDWYRNRIDGKQEVMIGYSDSGKDAG 603

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  gi|2499466   604 RFSAAWQLYKTQEQIVKIAKEFGVKLVIFHGRGGTVGRGGGPTHLALLSQ 653

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  gi|2499466   704 RPEWRELMDQMAVVATEEYRSVVFKEPRFVEYFRLATPELEFGRMNIGSR 753

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  gi|2499466   754 PSKRKPSGGIESLRAIPWIFSWTQTRFHLPVWLGFGAAFKHAIQKDSKNL 803

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+L+EmYk+WPFFRvt+DL+EmvFAKG PGiAaL+DkLLv+E+L+PFG+s
  gi|2499466   804 QMLQEMYKTWPFFRVTIDLVEMVFAKGNPGIAALNDKLLVSEDLRPFGES 853

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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  gi|2499466   854 LRANYEETKNYLLKIAGHKDLLEGDPYLKQGIRLRDPYITTLNVCQAYTL 903

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                    KRiRDP+y+vtlrPh+sKEyA+E+sk+adeL++Lnpt+++aPGLEDtLiL
  gi|2499466   904 KRIRDPNYHVTLRPHISKEYAAEPSKPADELIHLNPTSEYAPGLEDTLIL 953

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  gi|2499466   954 TMKGIAAGMQNTG    966

gi|10443872|gb|AAG17619.1|AF248080_1: domain 1 of 1, from 11 to 967: score 2674.9, E = 0
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gi|1044387    11    SIDAQLRLLVPGKVSEDDKLIEYDALLLDKFLDILQDLHGEGLKETV 57

                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                qECYElsAeYEGK+D+kKLeELG +LtsLdP+D+i++Aka++HmLnLAnL
gi|1044387    58 QECYELSAEYEGKHDPKKLEELGNVLTSLDPGDSIVIAKAFSHMLNLANL 107

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gi|1044387   108 AEEVQIAYRRRIKLKK-GDFADEASATTESDIEETFKKLVHKLKKSPEEV 156

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gi|1044387   157 FDALKNQTVDLVFTAHPTQSVRRSLLQKHGRIRDCLAQLYAKDITPDDKQ 206

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gi|1044387   207 ELDEALHREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

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gi|1044387   306 ARMMAANMYFSQIEDLMFEMSMWRCSDELRVRAEELHRSSSKR-DVKHYI 354

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gi|1044387   355 EFWKQVPPTEPYRVILGDVRDKLYNTRERARHLLAHDVSDIPEESVYTNV 404

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                E+FLEPLELCY+sLC CGD+viADGsLLD+LRqvstFGLsLv+LDiRqEs
gi|1044387   405 EQFLEPLELCYRSLCACGDRVIADGSLLDFLRQVSTFGLSLVRLDIRQES 454

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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gi|1044387   455 DRHTDVLDAITQHLEIGSYREWSEEKRQEWLLSELSGKRPLFGPDLPKTE 504

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                E++Dvld+f+vLAELP D+FGaYiismat+PsDvLAvELLqREC+vkq+L
gi|1044387   505 EIADVLDTFHVLAELPADCFGAYIISMATSPSDVLAVELLQRECHVKQPL 554

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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gi|1044387   555 RVVPLFEKLADLEAAPAAVARLFSIEWYKNRIDGKQEVMIGYSDSGKDAG 604

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLYkAqEE+i vAKk+GvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1044387   605 RLSAAWQLYKAQEELINVAKKFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 654

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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gi|1044387   655 PPETIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFCAATLEHGMNPPISP 704

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                +PEWR Lm+emAv AtE YR +v+KEPRFvEYFRlAtPElEYG+mniGsR
gi|1044387   705 RPEWRALMDEMAVYATEQYREIVFKEPRFVEYFRLATPELEYGRMNIGSR 754

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
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gi|1044387   755 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKYAIEKDIKNL 804

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                 +L+EmYk+WPFFRvt+DL+EmvFAKGDPGiAaL+DkLLv+E+L+ FG+s
gi|1044387   805 HMLQEMYKTWPFFRVTIDLVEMVFAKGDPGIAALNDKLLVSEDLWSFGES 854

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR++Y+Etk+lLLkiAGHkDlLEGDPYL+qrlRLRdsYittLnv+qAYtL
gi|1044387   855 LRANYEETKNLLLKIAGHKDLLEGDPYLRQRLRLRDSYITTLNVCQAYTL 904
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                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+vt rPh+sKEy +  sk+ade +kLnp +++aPGLEDtLiL
  gi|1044387   905 KRIRDPNYHVTFRPHISKEYSEPSSKPADEYIKLNPKSEYAPGLEDTLIL 954

                    tmKGiAAGmqntG<-*
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  gi|1044387   955 TMKGIAAGMQNTG    967

gi|228246|prf||1801241A: domain 1 of 1, from 11 to 966: score 2674.3, E = 0
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                       siDAqLRlLvPGKvsed+kL+eYDALLlDkFLDiLqDLHGedLkEav
  gi|228246|    11    SIDAQLRLLVPGKVSEDDKLVEYDALLLDKFLDILQDLHGEDLKEAV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    q CYElsAeYEGK+D+kKLeELG+ LtsLd +D+i++Aka++HmLnLAnL
  gi|228246|    58 QQCYELSAEYEGKHDPKKLEELGSLLTSLDTGDSIVIAKAFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEE ++AyRRRik+k  GDFaDEa+AttEsDiEEt+K+Lv klnKsPeEv
  gi|228246|   108 AEELQIAYRRRRIKLKS-GDFADEANATTESDIEETFKRLVHKLNKSPEEV 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+v+LvltAHPtqsvRRsLLqK++RiRnC+aqL+AKD+t++DK+
  gi|228246|   157 FDALKNQTVELVLTAHPTQSVRRSLLQKHGRIRNCIAQLYAKDITPDDKQ 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEALHREiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|228246|   207 ELDEALHREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     vDtALKniGinER PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|228246|   257 CVDTALKNIGINERFPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmm +n+Y+sq+EDLm E+smWRCn+ELRvRAEElyrta++d  vK+Yi
  gi|228246|   306 ARMMTSNMYFSQIEDLMIEMSMWRCNSELRVRAEELYRTARKD--VKHYI 353

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK +PP+ PYRviLGdvRDKLYntRER+RHLL  G s+i++eAvyt+v
  gi|228246|   354 EFWKRIPPNQPYRVILGDVRDKLYNTRERSRHLLVDGKSDIPDEAVYTNV 403

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+ LEPLELCY+sLC+CGD+viADGsLLD+LRqvstFGLsLvKLDiRqEs
  gi|228246|   404 EQLLEPLELCYRSLCDCGDHVIADGSLLDFLRQVSTFGLSLVKLDIRQES 453

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+t+vlDAit+HL+iGsYReWsEeKRqEWLlaEL+GKRPL+g+DLPktE
  gi|228246|   454 DRHTEVLDAITQHLGIGSYREWSEEKRQEWLLAELSGKRPLIGPDLPKTE 503

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    EvkD ld+f+vLAELP+D+FGaYiismat+ sDvLAvELLqRE ++k++L
  gi|228246|   504 EVKDCLDTFKVLAELPSDCFGAYIISMATSTSDVLAVELLQREYHIKHPL 553

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAa+ +LFs+DWY+nridGKqevm+GYsDsGKDAG
  gi|228246|   554 RVVPLFEKLADLEAAPAAMTRLFSMDWYRNRIDGKQEVMIGYSDSGKDAG 603

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    R+sAAWqLYk qE i+K+AK++GvKLv+FHGRGGtvGRGGGPtHLA+Lsq
  gi|228246|   604 RFSAAWQLYKTQEQIVKIAKEFGVKLVIFHGRGGTVGRGGGPTHLALLSQ 653

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGslRvtvqGEviE+sFGEE+LCFr+LqRF+AAtLEHGmnPP+sP
  gi|228246|   654 PPDTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFCAATLEHGMNPPISP 703

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    +PEWR+Lm++mAvvAtEEYRsvv+KEPRFvEYFRlAtPElE+G+mniGsR
  gi|228246|   704 RPEWRELMDQMAVVATEEYRSVVFKEPRFVEYFRLATPELEFGRMNIGSR 753

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                    P+KRkPsGGiesLRAiPWiF+WtqtRFHLPvWLG+GAAFKhAi+KD+Knl
  gi|228246|   754 PSKRKPSGGIESLRAIPWIFSWTQTRFHLPVWLGFGAAFKHAIQKDSKNL 803

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+L+EmYk+WPFFRvt+DL+EmvFAKG PGiAaL+DkLLv+E+L+PFG+
  gi|228246|   804 QMLQEMYKTWPFFRVTIDLVEMVFAKGNPGIAALNDKLLVSEDLRPFGEY 853

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Etk++LLkiAGHkDlLEGDPYLKq++RLRd+YittLnv+qAYtL
  gi|228246|   854 LRANYEETKNYLLKIAGHKDLLEGDPYLKQGIRLRDPYITTLNVCQAYTL 903

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+vtlrPh+sKEyA+E+sk+adeL++Lnpt+++aPGLEDtLiL
  gi|228246|   904 KRIRDPNYHVTLRPHISKEYAAEPSKPADELIHLNPTSEYAPGLEDTLIL 953

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|228246|   954 TMKGIAAGMQNTG    966

gi|27764449|emb|CAD60555.1|: domain 1 of 1, from 15 to 970: score 2649.3, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLR LvPGKvsed+kLieYDALL+D+FL iLqDLHG++L+E+v
  gi|2776444    15    SIDAQLRQLVPGKVSEDDKLIEYDALLVDRFLNILQDLHGPSLREFV 61

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE+sA+YEGK Dt KL+ELGakLt+L+PaDailvA++ilHmLnLAnL
  gi|2776444    62 QECYEVSADYEGKGDTTKLGELGAKLTGLAPADAILVASSILHMLNLANL 111

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A+RRR++k+k+G FaDE+sAttEsDiEEtlK+Lv+   KsPeEv
  gi|2776444   112 AEEVQIAHRRRNSKLKKGGFADEGSATTESDIEETLKRLVSEVGKSPEEV 161

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    FeALKnq+vDLv+tAHPtqs+RRsLLqKnaRiRnCL+qL AKD+t +DK+
  gi|2776444   162 FEALKNQTVDLVFTAHPTQSARRSLLQKNARIRNCLTQLNAKDITDDDKQ 211

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRRaqPtPqDEmR+GmsYiHEtvWkGvPKFLR
  gi|2776444   212 ELDEALQREIQAAFRTDEIRRAQPTPQDEMRYGMSYIHETVWKGVPKFLR 261

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinERlPY+v Li+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2776444   262 RVDTALKNIGINERLPYNVSLIRFSSWMGGDRDG-NPRVTPEVTRDVCLL 310

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlYi+q+E+LmFElsmWRCndELRvRAEEl++ + ++ v+KyYi
  gi|2776444   311 ARMMAANLYIDQIEELMFELSMWRCNDELRVRAEELHSSSGSK-VTKYYI 359

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP+EPYRviLG vRDKLYntRERaRHLLA G+seis e  +t +
  gi|2776444   360 EFWKQIPPNEPYRVILGHVRDKLYNTRERARHLLASGVSEISAESSFTSI 409

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFLEPLELCYksLC+CGDk+iADGsLLDlLRqv+tFGLsLvKLDiRqEs
  gi|2776444   410 EEFLEPLELCYKSLCDCGDKAIADGSLLDLLRQVFTFGLSLVKLDIRQES 459

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+tDv+DAittHL+iGsYReWsE+KRqEWLl+EL+GKRPLl++DLP+tE
  gi|2776444   460 ERHTDVIDAITTHLGIGSYREWSEDKRQEWLLSELRGKRPLLPPDLPQTE 509

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
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  gi|2776444   510 EIADVIGAFHVLAELPPDSFGPYIISMATAPSDVLAVELLQRECGVRQPL 559

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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  gi|2776444   560 PVVPLFERLADLQSAPASVERLFSVDWYMDRIKGKQQVMVGYSDSGKDAG 609

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLY+AqEE+++vAK+yGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|2776444   610 RLSAAWQLYRAQEEMAQVAKRYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 659
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                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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  gi|2776444   660 PPDTINGSIRVTVQGEVIEFCFGEEHLCFQTLQRFTAATLEHGMHPPVSP 709

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  gi|2776444   710 KPEWRKLMDEMAVVATEEYRSVVVKEARFVEYFRSATPETEYGRMNIGSR 759

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                    PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+AidKD++n+
  gi|2776444   760 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKFAIDKDVRNF 809

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q LkEmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLvaEeLkPFGk+
  gi|2776444   810 QVLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVAEELKPFGKQ 859

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRdkYvEt++lLL+iAGHkD+LEGDP+LKq+l LR++YittLnvfqAYtL
  gi|2776444   860 LRDKYVETQQLLLQIAGHKDILEGDPFLKQGLVLRNPYITTLNVFQAYTL 909

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP++kvt++P+lsKE+AdEn  k+++LvkLnp+++++PGLEDtLiL
  gi|2776444   910 KRIRDPNFKVTPQPPLSKEFADEN--KPAGLVKLNPASEYPPGLEDTLIL 957

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                    tmKGiAAGmqntG
  gi|2776444   958 TMKGIAAGMQNTG    970

gi|238624101|ref|NP_001154820.1|: domain 1 of 1, from 15 to 970: score 2646.7, E = 0
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                       siDAqLR LvPGKvsed+kLieYDALL+D+FL iLqDLHG++L+E+v
  gi|2386241    15    SIDAQLRQLVPGKVSEDDKLIEYDALLVDRFLNILQDLHGPSLREFV 61

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE+sA+YEGK Dt KL+ELGakLt+L+PaDailvA++ilHmLnLAnL
  gi|2386241    62 QECYEVSADYEGKGDTTKLGELGAKLTGLAPADAILVASSILHMLNLANL 111

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A+RRR++k+k+G FaDE+sAttEsDiEEtlK+Lv+   KsPeEv
  gi|2386241   112 AEEVQIAHRRRNSKLKKGGFADEGSATTESDIEETLKRLVSEVGKSPEEV 161

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|2386241   162 FEALKNQTVDLVFTAHPTQSARRSLLQKNARIRNCLTQLNAKDITDDDKQ 211

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                    ELDEAL REiqAAFRtDEiRRaqPtPqDEmR+GmsYiHEtvWkGvPKFLR
  gi|2386241   212 ELDEALQREIQAAFRTDEIRRAQPTPQDEMRYGMSYIHETVWKGVPKFLR 261

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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  gi|2386241   262 RVDTALKNIGINERLPYNVSLIRFSSWMGGDRDG-NPRVTPEVTRDVCLL 310

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|2386241   311 ARMMAANLYIDQIEELMFELSMWRCNDELRVRAEELHSSSGSK-VTKYYI 359

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP+EPYRviLG vRDKLYntRERaRHLLA G+seis e  +t +
  gi|2386241   360 EFWKQIPPNEPYRVILGHVRDKLYNTRERARHLLASGVSEISAESSFTSI 409

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFLEPLELCYksLC+CGDk+iADGsLLDlLRqv+tFGLsLvKLDiRqEs
  gi|2386241   410 EEFLEPLELCYKSLCDCGDKAIADGSLLDLLRQVFTFGLSLVKLDIRQES 459

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+tDv+DAittHL+iGsYReW+E+KRqEWLl+EL+GKRPLl++DLP+t+
  gi|2386241   460 ERHTDVIDAITTHLGIGSYREWPEDKRQEWLLSELRGKRPLLPPDLPQTD 509

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
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  gi|2386241   510 EIADVIGAFHVLAELPPDSFGPYIISMATAPSDVLAVELLQRECGVRQPL 559

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFE+LADL+ APA+ve+LFs+DWY+ ri GKq+vmvGYsDsGKDAG
  gi|2386241   560 PVVPLFERLADLQSAPASVERLFSVDWYMDRIKGKQQVMVGYSDSGKDAG 609

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLY+AqEE+++vAK+yGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|2386241   610 RLSAAWQLYRAQEEMAQVAKRYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 659

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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  gi|2386241   660 PPDTINGSIRVTVQGEVIEFCFGEEHLCFQTLQRFTAATLEHGMHPPVSP 709

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  gi|2386241   710 KPEWRKLMDEMAVVATEEYRSVVVKEARFVEYFRSATPETEYGRMNIGSR 759

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                    PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+AidKD++n+
  gi|2386241   760 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKFAIDKDVRNF 809

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                    q LkEmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLvaEeLkPFGk+
  gi|2386241   810 QVLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVAEELKPFGKQ 859

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRdkYvEt++lLL+iAGHkD+LEGDP+LKq+l LR++YittLnvfqAYtL
  gi|2386241   860 LRDKYVETQQLLLQIAGHKDILEGDPFLKQGLVLRNPYITTLNVFQAYTL 909

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                    KRiRDP++kvt++P+lsKE+AdEn  k+++LvkLnp+++++PGLEDtLiL
  gi|2386241   910 KRIRDPNFKVTPQPPLSKEFADEN--KPAGLVKLNPASEYPPGLEDTLIL 957

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                    tmKGiAAGmqntG
  gi|2386241   958 TMKGIAAGMQNTG    970

gi|162461756|ref|NP_001105418.1|: domain 1 of 1, from 15 to 970: score 2642.2, E = 0
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                       siDAqLR LvPGKvsed+kLieYDALL+D+FL iLqDLHG++L+E+v
  gi|1624617    15    SIDAQLRQLVPGKVSEDDKLIEYDALLVDRFLNILQDLHGPSLREFV 61

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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  gi|1624617    62 QECYEVSADYEGKGDTTKLGELGAKLTGLAPADAILVASSILHMLNLANL 111

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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  gi|1624617   112 AEEVQIAHRRRNSKLKKGGFADEGSATTESDIEETLKRLVSEVGKSPEEV 161

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|1624617   162 FEALKNQTVDLVFTAHPTQSARRSLLQKNARIRNCLTQLNAKDITDDDKQ 211

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|1624617   212 ELDEALQREIQAAFRTDEIRRAQPTPQAEMRYGMSYIHETVWKGVPKFLR 261

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinERlPY+v Li+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1624617   262 RVDTALKNIGINERLPYNVSLIRFSSWMGGDRDG-NPRVTPEVTRDVCLL 310

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlYi+q+E+LmFElsmWRCndELRvRAEEl++ + ++ v+KyYi
  gi|1624617   311 ARMMAANLYIDQIEELMFELSMWRCNDELRVRAEELHSSSGSK-VTKYYI 359

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP+EPYRviLG vRDKLYntRERaRHLLA G+seis e  +t +
  gi|1624617   360 EFWKQIPPNEPYRVILGHVRDKLYNTRERARHLLASGVSEISAESSFTSI 409
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                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFLEPLELCYksLC+CGDk+iADGsLLDlLRqv+tFGLsLvKLDiRqEs
  gi|1624617   410 EEFLEPLELCYKSLCDCGDKAIADGSLLDLLRQVFTFGLSLVKLDIRQES 459

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+tDv+DAittHL+iGsYReW+E+KRqEWLl+EL+GKRPLl++DLP+t+
  gi|1624617   460 ERHTDVIDAITTHLGIGSYREWPEDKRQEWLLSELRGKRPLLPPDLPQTD 509

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dv++af+vLAELP DsFG+YiismataPsDvLAvELLqRECgv+q+L
  gi|1624617   510 EIADVIGAFHVLAELPPDSFGPYIISMATAPSDVLAVELLQRECGVRQPL 559

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFE+LADL+ APA+ve+LFs+DWY+ ri GKq+vmvGYsDsGKDAG
  gi|1624617   560 PVVPLFERLADLQSAPASVERLFSVDWYMDRIKGKQQVMVGYSDSGKDAG 609

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLY+AqEE+++vAK+yGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1624617   610 RLSAAWQLYRAQEEMAQVAKRYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 659

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGs+RvtvqGEviEf FGEE+LCF++LqRFtAAtLEHGm+PPvsP
  gi|1624617   660 PPDTINGSIRVTVQGEVIEFCFGEEHLCFQTLQRFTAATLEHGMHPPVSP 709

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWRkLm+emAvvAtEEYRsvvvKE RFvEYFR+AtPE+EYG+mniGsR
  gi|1624617   710 KPEWRKLMDEMAVVATEEYRSVVVKEARFVEYFRSATPETEYGRMNIGSR 759

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+AidKD++n+
  gi|1624617   760 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKFAIDKDVRNF 809

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q LkEmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLvaEeLkPFGk+
  gi|1624617   810 QVLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVAEELKPFGKQ 859

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRdkYvEt++lLL+iAGHkD+LEGDP+LKq+l LR++YittLnvfqAYtL
  gi|1624617   860 LRDKYVETQQLLLQIAGHKDILEGDPFLKQGLVLRNPYITTLNVFQAYTL 909

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP++kvt++P+lsKE+AdEn  k+++LvkLnp+++++PGLEDtLiL
  gi|1624617   910 KRIRDPNFKVTPQPPLSKEFADEN--KPAGLVKLNPASEYPPGLEDTLIL 957

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|1624617   958 TMKGIAAGMQNTG    970

gi|212898592|gb|ACJ38542.1|: domain 1 of 1, from 15 to 970: score 2640.0, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLR LvPGKvsed+kLieYDALL+D+FL iLqDLHG++L+E+v
  gi|2128985    15    SIDAQLRQLVPGKVSEDDKLIEYDALLVDRFLNILQDLHGPSLREFV 61

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE+sA+YEGK Dt KL+ELGakLt+L+PaDailvA++ilHmLnLAnL
  gi|2128985    62 QECYEVSADYEGKGDTTKLGELGAKLTGLAPADAILVASSILHMLNLANL 111

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A+RRR++k+k+G FaDE+sAttEsDiEEtlK+Lv+   KsPeEv
  gi|2128985   112 AEEVQIAHRRRNSKLKKGGFADEGSATTESDIEETLKRLVSEVGKSPEEV 161

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    FeALKnq+vDLv+tAHPtqs+RRsLLqKnaRiRnCL+qL AKD+t +DK+
  gi|2128985   162 FEALKNQTVDLVFTAHPTQSARRSLLQKNARIRNCLTQLNAKDITDDDKQ 211

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRRaqPtPqDEmR+GmsYiHEtvWkGvPKFLR
  gi|2128985   212 ELDEALQREIQAAFRTDEIRRAQPTPQDEMRYGMSYIHETVWKGVPKFLR 261

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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                    RvDtALKniGinERlPY+v Li+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2128985   262 RVDTALKNIGINERLPYNVSLIRFSSWMGGDRDG-NPRVTPEVTRDVCLL 310

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlYi+q+E+LmFElsmWRCndELRvRAEEl++ + ++ v+KyYi
  gi|2128985   311 ARMMAANLYIDQIEELMFELSMWRCNDELRVRAEELHSSSGSK-VTKYYI 359

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    E WKq+PP+EPYRviLG vRDKLYntRERaRHLLA G+seis e  +t +
  gi|2128985   360 ELWKQIPPNEPYRVILGHVRDKLYNTRERARHLLASGVSEISAESSFTSI 409

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFLEPLELCYksLC+CGDk+iADGsLLDlLRqv+tFGLsLvKLDiRqEs
  gi|2128985   410 EEFLEPLELCYKSLCDCGDKAIADGSLLDLLRQVFTFGLSLVKLDIRQES 459

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+tDv+DAittHL+iGsYReWsE+KRqEWLl+EL+GKRPLl++DLP+tE
  gi|2128985   460 ERHTDVIDAITTHLGIGSYREWSEDKRQEWLLSELRGKRPLLPPDLPQTE 509

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dv++af+vLAELP DsFG+YiismataPsDvLAvELLqRECgv+q+L
  gi|2128985   510 EIADVIGAFHVLAELPPDSFGPYIISMATAPSDVLAVELLQRECGVRQPL 559

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFE+LA L+ APA+ve+LFs+DWY+ ri GKq+vmvGYsDsGKDAG
  gi|2128985   560 PVVPLFERLAYLQSAPASVERLFSVDWYMDRIKGKQQVMVGYSDSGKDAG 609

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLY+AqEE+++vAK+yGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|2128985   610 RLSAAWQLYRAQEEMAQVAKRYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 659

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGs+RvtvqGEviEf FGEE+LCF++LqRFtAAtLEHGm+PPvsP
  gi|2128985   660 PPDTINGSIRVTVQGEVIEFCFGEEHLCFQTLQRFTAATLEHGMHPPVSP 709

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWRkLm+emAvvAtEEYRsvvvKE RFvEYFR+AtPE+EYG+mniGsR
  gi|2128985   710 KPEWRKLMDEMAVVATEEYRSVVVKEARFVEYFRSATPETEYGRMNIGSR 759

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+AidKD++n+
  gi|2128985   760 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKFAIDKDVRNF 809

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q LkEmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLvaEeLkPFGk+
  gi|2128985   810 QVLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVAEELKPFGKQ 859

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRdkYvEt++lLL+iAGHkD+LEGDP+LKq+l LR++YittLnvfqAYtL
  gi|2128985   860 LRDKYVETQQLLLQIAGHKDILEGDPFLKQGLVLRNPYITTLNVFQAYTL 909

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP++kvt++P+lsKE+AdEn  k+++LvkLnp+++++PGLEDtLiL
  gi|2128985   910 KRIRDPNFKVTPQPPLSKEFADEN--KPAGLVKLNPASEYPPGLEDTLIL 957

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|2128985   958 TMKGIAAGMQNTG    970

gi|295855|emb|CAA33663.1|: domain 1 of 1, from 15 to 970: score 2637.5, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLR LvPGKvsed+kLieYDALL+D+FL iLqDLHG++L+E+v
  gi|295855|    15    SIDAQLRQLVPGKVSEDDKLIEYDALLVDRFLNILQDLHGPSLREFV 61

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE+sA+YEGK Dt KL+ELGakLt+L+PaDailvA++ilHmLnLAnL
  gi|295855|    62 QECYEVSADYEGKGDTTKLGELGAKLTGLAPADAILVASSILHMLNLANL 111

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A+RRR++k+k+G FaDE+sAttEsDiEEtlK+Lv+   KsPeEv
  gi|295855|   112 AEEVQIAHRRRRNSKLKKGGFADEGSATTESDIEETLKRLVSEVGKSPEEV 161
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                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    FeALKnq+vDLv+tAHPtqs+RRsLLqKnaRiRnCL+qL AKD+t +DK+
  gi|295855|   162 FEALKNQTVDLVFTAHPTQSARRSLLQKNARIRNCLTQLNAKDITDDDKQ 211

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRRaqPtPqDEmR+GmsYiHEtvWkGvPKFLR
  gi|295855|   212 ELDEALQREIQAAFRTDEIRRAQPTPQDEMRYGMSYIHETVWKGVPKFLR 261

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinERlPY+v Li+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|295855|   262 RVDTALKNIGINERLPYNVSLIRFSSWMGGDRDG-NPRVTPEVTRDVCLL 310

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlYi+q+E+LmFElsmWRCndELRvRAEEl++ + ++ v+KyYi
  gi|295855|   311 ARMMAANLYIDQIEELMFELSMWRCNDELRVRAEELHSSSGSK-VTKYYI 359

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP+EPYRviLG vRDKLYntRERaRHLLA G+seis e  +t +
  gi|295855|   360 EFWKQIPPNEPYRVILGHVRDKLYNTRERARHLLASGVSEISAESSFTSI 409

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFLEPLELCYksLC+CGDk+iADGsLLDlLRqv+tFGLsLvKLDiRqEs
  gi|295855|   410 EEFLEPLELCYKSLCDCGDKAIADGSLLDLLRQVFTFGLSLVKLDIRQES 459

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+tDv+DAittHL+iGsYReWsE+KRqEWLl+EL+GKRPLl++DLP+tE
  gi|295855|   460 ERHTDVIDAITTHLGIGSYREWSEDKRQEWLLSELRGKRPLLPPDLPQTE 509

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dv++af+vLAELP DsFG+YiismataPsDvLAvELLqRECgv+ ++
  gi|295855|   510 EIADVIGAFHVLAELPPDSFGPYIISMATAPSDVLAVELLQRECGVRPAV 559

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFE+LA L+ APA+ve+LFs+DWY+ ri GKq+vmvGYsDsGKDAG
  gi|295855|   560 PVVPLFERLASLQSAPASVERLFSVDWYMDRIKGKQQVMVGYSDSGKDAG 609

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLY+AqEE+++vAK+yGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|295855|   610 RLSAAWQLYRAQEEMAQVAKRYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 659

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGs+RvtvqGEviEf FGEE+LCF++LqRFtAAtLEHGm+PPvsP
  gi|295855|   660 PPDTINGSIRVTVQGEVIEFCFGEEHLCFQTLQRFTAATLEHGMHPPVSP 709

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWRkLm+emAvvAtEEYRsvvvKE RFvEYFR+AtPE+EYG+mniGsR
  gi|295855|   710 KPEWRKLMDEMAVVATEEYRSVVVKEARFVEYFRSATPETEYGRMNIGSR 759

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+AidKD++n+
  gi|295855|   760 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKFAIDKDVRNF 809

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q LkEmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLvaEeLkPFGk+
  gi|295855|   810 QVLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVAEELKPFGKQ 859

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRdkYvEt++lLL+iAGHkD+LEGDP+LKq+l LR++YittLnvfqAYtL
  gi|295855|   860 LRDKYVETQQLLLQIAGHKDILEGDPFLKQGLVLRNPYITTLNVFQAYTL 909

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP++kvt++P+lsKE+AdEn  k+++LvkLnp+++++PGLEDtLiL
  gi|295855|   910 KRIRDPNFKVTPQPPLSKEFADEN--KPAGLVKLNPASEYPPGLEDTLIL 957

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|295855|   958 TMKGIAAGMQNTG    970

gi|224121514|ref|XP_002330719.1|: domain 1 of 1, from 3 to 957: score 2623.3, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
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                  siDAqLRlL+PGKvsed+kLieYDALLlD+FLDiLqDLHGedLkE v
gi|2241215     3  SIDAQLRLLAPGKVSEDDKLIEYDALLLDRFLDILQDLHGEDLKETV 49

                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                qECYElsAeYEGK+D+kKLeELG++LtsLdP+D+i++Ak+++HmLnLAnL
gi|2241215    50 QECYELSAEYEGKHDPKKLEELGSVLTSLDPGDSIVIAKSFSHMLNLANL 99

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AEEv++AyRRR+k+kk GDFaDE +AttEsDiEEtlK+Lv+   KsPeEv
gi|2241215   100 AEEVQIAYRRRNKLKK-GDFADENNATTESDIEETLKRLVSEMKKSPEEV 148

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                F+ALKnq+v+Lv+tAHPtqsvRRsLLqK+aRiRnCLaqL+AKD+t++DK+
gi|2241215   149 FDALKNQTVELVFTAHPTQSVRRSLLQKHARIRNCLAQLYAKDITPDDKQ 198

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
gi|2241215   199 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 248

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
gi|2241215   249 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 297

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                aRmmAanlY+sq+EDLmFElsmWRC dELR RA+El+r ++rd   K+Yi
gi|2241215   298 ARMMAANLYYSQIEDLMFELSMWRCSDELRLRADELHRSSKRD--AKHYI 345

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                EFWKq+PP+EPYRviLG+ RDKLY tRER+R LL +Gisei+EeA + +v
gi|2241215   346 EFWKQIPPNEPYRVILGELRDKLYQTRERSRQLLSHGISEIPEEATFINV 395

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                E+FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
gi|2241215   396 EQFLEPLELCYRSLCSCGDRTIADGSLLDFLRQVSTFGLSLVRLDIRQES 445

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                +R+tDvlDAit+HLeiGsYReWsEe+RqEWLl+EL+GKRPL+g+DLPktE
gi|2241215   446 DRHTDVLDAITKHLEIGSYREWSEERRQEWLLSELRGKRPLFGPDLPKTE 495

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                E+ Dvld+f+v+AELP D FGaYiismataPsDvLAvELLqREC+vkq+L
gi|2241215   496 EISDVLDTFHVIAELPADNFGAYIISMATAPSDVLAVELLQRECHVKQPL 545

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                rvvPLFEkLADLeAAPAa+ +LFsiDWY+nri+G qevm+GYsDsGKDAG
gi|2241215   546 RVVPLFEKLADLEAAPAALVRLFSIDWYRNRINGIQEVMIGYSDSGKDAG 595

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                R+sAAWqLYkAqEE+iKvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|2241215   596 RFSAAWQLYKAQEELIKVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 645

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PPDti+GslRvtvqGEviE  FGEE+LCFr+LqRFtAAtLEHGm+PPvsP
gi|2241215   646 PPDTIHGSLRVTVQGEVIEKCFGEEHLCFRTLQRFTAATLEHGMHPPVSP 695

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                kPEWR Lm+emAvvAtEEYRs+v+KEPRFvEYFRlAtPE+EYG+mniGsR
gi|2241215   696 KPEWRALMDEMAVVATEEYRSIVFKEPRFVEYFRLATPEMEYGRMNIGSR 745

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KDi+nl
gi|2241215   746 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIIQKDIRNL 795

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                 +L+EmY+ WPFFRvt+DL+EmvFAKGDPGiAaL+DkLLv+E+L+ FG++
gi|2241215   796 HMLQEMYNAWPFFRVTIDLVEMVFAKGDPGIAALNDKLLVSEDLWAFGEK 845

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR++Y+Etk lLL+iAGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
gi|2241215   846 LRADYEETKGLLLQIAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 895
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                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y vt rPh+sKE   E s +adeLvkLnpt+++ PGLEDtLiL
  gi|2241215   896 KRIRDPNYNVTTRPHISKEIM-ESSNPADELVKLNPTSEYGPGLEDTLIL 944

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|2241215   945 TMKGIAAGMQNTG    957

gi|224114804|ref|XP_002316861.1|: domain 1 of 1, from 12 to 966: score 2618.6, E = 0
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                       siDAqLRlLvPGKvsed+kLieYDALLlD+FLDiLqDLHGedLkE v
  gi|2241148    12    SIDAQLRLLVPGKVSEDDKLIEYDALLLDRFLDILQDLHGEDLKETV 58

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYElsAeYEGK+D+kKLeELG++LtsLdP+D+i++Ak+++HmLnLAnL
  gi|2241148    59 QECYELSAEYEGKHDPKKLEELGSVLTSLDPGDSIVIAKSFSHMLNLANL 108

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRR+k+kk GDFaDE sAttEsDiEEtl++Lv+ l KsPeEv
  gi|2241148   109 AEEVQIAYRRRNKLKK-GDFADENSATTESDIEETLRRLVVDLKKSPEEV 157

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+vDLvltAHPtqsvRRsLLqK+aR+RnCLaqL+AKD+t+++K+
  gi|2241148   158 FDALKNQTVDLVLTAHPTQSVRRSLLQKHARLRNCLAQLYAKDITPNEKQ 207

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|2241148   208 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 257

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2241148   258 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 306

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq+EDLmFElsmWRC dELRvRA+ l+r ++rd   K+Yi
  gi|2241148   307 ARMMAANLYYSQIEDLMFELSMWRCSDELRVRADVLHRSSKRD--SKHYI 354

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP+EPYRviLG+ RD+LY tRER+R LL +Gise +EeA +t+v
  gi|2241148   355 EFWKQIPPNEPYRVILGELRDRLYQTRERSRQLLSHGISETPEEATFTNV 404

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|2241148   405 EQFLEPLELCYRSLCSCGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 454

                    eRqtDvlDAitthLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDv+DAit+HLeiGsYReWsEe+RqEWLl+EL+GKRPL+g+DLPktE
  gi|2241148   455 DRHTDVMDAITKHLEIGSYREWSEEQRQEWLLSELSGKRPLFGPDLPKTE 504

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+f+v+AELP+DsFGaYiismata sDvLAvELLqREC+vkq+L
  gi|2241148   505 EIADVLDTFHVIAELPSDSFGAYIISMATAASDVLAVELLQRECHVKQPL 554

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAa+ +LFsi+WY+ +i+GKqevm+GYsDsGKDAG
  gi|2241148   555 RVVPLFEKLADLEAAPAALSRLFSIEWYRDQINGKQEVMIGYSDSGKDAG 604

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    R+sAAWqLYkAqEE+iKvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2241148   605 RFSAAWQLYKAQEELIKVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 654

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRF+AAtLEHGm+PPvsP
  gi|2241148   655 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFAAATLEHGMHPPVSP 704

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAvvAtEEYRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|2241148   705 KPEWRALMDEMAVVATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 754

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
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                    +L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaL+DkLLv+ eL+PFG++
  gi|2241148   805 HMLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALNDKLLVSKELWPFGEK 854

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Etk lLL+iAGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|2241148   855 LRANYKETKSLLLQIAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 904

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y vt+rPhlsKE  + n k+adeLvkLnpt+ +aPG+EDtLiL
  gi|2241148   905 KRIRDPNYCVTPRPHLSKEIMESN-KPADELVKLNPTSDYAPGMEDTLIL 953

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|2241148   954 TMKGIAAGMQNTG    966

gi|155967407|gb|ABU41519.1|: domain 1 of 1, from 11 to 965: score 2616.4, E = 0
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                      siDAqLRlL+P Kvsed+kL+eYDALLlD+FLDiLqDLHGed++E v
  gi|1559674    11    SIDAQLRLLAPRKVSEDDKLVEYDALLLDRFLDILQDLHGEDIRETV 57

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qECYE+sA YE K+D++KLeELG +LtsLdP+D+i+v k+++HmLnLAnL
  gi|1559674    58 QECYEISAGYERKHDPQKLEELGKVLTSLDPGDSIVVTKSFSHMLNLANL 107

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++AyRRR k kk GDFaDE sAttEsD+EEt+KkLv++l KsPeEv
  gi|1559674   108 AEEVQIAYRRRTKSKK-GDFADENSATTESDMEETFKKLVVQLKKSPEEV 156

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   F+ALKnq+vDLvltAHPtqsvRRsLLqK+aRiRnCL+qL+AKD+t++DK+
  gi|1559674   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHARIRNCLTQLYAKDITPDDKQ 206

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|1559674   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALKniGinERlPY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1559674   257 RVDTALKNIGINERLPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmAanlY+sq+EDLmFElsmWRCn+ELR RA+ l+r +++d   K+Yi
  gi|1559674   306 ARMMAANLYFSQIEDLMFELSMWRCNEELRFRADALHRSSRKD--AKHYI 353

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWKq+PP+EPYRviLGdvRDKLYntRER+RHLL  Gis+i+EeA +t+v
  gi|1559674   354 EFWKQIPPNEPYRVILGDVRDKLYNTRERSRHLLTNGISDIPEEATFTNV 403

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   E+FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|1559674   404 EQFLEPLELCYRSLCACGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 453

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +R+tDvlDAit+HL+iGsYReWsEe+RqEWLl+EL+GKRPL+g+DLPktE
  gi|1559674   454 DRHTDVLDAITKHLGIGSYREWSEERRQEWLLSELRGKRPLFGPDLPKTE 503

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dvld+f+v+AELP D FGaYiismataPsDvLAvELLqREC vkq+L
  gi|1559674   504 EIADVLDTFHVIAELPPDNFGAYIISMATAPSDVLAVELLQRECRVKQPL 553

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAav +LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|1559674   554 RVVPLFEKLADLEAAPAAVSRLFSIDWYRNRINGKQEVMIGYSDSGKDAG 603

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE++KvAK+yGvKLv+FHGRGGtvGRGGGPtHLAiLsq
  gi|1559674   604 RLSAAWQLYKAQEELVKVAKQYGVKLVMFHGRGGTVGRGGGPTHLAILSQ 653
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                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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  gi|1559674   654 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 703

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                    kPEWR L++emA++At EYRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|1559674   704 KPEWRALLDEMAIIATKEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 753

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD Knl
  gi|1559674   754 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIIEKDRKNL 803

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+L+EmY++WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+EeL+PFG++
  gi|1559674   804 QMLQEMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEELWPFGER 853

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Etk lLL+iAGHkDlLEGDPYLKqrlRLRd+YittLnv qAYtL
  gi|1559674   854 LRANYEETKHLLLQIAGHKDLLEGDPYLKQRLRLRDAYITTLNVSQAYTL 903

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+vtlrPhlsKEy  E sk+a+eLvkLnp +++aPGLEDtLiL
  gi|1559674   904 KRIRDPDYHVTLRPHLSKEYT-ESSKPAAELVKLNPMSEYAPGLEDTLIL 952

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                    tmKGiAAGmqntG
  gi|1559674   953 TMKGIAAGMQNTG    965

gi|259506726|gb|ABK54024.2|: domain 1 of 1, from 12 to 967: score 2612.4, E = 0
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  gi|2595067    12    SIDAQLRLLVPRKVSEDDKLIEYDALLLDRFLDILQDLHGEDLKETV 58

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYEl+AeYEGK D++K  ELG +LtsLdP+D+i++Aka++HmLnLAnL
  gi|2595067    59 QECYELAAEYEGKNDPSKFKELGNVLTSLDPGDSIVIAKAFSHMLNLANL 108

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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  gi|2595067   109 AEELQIAHRRRRIKKLKKGDFADENSATTESDIEETFKRLVGELNKSPEEI 158

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  gi|2595067   159 FDALKNQTVDLVLTAHPTQSVRRSLLQKHARIRNCLAQLYAKDITPDDKQ 208

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                    ELDEAL REiqAAFRtDEiRR+qPtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|2595067   209 ELDEALQREIQAAFRTDEIRRTQPTPQDEMRAGMSYFHETIWKGVPKFLR 258

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  gi|2595067   259 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 307

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|2595067   308 ARMMAANLYYSQIEDLMFEMSMWRCSDELRHRADVLHRSSKKD--AKHYI 355

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
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  gi|2595067   356 EFWKQIPPNEPYRVILGDVRDKLYQTRERVRQLLAHGISDIPEEAVFTNV 405

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC CGD++iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|2595067   406 EQFLEPLELCYRSLCSCGDRAIADGSLLDFLRQVSTFGLSLVRLDIRQES 455

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|2595067   456 DRHTDVIDAITKHLEIGSYREWSEEKRQEWLLSELRGKRPLFGPDLPKTE 505

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                   rvvPLFEkLADLeAAPAa+++LFs+DWY+nri+GKqevm+GYsDsGKDAG
  gi|2595067   556 RVVPLFEKLADLEAAPAALARLFSVDWYRNRINGKQEVMIGYSDSGKDAG 605

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   R+sAAWqLYkAqEE+iKvAK+yG+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2595067   606 RFSAAWQLYKAQEELIKVAKQYGIKLTMFHGRGGTVGRGGGPTHLAILSQ 655

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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  gi|2595067   656 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPISP 705

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                   kPEWR Lm+emAv+At EYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|2595067   706 KPEWRALMDEMAVIATKEYRSIVFQEPRFVEYFRLATPEMEYGRMNIGSR 755

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                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KDiKnl
  gi|2595067   756 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIQKDIKNL 805

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                    +L+EmY+ WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+EeL+PFG++
  gi|2595067   806 HMLQEMYNLWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEELQPFGEK 855

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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  gi|2595067   856 LRANFAETKSLLLQVAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 905

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                   K iRDP+++v +rPhlsKEy +   k+a+eLv+Lnpt+++aPGLEDt+iL
  gi|2595067   906 KQIRDPNFHVKVRPHLSKEYMESR-KPAAELVRLNPTSEYAPGLEDTVIL 954

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                   tmKGiAAGmqntG
  gi|2595067   955 TMKGIAAGMQNTG    967

gi|2266947|gb|AAB80714.1|: domain 1 of 1, from 11 to 965: score 2610.3, E = 0
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  gi|2266947    11    SIDAQLRLLAPGKVSEDDKLVEYDAVLLDRFLDILQDLHGEDIRETV 57

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qECYElsAeYEGK+D+k LeELG +LtsLdP+D+i+v k+++HmLnL nL
  gi|2266947    58 QECYELSAEYEGKHDPKILEELGKVLTSLDPGDSIVVTKSFSHMLNLGNL 107

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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  gi|2266947   108 AEEVQIAYRRRRIKLKK-GDFADESSATTESDIEETFKRLVGQLNKSPEEV 156

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  gi|2266947   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLTQLYAKDITPDDKQ 206

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL REiqAAFRtDEiRR +PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|2266947   207 ELDEALQREIQAAFRTDEIRRNPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

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  gi|2266947   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

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                   aRmmAanlY+sq+EDLmFElsmWRC dELR+RA+El+r +++d   K+Yi
  gi|2266947   306 ARMMAANLYFSQIEDLMFELSMWRCSDELRIRADELHRSSKKD--AKHYI 353

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWKq+PP+EPYR+iLGdvRDKLYntRERaR LLA G+s+i+EeA +t+v
  gi|2266947   354 EFWKQIPPNEPYRIILGDVRDKLYNTRERARSLLANGFSDIPEEAAFTNV 403
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                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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  gi|2266947   404 EQFLEPLELCYRSLCACGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 453

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlDAit+HL+iGsYReW+Ee+RqEWLl+EL+GKRPL+g+DLPktE
  gi|2266947   454 DRHTDVLDAITKHLDIGSYREWPEERRQEWLLSELRGKRPLFGPDLPKTE 503

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
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  gi|2266947   504 EVADVLDTFHVISELPSDSFGAYIISMATAPSDVLAVELLQRECHVKQPL 553

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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  gi|2266947   554 RVVPLFEKLADLEAAPAAVARLFSIDWYRDRINGKQEVMIGYSDSGKDAG 603

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  gi|2266947   604 RLSAAWQLYKAQEELVKVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 653

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  gi|2266947   654 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 703

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  gi|2266947   704 NPEWRALMDEMAVVATKEYRSVVFQEPRFVEYFRLATPELEYGRMNIGSR 753

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  gi|2266947   754 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIQKDIKNL 803

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+Em ++WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+ eL+PFG++
  gi|2266947   804 HMLQEMHNQWPFFRVTMDLIEMVFAKGDPGIAALYDKLLVSKELWPFGEN 853

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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  gi|2266947   854 LRANYEDTKRLVLQVAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 903

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  gi|2266947   904 KRIRDPDYHVKVRPHLSREYM-ESSKAAAELVKLNPTSEYAPGLEDTLIL 952

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  gi|2266947   953 TMKGIAAGMQNTG    965

gi|255553993|ref|XP_002518037.1|: domain 1 of 1, from 11 to 965: score 2604.3, E = 0
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  gi|2555539    11    SIDAQLRLLAPRKVSEDDKLVEYDALLLDRFLDILQDLHGEDIRETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    q+CYElsAeYEGK+ ++KL ELG +LtsLdP+D+i+v k+++HmLnLAnL
  gi|2555539    58 QDCYELSAEYEGKHNPQKLAELGKVLTSLDPGDSIVVTKSFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRRik+kk GDFaDE sAttEsDiEEtlK+Lv++l KsPeEv
  gi|2555539   108 AEEVQIAYRRRIKLKK-GDFADENSATTESDIEETLKRLVVQLKKSPEEV 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|2555539   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHARIRDCLTQLYAKDITPDDKQ 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|2555539   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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                   aRmmAanlY+sq+EDLmFElsmWRCn+ELRvRA+El+rt+++d   K+Yi
  gi|2555539   306 ARMMAANLYFSQIEDLMFELSMWRCNEELRVRADELHRTSRKD--AKHYI 353

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWKq+PP EPYRviLGdvRDKLYntRER+R LLA Gis+i+EeA +t+v
  gi|2555539   354 EFWKQIPPSEPYRVILGDVRDKLYNTRERSRQLLANGISDIPEEATFTNV 403

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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  gi|2555539   404 EQFLEPLELCYRSLCACGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 453

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  gi|2555539   454 ERHTDVLDAITKHLGIGFYREWSEEHRQEWLLTELRGKRPLFGPDLPKTD 503

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  gi|2555539   504 EIADVLDTFHVIAELPADNFGAYIISMATAPSDVLAVELLQRECRVKQPL 553

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  gi|2555539   554 RVVPLFEKLADLEAAPAAVARLFSIDWYRNRINGKQEVMIGYSDSGKDAG 603

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
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                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|2555539   654 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 703

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  gi|2555539   704 KPEWRTLLDEMAVIATKEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 753

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  gi|2555539   754 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGPAFKHVIEKDVRNL 803

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  gi|2555539   804 HMLQEMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEELWPFGER 853

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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  gi|2555539   854 LRVNYEETKHLLLQVAGHKDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 903

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                   KRiRDP+y+vtlrPhlsKE+  E sk+a+eLvkLnp +++aPGLEDtLiL
  gi|2555539   904 KRIRDPDYHVTLRPHLSKEHM-ESSKPAAELVKLNPRSEYAPGLEDTLIL 952

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  gi|2555539   953 TMKGIAAGMQNTG    965

gi|255579064|ref|XP_002530381.1|: domain 1 of 1, from 11 to 965: score 2604.3, E = 0
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  gi|2555790    11    SIDAQLRLLVPAKVSEDDKLVEYDALLLDRFLDILQDLHGEDLKETV 57

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qECYElsAeYEGK+D++KL+ELG  LtsLdP+D+i++Ak+++HmLnLAnL
  gi|2555790    58 QECYELSAEYEGKHDPRKLDELGNLLTSLDPGDSIVIAKSFSHMLNLANL 107

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++AyRRR+k+kk GDFaDE sAttEsDiEEt+K+Lv  l KsPeEv
  gi|2555790   108 AEEVQIAYRRRRNKLKK-GDFADENSATTESDIEETFKRLVIDLKKSPEEV 156
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                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|2555790   157 FDALKNQTVDLVLTAHPTQSIRRSLLQKHARIRNCLAQLYAKDITPDDKQ 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR+ PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|2555790   207 ELDEALQREIQAAFRTDEIRRTAPTPQDEMRAGMSYFHETIWKGVPKFLR 256

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                    RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2555790   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq+EDLmFElsmWRC dELRvRA+El+r ++rd   K+Yi
  gi|2555790   306 ARMMAANLYYSQIEDLMFELSMWRCSDELRVRADELHRSSKRD--SKHYI 353

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  gi|2555790   354 EFWKQVPPSEPYRVILGDLRDKLYQTRERSRQMLSHGNSDIPEEATFTNV 403

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFG sLv+LDiRqEs
  gi|2555790   404 EQFLEPLELCYRSLCSCGDQPIADGSLLDFLRQVSTFGFSLVRLDIRQES 453

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  gi|2555790   454 DRHTDVIDTITKHLEIGSYREWSEERRQEWLLSELSGKRPLFGPDLQRTD 503

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  gi|2555790   504 EVADVLDTFHVIAELPADSFGAYIISMATAPSDVLAVELLQRECHVKQPL 553

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  gi|2555790   604 RFSAAWQLYKAQEELIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 653

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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  gi|2555790   654 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 703

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  gi|2555790   804 HMLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSQDLWSFGER 853

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  gi|2555790   854 LRTNYEETKRLLLQIAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 903

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  gi|2555790   904 KRIRDPNYNVTLRPHISKEIM-ESSKPADELVKLNPKSDYAPGLEDTLIL 952

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  gi|2555790   953 TMKGVAAGLQNTG    965

gi|972511|emb|CAA62469.1|: domain 1 of 1, from 11 to 965: score 2602.4, E = 0
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                   qECYElsAeYE K+D+kKLeELG +LtsLdP+D+i++Aka++HmLnLAnL
gi|972511|    58 QECYELSAEYEAKHDPKKLEELGNVLTSLDPGDSIVIAKAFSHMLNLANL 107

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++AyRRR k+kk+GDF DE++AttEsDiEEt+KkLv  l KsP+Ev
gi|972511|   108 AEEVQIAYRRRQKLKKKGDFGDESNATTESDIEETFKKLVGDLKKSPQEV 157

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gi|972511|   158 FDAIKNQTVDLVLTAHPTQSVRRSLLQKHGRIRDCLAQLYAKDITPDDKQ 207

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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gi|972511|   208 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 257

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gi|972511|   258 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 306

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gi|972511|   307 ARMMAANLYYSQIEDLMFELSMWRCNEELRVRADDLQRSSRRD--EKHYI 354

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gi|972511|   355 EFWKQVPPNEPYRVILGDVRDKLYQTRERARQLLGHGYSEIPEEATYTNI 404

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   E+FLEPLELCY+sLC CGD  iADGsLLD+LRqvstFGLsLv+LDiRqEs
gi|972511|   405 EQFLEPLELCYRSLCACGDLSIADGSLLDFLRQVSTFGLSLVRLDIRQES 454

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gi|972511|   555 RVVPLFEKLADLDAAPAAVARLFSIEWYRNRINGKQEVMIGYSDSGKDAG 604

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gi|972511|   605 RLSAAWQLYKAQEELIQVAKEFDVKLTMFHGRGGTVGRGGGPAHLAILSQ 654

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gi|972511|   655 PPETIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 704

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gi|972511|   755 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKYAIEKDIKNL 804

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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gi|972511|   805 RMLQEMYNAWPFFRVTIDLVEMVFAKGDPGIAALFDKLLVSEDLWSFGEL 854

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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gi|972511|   855 LRSKYEETKSLLLQIAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 904

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  gi|972511|   905 KRIRDPDYSVTPRPHISKEYMEAK--PATELVNLNPTSEYAPGLEDTLIL 952

                    tmKGiAAGmqntG<-*
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  gi|972511|   953 TMKGIAAGMQNTG    965

gi|1168761|sp|P29196.2|CAPP_SOLTU: domain 1 of 1, from 11 to 965: score 2602.4, E = 0
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  gi|1168761    11    SIDAQLRQLVPAKVSEDDKLVEYDALLLDRFLDILQDLHGEDLKETV 57

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  gi|1168761    58 QECYELSAEYEAKHDPKKLEELGNVLTSLDPGDSIVIAKAFSHMLNLANL 107

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  gi|1168761   108 AEEVQIAYRRRQKLKKKGDFGDESNATTESDIEETFKKLVGDLKKSPQEV 157

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  gi|1168761   158 FDAIKNQTVDLVLTAHPTQSVRRSLLQKHGRIRDCLAQLYAKDITPDDKQ 207

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  gi|1168761   208 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 257

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  gi|1168761   258 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 306

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  gi|1168761   307 ARMMAANLYYSQIEDLMFELSMWRCNEELRVRADDLQRSSRRD--EKHYI 354

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                    EFWKqvPP+EPYRviLGdvRDKLY tRERaR LL +G+sei+EeA yt++
  gi|1168761   355 EFWKQVPPNEPYRVILGDVRDKLYQTRERARQLLGHGYSEIPEEATYTNI 404

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                    E++Dvld+f+v+AELP D+FGaYiismataPsDvLAvELLqREC v+q+L
  gi|1168761   505 EIADVLDTFHVIAELPADCFGAYIISMATAPSDVLAVELLQRECRVRQPL 554

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                    rvvPLFEkLADL+AAPAav++LFsi+WY+nri+GKqevm+GYsDsGKDAG
  gi|1168761   555 RVVPLFEKLADLDAAPAAVARLFSIEWYRNRINGKQEVMIGYSDSGKDAG 604

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+i+vAK++ vKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1168761   605 RLSAAWQLYKAQEELIQVAKEFDVKLTMFHGRGGTVGRGGGPAHLAILSQ 654

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  gi|1168761   655 PPETIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 704

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                    kPEWR Lm+e+AvvAtE YRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|1168761   705 KPEWRALMDEIAVVATEKYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 754

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                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFK+Ai+KDiKnl
  gi|1168761   755 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKYAIEKDIKNL 804
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  gi|1168761   805 RMLQEMYNAWPFFRVTIDLVEMVFAKGDPGIAALFDKLLVSEDLWSFGEL 854

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR kY+Etk lLL+iAGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|1168761   855 LRSKYEETKSLLLQIAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 904

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                    KRiRDP+y vt+rPh+sKEy +    +a eLv Lnpt+++aPGLEDtLiL
  gi|1168761   905 KRIRDPDYSVTPRPHISKEYMEAK--PATELVNLNPTSEYAPGLEDTLIL 952

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                    tmKGiAAGmqntG
  gi|1168761   953 TMKGIAAGMQNTG    965

gi|149789414|gb|ABR29878.1|: domain 1 of 1, from 11 to 965: score 2598.1, E = 0
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  gi|1497894    11    SIDAQLRLLALRKVSEDDKLVEYDALLLDRFLDILQDLHGEDIRETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    q+CYElsAeYEGK+ ++KL ELG +LtsLdP+D+i+v k+++HmLnLAnL
  gi|1497894    58 QDCYELSAEYEGKHNPQKLAELGKVLTSLDPGDSIVVTKSFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRRik+kk GDFaDE sAttEsDiEEtlK+Lv++l KsPeEv
  gi|1497894   108 AEEVQIAYRRRIKLKK-GDFADENSATTESDIEETLKRLVVQLKKSPEEV 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|1497894   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHARIRDCLTQLYAKDITPDDKQ 206

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  gi|1497894   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1497894   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|1497894   306 ARMMAANLYFSQIEDLMFELSMWRCNEELRVRADELHRTSRKD--AKHYI 353

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                    EFWKq+PP EPYRviLGdvRDKLYntRER+R LLA Gis+i+EeA +t+v
  gi|1497894   354 EFWKQIPPSEPYRVILGDVRDKLYNTRERSRQLLANGISDIPEEATFTNV 403

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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  gi|1497894   404 EQFLEPLELCYRSLCACGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 453

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  gi|1497894   454 ERHTDVLDAITKHLGIGFYREWSEEHRQEWLLTELRGKRPLFGPDLPKTD 503

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  gi|1497894   504 EIADVLDTFHVIAELPADNFGAYIISMATAPSDVLAVELLQRECRVKQPL 553

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  gi|1497894   554 RVVPLFEKLADLEAAPAAVARLFSIDWYRNRINGKQEVMIGYSDSGKDAG 603

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  gi|1497894   604 RLSAAWQLYKAQEELVKVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 653

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                    kPEWR L++emAv+At EYRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|1497894   704 KPEWRTLLDEMAVIATKEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 753

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  gi|1497894   754 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGPAFKHVIEKDVRNL 803

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  gi|1497894   804 HMLQEMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEELWPFGER 853

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Etk lLL++AGHkDlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|1497894   854 LRVNYEETKHLLLQVAGHKDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 903

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+vtlrPhlsKE+  E sk+a+eLvkLnp +++aPGLEDtLiL
  gi|1497894   904 KRIRDPDYHVTLRPHLSKEHM-ESSKPAAELVKLNPRSEYAPGLEDTLIL 952

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|1497894   953 TMKGIAAGMQNTG    965

gi|157812633|gb|ABV80356.1|: domain 1 of 1, from 17 to 971: score 2594.7, E = 0
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                       siDAqLR LvP Kvsed+kL+eYDALLlD+FLDiLqDLHGedLkE v
  gi|1578126    17    SIDAQLRQLVPAKVSEDDKLVEYDALLLDRFLDILQDLHGEDLKETV 63

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYElsAeYEGK  +kKLeELG +LtsLdP+D+i++Aka++HmLnLA L
  gi|1578126    64 QECYELSAEYEGKSTPKKLEELGNVLTSLDPGDSIVIAKAFSHMLNLADL 113

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRRik+kk GDFaDE sAttEsDiEEtlK+Lv+ l KsPeEv
  gi|1578126   114 AEEVQIAYRRRIKLKK-GDFADENSATTESDIEETLKRLVVDLKKSPEEV 162

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|1578126   163 FDALKNQTVDLVFTAHPTQSVRRSLLQKHGRIRNCLAQLYAKDITPDDKQ 212

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEtvWkGvPKFLR
  gi|1578126   213 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETVWKGVPKFLR 262

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  gi|1578126   263 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVAPEVTRDVCLL 311

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|1578126   312 ARMMAANLYYSQIEDLMFELSMWRCSDELRVRADELHRSSRRD--AKHYI 359

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK+vPP+EPYRviLGdvRDKLY tRER+R +L +Gis+i+Ee  +t++
  gi|1578126   360 EFWKKVPPNEPYRVILGDVRDKLYQTRERSRQMLSHGISDIPEEETFTNI 409

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|1578126   410 EQFLEPLELCYRSLCSCGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 459

                    eRqtDvlDAitthLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|1578126   460 DRHTDVLDAITKHLEIGSCREWSEEQKQEWLLSELGGRRPLFGPDLPKTE 509

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                    E++Dvld+f vLAELP D FGaYiismataPsDvLAvELLqREC+vkq+L
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  gi|1578126   560 RVVPLFEKLADLEAAPAALARLFSIDWYRNRINGKQEVMIGYSDSGKDAG 609

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                    RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1578126   610 RLSAAWQLYKAQEELINVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 659

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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  gi|1578126   660 PPETIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 709

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  gi|1578126   710 KPEWRALMDEMAVVATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 759

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                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KDiKnl
  gi|1578126   760 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIQKDIKNL 809

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  gi|1578126   810 LMLQEMYNEWPFFRVTIDLVEMVLAKGDPGIAALYDKLLVSEELWSFGER 859

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +++Etk lLL+iAGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|1578126   860 LRTNFEETKSLLLQIAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 909

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                    KRiRDP+y v lrPh+s+E   E sk+adeLvkLnpt+++aPGLEDtLiL
  gi|1578126   910 KRIRDPNYSVKLRPHISREIM-ESSKPADELVKLNPTSEYAPGLEDTLIL 958

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                    tmKGiAAGmqntG
  gi|1578126   959 TMKGIAAGMQNTG    971

gi|149789409|gb|ABR29876.1|: domain 1 of 1, from 11 to 965: score 2593.1, E = 0
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  gi|1497894    11    SIDAQLRLLVPAKVSEDDKLVEYDALLLDRFLDILQDLHGEDLKETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYElsAeYEGK+D++KL+ELG  LtsLdP+D+i++Ak+++HmLnLAnL
  gi|1497894    58 QECYELSAEYEGKHDPRKLDELGNLLTSLDPGDSIVIAKSFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRR+k+kk GDFaDE sAttEsDiEEt+K+Lv  l KsPeEv
  gi|1497894   108 AEEVQIAYRRRRNKLKK-GDFADENSATTESDIEETFKRLVIDLKKSPEEV 156

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  gi|1497894   157 FDALKNQTVDLVLTAHPTQSIRRSLLQKHARIRNCLAQLYAKDITPDDKQ 206

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                    ELDEAL REiqAAFRtDEiRR+ PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|1497894   207 ELDEALQREIQAAFRTDEIRRTAPTPQDEMRAGMSYFHETIWKGVPKFLR 256

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  gi|1497894   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

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  gi|1497894   306 ARMMAANLYYSQIEDLMFELSMWRCSDELRVRADELHRSSKRD--SKHYI 353

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                    EFWKqvPP EPYRviLGd RDKLY tRER+R +L +G s+i+EeA +t+v
  gi|1497894   354 EFWKQVPPSEPYRVILGDLRDKLYQTRERSRQMLSHGNSDIPEEATFTNV 403

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                    E+FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFG sLv+LDiRqEs
  gi|1497894   404 EQFLEPLELCYRSLCSCGDQPIADGSLLDFLRQVSTFGFSLVRLDIRQES 453

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDv+D it+HLeiGsYReWsEe+RqEWLl+EL+GKRPL+g+DL +t+
  gi|1497894   454 DRHTDVMDTITKHLEIGSYREWSEERRQEWLLSELSGKRPLFGPDLQRTD 503

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  gi|1497894   504 EVADVLDTFHVIAELPADSFGAYIISMATAPSDVLAVELLQRECHVKQPL 553

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  gi|1497894   554 RVVPLFEKLADLEAAPAALARLFSIDWYRNRINGKQEVMIGYSDSGKDAG 603

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
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  gi|1497894   604 RFSAAWQLYKAQEELIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 653

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  gi|1497894   654 PPDTIHGSLRVTVQGEVNEQSCGEEHLCFRTLQRFTAATLEHGMHPPVSP 703

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  gi|1497894   704 KPEWRKLMDEMAVIATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 753

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  gi|1497894   754 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIQKDVRNL 803

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  gi|1497894   804 HMLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSQDLWSFGER 853

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Etk lLL+iAGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|1497894   854 LRTNYEETKRLLLQIAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 903

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y vtlrPh+sKE   E sk+adeLvkLnp + +aPGLEDtLiL
  gi|1497894   904 KRIRDPNYNVTLRPHISKEIM-ESSKPADELVKLNPKSDYAPGLEDTLIL 952

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                    tmKG+AAG+qntG
  gi|1497894   953 TMKGVAAGLQNTG    965

gi|225461660|ref|XP_002285441.1|: domain 1 of 1, from 11 to 963: score 2592.5, E = 0
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                       siDAqLRlLvP Kvsed+kL+eYDALLlD+FLDiLqDLHGedLkE v
  gi|2254616    11    SIDAQLRLLVPAKVSEDDKLVEYDALLLDRFLDILQDLHGEDLKETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYElsAeYEGK+D+kKLeELG +LtsLd +D+i++Ak+++HmLnLAnL
  gi|2254616    58 QECYELSAEYEGKHDPKKLEELGNVLTSLDAGDSIVIAKSFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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  gi|2254616   108 AEEVQIAYRRRRNKLKK-GDFADENNATTESDIEETLKKLVVQLKKSPEEV 156

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  gi|2254616   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLAQLYAKDITPDDKQ 206

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  gi|2254616   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

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  gi|2254616   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305
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  gi|2254616   306 ARMMAANLYYSQIEDLMFELSMWRCNDELRVRADELLRSSKKD--AKHYI 353

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  gi|2254616   354 EFWKQIPPSEPYRVILGEVRDKLYQTRERSRHLLAHGISDIPGEATYTNL 403

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  gi|2254616   404 EQFLEPLELCYRSLCACGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 453

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  gi|2254616   454 DRHTDVIDAITRHLEIGSYREWSEERRQEWLLSELSGKRPLFGPDLPKTE 503

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  gi|2254616   504 EIADVLDTFHVIAELPADNFGAYIISMATAPSDVLAVELLQRECHVKQPL 553

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  gi|2254616   554 RVVPLFEKLADLEAAPAAVARLFSIDWYKNRINGKQEVMIGYSDSGKDAG 603

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  gi|2254616   604 RLSAAWALYKAQEELIKVAKQYGIKLTMFHGRGGTVGRGGGPTHLAILSQ 653

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  gi|2254616   804 HLLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSKDLWSFGER 853

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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  gi|2254616   854 LRSNYEQTKSLLLQIAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQACTL 903

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  gi|2254616   951 TMKGIAAGMQNTG    963

gi|115581|sp|P16097.1|CAPP2_MESCR: domain 1 of 1, from 3 to 960: score 2585.0, E = 0
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  gi|115581|     3    SIDAQLRLLVPAKVSEDDKLVEYDALLLDRFLDILQDLHGEDIRETV 49

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE sAeYEGK+D+kKL+ELG++LtsLd +D+i+vAk+++HmLnLAnL
  gi|115581|    50 QECYERSAEYEGKHDPKKLDELGSVLTSLDAGDSIVVAKSFSHMLNLANL 99

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  gi|115581|   100 AEEVQIAYRRRIKKLKKGDLSDENSATTESDIEETFKRLVAELGKSPEEI 149

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  gi|115581|   200 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 249

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  gi|115581|   250 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 298

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  gi|115581|   299 ARMMAANLYFSQIEDLMFELSMWRCTDELRARADELHSSSRRD--AKHYI 346

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  gi|115581|   347 EFWKHIPPNEPYRVILGDVRDKLYNTRERSRQMLSHGVSDIPEDATYTSL 396

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  gi|115581|   397 EQFLEPLELCYGSLCACGDRPIADGTLLDFLRQVFTFGLSLVRLDIRQES 446

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  gi|115581|   447 DRHTDVMDAITQHLEIGSYKEWSEEKRQEWLLSELSGKRPLFGSDLPQTE 496

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  gi|115581|   547 RVVPLFEKLADLEAAPAAVARLFSIDWYKNRINGKQEVMIGYSDSGKDAG 596

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  gi|115581|   597 RLSAAWALYKAQEELVQVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 646

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  gi|115581|   647 PPETVNGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 696

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  gi|115581|   797 SVLQKMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEELWPFGER 846

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  gi|115581|   847 LRADFEETKGLILKIAGHKDLLEGDPYLRQRLRLRDSYITTLNALQAYTL 896

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  gi|115581|   897 KRIRDPNYNVQLRPHISKEYMDSTSnKPAAELVKLNPSSEYAPGLEDTLI 946

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  gi|115581|   947 LTMKGIAAGMQNTG    960

gi|45505269|gb|AAS67006.1|: domain 1 of 1, from 11 to 966: score 2584.5, E = 0
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                       siDAqLRlL+P Kvs+d+kL+eYDALLlD+FLDiLqDLHGed++  v
  gi|4550526    11    SIDAQLRLLAPRKVSDDDKLVEYDALLLDRFLDILQDLHGEDIRQTV 57
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gi|4550526    58 QDCYELSAEYEGEHKPEKLEELGNMLTGLDAGDSIVIAKSFSHMLNLANL 107

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AEEv++AyRRRik++k+GDFaDE sA tEsDiEEt+KkLv +l K+P+E+
gi|4550526   108 AEEVQIAYRRRIKLLKKGDFADENSAITESDIEETFKKLVAQLKKTPQEI 157

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gi|4550526   158 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLTQLYAKDITPDDKQ 207

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gi|4550526   208 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPQFLR 257

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gi|4550526   307 ARMMAANMYFSQIEDLMFELSMWRCTDELRVRAHELHRSSKRD--AKHYI 354

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gi|4550526   355 EFWKQIPPNEPYRVILGDVRDKLYNIRERARHLLANGTSDIPEETTFTNV 404

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gi|4550526   405 EQFLEPLELCYRSLCACGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 454

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gi|4550526   455 DRHTDVMDAITKHLDIGSYREWPEEKRQEWLLSELSGKRPLFGHDLPKTE 504

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gi|4550526   505 EITDVLETFRVISELPSDNFGAYIISMATSPSDVLAVELLQRECHVKQPL 554

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gi|4550526   555 RVVPLFEKLADLEAAPAAVARLFSIDWYRNRIDGKQEVMIGYSDSGKDAG 604

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gi|4550526   605 RLSAAWALYKAQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 654

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gi|4550526   655 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 704

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gi|4550526   705 KPEWRALMDEMAVIATKEYRSVVFKEPRFVEYFRCATPELEYGRMNIGSR 754

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gi|4550526   755 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGSAFKHVVEKDPKNL 804

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gi|4550526   805 QMLQDMYNQWPFFRVTLDLVEMVFAKGDPGIAALFDKLLVSEELRPFGEN 854

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gi|4550526   855 LRAKYEETKSFLLQVAGHKDILEGDPYLKQRLRLRDSYITTLNVLQAYTL 904

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  gi|4550526   905 KRIRDPDYHVKLRPHLSKDYM-ESSKPAAELVKLNPKSEYAPGLEDTLIL 953

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                   tmKGiAAGmqntG
  gi|4550526   954 TMKGIAAGMQNTG    966

gi|115610|sp|P27154.1|CAPP_TOBAC: domain 1 of 1, from 11 to 964: score 2580.8, E = 0
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  gi|115610|    11    SIDAQLRALVPGKVSEDDKLVEYDALLLDRFLDILQDLHGEDLKETV 57

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qECYElsAeYEGK+D+kKLeELG +LtsLdP+D+i++Aka++HmLnLAnL
  gi|115610|    58 QECYELSAEYEGKHDPKKLEELGNVLTSLDPGDSIVIAKAFSHMLNLANL 107

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++AyRRR k+k+ GDFaDE +AttEsDiEEt+KkLv  l KsP+Ev
  gi|115610|   108 AEEVQIAYRRRQKLKR-GDFADENNATTESDIEETFKKLVGDLKKSPQEV 156

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  gi|115610|   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRDCLAQLYAKDITPDDKQ 206

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  gi|115610|   257 RVDTALKNIGINERLPYNAPLIQFSSWMGGDRDG-NPRVTLEVTRDVCLL 305

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  gi|115610|   306 ARMMAANLYYSQIEELMFELSMWRCNDDLRIRAAELYRSSRRD--TKHYI 353

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  gi|115610|   404 EQFLEPLELCYRSLCECGDRPIADGSLLDFLRQVSTFGLSFVRLDIRQES 453

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  gi|115610|   454 DRHTDVLDAITQHLEIGSYREWSEERRQEWLLSELSGKRPLFGPDLPRTE 503

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  gi|115610|   504 EIADVLDTLHVIAELPSDCFGAYIISMATAPSDVLAVELLQRECHVKQPL 553

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  gi|115610|   554 RVVPLFEKLDDLESASAAVARLFSIEWYRNRINGKQEVMVGYSDSGKDAG 603

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  gi|115610|   604 RFSAAWQLYKAQEELIKVAKEHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 653

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  gi|115610|   654 PPDTIQGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 703

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                   kPEWR Lm+e+Av+AtE YRs+v+KEPRFvEY  lAtPElEYG+mniGsR
  gi|115610|   704 KPEWRALMDEIAVIATEKYRSIVFKEPRFVEYSALATPELEYGRMNIGSR 753

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFK+AidKDiKnl
  gi|115610|   754 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKYAIDKDIKNL 803
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                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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  gi|115610|   804 RMFHEMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEDLLPFGEL 853

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Et+ lLL+iAGHkDlLEGDPYLKqrlRLRdsYittLn +qAYtL
  gi|115610|   854 LRSNYEETRSLLLQIAGHKDLLEGDPYLKQRLRLRDSYITTLNLLQAYTL 903

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
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  gi|115610|   904 KRIRDPNYHVTLRPHISKDYMESK--SAAELVQLNPTSEYAPGLEDTLIL 951

                    tmKGiAAGmqntG<-*
                    tmKGiAAG+qntG
  gi|115610|   952 TMKGIAAGLQNTG    964

gi|223976187|gb|ACN32213.1|: domain 1 of 1, from 10 to 966: score 2578.6, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLR LvP Kvsed+kLieYDALLlD+FLDiLqDLHGedLkE v
  gi|2239761    10    SIDAQLRQLVPAKVSEDDKLIEYDALLLDRFLDILQDLHGEDLKETV 56

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YElsAeYEGK+D+kKL+ELG  +tsLd +D+i+vAk+++HmLnLAnL
  gi|2239761    57 QEVYELSAEYEGKHDSKKLDELGNLITSLDAGDSIVVAKSFSHMLNLANL 106

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A+RRRik+kk GDFaDE +AttEsDiEEtlKkLv+ l KsP+Ev
  gi|2239761   107 AEEVQIAHRRRRIKLKK-GDFADENNATTESDIEETLKKLVVELKKSPQEV 155

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    FeALKnq+vDLvltAHPtqsvRRsLLqK++RiRnCL+qL+AKDvt++DK+
  gi|2239761   156 FEALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLTQLYAKDVTPDDKQ 205

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+W GvPKFLR
  gi|2239761   206 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWTGVPKFLR 255

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R DtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2239761   256 RLDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 304

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq+EDLmFElsmWRCndELRvRA+El r +++d v K+Yi
  gi|2239761   305 ARMMAANLYYSQIEDLMFELSMWRCNDELRVRADELNRSSRKDAVAKHYI 354

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK +PP+EPYRv+LG+vRD+LY tRER+RHLLA+G sei+Ee  +t+v
  gi|2239761   355 EFWKIIPPNEPYRVLLGEVRDRLYQTRERSRHLLAHGHSEIPEEETFTNV 404

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFLEPLELCY+sLC CGD++iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|2239761   405 EEFLEPLELCYRSLCACGDRAIADGSLLDFLRQVSTFGLSLVRLDIRQES 454

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|2239761   455 DRHTDVLDAITKHLEIGSYQEWSEEKRQQWLLSELSGKRPLFGRDLPKTE 504

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E+kDvld+f+v+AELP D FGaYiismataPsDvLAvELLqREC+vk++L
  gi|2239761   505 EIKDVLDTFHVIAELPADNFGAYIISMATAPSDVLAVELLQRECHVKHPL 554

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAa+++LFs++WY+nri+GKqev +GYsDsGKDAG
  gi|2239761   555 RVVPLFEKLADLEAAPAALARLFSVEWYRNRINGKQEVTIGYSDSGKDAG 604

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    R+sAAWqLYkAqEE+iKvAK+yGvKL++FHGRGGtvGRGGGPt LAiLsq
  gi|2239761   605 RFSAAWQLYKAQEELIKVAKEYGVKLTMFHGRGGTVGRGGGPTRLAILSQ 654

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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  gi|2239761   655 PPDTIHGSLRVTVQGEVIEQSFGEQHLCFRTLQRYTAATLEHGMHPPISP 704

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                   kPEWR Lm++mAv+AtEEYRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|2239761   705 KPEWRALMDQMAVIATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 754

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKRkPsGGie+LRAiPWiFaWtqtRFHLPvWLG+G AF+h i KDiKnl
  gi|2239761   755 PAKRKPSGGIETLRAIPWIFAWTQTRFHLPVWLGFGEAFRHVIGKDIKNL 804

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY++WPFFRvtlDL+EmvFAKGDPGiAaLyDkLLv+ +L+ FG++
  gi|2239761   805 HMLQEMYNQWPFFRVTLDLVEMVFAKGDPGIAALYDKLLVSQDLWSFGEQ 854

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR k+ Etk+lLL++ GH+DlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|2239761   855 LRTKFDETKKLLLQVCGHRDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 904

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y v lrPh+sKEy  E sk+adeL+ Lnpt+++aPGLEDtLiL
  gi|2239761   905 KRIRDPNYNVSLRPHISKEYI-EISKPADELITLNPTSEYAPGLEDTLIL 953

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|2239761   954 TMKGIAAGMQNTG    966

gi|166714353|gb|ABY87944.1|: domain 1 of 1, from 13 to 968: score 2573.1, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      siDAqLRlL+P Kvs+d+kL+eYDALLlD+FLDiLqDLHGed++  v
  gi|1667143    13    SIDAQLRLLAPRKVSDDDKLVEYDALLLDRFLDILQDLHGEDIRQTV 59

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   q+CYElsAeYEGK+ t+KLeELG  Lt+Ld +D+i++Ak+++HmLnLAnL
  gi|1667143    60 QDCYELSAEYEGKHKTEKLEELGNMLTGLDAGDSIVIAKSFSHMLNLANL 109

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++AyRRRik++k+GDFaDE  A tEsDiEEt+K+Lv  l KsP+Ev
  gi|1667143   110 AEEVQIAYRRRIKLLKKGDFADENPAITESDIEETFKRLVTELKKSPQEV 159

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   F+ALKnq+vDLvltAHPtqs+RRsLLqK++R+RnCL+qL+AKD+t++DK+
  gi|1667143   160 FDALKNQTVDLVLTAHPTQSIRRSLLQKHGRVRNCLTQLYAKDITPDDKQ 209

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|1667143   210 ELDEALQREIQAAFRTDEIRRSPPTPQDEMRAGMSYFHETIWKGVPKFLR 259

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1667143   260 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 308

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmAanlY+sq+EDLmFElsmWRCndELRvRA+El+  ++rd   K+Yi
  gi|1667143   309 ARMMAANLYFSQIEDLMFELSMWRCNDELRVRADELHVSSRRD--AKHYI 356

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWKq+PP+EPYRviLGdvRDKLYntRERaR LLA G s+i+Ee  +t+v
  gi|1667143   357 EFWKQIPPNEPYRVILGDVRDKLYNTRERARQLLANGTSDIPEETTFTNV 406

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   E+FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLs+v+LDiRqEs
  gi|1667143   407 EQFLEPLELCYRSLCACGDRPIADGSLLDFLRQVSTFGLSMVRLDIRQES 456

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|1667143   457 DRHTDVMDAITKHLEIGSYREWSEERRQEWLLSELSGKRPLFGPDLPKTE 506

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dvl++f+v+AELP+D FGaYiismataPsDvLAvELLqREC+vkq+L
  gi|1667143   507 EIADVLETFHVIAELPSDNFGAYIISMATAPSDVLAVELLQRECHVKQPL 556
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                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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  gi|1667143   557 RVVPLFEKLADLESAPAAVARLFSIDWYRNRINGRQEVMIGYSDSGKDAG 606

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAW LYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1667143   607 RLSAAWALYKAQEELIKVAKDFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 656

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  gi|1667143   657 PPETIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 706

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  gi|1667143   707 KPEWRVLLDEMAVIATKEYRSIVFQEPRFVEYFRCATPELEYGRMNIGSR 756

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                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKhAi+KD Knl
  gi|1667143   757 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGSAFKHAIEKDPKNL 806

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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  gi|1667143   807 LMLQDMYNQWPFFRVTLDLIEMVFAKGDPGIASLYDKLLVSEELLPFGER 856

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR kY+Etk +LLk+AGH+DlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|1667143   857 LRTKYEETKSFLLKVAGHRDLLEGDPYLKQRLRLRDSYITTLNVLQAYTL 906

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+v lrPhlsKE+ + n k+a+eLvkLnp +++aPGLEDtLiL
  gi|1667143   907 KRIRDPDYHVKLRPHLSKEFMESN-KPAAELVKLNPKSEYAPGLEDTLIL 955

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|1667143   956 TMKGIAAGMQNTG    968

gi|399182|sp|Q02909.1|CAPP1_SOYBN: domain 1 of 1, from 11 to 967: score 2571.3, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLRlLvP Kvsed+kL+eYDALLlD+FLDiLqDLHGedLkE v
  gi|399182|    11    SIDAQLRLLVPAKVSEDDKLVEYDALLLDRFLDILQDLHGEDLKETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YElsAeYEGK+D+kKLeELG  +tsLd +D+i+vAk+++HmLnLAnL
  gi|399182|    58 QEVYELSAEYEGKHDPKKLEELGNLITSLDAGDSIVVAKSFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A+ RR+k+kk GDFaDE +AttEsDiEEtlKkLv+   KsP+Ev
  gi|399182|   108 AEEVQIAHSRRNKLKK-GDFADENNATTESDIEETLKKLVVDMKKSPQEV 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|399182|   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNNLTQLYAKDITPDDKQ 206

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                    ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvP FLR
  gi|399182|   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPTFLR 256

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|399182|   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq+EDLmFElsmWRCndELRvRA+El r ++++ v K+Yi
  gi|399182|   306 ARMMAANLYYSQIEDLMFELSMWRCNDELRVRADELNRSSKKNSVAKHYI 355

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
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  gi|399182|   356 EFWKAIPPNEPYRVLLGEVRNRLYQTRERSRHLLAHGYSDIPEEETFTNV 405

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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  gi|399182|   456 DRHTDVLDAITKHLEIGSYQEWSEEKRQQWLLSELSGKRPLFGPDLPQTE 505

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dvl++f+v+AELP D FGaYiismataPsDvLAvELLqREC+vk++L
  gi|399182|   506 EIRDVLETFHVIAELPLDNFGAYIISMATAPSDVLAVELLQRECHVKHPL 555

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAa+++LFs+DWY+nri+GKqevm+GYsDsGKDAG
  gi|399182|   556 RVVPLFEKLADLEAAPAALARLFSVDWYRNRINGKQEVMIGYSDSGKDAG 605

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   R+sAAWqLYkAqEE+i vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|399182|   606 RFSAAWQLYKAQEELIMVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 655

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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  gi|399182|   656 PPETIHGSLRVTVQGEVIEQSFGEQHLCFRTLQRFTAATLEHGMHPPISP 705

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                   kPEWR Lm+emAv+AtEEYRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|399182|   706 KPEWRALMDEMAVIATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 755

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKR+PsGGie+LRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD++n+
  gi|399182|   756 PAKRRPSGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIEKDVRNI 805

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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  gi|399182|   806 HVLQEMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDRLLVSEDLWSFGEQ 855

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR  Y+Etk+lLL++AGH+DlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|399182|   856 LRTMYEETKELLLQVAGHRDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 905

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                   KRiRDP+y v lrPh+sKE   E sk+adeL+ Lnpt+++aPGLEDtLiL
  gi|399182|   906 KRIRDPNYNVKLRPHISKE-SIEISKPADELITLNPTSEYAPGLEDTLIL 954

                   tmKGiAAGmqntG<-*
                   tmKGiAAG+qntG
  gi|399182|   955 TMKGIAAGLQNTG    967

gi|225446609|ref|XP_002280569.1|: domain 1 of 1, from 11 to 965: score 2565.8, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      siDAqLRlL+P Kvsed+kL+eYDALLlD+FLDiLq++HGedLkE v
  gi|2254466    11    SIDAQLRLLAPAKVSEDDKLVEYDALLLDRFLDILQEIHGEDLKETV 57

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qECYElsAeYEGK+D++KLeELG ++tsLd +D+i+vAk+++ mL LAnL
  gi|2254466    58 QECYELSAEYEGKHDPQKLEELGRVITSLDAGDSIVVAKSFSNMLTLANL 107

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++A+RRRik+kk GDF DE+sAttEsDiEEt+K+Lv++l KsPeEv
  gi|2254466   108 AEEVQIAFRRRRIKLKK-GDFHDESSATTESDIEETIKRLVVQLKKSPEEV 156

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  gi|2254466   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHARIRNCLAQLYAKDITPDDKQ 206

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  gi|2254466   207 ELDEALQREIQAAFRTDEIRRTAPTPQDEMRAGMSYFHETIWKGVPKFLR 256

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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  gi|2254466   257 RVDTALKNIGIDERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305
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                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|2254466   306 ARMMAANLYYSQIEDLMFELSMWRCNEELRARADELHRSSRRD--AKHYI 353

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKqvPP EPYRviLGdvRDKLY tRER+R LL  Gisei+EeA +t+v
  gi|2254466   354 EFWKQVPPSEPYRVILGDVRDKLYSTRERSRQLLSSGISEIPEEAAFTNV 403

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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  gi|2254466   404 EQFLEPLELCYRSLCACGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 453

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|2254466   454 DRHTDVMDAITKHLEIGSYREWSEERRQEWLLAELRGKRPLFGPDLPKTE 503

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+f+v+ ELP+D FGaYiismataPsDvLAvELLqREC+vk++L
  gi|2254466   504 EIADVLDTFHVISELPSDNFGAYIISMATAPSDVLAVELLQRECHVKKPL 553

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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  gi|2254466   554 RVVPLFEKLADLEAAPAAVARLFSIDWYRNRIDGKQEVMIGYSDSGKDAG 603

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                    R+sAAWqLYkAqE ++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2254466   604 RFSAAWQLYKAQEALVKVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 653

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  gi|2254466   854 LRTNYEETKRLLLQIAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 903

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  gi|2254466   904 KRIRDPNYHVMERPHLSKEIM-ESSKPAAELVKLNPTSEYAPGMEDTLIL 952

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  gi|2254466   953 TMKGIAAGLQNTG    965

gi|242061132|ref|XP_002451855.1|: domain 1 of 1, from 7 to 960: score 2565.3, E = 0
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  gi|2420611     7    SIDAQLRLLAPGKVSEDDKLVEYDALLVDRFLDILQDLHGPHLREFV 53

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYElsAeYE  +D  +L+ELG+kLtsL P+D+i+vA++++HmLnLAnL
  gi|2420611    54 QECYELSAEYENDRDEARLGELGSKLTSLPPGDSIVVASSFSHMLNLANL 103

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  gi|2420611   104 AEEVQVAQRRRIKLKR-GDFADEASAPTESDIEETLKRLVSQLGKSREEV 152

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  gi|2420611   203 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 252

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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  gi|2420611   253 RIDTALKNIGINERLPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 301

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|2420611   302 ARMMAANLYFSQIEDLMFELSMWRCSDELRIRADELHRSSKRA--AKHYI 349

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  gi|2420611   350 EFWKQVPPNEPYRVILGDVRDKLYYTRERSRHLLSSGISEIPEEATFTNV 399

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  gi|2420611   400 EQFLEPLELCYRSLCACGDKPIADGSLLDFLRQVSTFGLALVKLDIRQES 449

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  gi|2420611   450 DRHTDVLDSITTHLGIGSYAEWSEEKRQDWLLSELRGKRPLFGSDLPQTE 499

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  gi|2420611   500 ETADVLGTFHVLAELPADCFGAYIISMATAPSDVLAVELLQRECHVKQPL 549

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  gi|2420611   550 RVVPLFEKLADLEAAPAAVARLFSIDWYMNRINGKQEVMIGYSDSGKDAG 599

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  gi|2420611   600 RLSAAWQMYKAQEELIKVAKHYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 649

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  gi|2420611   650 PPDTIHGSLRVTVQGEVIEHSFGEELLCFRTLQRYTAATLEHGMHPPISP 699

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  gi|2420611   700 KPEWRALMDEMAVVATKEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 749

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  gi|2420611   750 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAIKHIMQKDIRNI 799

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  gi|2420611   800 HVLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAAVYDKLLVAEDLQSFGEQ 849

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Etk+lLL++AGHkD+LEGDPYLKqrlRLR+sYittLnv+qAYtL
  gi|2420611   850 LRKNYEETKELLLQVAGHKDVLEGDPYLKQRLRLRESYITTLNVCQAYTL 899

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
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  gi|2420611   900 KRIRDPSFQVSPQPPLSKEFTDES--QPVELVQLNQQSEYAPGLEDTLIL 947

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|2420611   948 TMKGIAAGMQNTG    960

gi|184097733|gb|ACC66283.1|: domain 1 of 1, from 10 to 966: score 2564.1, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLRlLvP Kvsed+kLieYDALLlD+FLDiLqDLHGedL+E v
  gi|1840977    10    SIDAQLRLLVPAKVSEDDKLIEYDALLLDRFLDILQDLHGEDLRETV 56
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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gi|1840977    57 QECYELSAEYEGKRDPKKLEELGNVLTSLDPGDSIVLAKSFSHMLNLANL 106

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AEEv++AyRRRikk+k+GDF DE sAttEsDiEEt+K+Lv  l KsP+Ev
gi|1840977   107 AEEVQIAYRRRIKKLKKGDFIDENSATTESDIEETFKRLVGDLGKSPQEV 156

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gi|1840977   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLAQLYAKDITPDDKQ 206

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gi|1840977   207 ELDEALQREIQAAFRTDEIRRTQPTPQDEMRAGMSYFHETIWKGVPKFLR 256

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gi|1840977   257 RVDTALKDLGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

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gi|1840977   306 ARMMAANLYFSQIEDLMFEISMFRCSDELRVRADELHTSSRKD--AKHYI 353

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gi|1840977   354 EFWKYIPPTEPYRVILGDVRDKLYNTRERSRQLLSHGVSDIPEDTTYTNV 403

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gi|1840977   404 EQFLEPLELCYRSLCACGDRSIADGSLLDFLRQVSTFGLSLVRLDIRQES 453

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gi|1840977   454 DRHTDVMDAITQHLEIGSYKEWSEEQRQEWLLSELSGKRPLFGPDLPKTE 503

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gi|1840977   504 EIADVLDTFHVIAELPADCFGAYIISMATSPSDVLAVELLQRECHVKVPL 553

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gi|1840977   554 RVVPLFEKLADLEAAPAAVSRLFSIEWYKNRINGKQEVMIGYSDSGKDAG 603

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gi|1840977   604 RLSAAWALYKAQEELVKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 653

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gi|1840977   704 KPEWRTLLDAMAVAATEKYRSIVFKEPRFVEYFRLATPETALGSMNIGSR 753

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gi|1840977   754 PSKREASGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAIQKDSQNL 803

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gi|1840977   804 YMLEQMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEELCPFGEQ 853

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gi|1840977   854 LGSDYEETKKLLLQVAGHKEILEGDPHLRQRLRLRDPYITTLNVCQAYTL 903

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gi|1840977   904 KRIRDPNFHVTVRPHISKDYMESTDKPAAELVKLNPSSEYAPGLEDTLIL 953
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  gi|1840977   954 TMKGIAAGMQNTG    966

gi|115587|sp|P29195.1|CAPP1_SORBI: domain 1 of 1, from 7 to 960: score 2562.2, E = 0
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  gi|115587|     7    SIDAQLRLLAPGKVSEDDKLVEYDALLVDRFLDILQDLHGPHLREFV 53

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                  qECYElsAeYE  +D  +L+ELG+kLtsL P+D+i+vA++++HmLnLAnL
  gi|115587|    54 QECYELSAEYENDRDEARLGELGSKLTSLPPGDSIVVASSFSHMLNLANL 103

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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  gi|115587|   104 AEEVQVAQRRRIKLKR-GDFADEASAPTESDIEETLKRLVSQLGKSREEV 152

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  gi|115587|   153 FDALKNQTVDLVFTAHPTQSVRRSLLQKHGRIRNCLRQLYAKDITADDKQ 202

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|115587|   203 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 252

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  gi|115587|   253 RIDTALKNIGINERLPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 301

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  gi|115587|   302 ARMMAANLYFSQIEDLMFELSMWRCSDELRIRADELHRSSKRA--AKHYI 349

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  gi|115587|   350 EFWKQVPPNEPYRVILGDVRDKLYYTRERSRHLLSSGISEIPEEATFTNV 399

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  gi|115587|   400 EQFLEPLELCYRSLCACGDKPIADGSLLDFLRQVFNFGLALVKLDIRQES 449

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  gi|115587|   450 DRHTDVLDSITTHLGIGSYAEWSEEKRQDWLLSELRGKRPLFGSDLPQTE 499

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  gi|115587|   500 ETADVLGTFHVLAELPADCFGAYIISMATAPSDVLAVELLQRECHVKQPL 549

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  gi|115587|   550 RVVPLFEKLADLEAAPAAVARLFSIDWYMNRINGKQEVMIGYSDSGKDAG 599

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  gi|115587|   600 RLSAAWQMYKAQEELIKVAKHYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 649

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  gi|115587|   650 PPDTIHGSLRVTVQGEVIEHSFGEELLCFRTLQRYTAATLEHGMHPPISP 699

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  gi|115587|   700 KPEWRALMDEMAVVATKEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 749

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  gi|115587|   750 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAIKHIMQKDIRNI 799

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  gi|115587|   800 HVLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAAVYDKLLVAEDLQSFGEQ 849

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  gi|115587|   850 LRKNYEETKELLLQVAGHKDVLEGDPYLKQRLRLRESYITTLNVCQAYTL 899

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  gi|115587|   900 KRIRDPSFQVSPQPPLSKEFTDES--QPVELVQLNQQSEYAPGLEDTLIL 947

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                    tmKGiAAGmqntG
  gi|115587|   948 TMKGIAAGMQNTG    960

gi|162458095|ref|NP_001105503.1|: domain 1 of 1, from 7 to 960: score 2561.5, E = 0
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  gi|1624580     7    SIDAQLRLLAPGKVSEDDKLVEYDALLVDRFLDILQDLHGPHLREFV 53

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  gi|1624580    54 QECYELSAEYENDRDEARLGELGSKLTSLPPGDSIVVASSFSHMLNLANL 103

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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  gi|1624580   104 AEEVQIAHRRRRIKLKR-GDFADEASAPTESDIEETLKRLVSQLGKSREEV 152

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                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|1624580   203 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 252

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  gi|1624580   253 RIDTALKNIGINERLPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 301

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                    aRmmAanlY+sq+EDLmFElsmWRC dELR+RA+El+r +++    K+Yi
  gi|1624580   302 ARMMAANLYFSQIEDLMFELSMWRCSDELRIRADELHRSSRKA--AKHYI 349

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  gi|1624580   350 EFWKQVPPNEPYRVILGDVRDKLYYTRERSRHLLTSGISEILEEATFTNV 399

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  gi|1624580   400 EQFLEPLELCYRSLCACGDKPIADGSLLDFLRQVSTFGLALVKLDIRQES 449

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  gi|1624580   450 DRHTDVLDSITTHLGIGSYAEWSEEKRQDWLLSELRGKRPLFGSDLPQTE 499

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  gi|1624580   500 ETADVLGTFHVLAELPADCFGAYIISMATAPSDVLAVELLQRECHVKHPL 549

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  gi|1624580   550 RVVPLFEKLADLEAAPAAVARLFSIDWYMDRINGKQEVMIGYSDSGKDAG 599

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  gi|1624580   600 RLSAAWQMYKAQEELIKVAKHYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 649

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  gi|1624580   800 HILREMYNEWPFFRVTLDLLEMVFAKGDPGIAAVYDKLLVADDLQSFGEQ 849

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  gi|1624580   850 LRKNYEETKELLLQVAGHKDVLEGDPYLKQRLRLRESYITTLNVCQAYTL 899

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  gi|1624580   900 KRIRDPSFQVSPQPPLSKEFTDES--QPAELVQLNQQSEYAPGLEDTLIL 947

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  gi|1624580   948 TMKGIAAGMQNTG    960

gi|6688531|emb|CAB65170.1|: domain 1 of 1, from 11 to 964: score 2560.4, E = 0
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  gi|6688531    11    SIDAQLRQLVPAKVSEDDKLVEYDALLLDRFLDILQDLHGEDLKGTV 57

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  gi|6688531    58 QDCYELSAEYEAKHDPKKLEELGNVLTSLVPGDSIVIAKAFSHMLNLANL 107

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  gi|6688531   108 AEEVQIAYRRRQKLKKKGDFGDESNATTESDIEETFKKLVGDLKKSPQEV 157

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  gi|6688531   158 FDAIKNQTVDLVLTAHPTQSVRRSLLQKHGRIRDCLAQLYAKDITPDDKQ 207

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  gi|6688531   208 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 257

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  gi|6688531   258 RVDTALKNIGIDERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 306

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  gi|6688531   307 ARMMAANLYYSQIEDLMFELSMWRCSEELRVRAHKLQRSWRDE---KHYI 353

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  gi|6688531   354 EFWKQVPPNEPYRVILGDVRDKLYQTRELARQLLGHGYSEIPEEATYTNI 403

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  gi|6688531   404 EQFLEPLELCYSSLCACGDLSIADGSLLDFLRQVSTFGLSLVRLDIRQES 453

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  gi|6688531   454 DRHTDVLDAITQHLEIGSYREWSEERRQEWLLSELSGKRPLFGRDLPKTE 503

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  gi|6688531   504 EIADVLDTFHVIAELPADCFGAYIISMATAPSDVLAVELLQRECRVRQPL 553

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  gi|6688531   604 RLSASWQLYKAQEELIQVAKEFDVKLTMFHGRGGTVGRGGGPAHLAILSQ 653

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  gi|6688531   654 PPETIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 703

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  gi|6688531   704 KPEWRALMDEIAVVATEKYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 753

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  gi|6688531   754 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKYAIEKDIKNL 803

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  gi|6688531   804 RMLQEMYNAWPFFRVTIDLVEMVFAKGDPGIAALFDKLLVSEDLLSFGEL 853

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                    LR +Y+Etk lLL+iAGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|6688531   854 LRSNYEETKSLLLQIAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 903

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  gi|6688531   904 KRIRDPDYSVTPRPHISKEYMESK--PATELVNLNPTSEYAPGLEDTLIL 951

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  gi|6688531   952 TMKGIAAGMQNTG    964

gi|12697498|emb|CAC28225.1|: domain 1 of 1, from 11 to 961: score 2560.2, E = 0
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  gi|1269749    11    SIDAQLRLLVPAKVSEDDKLVEYDALLLDRFLDILQDLHGEDLKETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YElsAeYEGK+D+kKLeELG  +tsLd +D+i+vAk+++HmLnLAnL
  gi|1269749    58 QEVYELSAEYEGKHDPKKLEELGNLITSLDAGDSIVVAKSFSHMLNLANL 107

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  gi|1269749   108 AEEVQIAHRRRNKLKK-GDFADESNATTESDIEETLKKLVGEMKKSPQEV 156

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  gi|1269749   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRVRNCLTQLYAKDITPDDKQ 206

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  gi|1269749   306 ARMMAANLYYSQIEDLMFELSMWRCNDELRVRADELNRSSKKDAVAKHYI 355

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  gi|1269749   356 EFWKIIPPSEPYRVVLGEVRDRLYQTRERSRHLLAHGYSDIPEEETFTNL 405

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  gi|1269749   406 EEFLEPLELCYRSLCACGDRAIADGTLLDFLRQVSTFGLSLVRLDIRQES 455
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  gi|1269749   456 DRHTDVLDAITKHLEIGSYQEWSEEKRQQWLLSELSGKRPLFGPDLPQTE 505

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  gi|1269749   506 EIRDVLDTFHVIAELPPDNFGAYIISMATTPSDVLAVELLQRECHIKHPL 555

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  gi|1269749   606 RFSAAWQLYKAQEELIKVAKKFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 655

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  gi|1269749   706 KPEWRAMMDQMAVIATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 755

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  gi|1269749   756 PAKRRPSGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKKVIEKDVRNL 805

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  gi|1269749   806 HMLQEMYNQWPFFRVTLDLVEMVFAKGDPGIASLNDRLLVSKDLWPFGEQ 855

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  gi|1269749   856 LRNKYEETKKLLLQVAGHREILEGDPYLKQRLRLRDSYITTLNAFQAYTL 905

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                    KRiRDP+y v ++P +sKE A E        v Lnpt+++aPGLEDtLiL
  gi|1269749   906 KRIRDPNYNVKVKPRISKESAVEL-------VTLNPTSEYAPGLEDTLIL 948

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|1269749   949 TMKGIAAGMQNTG    961

gi|218190390|gb|EEC72817.1|: domain 1 of 1, from 15 to 968: score 2559.5, E = 0
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  gi|2181903    15    SIDAQLRLLAPGKVSEDDKLVEYDALLVDRFLDILQDLHGPHLREFV 61

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  gi|2181903    62 QECYELSAEYENDRDEARLDELGRKLTSLPPGDSIVVSSSFSHMLNLANL 111

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  gi|2181903   112 AEEVQIAHRRRRIKLKR-GDFADEASAPTESDIEETLKRLVTQLGKSREEV 160

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  gi|2181903   161 FDALKNQTVDLVFTAHPTQSVRRSLLQKHGRIRNCLRQLYAKDITADDKQ 210

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  gi|2181903   211 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 260

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  gi|2181903   261 RIDTALKNIGINERLPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 309

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  gi|2181903   358 EFWKQIPPNEPYRVILGGVRDKLYYTRERTRHLLTTGVSEIPEEATFTNV 407

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  gi|2181903   408 EEFLEPLELCYRSLCACGDKPIADGSLLDFLRQVSTFGLALVKLDIRQES 457

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  gi|2181903   458 DRHTDVLDAITTYLGIGSYAEWSEEKRQDWLLSELRGKRPLFGPDLPQTE 507

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  gi|2181903   508 EIADVLGTFHVLAELPADCFGAYIISMATAPSDVLAVELLQRECHIKQPL 557

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  gi|2181903   708 KPEWRALMDEMAVVATKEYRSIVFKEPRFVEYFRSATPETEYGRMNIGSR 757

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++KDi+n+
  gi|2181903   758 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHIMQKDIRNI 807

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva +L+ FG++
  gi|2181903   808 HTLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVAGDLQSFGEQ 857

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++++Etk+lLL++AGHkD+LEGDPYLKqrlRLR+sYittLnv+qAYtL
  gi|2181903   858 LRNNFEETKQLLLQVAGHKDILEGDPYLKQRLRLRESYITTLNVCQAYTL 907

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPs++v ++P lsKE+ d n  +++eLv+Ln ++++aPGLEDtLiL
  gi|2181903   908 KRIRDPSFEVMPQPALSKEFVDSN--QPAELVQLNAASEYAPGLEDTLIL 955

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|2181903   956 TMKGIAAGMQNTG    968

gi|40354190|gb|AAR84575.1|: domain 1 of 1, from 8 to 961: score 2558.3, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLRlL+PGKvsed+kL+eYDALL+D+FLDiLqDLHG+ L+E+v
  gi|4035419     8    SIDAQLRLLAPGKVSEDDKLVEYDALLVDRFLDILQDLHGPHLREFV 54

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYElsAeYE  +D  +L+ELG+kLtsL P+D+i+vA++++HmLnLAnL
  gi|4035419    55 QECYELSAEYENDRDEARLGELGSKLTSLPPGDSIVVASSFSHMLNLANL 104

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A+RRRik+k+ GDFaDEasA tEsDiEEtlK+Lv++l Ks eEv
  gi|4035419   105 AEEVQIAHRRRIKLKR-GDFADEASAPTESDIEETLKRLVSQLGKSREEV 153

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+vDLv+tAHPtq vRRsLLqK++RiRnCL qL+AKD+t +DK+
  gi|4035419   154 FDALKNQTVDLVFTAHPTQPVRRSLLQKHGRIRNCLRQLYAKDITADDKQ 203
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                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|4035419   204 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 253

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R+DtALKniGinERlPY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|4035419   254 RIDTALKNIGINERLPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 302

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq+EDLmFElsmWRC dELR+RA+El r ++r    K+Yi
  gi|4035419   303 ARMMAANLYFSQIEDLMFELSMWRCSDELRIRADELRRSSKRA--AKHYI 350

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKqvPP+EPYRviLGdvRDKLY tRER+RHLL tGisei+EeA +t+v
  gi|4035419   351 EFWKQVPPNEPYRVILGDVRDKLYYTRERSRHLLTTGISEIPEEATFTNV 400

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC CGDk iADGsLLD+LRqvstFGL+LvKLDiRqEs
  gi|4035419   401 EQFLEPLELCYRSLCACGDKPIADGSLLDFLRQVSTFGLALVKLDIRQES 450

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlD it+HL+iGsY eWsEeKRq+WLl+EL+GKRPL+gsDLP tE
  gi|4035419   451 DRHTDVLDSITKHLGIGSYAEWSEEKRQDWLLSELSGKRPLFGSDLPLTE 500

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E +Dvl+af+vLAELP D+FGaYi+smataPsDvLAvELLqREC+vk++L
  gi|4035419   501 ETADVLGAFHVLAELPADCFGAYIVSMATAPSDVLAVELLQRECHVKHPL 550

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADL+ APAav++LFsiDWY+ ri+GKqevm+GYsDsGKDAG
  gi|4035419   551 RVVPLFEKLADLKSAPAAVARLFSIDWYMDRINGKQEVMIGYSDSGKDAG 600

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWq+YkAqEE+iKvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|4035419   601 RLSAAWQMYKAQEELIKVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 650

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE sFGEE+LCFr+LqR+tAAtLEHGm+PP+sP
  gi|4035419   651 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRYTAATLEHGMHPPISP 700

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emA+vAt EYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|4035419   701 KPEWRALMDEMAIVATKEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 750

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWi aWtqtRFHLPvWLG+GAAFKh ++KDi+n+
  gi|4035419   751 PSKRKPSGGIESLRAIPWISAWTQTRFHLPVWLGFGAAFKHLMQKDIRNI 800

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAa+yDkLLvaE+L+ FG++
  gi|4035419   801 HTLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAAVYDKLLVAEDLQSFGEQ 850

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Etk+lLL++AGHkD+LEGDPYLKqrlRLR+sYittLnv+qAYtL
  gi|4035419   851 LRKNYEETKELLLQVAGHKDVLEGDPYLKQRLRLRESYITTLNVCQAYTL 900

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP ++v ++P lsKE+ dE   ++++Lv+Lnp +++aPGLEDtLiL
  gi|4035419   901 KRIRDPGFQVSPQPALSKEFTDES--QPAQLVQLNPESEYAPGLEDTLIL 948

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|4035419   949 TMKGIAAGMQNTG    961

gi|15219272|ref|NP_175738.1|: domain 1 of 1, from 11 to 967: score 2557.3, E = 0
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                       siD  LR LvPGKvsed+kL+eYDALLlD+FLDiLqDLHGedL+E v
  gi|1521927    11    SIDVHLRQLVPGKVSEDDKLVEYDALLLDRFLDILQDLHGEDLRETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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                qE YE sAeYEGK+++kKLeELG++LtsLdP+D+i++Aka++HmLnLAnL
gi|1521927    58 QELYEHSAEYEGKHEPKKLEELGSVLTSLDPGDSIVIAKAFSHMLNLANL 107

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AEEv++AyRRRikk+k+GDF DE+sAttEsD+EEt+KkLv  lnKsPeE+
gi|1521927   108 AEEVQIAYRRRIKKLKKGDFVDESSATTESDLEETFKKLVGDLNKSPEEI 157

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                F+ALKnq+vDLvltAHPtqsvRRsLLqK++RiR CLaqL+AKD+t++DK+
gi|1521927   158 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRDCLAQLYAKDITPDDKQ 207

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                ELDEAL REiqAAFRtDEi+R++PtPqDEmRaGmsY+HEt+WkGvPKFLR
gi|1521927   208 ELDEALQREIQAAFRTDEIKRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 257

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                RvDtALKniGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
gi|1521927   258 RVDTALKNIGIEERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 306

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                aRmmAa +Y++q+EDLmFE+smWRCndELR+RA+E++  +++d   K+Yi
gi|1521927   307 ARMMAATMYFNQIEDLMFEMSMWRCNDELRARADEVHANSRKD-AAKHYI 355

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                EFWK +P tEPYRviLGdvRDKLY tRERa  LL  G s+++ eA + ++
gi|1521927   356 EFWKSIPTTEPYRVILGDVRDKLYHTRERAHQLLSNGHSDVPVEATFINL 405

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                E+FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
gi|1521927   406 EQFLEPLELCYRSLCSCGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 455

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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gi|1521927   456 DRHTDVLDAITTHLDIGSYREWSEERRQEWLLSELSGKRPLFGSDLPKTE 505

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                E++Dvld+f+v+AELP DsFGaYiismataPsDvLAvELLqREC vkq+L
gi|1521927   506 EIADVLDTFHVIAELPADSFGAYIISMATAPSDVLAVELLQRECRVKQPL 555

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                rvvPLFEkLADLeAAPAav++LFs+DWY+nri+GKqevm+GYsDsGKDAG
gi|1521927   556 RVVPLFEKLADLEAAPAAVARLFSVDWYKNRINGKQEVMIGYSDSGKDAG 605

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1521927   606 RLSAAWQLYKAQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 655

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PPDtinGslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PP+sP
gi|1521927   656 PPDTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPISP 705

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                kPEWR L++emAvvAtEEYRsvv++EPRFvEYFRlAtPElEYG+mniGsR
gi|1521927   706 KPEWRALLDEMAVVATEEYRSVVFQEPRFVEYFRLATPELEYGRMNIGSR 755

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G A +h i+KD++nl
gi|1521927   756 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGSAIRHVIEKDVRNL 805

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                 +L++mY+ WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+EeL+PFG++
gi|1521927   806 HMLQDMYQHWPFFRVTIDLIEMVFAKGDPGIAALYDKLLVSEELWPFGEK 855

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR++++Etk+l+L+ AGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
gi|1521927   856 LRANFEETKKLILQTAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 905

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                KRiRDPsy+vtlrPh+sKE A E sk+a eL++Lnpt+++aPGLEDtLiL
gi|1521927   906 KRIRDPSYHVTLRPHISKEIA-ESSKPAKELIELNPTSEYAPGLEDTLIL 954
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                    tmKGiAAGmqntG<-*
                    tmKGiAAG+qntG
  gi|1521927   955 TMKGIAAGLQNTG    967

gi|1705587|sp|P51061.1|CAPP2_SOYBN: domain 1 of 1, from 11 to 967: score 2556.7, E = 0
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  gi|1705587    11    SIDAQLRQLAPAKVSEDDKLIEYDALLLDRFLDILQDLHGEDLKETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YElsAeYEGK+D+kKLeELG  +tsLd +D+ilvAk+++HmLnLAnL
  gi|1705587    58 QEVYELSAEYEGKHDPKKLEELGNLITSLDAGDSILVAKSFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++  RRR+k+kk GDFaDE +AttEsDiEEtlKkLv  l KsP+Ev
  gi|1705587   108 AEEVQISRRRRNKLKK-GDFADENNATTESDIEETLKKLVFDLKKSPQEV 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|1705587   157 FDALKNQTVDLVLTAHPTQSIRRSLLQKHGRIRNCLSQLYAKDITPDDKQ 206

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  gi|1705587   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWNGVPRFLR 256

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                    RvDtAL niGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1705587   257 RVDTALNNIGIKERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

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  gi|1705587   306 ARMMAANLYYSQIEDLMFELSMWRCNDELRVRAEELHRSSKKDEVAKHYI 355

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK+vPP+EPYRv+LG+vRD+LY tRER+RHLL  G+s+i+EeA +t+v
  gi|1705587   356 EFWKKVPPNEPYRVVLGEVRDRLYQTRERSRHLLSNGYSDIPEEATFTNV 405

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFLE LELCY+sLC CGD++iADGsLLD++RqvstFGLsLv+LDiRqEs
  gi|1705587   406 EEFLESLELCYRSLCACGDRAIADGSLLDFMRQVSTFGLSLVRLDIRQES 455

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|1705587   456 DRHTDVLDAITKHLEIGSYQEWSEEKRQEWLLSELSGKRPLFGPDLPQTE 505

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+f+v+AELP D FGaYiismataPsDvLAvELLqREC++k++L
  gi|1705587   506 EIRDVLDTFHVIAELPPDNFGAYIISMATAPSDVLAVELLQRECHIKHPL 555

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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  gi|1705587   556 RVVPLFEKLADLEAAPAALARLFSIDWYRNRINGKQEVMIGYSDSGKDAG 605

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    R+sAAWqLYkAqEE+i vAKk+GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1705587   606 RFSAAWQLYKAQEELINVAKKFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 655

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGE +LCFr+LqRFtAAtLEHGm+PP+sP
  gi|1705587   656 PPDTIHGSLRVTVQGEVIEQSFGEQHLCFRTLQRFTAATLEHGMHPPISP 705

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  gi|1705587   706 KPEWRALMDQMAVIATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 755

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
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  gi|1705587   756 PAKRRPSGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKKVIEENVKNL 805

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY++WPFFRvtlDL+EmvFAKGDP iAaL+D+LLv+ +L+PFG++
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                   LR+kY+Et++lLL++AGHk++LEGDPYLKqrlRLR + ittLn++qAYtL
  gi|1705587   856 LRNKYEETRKLLLQVAGHKEILEGDPYLKQRLRLRHAPITTLNIVQAYTL 905

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y v +rP +sKE  +E sk adeLvkLnpt+++aPGLEDtLiL
  gi|1705587   906 KRIRDPNYNVKVRPRISKE-SAEASKSADELVKLNPTSEYAPGLEDTLIL 954

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|1705587   955 TMKGIAAGMQNTG    967

gi|37785629|gb|AAP43628.1|: domain 1 of 1, from 11 to 963: score 2556.2, E = 0
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                      siDAqLRlL+PGKvsed+kLieYDALLlD+FLDiLqDLHGed++E+v
  gi|3778562    11    SIDAQLRLLAPGKVSEDDKLIEYDALLLDRFLDILQDLHGEDVREFV 57

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qECYE++A+Y+G + t+KLeELG  LtsLdP+D+i+v k+++ mL LAnL
  gi|3778562    58 QECYEVAADYDGNRNTEKLEELGNMLTSLDPGDSIVVTKSFSNMLSLANL 107

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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  gi|3778562   108 AEEVQIAYRRRIKKLKKGDFADEASATTESDIEETLKRLLQLN-KTPEEV 156

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  gi|3778562   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKFGRIRDCLTQLYAKDITPDDKQ 206

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  gi|3778562   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

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  gi|3778562   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

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                   aRmmAanlY+sq+EDLmFE+smWRCn+ELRvRAE  +r a+rd   K+Yi
  gi|3778562   306 ARMMAANLYFSQIEDLMFEMSMWRCNEELRVRAER-QRCAKRD--AKHYI 352

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWKq+P +EPYR iLGdvRDKLYntRERaR LL  G+s+++E+Av+t v
  gi|3778562   353 EFWKQIPANEPYRAILGDVRDKLYNTRERARQLLSSGVSDVPEDAVFTSV 402

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   ++FLEPLELCY+sLC+CGD+ iADGsLLD+LRqvstFGL+LvKLDiRqEs
  gi|3778562   403 DQFLEPLELCYRSLCDCGDRPIADGSLLDFLRQVSTFGLALVKLDIRQES 452

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|3778562   453 DRHTDVLDAITTHLGIGSYKEWSEDKRQEWLLSELSGKRPLFGPDLPKTE 502

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                   Ev+Dvld+f+v+ ELP+DsFGaYiismataPsDvLAvELLqRECg+  +L
  gi|3778562   503 EVADVLDTFKVISELPSDSFGAYIISMATAPSDVLAVELLQRECGITDPL 552

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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  gi|3778562   553 RVVPLFEKLADLESAPAAVARLFSIEWYRNRINGKQEVMIGYSDSGKDAG 602

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYk qEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|3778562   603 RLSAAWQLYKTQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 652

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+G lRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|3778562   653 PPDTIHGQLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 702
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                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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  gi|3778562   703 KPEWRVLMDEMAIIATEEYRSVVFKEPRFVEYFRLATPELEYGRMNIGSR 752

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                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFK  i+KD Knl
  gi|3778562   753 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKRVIQKDNKNL 802

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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  gi|3778562   803 NMLKEMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDRLLVSEELQPFGEQ 852

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Et+ lLL++AGHkD+LEGDPYL+qrl LRd+YittLnv+qAYtL
  gi|3778562   853 LRVNYQETRRLLLQVAGHKDILEGDPYLRQRLQLRDPYITTLNVCQAYTL 902

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    K iRDPs++v +rPhlsK+y +    +a+eLvkLnp +++aPGLEDt+iL
  gi|3778562   903 KQIRDPSFHVKVRPHLSKDYMESS--PAAELVKLNPKSEYAPGLEDTVIL 950

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|3778562   951 TMKGIAAGMQNTG    963

gi|15232442|ref|NP_188112.1|: domain 1 of 1, from 11 to 968: score 2555.0, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLR LvP Kvsed+kL+eYDALLlD+FLDiLqDLHGedL+E v
  gi|1523244    11    SIDAQLRQLVPAKVSEDDKLVEYDALLLDRFLDILQDLHGEDLRETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YElsAeYEGK++++KLeELG++LtsLdP+D+i++ ka++HmLnLAnL
  gi|1523244    58 QELYELSAEYEGKREPSKLEELGSVLTSLDPGDSIVISKAFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A+RRRikk+k+GDF DE+sAttEsDiEEt+K+Lv+ l KsPeE+
  gi|1523244   108 AEEVQIAHRRRIKKLKKGDFVDESSATTESDIEETFKRLVSDLGKSPEEI 157

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+vDLvltAHPtqsvRRsLLqK++RiR CLaqL+AKD+t++DK+
  gi|1523244   158 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRDCLAQLYAKDITPDDKQ 207

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDE L REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|1523244   208 ELDESLQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 257

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1523244   258 RVDTALKNIGIDERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 306

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY++q+E LmFElsmWRC dE RvRA+El+r +++d   K+Yi
  gi|1523244   307 ARMMAANLYYNQIENLMFELSMWRCTDEFRVRADELHRNSRKD-AAKHYI 355

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK +PPtEPYRviLGdvRDKLY tRER+R LL  Gis+i+EeA +t+v
  gi|1523244   356 EFWKTIPPTEPYRVILGDVRDKLYHTRERSRQLLSNGISDIPEEATFTNV 405

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC CGD  iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|1523244   406 EQFLEPLELCYRSLCSCGDSPIADGSLLDFLRQVSTFGLSLVRLDIRQES 455

                    eRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    eR+tDvlDAit+HL+iG+sYR+WsEe RqEWLlaEL+GKRPL+g+DLPkt
  gi|1523244   456 ERHTDVLDAITKHLDIGsSYRDWSEEGRQEWLLAELSGKRPLFGPDLPKT 505

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    EE+ Dvld+f+v+ ELP+D+FGaYiismat+PsDvLAvELLqREC+vk++
  gi|1523244   506 EEISDVLDTFKVISELPSDCFGAYIISMATSPSDVLAVELLQRECHVKNP 555

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
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                   GRlsAAW LYkAqEE++KvAKkyGvKL++FHGRGGtvGRGGGPtHLAiLs
  gi|1523244   606 GRLSAAWELYKAQEELVKVAKKYGVKLTMFHGRGGTVGRGGGPTHLAILS 655

                   qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                   qPPDt+nGslRvtvqGEviE+sFGE +LCFr+LqRFtAAtLEHGmnPP+s
  gi|1523244   656 QPPDTVNGSLRVTVQGEVIEQSFGEAHLCFRTLQRFTAATLEHGMNPPIS 705

                   PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
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  gi|1523244   706 PKPEWRALLDEMAVVATEEYRSVVFQEPRFVEYFRLATPELEYGRMNIGS 755

                   RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                   RP+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF++Ai+KD++n
  gi|1523244   756 RPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRYAIKKDVRN 805

                   lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                   l +L++mYk+WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+ FG+
  gi|1523244   806 LHMLQDMYKQWPFFRVTIDLIEMVFAKGDPGIAALYDKLLVSEDLWAFGE 855

                   sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                   +LR+++ Etk+l+L+ AGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYt
  gi|1523244   856 KLRANFDETKNLVLQTAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYT 905

                   LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                   LKRiRD +y vtlrPh+sKE  +   k a+eLvkLnpt+++aPGLEDtLi
  gi|1523244   906 LKRIRDANYNVTLRPHISKEIMQSS-KSAQELVKLNPTSEYAPGLEDTLI 954

                   LtmKGiAAGmqntG<-*
                   LtmKGiAAG+qntG
  gi|1523244   955 LTMKGIAAGLQNTG    968

gi|115445275|ref|NP_001046417.1|: domain 1 of 1, from 15 to 968: score 2554.8, E = 0
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                      siDAqLRlL+PGKvsed+kL+eYDALL+D+FLDiLqDLHG+ L+E+v
  gi|1154452    15    SIDAQLRLLAPGKVSEDDKLVEYDALLVDRFLDILQDLHGPHLREFV 61

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qECYElsAeYE  +D  +L+ELG kLtsL P+D+i+v ++++HmLnLAnL
  gi|1154452    62 QECYELSAEYENDRDEARLDELGRKLTSLPPGDSIVVSSSFSHMLNLANL 111

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++A+RRRik+k+ GDFaDEasA tEsDiEEtlK+Lv +l Ks eEv
  gi|1154452   112 AEEVQIAHRRRRIKLKR-GDFADEASAPTESDIEETLKRLVTQLGKSREEV 160

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   F+ALKnq+vDLv+tAHPtqsvRRsLLqK++RiRnCL qL+AKD+t +DK+
  gi|1154452   161 FDALKNQTVDLVFTAHPTQSVRRSLLQKHGRIRNCLRQLYAKDITADDKQ 210

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|1154452   211 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 260

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   R+DtALKniGinERlPY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1154452   261 RIDTALKNIGINERLPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 309

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmAanlY+sq+EDLmFElsmWRC dELR+RA++l+  +++    K+Yi
  gi|1154452   310 ARMMAANLYFSQIEDLMFELSMWRCSDELRIRADDLHCSSRKA--AKHYI 357

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWKq+PP+EPYRviLG vRDKLY tRER+RHLL tG+sei+EeA +t+v
  gi|1154452   358 EFWKQIPPNEPYRVILGGVRDKLYYTRERTRHLLTTGVSEIPEEATFTNV 407

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   EeFLEPLELCY+sLC CGDk iADGsLLD+LRqvstFGL+LvKLDiRqEs
  gi|1154452   408 EEFLEPLELCYRSLCACGDKPIADGSLLDFLRQVSTFGLALVKLDIRQES 457
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                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|1154452   458 DRHTDVLDAITTYLGIGSYAEWSEEKRQDWLLSELRGKRPLFGPDLPQTE 507

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvl++f+vLAELP D+FGaYiismataPsDvLAvELLqREC++kq+L
  gi|1154452   508 EIADVLGTFHVLAELPADCFGAYIISMATAPSDVLAVELLQRECHIKQPL 557

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAav++LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|1154452   558 RVVPLFEKLADLEAAPAAVARLFSIDWYMNRINGKQEVMIGYSDSGKDAG 607

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWq+YkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1154452   608 RLSAAWQMYKAQEELVKVAKHYGVKLTMFHGRGGTVGRGGGPSHLAILSQ 657

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|1154452   658 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPISP 707

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAvvAt EYRs+v+KEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1154452   708 KPEWRALMDEMAVVATKEYRSIVFKEPRFVEYFRSATPETEYGRMNIGSR 757

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++KDi+n+
  gi|1154452   758 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHIMQKDIRNI 807

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva +L+ FG++
  gi|1154452   808 HTLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVAGDLQSFGEQ 857

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++++Etk+lLL++AGHkD+LEGDPYLKqrlRLR+sYittLnv+qAYtL
  gi|1154452   858 LRNNFEETKQLLLQVAGHKDILEGDPYLKQRLRLRESYITTLNVCQAYTL 907

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPs++v  +P lsKE+ d n  +++eLv+Ln ++++aPGLEDtLiL
  gi|1154452   908 KRIRDPSFEVMSQPALSKEFVDSN--QPAELVQLNAASEYAPGLEDTLIL 955

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|1154452   956 TMKGIAAGMQNTG    968

gi|9828445|gb|AAG00180.1|AF271995_1: domain 1 of 1, from 6 to 959: score 2554.8, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLRlL+PGKvsed+kL+eYDALL+D+FLDiLqDLHG+ L+E+v
  gi|9828445     6    SIDAQLRLLAPGKVSEDDKLVEYDALLVDRFLDILQDLHGPHLREFV 52

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYElsAeYE  +D  +L+ELG kLtsL P+D+i+v ++++HmLnLAnL
  gi|9828445    53 QECYELSAEYENDRDEARLDELGRKLTSLPPGDSIVVSSSFSHMLNLANL 102

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A+RRRik+k+ GDFaDEasA tEsDiEEtlK+Lv +l Ks eEv
  gi|9828445   103 AEEVQIAHRRRRIKLKR-GDFADEASAPTESDIEETLKRLVTQLGKSREEV 151

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+vDLv+tAHPtqsvRRsLLqK++RiRnCL qL+AKD+t +DK+
  gi|9828445   152 FDALKNQTVDLVFTAHPTQSVRRSLLQKHGRIRNCLRQLYAKDITADDKQ 201

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|9828445   202 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 251

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R+DtALKniGinERlPY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|9828445   252 RIDTALKNIGINERLPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 300

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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                   EFWKq+PP+EPYRviLG vRDKLY tRER+RHLL tG+sei+EeA +t+v
  gi|9828445   349 EFWKQIPPNEPYRVILGGVRDKLYYTRERTRHLLTTGVSEIPEEATFTNV 398

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   EeFLEPLELCY+sLC CGDk iADGsLLD+LRqvstFGL+LvKLDiRqEs
  gi|9828445   399 EEFLEPLELCYRSLCACGDKPIADGSLLDFLRQVSTFGLALVKLDIRQES 448

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +R+tDvlDAitt L+iGsY eWsEeKRq+WLl+EL+GKRPL+g+DLP+tE
  gi|9828445   449 DRHTDVLDAITTYLGIGSYAEWSEEKRQDWLLSELRGKRPLFGPDLPQTE 498

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dvl++f+vLAELP D+FGaYiismataPsDvLAvELLqREC++kq+L
  gi|9828445   499 EIADVLGTFHVLAELPADCFGAYIISMATAPSDVLAVELLQRECHIKQPL 548

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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  gi|9828445   549 RVVPLFEKLADLEAAPAAVARLFSIDWYMNRINGKQEVMIGYSDSGKDAG 598

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWq+YkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|9828445   599 RLSAAWQMYKAQEELVKVAKHYGVKLTMFHGRGGTVGRGGGPSHLAILSQ 648

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|9828445   649 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPISP 698

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emAvvAt EYRs+v+KEPRFvEYFR+AtPE+EYG+mniGsR
  gi|9828445   699 KPEWRALMDEMAVVATKEYRSIVFKEPRFVEYFRSATPETEYGRMNIGSR 748

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++KDi+n+
  gi|9828445   749 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHIMQKDIRNI 798

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva +L+ FG++
  gi|9828445   799 HTLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVAGDLQSFGEQ 848

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++++Etk+lLL++AGHkD+LEGDPYLKqrlRLR+sYittLnv+qAYtL
  gi|9828445   849 LRNNFEETKQLLLQVAGHKDILEGDPYLKQRLRLRESYITTLNVCQAYTL 898

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPs++v  +P lsKE+ d n  +++eLv+Ln ++++aPGLEDtLiL
  gi|9828445   899 KRIRDPSFEVMSQPALSKEFVDSN--QPAELVQLNAASEYAPGLEDTLIL 946

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|9828445   947 TMKGIAAGMQNTG    959

gi|23503558|dbj|BAC20365.1|: domain 1 of 1, from 11 to 967: score 2554.8, E = 0
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                      siDAqLR LvP Kvsed+kL+eYDALLlD+FLDiLqDLHGedL+E v
  gi|2350355    11    SIDAQLRQLVPAKVSEDDKLVEYDALLLDRFLDILQDLHGEDLRETV 57

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qE YElsAeYE K+++++Le LG  +tsLd +D+i+vAk++ HmLnLAnL
  gi|2350355    58 QEVYELSAEYERKHEPQRLEVLGNLITSLDAGDSIVVAKSFAHMLNLANL 107

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++A+RRRik+kk GDFaDE++AttEsDiEEt+KkLv    KsP+Ev
  gi|2350355   108 AEEVQIAHRRRIKLKK-GDFADEGNATTESDIEETFKKLVGEMKKSPQEV 156

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   F+ LKnq+vDLvltAHPtqsvRRsLLqK++RiRnCL+qL+AKD+t++DK+
  gi|2350355   157 FDELKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLTQLYAKDITPDDKQ 206
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                    RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2350355   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|2350355   306 ARMMAANLYYSQIEDLMFELSMWRCNDELRVRAEELTSSSNKDAVAKHYI 355

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                    EFWK +PP EPYRv+LG+vR +LY tRER+RHLLA  +s+i Ee  +t+v
  gi|2350355   356 EFWKNIPPSEPYRVVLGEVRNRLYQTRERSRHLLANEYSDILEEHTFTNV 405

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  gi|2350355   406 EEFLEPLELCYRSLCACGDRAIADGSLLDFLRQVSTFGLSLVRLDIRQES 455

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  gi|2350355   456 DRLTDVLDAITKHLGIGSYLEWSEEKRQQWLLSELSGKRPLFGPDLPQTE 505

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                    E+kDvld+f+v+AELP+D FGaYiismataPsDvLAvELLqREC+vk++L
  gi|2350355   506 EIKDVLDTFHVIAELPSDNFGAYIISMATAPSDVLAVELLQRECHVKNPL 555

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  gi|2350355   556 RVVPLFEKLADLETAPAALARLFSVEWYRNRINGKQEVMIGYSDSGKDAG 605

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  gi|2350355   606 RFSAAWQLYKAQEELIKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 655

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  gi|2350355   656 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHGMHPPISP 705

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  gi|2350355   806 NMLQEMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDRLLVSEDLWSFGEQ 855

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  gi|2350355   906 KRIRDPNYNVKLRPHISKE-AIDVSKPADELVTLNPTSEYAPGLEDTLIL 954

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  gi|2350355   955 TMKGIAAGMQNTG    967

gi|240254631|ref|NP_850373.4|: domain 1 of 1, from 11 to 963: score 2554.7, E = 0
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  gi|2402546    11    SIDAQLRLLAPGKVSEDDKLIEYDALLLDRFLDILQDLHGEDVREFV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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                 AEEv++AyRRRikk+k+GDFaDEasAttEsDiEEtlK+L  +  K+PeEv
gi|2402546   108 AEEVQIAYRRRIKKLKKGDFADEASATTESDIEETLKRLLQLN-KTPEEV 156

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gi|2402546   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKFGRIRDCLTQLYAKDITPDDKQ 206

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gi|2402546   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

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gi|2402546   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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gi|2402546   306 ARMMAANLYFSQIEDLMFEMSMWRCNEELRVRAER-QRCAKRD--AKHYI 352

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gi|2402546   353 EFWKQIPANEPYRAILGDVRDKLYNTRERARQLLSSGVSDVPEDAVFTSV 402

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gi|2402546   403 DQFLEPLELCYRSLCDCGDRPIADGSLLDFLRQVSTFGLALVKLDIRQES 452

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gi|2402546   603 RLSAAWQLYKTQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 652

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gi|2402546   653 PPDTIHGQLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 702

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gi|2402546   753 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKRVIQKDSKNL 802

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gi|2402546   803 NMLKEMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDRLLVSEELQPFGEQ 852

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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gi|2402546   853 LRVNYQETRRLLLQVAGHKDILEGDPYLRQRLQLRDPYITTLNVCQAYTL 902

                 KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                 K iRDPs++v +rPhlsK+y +    +a+eLvkLnp +++aPGLEDt+iL
gi|2402546   903 KQIRDPSFHVKVRPHLSKDYMESS--PAAELVKLNPKSEYAPGLEDTVIL 950

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  gi|2402546   951 TMKGIAAGMQNTG    963

gi|242048870|ref|XP_002462179.1|: domain 1 of 1, from 13 to 967: score 2553.8, E = 0
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  gi|2420488    13    SIDAQLRMLVPGKVSEDDKLIEYDALLLDRFLDILQDLHGDDLKEMV 59

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE++AeYE K+D +KL+ELG  +tsLdP+D+i++Ak+++HmLnLAnL
  gi|2420488    60 QECYEVAAEYETKHDLQKLDELGKMITSLDPGDSIVIAKSFSHMLNLANL 109

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRRik+kk GDFaDE sA tEsDiEEtlK+Lv+ l KsP+Ev
  gi|2420488   110 AEEVQIAYRRRRIKLKK-GDFADENSAITESDIEETLKRLVVDLKKSPAEV 158

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|2420488   159 FDALKSQTVDLVLTAHPTQSVRRSLLQKHSRIRNCLVQLYSKDITPDDKQ 208

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  gi|2420488   209 ELDEALQREIQAAFRTDEIRRTQPTPQDEMRAGMSYFHETIWKGVPKFLR 258

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  gi|2420488   259 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 307

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  gi|2420488   308 ARMMASNLYCSQIEDLMFELSMWRCSDELRMRADELHRSTKKD--AKHYI 355

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  gi|2420488   356 EFWKKVPPNEPYRVILSDVRDKLYNTRERSRELLSSGHSDIPEEATLTTV 405

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+ LEPLELCY+sLC CGD+viADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|2420488   406 EQLLEPLELCYRSLCACGDRVIADGSLLDFLRQVSTFGLSLVRLDIRQES 455

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  gi|2420488   456 DRHTDVLDAITTYLGIGSYREWPEERRQEWLLSELNGKRPLFGPDLPKTE 505

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                    E++Dvld+f+v+AELP D FGaYiismataPsDvLAvELLqREC+vk +L
  gi|2420488   506 EIADVLDTFHVIAELPADNFGAYIISMATAPSDVLAVELLQRECHVKTPL 555

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  gi|2420488   556 RVVPLFEKLADLEAAPAALARLFSIDWYRQRINGKQEVMIGYSDSGKDAG 605

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  gi|2420488   606 RLSAAWQLYKAQEELIKVAKDFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 655

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  gi|2420488   656 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPNAP 705

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  gi|2420488   756 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHVLQKDIRNL 805

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  gi|2420488   806 HMLQEMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELRPLGEK 855
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                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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  gi|2420488   856 LRANYEETQKLLLQVAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 905

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+v lrPhlsKE  d   k a eLvkLnp++++aPGLEDtLiL
  gi|2420488   906 KRIRDPDYHVALRPHLSKEIMDPT-KAASELVKLNPGSEYAPGLEDTLIL 954

                    tmKGiAAGmqntG<-*
                    tmKGiAAG+qntG
  gi|2420488   955 TMKGIAAGLQNTG    967

gi|222423984|dbj|BAH19953.1|: domain 1 of 1, from 11 to 967: score 2553.6, E = 0
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                       siD  LR LvPGKvsed+kL+eYDALLlD+FLDiLqDLHGedL+E v
  gi|2224239    11    SIDVHLRQLVPGKVSEDDKLVEYDALLLDRFLDILQDLHGEDLRETV 57

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                    qE YE sAeYEGK+++kKLeELG++LtsLdP+D+i++Aka++HmLnLAnL
  gi|2224239    58 QELYEHSAEYEGKHEPKKLEELGSVLTSLDPGDSIVIAKAFSHMLNLANL 107

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  gi|2224239   108 AEEVQIAYRRRIKKLKKGDFVDESSATTESDLEETFKKLVGDLNKSPEEI 157

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  gi|2224239   158 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRDCLAQLYAKDITPDDKQ 207

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  gi|2224239   307 ARMMAATMYFNQIEDLIFEMSMWRCNDELRARADEVHANSRKD-AAKHYI 355

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  gi|2224239   356 EFWKSIPTTEPYRVILGDVRDKLYHTRERAHQLLSNGHSDVPVEATFINL 405

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|2224239   406 EQFLEPLELCYRSLCSCGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 455

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|2224239   456 DRHTDVLDAITTHLDIGSYREWSEERRQEWLLSELSGKRPLFGSDLPKTE 505

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  gi|2224239   506 EIADVLDTFHVIAELPADSFGAYIISMATAPSDVLAVELLQRECRVKQPL 555

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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  gi|2224239   556 RVVPLFEKLADLEAAPAAVARLFSVDWYKNRINGKQEVMIGYSDSGKDAG 605

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  gi|2224239   606 RLSAAWQLYKAQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 655

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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  gi|2224239   656 PPDTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPISP 705

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                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G A +h i+KD++nl
  gi|2224239   756 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGSAIRHVIEKDVRNL 805

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  gi|2224239   806 HMLQDMYQHWPFFRVTIDLIEMVFAKGDPGIAALYDKLLVSEELWPFGEK 855

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++++Etk+l+L+ AGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|2224239   856 LRANFEETKKLILQTAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 905

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
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  gi|2224239   906 KRIRDPSYHVTLRPHISKEIA-ESSKPAKELIELNPTSEYAPGLEDTLIL 954

                    tmKGiAAGmqntG<-*
                    tmKGiAAG+qntG
  gi|2224239   955 TMKGIAAGLQNTG    967

gi|226320260|gb|ACO48251.1|: domain 1 of 1, from 11 to 969: score 2553.2, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLR L+P Kvsed+kLieYDALLlD+FLDiLqDLHGedL+E v
  gi|2263202    11    SIDAQLRQLAPAKVSEDDKLIEYDALLLDRFLDILQDLHGEDLRETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YElsAeYEGK+D+kKLeELG ++tsLd +D+i+vAk+++HmLnLAnL
  gi|2263202    58 QEVYELSAEYEGKHDPKKLEELGKVITSLDAGDSIVVAKSFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A+RRR+k+kk GDF D  +AttEsDiEEtlKkLvl l KsP+Ev
  gi|2263202   108 AEEVQIAHRRRNKLKK-GDFVDVNNATTESDIEETLKKLVLNLKKSPQEV 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+vDLvltAHPtqs+RRsLLqK++RiRnCL+qL+AKD+t++DK+
  gi|2263202   157 FDALKNQTVDLVLTAHPTQSIRRSLLQKHGRIRNCLSQLYAKDITPDDKQ 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+W GvPKFLR
  gi|2263202   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWMGVPKFLR 256

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R DtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2263202   257 RLDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq+EDLmFElsmWRCndELRvRA+El+   ++d v K+Yi
  gi|2263202   306 ARMMAANLYYSQIEDLMFELSMWRCNDELRVRADELHGSFKKDEVAKHYI 355

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK++P +EPYRviLGdvRD+LY tRER+RHLLA+G+s+i+EeA +t+v
  gi|2263202   356 EFWKKIPANEPYRVILGDVRDRLYKTRERSRHLLAQGYSDIPEEASFTNV 405

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFLEPLELCY+sLC CGD++iADG LLD+LRqvstFGLsLv+LDiRqEs
  gi|2263202   406 EEFLEPLELCYRSLCACGDRAIADGTLLDFLRQVSTFGLSLVRLDIRQES 455

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDv+DAit+HL+iGsY eWsEeKRqEWLl EL+GKRPL+g+DLP tE
  gi|2263202   456 DRHTDVMDAITKHLGIGSYQEWSEEKRQEWLLEELSGKRPLFGPDLPTTE 505

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+f+v+AELP D FGaYiismataPsDvLAvELLqREC +k++L
  gi|2263202   506 EIRDVLDTFHVIAELPADNFGAYIISMATAPSDVLAVELLQRECRIKHPL 555

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAa+++LFs++WY+nri+GKq+vm+GYsDsGKDAG
  gi|2263202   556 RVVPLFEKLADLEAAPAALARLFSVEWYRNRINGKQDVMIGYSDSGKDAG 605
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                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    R+sAAWqLYkAqE++iKvAKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2263202   606 RFSAAWQLYKAQEDLIKVAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 655

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDt++GslRvtvqGEviE+sFGE +LCFr+LqRFtAAtLEHGmn P++P
  gi|2263202   656 PPDTVHGSLRVTVQGEVIEQSFGEQHLCFRTLQRFTAATLEHGMNAPIAP 705

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR+Lm+emAv+AtEEYRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|2263202   706 KPEWRQLMDEMAVIATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 755

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkPsGGie+LRAiPWiFaWtqtRFHLPvWLG+GAAFK  i+KD++nl
  gi|2263202   756 PAKRKPSGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKNVIQKDVRNL 805

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY++WPFFRvt+DL+EmvFAKGDPGiAaL+D+LLv+ +L+PFG++
  gi|2263202   806 NMLQEMYNNWPFFRVTIDLVEMVFAKGDPGIAALNDRLLVSKDLWPFGEQ 855

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR+kY+Etk+lLL++AGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
  gi|2263202   856 LRNKYEETKKLLLQVAGHKDLLEGDPYLKQRLRLRDSYITTLNVFQAYTL 905

                    KRiRDPsykvt..lrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    KRiRDP+y v  ++rP +sKE  d   k adeLv Lnpt+++aPGLEDtL
  gi|2263202   906 KRIRDPNYNVNvrPRPRISKESLDIS-KSADELVSLNPTSEYAPGLEDTL 954

                    iLtmKGiAAGmqntG<-*
                    iLtmKGiAAGmqnt
  gi|2263202   955 ILTMKGIAAGMQNTS    969

gi|20141087|gb|AAK58635.2|AF271161_1: domain 1 of 1, from 16 to 970: score 2550.1, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s+DAqLR+L+P Kvsed++L+eYDALLlD+FL+iLqDLHGedL+E v
  gi|2014108    16    SVDAQLRMLAPSKVSEDDNLVEYDALLLDRFLEILQDLHGEDLRETV 62

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    q CYElsAeYE   D++KLeELG  LtsLdP+D+i+vA++++HmLnL nL
  gi|2014108    63 QSCYELSAEYESTLDPQKLEELGNMLTSLDPGDSIVVASSFSHMLNLGNL 112

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A+RRRik+kk GDFaDE sA tEsDiEEtlKkLv++l KsP+Ev
  gi|2014108   113 AEEVQIAFRRRIKLKK-GDFADENSAATESDIEETLKKLVVQLKKSPQEV 161

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+vDLvltAHPtqs+RRsLLqK++RiRnCLaqL+AKDvt++DK+
  gi|2014108   162 FDALKNQTVDLVLTAHPTQSIRRSLLQKHSRIRNCLAQLYAKDVTPDDKQ 211

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|2014108   212 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 261

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtAL+niGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2014108   262 RVDTALRNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 310

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq+EDLmFElsmWRC dELRvRA  l+r +++    K+Yi
  gi|2014108   311 ARMMAANLYYSQIEDLMFELSMWRCSDELRVRATALHRSSRSV--AKHYI 358

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP+EPYRviLG+vRDKLY tRERaR LL  G+s+i+Ee  +t++
  gi|2014108   359 EFWKQIPPNEPYRVILGEVRDKLYKTRERARQLLSNGFSDIPEESTFTNI 408

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLs+vKLDiRqEs
  gi|2014108   409 EEFLEPLELCYRSLCSCGDQPIADGSLLDFLRQVSTFGLSIVKLDIRQES 458

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|2014108   459 DRHTDVLDAITNHLGIGSYRDWSEEKRQEWLLSELRGKRPLFGPDLPKTD 508

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+++v+AELP D FGaYiismataPsDvLAvELLqREC+vk++L
  gi|2014108   509 EIADVLDTMHVIAELPFDNFGAYIISMATAPSDVLAVELLQRECHVKKPL 558

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLe APAav++LFsiDWY nri+GKqevm+GYsDsGKDAG
  gi|2014108   559 RVVPLFEKLADLETAPAAVARLFSIDWYLNRINGKQEVMIGYSDSGKDAG 608

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+iKvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2014108   609 RLSAAWQLYKAQEELIKVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 658

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGs+RvtvqGEviE+sFGEE LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2014108   659 PPDTINGSIRVTVQGEVIEQSFGEERLCFRTLQRFTAATLEHGMHPPLSP 708

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAvvAt+EYRs+v+K+PRFvEYFR+AtPElEYG+mniGsR
  gi|2014108   709 KPEWRALMDEMAVVATDEYRSIVFKDPRFVEYFRSATPELEYGRMNIGSR 758

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KR+PsGGiesLRAiPWiFaWtqt+FHLPvWLG+G AFKh idKD Knl
  gi|2014108   759 PSKRRPSGGIESLRAIPWIFAWTQTKFHLPVWLGFGSAFKHVIDKDPKNL 808

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAa+yDkLLv+ +L PFG++
  gi|2014108   809 QMLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAAMYDKLLVSKDLLPFGER 858

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR+kY Etk+lLLk+AGHkDlLEGDPYL+qrl LRdsYittLn +qAYtL
  gi|2014108   859 LREKYTETKNLLLKVAGHKDLLEGDPYLRQRLQLRDSYITTLNACQAYTL 908

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP y v lrPhlsKE  d   k a+eLvkLnp++++aPGLEDtLiL
  gi|2014108   909 KRIRDPGYNVQLRPHLSKEMVDSS-KSAAELVKLNPGSEYAPGLEDTLIL 957

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|2014108   958 TMKGIAAGMQNTG    970

gi|399183|sp|Q02735.1|CAPP_MEDSA: domain 1 of 1, from 10 to 966: score 2549.9, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLR LvP Kvsed+kLieYDALLlD+FLDiLqDLHGedLk+ v
  gi|399183|    10    SIDAQLRQLVPAKVSEDDKLIEYDALLLDRFLDILQDLHGEDLKDSV 56

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YElsAeYE K+D+kKLeELG  +ts d +D+i+vAk+++HmLnLAnL
  gi|399183|    57 QEVYELSAEYERKHDPKKLEELGNLITSFDAGDSIVVAKSFSHMLNLANL 106

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A+RRR+k+kk GDF DE++AttEsDiEEtlKkLv    KsP+Ev
  gi|399183|   107 AEEVQIAHRRRNKLKK-GDFRDESNATTESDIEETLKKLVFDMKKSPQEV 155

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+vDLvltAHPtqsvRRsLLqK++R+RnCL+qL+AKD+t++DK+
  gi|399183|   156 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRVRNCLSQLYAKDITPDDKQ 205

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEi+R++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|399183|   206 ELDEALQREIQAAFRTDEIKRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 255

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                    RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|399183|   256 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 304

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq+EDLmFElsmWRCndELRvRAEEl+r +++d v K+Yi
  gi|399183|   305 ARMMAANLYYSQIEDLMFELSMWRCNDELRVRAEELHRNSKKDEVAKHYI 354
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                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
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  gi|399183|   355 EFWKKIPLNEPYRVVLGEVRDKLYRTRERSRYLLAHGYCEIPEEATFTNV 404

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    +eFLEPLELCY+sLC CGD++iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|399183|   405 DEFLEPLELCYRSLCACGDRAIADGSLLDFLRQVSTFGLSLVRLDIRQES 454

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDv+DAit+HLeiGsY eWsEeKRqEWLl+EL GKRPL+g+DLP+t+
  gi|399183|   455 DRHTDVMDAITKHLEIGSYQEWSEEKRQEWLLSELIGKRPLFGPDLPQTD 504

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+frv+AELP+D FGaYiismataPsDvLAvELLqREC+v+++L
  gi|399183|   505 EIRDVLDTFRVIAELPSDNFGAYIISMATAPSDVLAVELLQRECKVRNPL 554

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkL DLe APAa+++LFsiDWYinridGKqevm+GYsDsGKDAG
  gi|399183|   555 RVVPLFEKLDDLESAPAALARLFSIDWYINRIDGKQEVMIGYSDSGKDAG 604

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    R+sAAWqLYkAqE++iKvA+k+GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|399183|   605 RFSAAWQLYKAQEDLIKVAQKFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 654

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP+ti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PP sP
  gi|399183|   655 PPETIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPSSP 704

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm++mAv+AtEEYRs+v+KEPRFvEYFRlAtPE+EYG+mniGsR
  gi|399183|   705 KPEWRALMDQMAVIATEEYRSIVFKEPRFVEYFRLATPEMEYGRMNIGSR 754

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+PsGGie+LRAiPWiFaWtqtRFHLPvWLG+GAAF+  ++KD+Knl
  gi|399183|   755 PAKRRPSGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFRQVVQKDVKNL 804

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY++WPFFRvt+DL+EmvFAKGDPGiAaL+D+LLv+ +L+PFG++
  gi|399183|   805 HMLQEMYNQWPFFRVTIDLVEMVFAKGDPGIAALNDRLLVSKDLWPFGEQ 854

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR kY+Etk+lLL++A Hk++LEGDPYLKqrlRLRdsYittLnvfqAYtL
  gi|399183|   855 LRSKYEETKKLLLQVAAHKEVLEGDPYLKQRLRLRDSYITTLNVFQAYTL 904

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+ykv +rP++sKE  +E sk+adeLv Lnpt+++aPGLEDtLiL
  gi|399183|   905 KRIRDPNYKVEVRPPISKE-SAETSKPADELVTLNPTSEYAPGLEDTLIL 953

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|399183|   954 TMKGIAAGMQNTG    966

gi|25901017|dbj|BAC41249.1|: domain 1 of 1, from 11 to 967: score 2549.7, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLR L+P Kvsed+kLieYDALLlD+FLDiLqDLHGedLkE v
  gi|2590101    11    SIDAQLRQLAPAKVSEDDKLIEYDALLLDRFLDILQDLHGEDLKETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YElsAeYEGK+D+kKLeELG  +tsLd +D+ilvAk+++HmLnLAnL
  gi|2590101    58 QEVYELSAEYEGKHDPKKLEELGNLITSLDAGDSILVAKSFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++  RRR+k+kk GDFaDE +AttEsDiEEtlKkLv  l KsP+Ev
  gi|2590101   108 AEEVQISRRRRNKLKK-GDFADENNATTESDIEETLKKLVFGLKKSPQEV 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+vDLvltAHPtqs+RRsLLqK++RiRnCL+qL+AKD+t++DK+
  gi|2590101   157 FDALKNQTVDLVLTAHPTQSIRRSLLQKHGRIRNCLSQLYAKDITPDDKQ 206

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  gi|2590101   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWNGVPRFLR 256

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtAL niGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2590101   257 RVDTALNNIGIKERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq+EDLmFElsmWRCndELRvRAEEl+r +++d v K+Yi
  gi|2590101   306 ARMMAANLYYSQIEDLMFELSMWRCNDELRVRAEELHRSSKKDEVAKHYI 355

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK+vPP+EPYRv+LG+vRD+LY tRER+RHLL  G+s+i+EeA +t+v
  gi|2590101   356 EFWKKVPPNEPYRVVLGEVRDRLYQTRERSRHLLSNGYSDIPEEATFTNV 405

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFLE LELCY+sLC CGD++iADGsLLD++RqvstFGLsLv+LDiRqEs
  gi|2590101   406 EEFLESLELCYRSLCACGDRAIADGSLLDFMRQVSTFGLSLVRLDIRQES 455

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlDAit+HLeiGsY eWsEeKRqEWLl+EL+GKRPL+g+DLP+tE
  gi|2590101   456 DRHTDVLDAITKHLEIGSYQEWSEEKRQEWLLSELSGKRPLFGPDLPQTE 505

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+f+v+AELP D FGaYiismataPsDvLAvELLqREC++k++L
  gi|2590101   506 EIRDVLDTFHVIAELPPDNFGAYIISMATAPSDVLAVELLQRECHIKHPL 555

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAa+++LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|2590101   556 RVVPLFEKLADLEAAPAALARLFSIDWYRNRINGKQEVMIGYSDSGKDAG 605

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    R+sAAWqLYkAqEE+i vAKk+G+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2590101   606 RFSAAWQLYKAQEELINVAKKFGIKLTMFHGRGGTVGRGGGPTHLAILSQ 655

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGE +LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2590101   656 PPDTIHGSLRVTVQGEVIEQSFGEQHLCFRTLQRFTAATLEHGMHPPISP 705

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm++mAv+AtEEYRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|2590101   706 KPEWRALMDQMAVIATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 755

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkPsGGie+LRAiPWiFaWtqtRFHLPvWLG+GAAFK  i+K + nl
  gi|2590101   756 PAKRKPSGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKEVIEKNVNNL 805

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY++WPFFRvtlDL+EmvFAKGDP iA+L+D+LLv+ +L+ FG++
  gi|2590101   806 NMLQEMYNQWPFFRVTLDLVEMVFAKGDPKIAGLNDRLLVSKDLWLFGDQ 855

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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  gi|2590101   856 LRNKYEETKKLLLQVAGHKEILEGDPYLKQRLRLRHAPITTLNIVQAYTL 905

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y v +rP +sKE  +E sk adeL+kLnpt+++aPGLEDtLiL
  gi|2590101   906 KRIRDPNYNVKVRPRISKE-SAEASKSADELIKLNPTSEYAPGLEDTLIL 954

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|2590101   955 TMKGIAAGMQNTG    967

gi|28416715|gb|AAO42888.1|: domain 1 of 1, from 11 to 968: score 2549.5, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLR LvP Kvsed+kL+eYDALLlD+FLDiLqDLHGedL+E v
  gi|2841671    11    SIDAQLRQLVPAKVSEDDKLVEYDALLLDRFLDILQDLHGEDLRETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YElsAeYEGK++++KLeELG++LtsLdP+D+i++ ka++HmLnLAnL
  gi|2841671    58 QELYELSAEYEGKREPSKLEELGSVLTSLDPGDSIVISKAFSHMLNLANL 107
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                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AEEv++A+RRRikk+k+GDF DE+sAttEsDiEEt+K+Lv+ l KsPeE+
gi|2841671   108 AEEVQIAHRRRIKKLKKGDFVDESSATTESDIEETFKRLVSDLGKSPEEI 157

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                F+ALKnq+vDLvltAHPtqsvRRsLLqK++RiR CLaqL+AKD+t++DK+
gi|2841671   158 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRDCLAQLYAKDITPDDKQ 207

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                ELDE L REiqAAFRtDEiRR++PtPqDEmRaGmsY+ Et+WkGvPKFLR
gi|2841671   208 ELDESLQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFRETIWKGVPKFLR 257

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                RvDtALKniGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
gi|2841671   258 RVDTALKNIGIDERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 306

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                aRmmAanlY++q+E LmFElsmWRC dE RvRA+El+r +++d   K+Yi
gi|2841671   307 ARMMAANLYYNQIENLMFELSMWRCTDEFRVRADELHRNSRKD-AAKHYI 355

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                EFWK +PPtEPYRviLGdvRDKLY tRER+R LL  Gis+i+EeA +t+v
gi|2841671   356 EFWKTIPPTEPYRVILGDVRDKLYHTRERSRQLLSNGISDIPEEATFTNV 405

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                E+FLEPLELCY+sLC CGD  iADGsLLD+LRqvstFGLsLv+LDiRqEs
gi|2841671   406 EQFLEPLELCYRSLCSCGDSPIADGSLLDFLRQVSTFGLSLVRLDIRQES 455

                eRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                eR+tDvlDAit+HL+iG+sYR+WsEe RqEWLlaEL+GKRPL+g+DLPkt
gi|2841671   456 ERHTDVLDAITKHLDIGsSYRDWSEEGRQEWLLAELSGKRPLFGPDLPKT 505

                EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                EE+ Dvld+f+v+ ELP+D+FGaYiismat+PsDvLAvELLqREC+vk++
gi|2841671   506 EEISDVLDTFKVISELPSDCFGAYIISMATSPSDVLAVELLQRECHVKNP 555

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gi|2841671   556 LRVVPLFEKLADLEAAPAAVARLFSIDWYKNRINGKQEVMIGYSDSGKDA 605

                GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                GRlsAAW LYkAqEE++KvAKkyGvKL++FHGRGGtvGRGGGPtHLAiLs
gi|2841671   606 GRLSAAWELYKAQEELVKVAKKYGVKLTMFHGRGGTVGRGGGPTHLAILS 655

                qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                qPPDt+nGslRvtvqGEviE+sFGE +LCFr+LqRFtAAtLEHGmnPP+s
gi|2841671   656 QPPDTVNGSLRVTVQGEVIEQSFGEAHLCFRTLQRFTAATLEHGMNPPIS 705

                PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
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gi|2841671   706 PKPEWRALLDEMAVVATEEYRSVVFQEPRFVEYFRLATPELEYGRMNIGS 755

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                RP+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF++Ai+KD++n
gi|2841671   756 RPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRYAIKKDVRN 805

                lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                l +L++mYk+WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+ FG+
gi|2841671   806 LHMLQDMYKQWPFFRVTIDLIEMVFAKGDPGIAALYDKLLVSEDLWAFGE 855

                sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                +LR+++ Etk+l+L+ AGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYt
gi|2841671   856 KLRANFDETKNLVLQTAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYT 905

                LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                LKRiRD +y vtlrPh+sKE  +   k a+eLvkLnpt+++aPGLEDtLi
gi|2841671   906 LKRIRDANYNVTLRPHISKEIMQSS-KSAQELVKLNPTSEYAPGLEDTLI 954

                LtmKGiAAGmqntG<-*
                LtmKGiAAG+qntG
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  gi|2841671   955 LTMKGIAAGLQNTG    968

gi|2626743|dbj|BAA23419.1|: domain 1 of 1, from 11 to 967: score 2547.8, E = 0
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                     siDAqLR L+P Kvsed+kLieYDALLlD+FLDiLqDLHGedLkE v
  gi|2626743    11    SIDAQLRQLAPAKVSEDDKLIEYDALLLDRFLDILQDLHGEDLKETV 57

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                  qE YElsAeYEGK+D+kKLeELG  +tsLd +D+ilvAk+++HmLnLAnL
  gi|2626743    58 QEVYELSAEYEGKHDPKKLEELGNLITSLDAGDSILVAKSFSHMLNLANL 107

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AEEv++  RRR+k+kk GDFaDE +AttEsDiEEtlKkLv  l KsP+Ev
  gi|2626743   108 AEEVQISRRRRNKLKK-GDFADENNATTESDIEETLKKLVFGLKKSPQEV 156

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                  F+ALKnq+vDLvltAHPtqs+RRsLLqK++RiRnCL+qL+AKD+t++DK+
  gi|2626743   157 FDALKNQTVDLVLTAHPTQSIRRSLLQKHGRIRNCLSQLYAKDITPDDKQ 206

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                  ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+W+GvP+FLR
  gi|2626743   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWNGVPRFLR 256

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                  RvDtAL niGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2626743   257 RVDTALNNIGIKERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                  aRmmAanlY+sq+EDLmFElsmWRCndELRvRAEEl+r +++d v K+Yi
  gi|2626743   306 ARMMAANLYYSQIEDLMFELSMWRCNDELRVRAEELHRSSKKDEVAKHYI 355

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                  EFWK+vPP+EPYRv+LG+vRD+LY tRER+RHLL  G+s+i+EeA +t+v
  gi|2626743   356 EFWKKVPPNEPYRVVLGEVRDRLYQTRERSRHLLSNGYSDIPEEATFTNV 405

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                  EeFLE LELCY+sLC CGD++iADGsLLD++RqvstFGLsLv+LDiRqEs
  gi|2626743   406 EEFLESLELCYRSLCACGDRAIADGSLLDFMRQVSTFGLSLVRLDIRQES 455

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  +R+tDvlDAit+HLeiGsY eWsEeKRqEWLl+EL+GKRPL+g+DLP+tE
  gi|2626743   456 DRHTDVLDAITKHLEIGSYQEWSEEKRQEWLLSELSGKRPLFGPDLPQTE 505

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++Dvld+f+v+AELP D FGaYiismataPsDvLAvELLqREC++k++L
  gi|2626743   506 EIRDVLDTFHVIAELPPDNFGAYIISMATAPSDVLAVELLQRECHIKHPL 555

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLeAAPAa+++LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|2626743   556 RVVPLFEKLADLEAAPAALARLFSIDWYRNRINGKQEVMIGYSDSGKDAG 605

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  R+sAAWqLYkAqEE+i vAKk+G+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2626743   606 RFSAAWQLYKAQEELINVAKKFGIKLTMFHGRGGTVGRGGGPTHLAILSQ 655

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGE +LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2626743   656 PPDTIHGSLRVTVQGEVIEQSFGEQHLCFRTLQRFTAATLEHGMHPPISP 705

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm++mAv+AtEEYRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|2626743   706 KPEWRALMDQMAVIATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 755

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKRkPsGGie+LRAiPWiFaWtqtRFHLPvWLG+GAAFK  i+K + nl
  gi|2626743   756 PAKRKPSGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKEVIEKNVNNL 805

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+EmY++WPFFRvtlDL+EmvFAKGDP iA+L D+LLv+ +L+ FG++
  gi|2626743   806 NMLQEMYNQWPFFRVTLDLVEMVFAKGDPKIAGLKDRLLVSKDLWRFGDQ 855
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                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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  gi|2626743   856 LRNKYEETKKLLLQVAGHKEILEGDPYLKQRLRLRHAPITTLNIVQAYTL 905

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y v +rP +sKE  +E sk adeL+kLnpt+++aPGLEDtLiL
  gi|2626743   906 KRIRDPNYNVKVRPRISKE-SAEASKSADELIKLNPTSEYAPGLEDTLIL 954

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|2626743   955 TMKGIAAGMQNTG    967

gi|26800701|emb|CAD58726.1|: domain 1 of 1, from 11 to 963: score 2547.1, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLRlL+PGKvsed+kLieYDALLlD+FLDiLqDLHGed++E+v
  gi|2680070    11    SIDAQLRLLAPGKVSEDDKLIEYDALLLDRFLDILQDLHGEDVREFV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE++A+Y+G + t+KLeELG  LtsLdP+D+i+v k+++ mL LAnL
  gi|2680070    58 QECYEVAADYDGNRNTEKLEELGNMLTSLDPGDSIVVTKSFSNMLSLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRRikk+k+GDFaDEasAttEsDiEEtlK+L  +  K+PeEv
  gi|2680070   108 AEEVQIAYRRRIKKLKKGDFADEASATTESDIEETLKRLLQLN-KTPEEV 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+vDLvltAHPtqsvRRsLLqK +RiR CL+qL+AKD+t++DK+
  gi|2680070   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKFGRIRDCLTQLYAKDITPDDKQ 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|2680070   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2680070   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq+EDLmFE+smWRCn+ELRvRAE  +r a+rd   K+Yi
  gi|2680070   306 ARMMAANLYFSQIEDLMFEMSMWRCNEELRVRAER-QRCAKRD--AKHYI 352

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+P +EPYR iLGdvRDKLYntRERaR LL  G+s+++E+Av+t v
  gi|2680070   353 EFWKQIPANEPYRAILGDVRDKLYNTRERARQLLSSGVSDVPEDAVFTSV 402

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    ++FLEPLELCY+sLC+CGD+ iADGsLLD+LRqvstFGL+LvKLDiRqEs
  gi|2680070   403 DQFLEPLELCYRSLCDCGDRPIADGSLLDFLRQVSTFGLALVKLDIRQES 452

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+ DvlDAittHL+iGsY+eWsE+KRqEWLl+EL+GKRPL+g+DLPktE
  gi|2680070   453 ERHSDVLDAITTHLGIGSYKEWSEDKRQEWLLSELSGKRPLFGPDLPKTE 502

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvld+f+v+ ELP+DsFGaYiismataPsDvLAvELLqRECg+  +L
  gi|2680070   503 EVADVLDTFKVISELPSDSFGAYIISMATAPSDVLAVELLQRECGITDPL 552

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLe APAav++LFsi+WY+nri+GKqevm+GYsDsGKDAG
  gi|2680070   553 RVVPLFEKLADLESAPAAVARLFSIEWYRNRINGKQEVMIGYSDSGKDAG 602

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYk qEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2680070   603 RLSAAWQLYKTQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 652

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+G lRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|2680070   653 PPDTIHGQLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 702

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emA++AtEEYRsvv+KEPRFvEYFRlAtPElEYG+mniGsR
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  gi|2680070   703 KPEWRVLMDEMAIIATEEYRSVVFKEPRFVEYFRLATPELEYGRMNIGSR 752

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiP iFaWtqtRFHLPvWLG+G AFK  i+KD+Knl
  gi|2680070   753 PSKRKPSGGIESLRAIPRIFAWTQTRFHLPVWLGFGGAFKRVIQKDSKNL 802

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +LkEmY++WPFFRvt+DL+EmvFAKGDPGiAaLyD+LLv+EeL+PFG++
  gi|2680070   803 NMLKEMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDRLLVSEELQPFGEQ 852

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR +Y+Et+ lLL++AGHkD+LEGDPYL+qrl LRd+YittLnv+qAYtL
  gi|2680070   853 LRVNYQETRRLLLQVAGHKDILEGDPYLRQRLQLRDPYITTLNVCQAYTL 902

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   K iRDPs++v +rPhlsK+y +    +a+eLvkLnp +++aPGLEDt+iL
  gi|2680070   903 KQIRDPSFHVKVRPHLSKDYMESS--PAAELVKLNPKSEYAPGLEDTVIL 950

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|2680070   951 TMKGIAAGMQNTG    963

gi|14279574|gb|AAK58637.1|AF271163_1: domain 1 of 1, from 16 to 970: score 2545.4, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      s+DAqLR+L+P Kvsed++L+eYDALLlD+FL+iLqDLHGedL+E v
  gi|1427957    16    SVDAQLRMLAPSKVSEDDNLVEYDALLLDRFLEILQDLHGEDLRETV 62

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   q CYElsAeYE   D++KLeELG  LtsLdP+D+i+vA++++HmLnL nL
  gi|1427957    63 QSCYELSAEYESTLDPQKLEELGNMLTSLDPGDSIVVASSFSHMLNLGNL 112

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++A+RRRik+kk GDFaDE sA tEsDiEEtlKkLv++l KsP+Ev
  gi|1427957   113 AEEVQIAFRRRRIKLKK-GDFADENSAATESDIEETLKKLVVQLKKSPQEV 161

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   F+ALKnq+vDLvltAHPtqs+RRsLLqK++RiRn LaqL+AKDvt++DK+
  gi|1427957   162 FDALKNQTVDLVLTAHPTQSIRRSLLQKHSRIRNSLAQLYAKDVTPDDKQ 211

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|1427957   212 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 261

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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  gi|1427957   262 RVDTALRNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 310

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmAanlY+sq+EDLmFElsmWRC dELRvRA  l+r +++    K+Yi
  gi|1427957   311 ARMMAANLYYSQIEDLMFELSMWRCSDELRVRATALHRSSRSV--AKHYI 358

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWKq+PP+EPYRviLG+vRDKLY tRERaR LL  G+s+i+Ee  +t++
  gi|1427957   359 EFWKQIPPNEPYRVILGEVRDKLYKTRERARQLLSNGFSDIPEESTFTNI 408

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   EeFLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLs+vKLDiRqEs
  gi|1427957   409 EEFLEPLELCYRSLCSCGDQPIADGSLLDFLRQVSTFGLSIVKLDIRQES 458

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +R+tDvlDAit HL+iGsYR+WsEeKRqEWLl+EL+GKRPL+g+DLPkt+
  gi|1427957   459 DRHTDVLDAITNHLGIGSYRDWSEEKRQEWLLSELRGKRPLFGPDLPKTD 508

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dvld+++v+AELP D FGaYiismataPsDvLAvELLqREC+vk++L
  gi|1427957   509 EIADVLDTMHVIAELPFDNFGAYIISMATAPSDVLAVELLQRECHVKKPL 558

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLe APAav++LFsiDWY nri+GKqevm+GYsDsGKDAG
  gi|1427957   559 RVVPLFEKLADLETAPAAVARLFSIDWYLNRINGKQEVMIGYSDSGKDAG 608
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                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+iKvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1427957   609 RLSAAWQLYKAQEELIKVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 658

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGs+RvtvqGEviE+sFGEE LCFr+LqRFtAAtLEHGm+PP+sP
  gi|1427957   659 PPDTINGSIRVTVQGEVIEQSFGEERLCFRTLQRFTAATLEHGMHPPLSP 708

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAvvAt+EYRs+v+K+PRFvEYFR+AtPElEYG+mniGsR
  gi|1427957   709 KPEWRALMDEMAVVATDEYRSIVFKDPRFVEYFRSATPELEYGRMNIGSR 758

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KR+PsGGiesLRAiPW+FaWtqt+FHLPvWLG+G AFKh idKD Knl
  gi|1427957   759 PSKRRPSGGIESLRAIPWVFAWTQTKFHLPVWLGFGSAFKHVIDKDPKNL 808

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAa+yDkLLv+ +L PFG++
  gi|1427957   809 QMLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAAMYDKLLVSKDLLPFGER 858

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR+kY Etk+lLLk+AGHkDlLEGDPYL+qrlRLRdsYittLn +qAYtL
  gi|1427957   859 LREKYTETKNLLLKVAGHKDLLEGDPYLRQRLRLRDSYITTLNACQAYTL 908

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP y v lrPhlsKE  d   k a+eLvkLnp++++aPGLEDtLiL
  gi|1427957   909 KRIRDPGYNVQLRPHLSKEMVDSS-KSAAELVKLNPGSEYAPGLEDTLIL 957

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|1427957   958 TMKGIAAGMQNTG    970

gi|4033351|emb|CAA11415.1|: domain 1 of 1, from 11 to 964: score 2545.2, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s+D  LR LvPGKvsed+kL+eYDALLlD+FLDiLq+LHGedL+E v
  gi|4033351    11    SMDVHLRQLVPGKVSEDDKLVEYDALLLDRFLDILQELHGEDLRETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YE sAeYEGK+++kKLeELG +LtsLdP+D+i++Aka++HmLnLAnL
  gi|4033351    58 QELYEHSAEYEGKHEPKKLEELGNVLTSLDPGDSIVIAKAFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRRikk+k+GDF DE+sAttEsD+EEt+KkLv  lnKsPeE+
  gi|4033351   108 AEEVQIAYRRRIKKLKKGDFVDESSATTESDLEETFKKLVGDLNKSPEEI 157

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+vDLvltAHPtqsvRRsLLqK++RiR CLaqL+AKD+t++DK+
  gi|4033351   158 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRDCLAQLYAKDITPDDKQ 207

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEi+R++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|4033351   208 ELDEALQREIQAAFRTDEIKRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 257

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|4033351   258 RVDTALKNIGIEERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 306

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAa +Y++q+EDLmFElsmWRCndELRvRA+El+   ++d   K+Yi
  gi|4033351   307 ARMMAATMYFNQIEDLMFELSMWRCNDELRVRADELHVNRRKD-AAKHYI 355

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK +PPtEPYRv+LGdvRDKLY tRERaR LL  G s+++EeA + ++
  gi|4033351   356 EFWKSIPPTEPYRVVLGDVRDKLYHTRERARQLLSNGTSDVPEEATFNNL 405

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|4033351   406 EEFLEPLELCYRSLCSCGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 455

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlDAittHLeiGsYReWsEe+RqEWLl+EL+GKRPL+gsDLPktE
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  gi|4033351   456 DRHTDVLDAITTHLEIGSYREWSEERRQEWLLSELSGKRPLFGSDLPKTE 505

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dvld+f+v+AELP+DsFGaYiismataPsDvLAvELLqREC+vk++L
  gi|4033351   506 EIADVLDTFHVIAELPSDSFGAYIISMATAPSDVLAVELLQRECHVKRPL 555

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAav++LFs+DWY+nri+GKqevm+GYsDsGKDAG
  gi|4033351   556 RVVPLFEKLADLEAAPAAVARLFSVDWYKNRINGKQEVMIGYSDSGKDAG 605

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGR GGPtHLAiLsq
  gi|4033351   606 RLSAAWQLYKAQEELVKVAKEYGVKLTMFHGRGGTVGRRGGPTHLAILSQ 655

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PPvsP
  gi|4033351   656 PPDTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPVSP 705

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR+L++emAvvAtEEYRsvv++EPRFvEYFRlAtPElEYG+mniGsR
  gi|4033351   706 KPEWRELLDEMAVVATEEYRSVVFQEPRFVEYFRLATPELEYGRMNIGSR 755

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAA +h ++KD+Knl
  gi|4033351   756 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAIRHVVEKDVKNL 805

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L++mY+ WPFFR+t+DL+EmvFAKGDPGiAaLyDkLLv+EeL+PFG++
  gi|4033351   806 HMLQDMYQHWPFFRITIDLIEMVFAKGDPGIAALYDKLLVSEELWPFGEK 855

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++++Etk+l+L+ AGHkDlLEGDPYLKqrlRLR+sYittLnv+qAYtL
  gi|4033351   856 LRANFEETKKLVLQTAGHKDLLEGDPYLKQRLRLRNSYITTLNVCQAYTL 905

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPsy vtlrPh+sKE A+       eL++Lnpt+++aPGLEDtLiL
  gi|4033351   906 KRIRDPSYNVTLRPHISKEIAESS----KELIELNPTSEYAPGLEDTLIL 951

                   tmKGiAAGmqntG<-*
                   tmKG+AAG+qntG
  gi|4033351   952 TMKGVAAGLQNTG    964

gi|115583|sp|P29194.1|CAPP2_SORBI: domain 1 of 1, from 6 to 960: score 2544.9, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      siDAqLR+LvPGKvsed+kLieYDALLlD+FLDiLqDLHG+dLkE+v
  gi|115583|     6    SIDAQLRMLVPGKVSEDDKLIEYDALLLDRFLDILQDLHGDDLKEMV 52

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qECYE++AeYE K+D +KL+ELG  +tsLdP+D+i++Ak+++HmLnLAnL
  gi|115583|    53 QECYEVAAEYETKHDLQKLDELGKMITSLDPGDSIVIAKSFSHMLNLANL 102

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++AyRRRik+kk GDFaDE sA tEsDiEEtlK+Lv+ l KsP+Ev
  gi|115583|   103 AEEVQIAYRRRIKLKK-GDFADENSAITESDIEETLKRLVVDLKKSPAEV 151

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   F+ALK q+vDLvltAHPtqsvRRsLLqK++RiRnCL qL+ KD+t++DK+
  gi|115583|   152 FDALKSQTVDLVLTAHPTQSVRRSLLQKHSRIRNCLVQLYSKDITPDDKQ 201

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL REiqAAFRtDEiRR+qPtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|115583|   202 ELDEALQREIQAAFRTDEIRRTQPTPQDEMRAGMSYFHETIWKGVPKFLR 251

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|115583|   252 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 300

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmA+nlY sq+EDLmFElsmWRC dELR RA+El+r  ++d   K+Yi
  gi|115583|   301 ARMMASNLYCSQIEDLMFELSMWRCSDELRMRADELHRSTKKD--AKHYI 348
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                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK+vPP+EPYRviL dvRDKLYntRER+R LL  G s+i+EeA  t v
  gi|115583|   349 EFWKKVPPNEPYRVILSDVRDKLYNTRERSRELLSSGHSDIPEEATLTTV 398

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+ LEPLELCY+sLC CGD+viADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|115583|   399 EQLLEPLELCYRSLCACGDRVIADGSLLDFLRQVSTFGLSLVRLDIRQES 448

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlDAitt L+iGsYReW+Ee+RqEWLl+EL GKRPL+g+DLPktE
  gi|115583|   449 DRHTDVLDAITTYLGIGSYREWPEERRQEWLLSELNGKRPLFGPDLPKTE 498

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+f+v+AELP D FGaYiismataPsDvLAvELLqREC+vk +L
  gi|115583|   499 EIADVLDTFHVIAELPADNFGAYIISMATAPSDVLAVELLQRECHVKTPL 548

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAa+++LFsiDWY+ ri+GKqevm+GYsDsGKDAG
  gi|115583|   549 RVVPLFEKLADLEAAPAALARLFSIDWYRQRINGKQEVMIGYSDSGKDAG 598

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|115583|   599 RLSAAWQLYKAQEELIKVAKDFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 648

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+L Fr+LqRFtAAtLEHGm+PP +P
  gi|115583|   649 PPDTIHGSLRVTVQGEVIEQSFGEEHLSFRTLQRFTAATLEHGMHPPNAP 698

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emAvvAtEEYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|115583|   699 KPEWRTLLDEMAVVATEEYRSIVFQEPRFVEYFRLATPETEYGRMNIGSR 748

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++KDi+nl
  gi|115583|   749 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHVLQKDIRNL 798

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL+P G++
  gi|115583|   799 HMLQEMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELRPLGEK 848

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Et++lLL++AGH+DlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|115583|   849 LRANYEETQKLLLQVAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 898

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+v lrPhlsKE  d   k a eLvkLnp++++aPGLEDtLiL
  gi|115583|   899 KRIRDPDYHVALRPHLSKEIMDPT-KAASELVKLNPGSEYAPGLEDTLIL 947

                    tmKGiAAGmqntG<-*
                    tmKGiAAG+qntG
  gi|115583|   948 TMKGIAAGLQNTG    960

gi|242078871|ref|XP_002444204.1|: domain 1 of 1, from 10 to 964: score 2540.4, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLR+L+P K sed+kL+eYDALLlD+FLDiLqDLHGedL+E v
  gi|2420788    10    SIDAQLRMLAPAKLSEDDKLVEYDALLLDRFLDILQDLHGEDLRELV 56

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE++AeYE K+D++KL+ELG  LtsLdP+D+i+ Aka++HmLnLAnL
  gi|2420788    57 QECYEIAAEYERKHDSEKLDELGNMLTSLDPGDSIVTAKAFSHMLNLANL 106

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRRik+kk GDFaDE sA tEsDiEEt+K+Lv+ l KsP+Ev
  gi|2420788   107 AEEVQIAYRRRIKLKK-GDFADENSALTESDIEETFKRLVVDLKKSPAEV 155

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALK q+vDLvltAHPtqsvRRsLLqK++RiRnCL qL  KD+t++DK+
  gi|2420788   156 FDALKSQTVDLVLTAHPTQSVRRSLLQKHSRIRNCLVQLCSKDITPDDKQ 205

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR+qPtPqDEmRaGmsY+HEt+WkGvPKFLR
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  gi|2420788   206 ELDEALQREIQAAFRTDEIRRTQPTPQDEMRAGMSYFHETIWKGVPKFLR 255

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                   RvDtALKniGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2420788   256 RVDTALKNIGIDERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 304

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmAanlY sq+E LmFElsmWRCndELR+ A+El+r +++d   K+Yi
  gi|2420788   305 ARMMAANLYCSQIENLMFELSMWRCNDELRAQADELHRSSKKD--AKHYI 352

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWK+vPP EPYRviLGd RDKLYntRERaR LL  G+s+i+Ee   t+v
  gi|2420788   353 EFWKKVPPSEPYRVILGDLRDKLYNTRERARQLLSSGYSDIPEESTVTNV 402

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   E+FLEPLELCY+sLC CGD+viADGsLLD+LRqvstFGL Lv+LDiRqEs
  gi|2420788   403 EQFLEPLELCYRSLCACGDRVIADGSLLDFLRQVSTFGLCLVRLDIRQES 452

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +R+tDvlDAitt L+iGsYReWsEe+RqEWLl+EL GKRPL+g+DLP t+
  gi|2420788   453 DRHTDVLDAITTYLGIGSYREWSEERRQEWLLSELNGKRPLFGPDLPTTD 502

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dvld+frv+AELP D FGaYiismataPsDvLAvELLqREC+vk +L
  gi|2420788   503 EIADVLDTFRVIAELPADNFGAYIISMATAPSDVLAVELLQRECHVKTPL 552

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLe APAa+++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|2420788   553 RVVPLFEKLADLEGAPAALARLFSVDWYRERINGKQEVMIGYSDSGKDAG 602

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+iKvAKk+GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2420788   603 RLSAAWQLYKAQEELIKVAKKFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 652

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2420788   653 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 702

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L++emAvvAt EYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|2420788   703 KPEWRALLDEMAVVATKEYRSIVFQEPRFVEYFRLATPEMEYGRMNIGSR 752

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|2420788   753 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHILEKDIRNL 802

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+ eL+P G++
  gi|2420788   803 HMLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSSELWPLGEK 852

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Etk lLL++AGHkDlLEGD YLKqrlRLRd+YittLnv+qAYt+
  gi|2420788   853 LRANYEETKRLLLQVAGHKDLLEGDLYLKQRLRLRDAYITTLNVCQAYTM 902

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y+vtlrPhlsKE  d n k+a+eLvkLnpt+++aPGLEDtLiL
  gi|2420788   903 KRIRDPDYHVTLRPHLSKEIMDWN-KPAAELVKLNPTSEYAPGLEDTLIL 951

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|2420788   952 TMKGIAAGMQNTG    964

gi|224068767|ref|XP_002302820.1|: domain 1 of 1, from 11 to 965: score 2539.8, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      siDAqLRlL+PGKvsed+kL+eYDALLlD+FLDiLqDLHG+d++E v
  gi|2240687    11    SIDAQLRLLAPGKVSEDDKLVEYDALLLDRFLDILQDLHGKDIRETV 57

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    +CYElsAeYE K+D++KLeELG ++tsLdP+D+i+v k+++HmLnLAnL
  gi|2240687    58 HDCYELSAEYEAKHDPQKLEELGRVITSLDPGDSIVVTKSFSHMLNLANL 107
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                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AEEv++A RRRik+kk GDFaDE sAttEsDiEEtl +Lv +lnKsPeEv
gi|2240687   108 AEEVQIASRRRIKLKK-GDFADENSATTESDIEETLNRLVGQLNKSPEEV 156

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                FeALKnq+vDLvltAHPtqsvRRsLLqK+aRiRnCL+qL+AKD+t+ DK+
gi|2240687   157 FEALKNQTVDLVLTAHPTQSVRRSLLQKHARIRNCLTQLYAKDITPYDKQ 206

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
gi|2240687   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                R DtALKniGi ER+PY++P+i+FssWmGGDRDG nPRvtPEvtRDvCLL
gi|2240687   257 RLDTALKNIGIKERVPYNAPVIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                aRmmAanlY+sq+EDLmFElsmWRCn+ELRvRA+El++ ++r    K+Yi
gi|2240687   306 ARMMAANLYFSQIEDLMFELSMWRCNEELRVRADELHSSSKRY--AKHYI 353

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                EFWKq+PP+EPYRv+LG+vRDKLYntRER+R LLA G s+i+E+  +t+
gi|2240687   354 EFWKQIPPNEPYRVVLGNVRDKLYNTRERSRQLLANGKSDIPEDSTFTNA 403

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                E+ LEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
gi|2240687   404 EQILEPLELCYRSLCACGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 453

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                +R+t vlDAit+HL+iGsYReWsEe R+EWLl+EL+GKRPL+g+DLPktE
gi|2240687   454 DRHTAVLDAITKHLGIGSYREWSEEHRREWLLSELRGKRPLFGPDLPKTE 503

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                E++Dvld+f+v+AELP D FGaYiismat+PsDvLAvELLqREC+v+q+L
gi|2240687   504 EIADVLDTFHVIAELPPDNFGAYIISMATSPSDVLAVELLQRECHVQQSL 553

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                rvvPLFEkLADLeAAPAa++ LFsi WY+ ri GKqevm+GYsDsGKDAG
gi|2240687   554 RVVPLFEKLADLEAAPAAMACLFSINWYRDRIKGKQEVMIGYSDSGKDAG 603

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|2240687   604 RLSAAWQLYKAQEELVKVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 653

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
gi|2240687   654 PPDTIHGSLRVTVQGEVIEKSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 703

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                k EWR Lm+emA+vAt EYRs+v++EPRFvEYFRlAtPElEYG+mniGsR
gi|2240687   704 KSEWRALMDEMAIVATKEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 753

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD Knl
gi|2240687   754 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIQKDTKNL 803

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  L+EmY++WPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL+PFG++
gi|2240687   804 HTLQEMYNQWPFFRVTIDLVEMVFAKGGPGIAALYDKLLVSEELRPFGDR 853

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR++Y+E k +LL+iAGHkDlLEGDPYLKqrlRLRd+YittLnv+qAYtL
gi|2240687   854 LRANYEENKLFLLQIAGHKDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 903

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                K iRDP+y+vt+rPhlsK+y +   k+a+eLvkLnpt+++aPGLEDtLiL
gi|2240687   904 KQIRDPDYHVTVRPHLSKDYMEST-KPAAELVKLNPTSEYAPGLEDTLIL 952

                tmKGiAAGmqntG<-*
                tmKGiAAG+qntG
gi|2240687   953 TMKGIAAGLQNTG    965
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gi|51574149|gb|AAU07998.1|: domain 1 of 1, from 12 to 968: score 2537.8, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      siDAqLR L+P Kvsed+kLieYDALLlD+FLDiLqDLHGedLk  v
  gi|5157414    12    SIDAQLRQLAPAKVSEDDKLIEYDALLLDRFLDILQDLHGEDLKNTV 58

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   q+ YEls eYEGK+D+kKLeE+G  +tsLd +D+i+vAk+++HmLnLAnL
  gi|5157414    59 QDVYELSSEYEGKHDPKKLEEIGNAITSLDAGDSIVVAKSFSHMLNLANL 108

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++ +RRR+k+kk G FaDE++AttEsDiEEtlK+Lv  l KsP+Ev
  gi|5157414   109 AEEVQISHRRRNKLKK-GNFADETNATTESDIEETLKRLVFDLKKSPQEV 157

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   F+ALKnq+vDLvltAHPtqs+RRsLLqK+aRiRnCL+qL+AKD+t++DK+
  gi|5157414   158 FDALKNQTVDLVLTAHPTQSIRRSLLQKHARIRNCLSQLYAKDITPDDKQ 207

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDE L REiqAAFRtDEi+R++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|5157414   208 ELDESLQREIQAAFRTDEIKRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 257

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   R+DtALKniGinER+P ++P+i+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|5157414   258 RIDTALKNIGINERVPHNAPVIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 306

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmA+n+Y+sq+EDLmFElsmWRC dELR RA+El+r + +d v K+Yi
  gi|5157414   307 ARMMASNMYYSQIEDLMFELSMWRCSDELRDRADELHRSSNKDEVAKHYI 356

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWK+vPP+EPYRv+LG+vRD+LY tRER+RHLLA+G+s+i+EeA +t+v
  gi|5157414   357 EFWKKVPPNEPYRVVLGEVRDRLYQTRERSRHLLAHGYSDIPEEATFTNV 406

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   EeFLEPLE+CY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|5157414   407 EEFLEPLEVCYRSLCACGDRSIADGSLLDFLRQVSTFGLSLVRLDIRQES 456

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|5157414   457 DRHTDVMDAITKHLEIGSYQEWSEEKRQEWLLSELCGKRPLFGPDLPKTE 506

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dvld+f+vLAELP D FGaYiismataPsDvLAvELLqREC++k++L
  gi|5157414   507 EIRDVLDTFHVLAELPPDNFGAYIISMATAPSDVLAVELLQRECHIKHPL 556

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAa+++LFs+DWY+nridGKqevm+GYsDsGKDAG
  gi|5157414   557 RVVPLFEKLADLEAAPAALARLFSVDWYKNRIDGKQEVMIGYSDSGKDAG 606

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   R+sAAWqLYkAqE++iKvA k+GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|5157414   607 RFSAAWQLYKAQEDLIKVAEKFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 656

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP ti+GslRvtvqGEviE+sFGE +LCFr+LqR+tAAtLEHGmnPP+sP
  gi|5157414   657 PPGTIHGSLRVTVQGEVIEQSFGEQHLCFRTLQRYTAATLEHGMNPPISP 706

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                   kPEWR Lm++mAvvAtEEYRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|5157414   707 KPEWRALMDQMAVVATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 756

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKR+P GGie+LRAiPWiFaWtqtRFHLPvWLG+G AFK  i+KD  nl
  gi|5157414   757 PAKRRPTGGIETLRAIPWIFAWTQTRFHLPVWLGFGKAFKQVIEKDAGNL 806

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY++WPFFRvt+DL+EmvFAKGDPGiAaL+D+LLv+ +L+PFG++
  gi|5157414   807 LMLQEMYNQWPFFRVTIDLVEMVFAKGDPGIAALNDRLLVSKDLWPFGEQ 856

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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                    LR kY+Etk+ LL++A HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
  gi|5157414   857 LRKKYEETKNHLLQVAAHKDLLEGDPYLKQRLRLRDSYITTLNVFQAYTL 906

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP++ v +rPh+sK+y  E sk a eLv Lnpt+++aPGLED LiL
  gi|5157414   907 KRIRDPNFNVPPRPHISKDYL-EKSKSATELVSLNPTSEYAPGLEDSLIL 955

                    tmKGiAAGmqntG<-*
                     mKGiAAGmqntG
  gi|5157414   956 SMKGIAAGMQNTG    968

gi|115476100|ref|NP_001061646.1|: domain 1 of 1, from 10 to 964: score 2536.9, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLR+L+P K sed+kL+eYDALLlD+FLDiLqDLHG+dL+E v
  gi|1154761    10    SIDAQLRMLAPAKLSEDDKLVEYDALLLDRFLDILQDLHGDDLRELV 56

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE++AeYEGK+D++KL+ELG  LtsLdP+D+i++Aka++HmLnLAnL
  gi|1154761    57 QECYEIAAEYEGKHDSQKLDELGNMLTSLDPGDSIVMAKAFSHMLNLANL 106

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRRik+kk GDFaDE sA tEsDiEEt+K+Lv+ l KsP+Ev
  gi|1154761   107 AEEVQIAYRRRIKLKK-GDFADENSALTESDIEETFKRLVVDLKKSPAEV 155

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALK q+vDLvltAHPtqsvRRsLLqK++RiRnCL qL+ KD+t++DK+
  gi|1154761   156 FDALKSQTVDLVLTAHPTQSVRRSLLQKHSRIRNCLVQLYSKDITPDDKQ 205

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR+qPtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|1154761   206 ELDEALQREIQAAFRTDEIRRTQPTPQDEMRAGMSYFHETIWKGVPKFLR 255

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R DtALKniGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1154761   256 RLDTALKNIGIDERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 304

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmA+nlY sq+EDLmFElsmWRCndELR+RA+El+  +++d   K+Yi
  gi|1154761   305 ARMMASNLYCSQIEDLMFELSMWRCNDELRARADELHLSSKKD--AKHYI 352

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK+vPP EPYRv+LGdvRDKLYntRERaR LL  G+s+i+Ee   t v
  gi|1154761   353 EFWKKVPPSEPYRVVLGDVRDKLYNTRERARQLLSSGYSDIPEETTLTSV 402

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC+CGD+viADG LLD+LRqvstFGL Lv+LDiRqEs
  gi|1154761   403 EQFLEPLELCYRSLCDCGDRVIADGTLLDFLRQVSTFGLCLVRLDIRQES 452

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlDAitt L+iGsYReWsEe+Rq+WLl+EL GKRPL+g+DLPkt+
  gi|1154761   453 DRHTDVLDAITTYLGIGSYREWSEERRQDWLLSELNGKRPLFGPDLPKTD 502

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+frv+AELP D FGaYiismataPsDvLAvELLqREC+vk +L
  gi|1154761   503 EIADVLDTFRVIAELPADNFGAYIISMATAPSDVLAVELLQRECHVKTPL 552

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLe APAav++LFsiDWY+ ri+GKqevm+GYsDsGKDAG
  gi|1154761   553 RVVPLFEKLADLESAPAAVARLFSIDWYRERINGKQEVMIGYSDSGKDAG 602

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYk qEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1154761   603 RLSAAWQLYKSQEELINVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 652

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP++P
  gi|1154761   653 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPIAP 702

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emAvvAt EYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|1154761   703 KPEWRALLDEMAVVATKEYRSIVFQEPRFVEYFRLATPEMEYGRMNIGSR 752
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                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++KDi+nl
  gi|1154761   753 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGSAFKHILEKDIRNL 802

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+EeL+P G++
  gi|1154761   803 HMLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEELWPLGEK 852

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++ +Etk+lLL++AGHkDlLEGD YLKqrlRLR++YittLnv+qAYt+
  gi|1154761   853 LRANCEETKQLLLQVAGHKDLLEGDLYLKQRLRLRNAYITTLNVCQAYTM 902

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+vtlrPh+sKE  d   k+a+eLvkLnpt+++aPGLEDtLiL
  gi|1154761   903 KRIRDPDYHVTLRPHMSKEIMDWS-KPAAELVKLNPTSEYAPGLEDTLIL 951

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|1154761   952 TMKGIAAGMQNTG    964

gi|25901015|dbj|BAC41248.1|: domain 1 of 1, from 11 to 967: score 2535.5, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLR L+P Kvsed+kLieYDALLlD+FLDiLq    e+LkE v
  gi|2590101    11    SIDAQLRQLAPAKVSEDDKLIEYDALLLDRFLDILQGFTWENLKETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YElsAeYEGK+D+kKLeELG  +tsLd +D+ilvAk+++HmLnLAnL
  gi|2590101    58 QEVYELSAEYEGKHDPKKLEELGNLITSLDAGDSILVAKSFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++  RRR+k+kk GDFaDE +AttEsDiEEtlKkLv  l KsP+Ev
  gi|2590101   108 AEEVQISRRRRNKLKK-GDFADENNATTESDIEETLKKLVFDLKKSPQEV 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|2590101   157 FDALKNQTVDLVLTAHPTQSIRRSLLQKHGRIRNCLSQLYAKDITPDDKQ 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|2590101   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWNGVPRFLR 256

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  gi|2590101   257 RVDTALNNIGIKERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|2590101   306 ARMMAANLYYSQIEDLMFELSMWRCNDELRVRAEELHRSSKKDEVAKHYI 355

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK+vPP+EPYRv+LG+vRD+LY tRER+RHLL  G+s+i+EeA +t+v
  gi|2590101   356 EFWKKVPPNEPYRVVLGEVRDRLYQTRERSRHLLSNGYSDIPEEATFTNV 405

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFLE LELCY+sLC CGD++iADGsLLD++RqvstFGLsLv+LDiRqEs
  gi|2590101   406 EEFLESLELCYRSLCACGDRAIADGSLLDFMRQVSTFGLSLVRLDIRQES 455

                    eRqtDvlDAitthLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlDAit+HLeiGsY eWsEeKRqEWLl+EL+GKRPL+g+DLP+tE
  gi|2590101   456 DRHTDVLDAITKHLEIGSYQEWSEEKRQEWLLSELSGKRPLFGPDLPQTE 505

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+f+v+AELP D FGaYiismataPsDvLAvELLqREC++k++L
  gi|2590101   506 EIRDVLDTFHVIAELPPDNFGAYIISMATAPSDVLAVELLQRECHIKHPL 555

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAa+++LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|2590101   556 RVVPLFEKLADLEAAPAALARLFSIDWYRNRINGKQEVMIGYSDSGKDAG 605

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
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                    R+sAAWqLYkAqEE+i vAKk+GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2590101   606 RFSAAWQLYKAQEELINVAKKFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 655

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGE +LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2590101   656 PPDTIHGSLRVTVQGEVIEQSFGEQHLCFRTLQRFTAATLEHGMHPPISP 705

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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  gi|2590101   706 KPEWRALMDQMAVIATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 755

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+PsGGie+LRAiPWiFaWtqtRFHLPvWLG+GAAFK  i+  +Knl
  gi|2590101   756 PAKRRPSGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKKVIEENVKNL 805

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY++WPFFRvtlDL+EmvFAKGDP iAaL+D+LLv+ +L+PFG++
  gi|2590101   806 NMLQEMYNQWPFFRVTLDLVEMVFAKGDPKIAALNDRLLVSKDLWPFGDQ 855

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR+kY+Et++lLL++AGHk++LEGDPYLKqrlRLR + ittLn++qAYtL
  gi|2590101   856 LRNKYEETRKLLLQVAGHKEILEGDPYLKQRLRLRHAPITTLNIVQAYTL 905

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y v +rP +sKE A+   k adeLvkLnpt+++aPGLEDtLiL
  gi|2590101   906 KRIRDPNYNVKVRPRISKESAEAX-KSADELVKLNPTSEYAPGLEDTLIL 954

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|2590101   955 TMKGIAAGMQNTG    967

gi|829295|emb|CAA27270.1|: domain 1 of 1, from 1 to 935: score 2534.0, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                          eYDALL+D+FL iLqDLHG++L+E+v
  gi|829295|     1    ---------------------EYDALLVDRFLNILQDLHGPSLREFV 26

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE+sA+YEGK Dt KL+ELGakLt+L+PaDailvA++ilHmLnLAnL
  gi|829295|    27 QECYEVSADYEGKGDTTKLGELGAKLTGLAPADAILVASSILHMLNLANL 76

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A+RRR++k+k+G FaDE+sAttEsDiEEtlK+Lv+   KsPeEv
  gi|829295|    77 AEEVQIAHRRRRNSKLKKGGFADEGSATTESDIEETLKRLVSEVGKSPEEV 126

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    FeALKnq+vDLv+tAHPtqs+RRsLLqKnaRiRnCL+qL AKD+t +DK+
  gi|829295|   127 FEALKNQTVDLVFTAHPTQSARRSLLQKNARIRNCLTQLNAKDITDDDKQ 176

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRRaqPtPqDEmR+GmsYiHEtvWkGvPKFLR
  gi|829295|   177 ELDEALQREIQAAFRTDEIRRAQPTPQDEMRYGMSYIHETVWKGVPKFLR 226

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinERlPY+v Li+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|829295|   227 RVDTALKNIGINERLPYNVSLIRFSSWMGGDRDG-NPRVTPEVTRDVCLL 275

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlYi+q+E+LmFElsmWRCnd++RvRAEEl++ + ++ v+KyYi
  gi|829295|   276 ARMMAANLYIDQIEELMFELSMWRCNDDVRVRAEELHSSSGSK-VTKYYI 324

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP+EPYRviLG vRDKLYntRERaRHLLA G+seis e  +t +
  gi|829295|   325 EFWKQIPPNEPYRVILGHVRDKLYNTRERARHLLASGVSEISAESSFTSI 374

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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  gi|829295|   375 EEFLEPLELCYKSLCDCGDKAIADGSLLDLLRQVFTFGLSLVKLDIRQES 424

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+tDv+DAittHL+iGsYReWsE+KRqEWLl+EL+GKRPLl++DLP+t+
  gi|829295|   425 ERHTDVIDAITTHLGIGSYREWSEDKRQEWLLSELRGKRPLLPPDLPQTD 474
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  gi|829295|   475 EIADVIGAFHVLAELPPDSFGPYIISMATAPSDVLAVELLQRECGVRPAV 524

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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  gi|829295|   525 PVVPLFERLASLQLRPASVERLFSVDWYMDRIKGKQQVMVGYSDSGKDAG 574

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLY+AqEE+++vAK+yGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|829295|   575 RLSAAWQLYRAQEEMAQVAKRYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 624

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGs+RvtvqGEviEf FGEE+L F++LqRFtAAtLEHGm+PPvsP
  gi|829295|   625 PPDTINGSIRVTVQGEVIEFCFGEEHLSFQTLQRFTAATLEHGMHPPVSP 674

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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  gi|829295|   675 KPEWRKLMDEMAVVATEEYRSVVVKEPRFVEYFRSATPETEYGRMNIGSR 724

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+AidKD++n+
  gi|829295|   725 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKFAIDKDVRNF 774

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q LkEmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLvaEeLkPFGk+
  gi|829295|   775 QVLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVAEELKPFGKQ 824

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRdkYvEt++lLL+iAGHkD+LEGDP+LKq+l LR++YittLnvfqAYtL
  gi|829295|   825 LRDKYVETQQLLLQIAGHKDILEGDPFLKQGLVLRNPYITTLNVFQAYTL 874

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
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  gi|829295|   875 KRIRDPNFKVTPQPPLSKEFADEN--KPAGLVKLNPASEYPPGLEDTLIL 922

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                    tmKGi AGmqntG
  gi|829295|   923 TMKGIRAGMQNTG    935

gi|24636262|sp|Q9AU12.1|CAPP_PHAVU: domain 1 of 1, from 11 to 968: score 2532.8, E = 0
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  gi|2463626    11    SIDAQLRQLAPSKVSEDDKLIEYDALLLDRFLDILQNLHGEDLKETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YElsAeYEGK+D+kKLeELG ++tsLd +D+i+vAk+++HmLnLAnL
  gi|2463626    58 QEVYELSAEYEGKHDPKKLEELGNVITSLDAGDSIVVAKSFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++  RRR+k+kk GDFaDE +AttEsDiEEtlKkLv  l KsP+Ev
  gi|2463626   108 AEEVQISRRRRNKLKK-GDFADENNATTESDIEETLKKLVFELKKSPQEV 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+vDLvltAHPtqsvRRsLLqK+aRiRnCL++L+AKD+t++DK+
  gi|2463626   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHARIRNCLSKLYAKDITPDDKQ 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+W+GvP FLR
  gi|2463626   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWNGVPSFLR 256

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtAL niGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2463626   257 RVDTALNNIGIKERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAan+Y+sq+EDLmFElsmWRCndELRv A+E++r + +d v K+Yi
  gi|2463626   306 ARMMAANMYYSQIEDLMFELSMWRCNDELRVHADEVHRSSNKDEVAKHYI 355

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  gi|2463626   356 EFWKKVPTNEPYRVVLGEVRDRLYQTRERSRHLLSNGYSDIPEENTFTSV 405

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFL PLELCY+sLC CGD++iADGsLLD+LRqvstFGLs+v+LDiRqEs
  gi|2463626   406 EEFLQPLELCYRSLCACGDRAIADGSLLDFLRQVSTFGLSIVRLDIRQES 455

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlDAit+HLeiGsY eWsEeKRqEWLl+EL+GKRPL+g+DLP+tE
  gi|2463626   456 DRHTDVLDAITKHLEIGSYQEWSEEKRQEWLLSELSGKRPLFGPDLPQTE 505

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+f+v+AELP D FGaYiismataPsDvLAvELLqREC+vk++L
  gi|2463626   506 EIRDVLDTFHVIAELPPDNFGAYIISMATAPSDVLAVELLQRECHVKHPL 555

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAa+++LFs+DWY+nridGKqevm+GYsDsGKDAG
  gi|2463626   556 RVVPLFEKLADLEAAPAALARLFSVDWYKNRIDGKQEVMIGYSDSGKDAG 605

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    R+sAAWqLYkAqEE++KvAKk+G+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2463626   606 RFSAAWQLYKAQEELVKVAKKFGIKLTMFHGRGGTVGRGGGPTHLAILSQ 655

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+ FGE +LCFr+LqRFtAAtLEHGmnPP+sP
  gi|2463626   656 PPDTIHGSLRVTVQGEVIEQCFGEQHLCFRTLQRFTAATLEHGMNPPISP 705

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  gi|2463626   706 KPEWRAMMDQMAVIATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 755

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi.Kn
                    PaKR+PsGGie+LRAiPWiFaWtqtRFHLPvWLG+GAAFK  +dK  +Kn
  gi|2463626   756 PAKRRPSGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKQVLDKNAkKN 805

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l +L+EmY++WPFFRvtlDL+EmvFAKGDP i aL+D+LLv+ +L+PFG+
  gi|2463626   806 LSMLQEMYNQWPFFRVTLDLVEMVFAKGDPKIGALNDRLLVSKDLWPFGD 855

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
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  gi|2463626   856 QLRNKYEETKKLLLQVAGHKEILEGDPYLKQRLRLRHSPITTLNVFQAYT 905

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    LKRiRDP+ykv  rP +sKE  +E sk adeL+kLnpt+++aPGLEDtLi
  gi|2463626   906 LKRIRDPNYKVKARPRISKE-SAEASKSADELIKLNPTSEYAPGLEDTLI 954

                    LtmKGiAAGmqntG<-*
                    LtmKGiAAGmqntG
  gi|2463626   955 LTMKGIAAGMQNTG    968

gi|4033349|emb|CAA11414.1|: domain 1 of 1, from 11 to 964: score 2532.7, E = 0
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                       s+D  LR LvPGKvsed+kL+eYDALLlD+FLDiLq+LHGedL+E v
  gi|4033349    11    SMDVHLRQLVPGKVSEDDKLVEYDALLLDRFLDILQELHGEDLRETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YE sAeYEGK+++kKLeELG +LtsLdP+D+i++Aka++HmLnLAnL
  gi|4033349    58 QELYEHSAEYEGKHEPKKLEELGNVLTSLDPGDSIVIAKAFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRRikk+k+GDF DE+sAttEsD+EEt+KkLv  lnKsPeE+
  gi|4033349   108 AEEVQIAYRRRIKKLKKGDFVDESSATTESDLEETFKKLVGDLNKSPEEI 157

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                    F+ALKnq+vDLvltAHP qsvRRsLLqK++RiR CLaqL+AKD+t++DK+
  gi|4033349   158 FDALKNQTVDLVLTAHPPQSVRRSLLQKHGRIRDCLAQLYAKDITPDDKQ 207

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEi+R++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|4033349   208 ELDEALQREIQAAFRTDEIKRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 257
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                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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  gi|4033349   258 RVDTALKNIGIEERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 306

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|4033349   307 ARMMAATMYFNQIEDLMFELSMWRCNDELRVRADELHVNRRKD-AAKHYI 355

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK +P tEPYRv+LGdvRDKLY tRERaR LL  G s+++EeA + ++
  gi|4033349   356 EFWKSIPTTEPYRVVLGDVRDKLYHTRERARQLLSNGTSDVPEEATFNNL 405

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|4033349   406 EDFLEPLELCYRSLCSCGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 455

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                    +R+tDvlDAittHL+iGsYReWsEe+RqEWLl+EL+GKRPL+gsDLPktE
  gi|4033349   456 DRHTDVLDAITTHLDIGSYREWSEERRQEWLLSELSGKRPLFGSDLPKTE 505

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  gi|4033349   506 EIADVLDTFHVIAELPSDSFGAYIISMATAPSDVLAVELLQRECHVKRPL 555

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  gi|4033349   556 RVVPLFEKLADLEAAPAAVARLFSVDWYKNRINGKQEVMIGYSDSGKDAG 605

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|4033349   606 RLSAAWQLYKAQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 655

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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  gi|4033349   656 PPDTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPVSP 705

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  gi|4033349   706 KPEWRALLDEMADVATEEYRSVVFQEPRFVEYFRLATPELEYGRMNIGSR 755

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
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  gi|4033349   756 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAIRHVVEKDVKNL 805

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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  gi|4033349   806 HMLQDMYKNWPFFRVTIDLIEMVFAKGDPGIAALYDKLLVSEELWPFGDK 855

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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  gi|4033349   856 LRANFEETKKLVLQTAGHKDLLEGDPYLKQRLRLRNSYITTLNVCQAYTL 905

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                    KRiRDPsy+vtlrPh+sKE A+       eL++Lnpt+++aPGLEDtLiL
  gi|4033349   906 KRIRDPSYHVTLRPHISKEIAESS----KELIELNPTSEYAPGLEDTLIL 951

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                    tmKG+AAG+qntG
  gi|4033349   952 TMKGVAAGLQNTG    964

gi|14279572|gb|AAK58636.1|AF271162_1: domain 1 of 1, from 14 to 968: score 2530.3, E = 0
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                       s+DAqLR+L+P Kvsed++L+eYDALLlD+FLDiLqDLHGedL+E v
  gi|1427957    14    SVDAQLRMLAPSKVSEDDNLVEYDALLLDRFLDILQDLHGEDLRETV 60

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    q CYElsAeYE    ++KLeELG  LtsLdP+D+i+vA++++HmLnL nL
  gi|1427957    61 QSCYELSAEYESTLNPEKLEELGKMLTSLDPGDSIVVASSFSHMLNLGNL 110

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gi|1427957   111 AEEVQIAFRRRIKLKK-GDFADENSATTESDIEETLRKMVVQLKKSPQEV 159

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gi|1427957   160 FDALKNQTVDLVLTAHPTQSIRRSLLQKHSRIRNCLAQLYAKDVTPDDKQ 209

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gi|1427957   210 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 259

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gi|1427957   260 RVDTALRNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 308

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gi|1427957   309 ARMMAANLYYSQIEDLMFELSMWRCSDELRVRATEIHGSSKSV--AKHYI 356

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
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gi|1427957   357 EFWKQIPPHEPYRVVLGEVRDKLYKTRERARQLLANGFSDIPEETTFTNI 406

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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gi|1427957   407 EQFLEPLELCYRSLCSCGDQPIADGSLLDFLRQVSTFGLSLVKLDIRQES 456

                eRqtDvlDAitthLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                eR+tDv+DAit HL+iGsYR WsEeKRqEWLl+EL+GKRPL+g+DLPktE
gi|1427957   457 ERHTDVMDAITNHLGIGSYRAWSEEKRQEWLLSELRGKRPLFGPDLPKTE 506

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                E++Dvlda++v+AELP D FGaYiismataPsDvLAvELLqREC+vk++L
gi|1427957   507 EIADVLDAMHVIAELPFDNFGAYIISMATAPSDVLAVELLQRECHVKKPL 556

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                rvvPLFEkLADLe APA+v++LFsiDWY nridGKqevm+GYsDsGKDAG
gi|1427957   557 RVVPLFEKLADLETAPASVARLFSIDWYLNRIDGKQEVMIGYSDSGKDAG 606

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLYkAqEE+i+vAKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1427957   607 RLSAAWQLYKAQEELIQVAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 656

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PP+tinGs+RvtvqGEviE+sFGEE LCFr+LqRFtAAtLEHGm PP+sP
gi|1427957   657 PPETINGSIRVTVQGEVIEQSFGEERLCFRTLQRFTAATLEHGMRPPISP 706

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                kPEWR Lm+emAvvAt+EYRs+v+K+PRFvEYFR+AtPElEYG+mniGsR
gi|1427957   707 KPEWRALMDEMAVVATDEYRSIVFKDPRFVEYFRSATPELEYGRMNIGSR 756

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+KRkPsGGiesLRAiPWiFaWtqt+FHLPvWLG+G AFKh i KD Knl
gi|1427957   757 PSKRKPSGGIESLRAIPWIFAWTQTKFHLPVWLGFGSAFKHVIGKDPKNL 806

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                q+L+EmY+eWPFFRvt+DL+EmvFAKGDP iAa+yDkLLv+ +L+PFG+
gi|1427957   807 QMLQEMYNEWPFFRVTIDLVEMVFAKGDPVIAAMYDKLLVSKDLQPFGEC 856

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR+kY EtkdlLLk+AGHkDlLEGDPYLKqrl LRdsYit Ln +qAYtL
gi|1427957   857 LREKYTETKDLLLKVAGHKDLLEGDPYLKQRLQLRDSYITALNACQAYTL 906

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                KRiRDP y v  rPhlsK+  +   k a+eLvkLnp++++aPGLEDtLiL
gi|1427957   907 KRIRDPGYNVQARPHLSKDMVNNG-KSAAELVKLNPGSEYAPGLEDTLIL 955

                tmKGiAAGmqntG<-*
                tmKGiAAGmqntG
gi|1427957   956 TMKGIAAGMQNTG    968
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gi|162458345|ref|NP_001105438.1|: domain 1 of 1, from 13 to 967: score 2529.8, E = 0
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                     siDAqLR+LvPGKvsed+kLieYDALLlD+FLDiLqDLHG+dLkE+v
  gi|1624583    13    SIDAQLRMLVPGKVSEDDKLIEYDALLLDRFLDILQDLHGDDLKEMV 59

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                  qECYE++AeYE K+D +KL+ELG  +tsLdP+D+i++Ak+++HmLnLAnL
  gi|1624583    60 QECYEVAAEYETKHDLQKLDELGKMITSLDPGDSIVIAKSLSHMLNLANL 109

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AEEv++AyRRRik+kk GDFaDE sA tEsDiEEtlK+Lv+ l KsP+Ev
  gi|1624583   110 AEEVQIAYRRRIKLKK-GDFADENSAITESDIEETLKRLVVDLKKSPAEV 158

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                  F+ALK q+vDLvltAHPtqsvRRsLLqK++RiRnCL qL+ KD+t++DK+
  gi|1624583   159 FDALKSQTVDLVLTAHPTQSVRRSLLQKHSRIRNCLVQLYSKDITPDDKQ 208

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                  ELDEAL REiqAAFRtDEiRR+qPtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|1624583   209 ELDEALQREIQAAFRTDEIRRTQPTPQDEMRAGMSYFHETIWKGVPKFLR 258

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                  RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1624583   259 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 307

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                  aRmmA+nlY sq+EDLmFElsmWRC dELR RA+ l+   ++d   K+Yi
  gi|1624583   308 ARMMASNLYCSQIEDLMFELSMWRCSDELRMRADVLHLSTKKD--AKHYI 355

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                  EFWK+vPP+EPYRviL dvRDKLYntRER+R LL  G s+i+EeA  t+v
  gi|1624583   356 EFWKKVPPNEPYRVILSDVRDKLYNTRERSRELLSSGHSDIPEEATLTNV 405

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                  E+ LEPLELCY+sLC CGD viADG LLD+LRqvstFGLsLv+LDiRqEs
  gi|1624583   406 EQLLEPLELCYRSLCACGDSVIADGTLLDFLRQVSTFGLSLVRLDIRQES 455

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  +R+tDvlDAitt L+iGsYReW Ee+RqEWLl+EL GKRPL+gsDLPktE
  gi|1624583   456 DRHTDVLDAITTYLGIGSYREWTEERRQEWLLSELNGKRPLFGSDLPKTE 505

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E+ Dvld+f+v+AELP+D FGaYiismataPsDvLAvELLqREC+vk +L
  gi|1624583   506 EISDVLDTFHVIAELPSDNFGAYIISMATAPSDVLAVELLQRECHVKTPL 555

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLeAAPAa+++LFsiDWY+ ri+GKqevm+GYsDsGKDAG
  gi|1624583   556 RVVPLFEKLADLEAAPAALARLFSIDWYRQRINGKQEVMIGYSDSGKDAG 605

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1624583   606 RLSAAWQLYKAQEELIKVAKDFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 655

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP +P
  gi|1624583   656 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPNAP 705

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++emAvvAtEEYRs+v+KEPRFvEYFRlAtPE+EYG+mniGsR
  gi|1624583   706 KPEWRALLDEMAVVATEEYRSIVFKEPRFVEYFRLATPETEYGRMNIGSR 755

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGi+sLRAiPWiFaWtqtRFHLPvWLG+GAAFK  ++KDi+nl
  gi|1624583   756 PSKRKPSGGIDSLRAIPWIFAWTQTRFHLPVWLGFGAAFKNVLQKDIRNL 805

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+EmY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL+P G++
  gi|1624583   806 HMLQEMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELHPLGEK 855

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y+Et++lLL++AGH+DlLEGD YLKqrlRLRd+YittLnv+qAYtL
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  gi|1624583   856 LRANYEETQKLLLQVAGHRDLLEGDLYLKQRLRLRDAYITTLNVCQAYTL 905

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y+v lrPhlsKE  d   k a+++vkLnp++++aPGLEDtLiL
  gi|1624583   906 KRIRDPDYHVALRPHLSKEIMDST-KAAADVVKLNPGSEYAPGLEDTLIL 954

                   tmKGiAAGmqntG<-*
                   tmKGiAAG+qntG
  gi|1624583   955 TMKGIAAGLQNTG    967

gi|226320258|gb|ACO48250.1|: domain 1 of 1, from 11 to 966: score 2528.2, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      siDAqLRlL+P Kvs+d+kL+eYDALLlD+FLDiLqDLHG d++E v
  gi|2263202    11    SIDAQLRLLAPSKVSDDDKLVEYDALLLDRFLDILQDLHGLDIRETV 57

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   q+CYElsAeYEG  D++KLeELG  Lt+Ld +D+i+vAk+++HmLnLAnL
  gi|2263202    58 QDCYELSAEYEGENDPHKLEELGNMLTGLDAGDSIVVAKSFSHMLNLANL 107

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++AyRRRik++k+GDF DE sA tEsD+EEt+K+Lv + nK+P+Ev
  gi|2263202   108 AEEVQIAYRRRIKLLKKGDFVDENSAITESDLEETFKRLVNQMNKTPQEV 157

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   F+ALKnq+vDLvltAHPtqsvRRsLLqK++RiRnCL+qL+AKD+t++D++
  gi|2263202   158 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLTQLYAKDITPDDRQ 207

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkG+PKFLR
  gi|2263202   208 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGIPKFLR 257

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALKniGinER+PY +P+i+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2263202   258 RVDTALKNIGINERVPYSAPVIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 306

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmAanlY+sq+EDLmFElsmWRC dELRv  +El r +++d   K+Yi
  gi|2263202   307 ARMMAANLYFSQIEDLMFELSMWRCSDELRVHVDELLRSSKSD--AKHYI 354

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWKqvPP+EPYRviLGdvRDKLYntRE aR LLA G sei+Ee  +t+v
  gi|2263202   355 EFWKQVPPNEPYRVILGDVRDKLYNTREHARQLLANGTSEIPEETTFTNV 404

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   E+FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|2263202   405 EQFLEPLELCYRSLCACGDQPIADGSLLDFLRQVSTFGLSLVRLDIRQES 454

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +R+tDv+DAit HLe+GsYReWsEe+Rq WLl+EL+G+RPL+g+DLPktE
  gi|2263202   455 DRHTDVMDAITNHLELGSYREWSEERRQQWLLSELSGRRPLYGPDLPKTE 504

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E+ Dvl++frv+AELP+DsFGaYiismata sDvLAvELLqREC+vkq+L
  gi|2263202   505 EITDVLETFRVIAELPSDSFGAYIISMATAASDVLAVELLQRECHVKQPL 554

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAP a++ LFsiDWY+nridGKqevm+GYsDsGKDAG
  gi|2263202   555 RVVPLFEKLADLEAAPSALACLFSIDWYRNRIDGKQEVMIGYSDSGKDAG 604

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAW LYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2263202   605 RLSAAWALYKAQEELIKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 654

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+ PvsP
  gi|2263202   655 PPDTIHGSLRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHSPVSP 704

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emAv+At EYRsvv++EPRFvEYFR AtPElEYG+mniGsR
  gi|2263202   705 KPEWRALMDEMAVIATKEYRSVVFQEPRFVEYFRCATPELEYGRMNIGSR 754
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                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh i+KD Knl
  gi|2263202   755 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGKAFKHVIEKDPKNL 804

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+L++mY++WPFFRvtlDL+EmvFAKGDPGiAaLyDkLLv+EeL+ FG++
  gi|2263202   805 QMLRDMYNQWPFFRVTLDLVEMVFAKGDPGIAALYDKLLVSEELWLFGER 854

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    L+ kY+Etk lLL++AGHkDlLEGDPYLKqrlR+RdsYittLnv+qAYtL
  gi|2263202   855 LKSKYEETKSLLLQVAGHKDLLEGDPYLKQRLRIRDSYITTLNVLQAYTL 904

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+v l+Phl K+y  E sk+a+eLvkLnp +++aPGLEDtLiL
  gi|2263202   905 KRIRDPDYHVNLKPHLCKDYT-ESSKPAAELVKLNPKSEYAPGLEDTLIL 953

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|2263202   954 TMKGIAAGMQNTG    966

gi|30088841|gb|AAP06951.1|: domain 1 of 1, from 8 to 961: score 2527.6, E = 0
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                       siDAqLRlL+PGKvsed+kL+eYDALL+D+FLDiLqDLHG+ L+E+v
  gi|3008884     8    SIDAQLRLLAPGKVSEDDKLVEYDALLVDRFLDILQDLHGPHLREFV 54

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYElsAeYE  +D  +L+ELG+kLtsL P+++i+vA++++HmLnLAnL
  gi|3008884    55 QECYELSAEYENDRDEARLGELGSKLTSLPPGESIVVASSFSHMLNLANL 104

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A+RRRik+k+ GDFaDEasA tEsDiEEtlK+Lv++l Ks eEv
  gi|3008884   105 AEEVQIAHRRRIKLKR-GDFADEASAPTESDIEETLKRLVSQLGKSREEV 153

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+vDLv+tAHPtqsvRRsLLqK++RiRnCL qL+AKD+t +DK+
  gi|3008884   154 FDALKNQTVDLVFTAHPTQSVRRSLLQKHGRIRNCLRQLYAKDITADDKQ 203

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|3008884   204 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 253

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R+DtALKniGinERlPY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|3008884   254 RIDTALKNIGINERLPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 302

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq+EDLmFElsmWRC dELR+RA++l+r  +r     +Yi
  gi|3008884   303 ARMMAANLYFSQIEDLMFELSMWRCSDELRIRADDLHRSTKRA--AEHYI 350

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKqvPP+EPYRviLGdvRDKLY tRER+RHLL tGisei+E+A +t+v
  gi|3008884   351 EFWKQVPPNEPYRVILGDVRDKLYYTRERSRHLLTTGISEIPEDATFTNV 400

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC CGDk iADGsLLD+LRqvstFGL+LvKLDiRqEs
  gi|3008884   401 EQFLEPLELCYRSLCACGDKPIADGSLLDFLRQVSTFGLALVKLDIRQES 450

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlD ittH +iGsY eWsEeKRq+WLl+EL+GKRPL+gsDLP tE
  gi|3008884   451 DRHTDVLDSITTHPGIGSYAEWSEEKRQDWLLSELRGKRPLFGSDLPLTE 500

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E +Dvl++f+vLAELP D+FGaYiismataPsDvLAvELLqREC+vkq+L
  gi|3008884   501 ETADVLGTFHVLAELPTDCFGAYIISMATAPSDVLAVELLQRECHVKQPL 550

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAav++LFsi WY+nri+GKqevm+GYsDsGKDAG
  gi|3008884   551 RVVPLFEKLADLEAAPAAVARLFSIGWYMNRINGKQEVMIGYSDSGKDAG 600

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsA Wq+YkAqEE+iKvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
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  gi|3008884   601 RLSATWQMYKAQEELIKVAKHYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 650

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE sFGEE LCFr+LqR+tAAtLEHGm+PP+sP
  gi|3008884   651 PPDTIHGSLRVTVQGEVIEHSFGEELLCFRTLQRYTAATLEHGMHPPISP 700

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emA+vAt EYRs+v++EPRFvEYF +AtPE+EYG+mni sR
  gi|3008884   701 KPEWRALMDEMAIVATKEYRSIVFQEPRFVEYFGSATPETEYGRMNIDSR 750

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KR+PsGGiesLRAiPWiFaWtqtRFH PvWLG+GAAFKh ++KDi+n
  gi|3008884   751 PSKRRPSGGIESLRAIPWIFAWTQTRFHPPVWLGFGAAFKHIMQKDIRNT 800

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     LkEmY+eWPF RvtlDLlEmvFAKGDPGiAa+yDkLLva++L+ FG++
  gi|3008884   801 HTLKEMYNEWPFSRVTLDLLEMVFAKGDPGIAAVYDKLLVADDLQSFGEQ 850

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR +Y+Etk+lLL++AGHkD+LEGDPYLKqrlRLR+sYittLnv+qAYtL
  gi|3008884   851 LRKNYEETKELLLQVAGHKDVLEGDPYLKQRLRLRESYITTLNVCQAYTL 900

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPs++v ++P lsKE+ dE   +++eLv+Lnp +++aPGLE tLiL
  gi|3008884   901 KRIRDPSFQVSPQPALSKEFVDES--QPAELVRLNPESEYAPGLENTLIL 948

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|3008884   949 TMKGIAAGMQNTG    961

gi|51574151|gb|AAU07999.1|: domain 1 of 1, from 12 to 968: score 2526.5, E = 0
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                      siDAqLR L+P Kvsed+kLieYDALLlD+FLDiLqDLHGedLk+ v
  gi|5157415    12    SIDAQLRQLAPAKVSEDDKLIEYDALLLDRFLDILQDLHGEDLKDTV 58

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qE YEls +YEGK+D+kKLeE+G ++tsLd +D+i+vAk+++HmLnLAnL
  gi|5157415    59 QEVYELSSQYEGKHDPKKLEEIGNVITSLDAGDSIVVAKSFSHMLNLANL 108

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++ +RRR+k+kk G FaDE++AttEsDiEEtlK+Lv  l KsP Ev
  gi|5157415   109 AEEVQISHRRRNKLKK-GNFADETNATTESDIEETLKRLVFDLKKSPHEV 157

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   F+ALK q+vDLvltAHPtqs+RRsLLqK+aRiR CL+ L+AKD+t++DKk
  gi|5157415   158 FDALKSQTVDLVLTAHPTQSIRRSLLQKHARIRDCLSHLYAKDITPDDKK 207

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL REiqAAFRtDEi+R++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|5157415   208 ELDEALQREIQAAFRTDEIKRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 257

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALKniGinE +P ++P+i+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|5157415   258 RVDTALKNIGINECIPHNAPVIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 306

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmAan+Y+sq+EDLmFElsmWRC dELR RA+El+r + +d v K+Yi
  gi|5157415   307 ARMMAANMYYSQIEDLMFELSMWRCSDELRNRADELHRSSNKDEVAKHYI 356

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                   EFWK+vP +EPYRv+LG+vRD+LY tRER+RHLLA+G+s+i+EeA +t+v
  gi|5157415   357 EFWKKVPANEPYRVVLGEVRDRLYQTRERSRHLLAHGYSDIPEEATFTNV 406

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   EeFLEPLE+CY+sLC CGD+ iADGsLLD+LRq+stFGLsLv+LDiRqEs
  gi|5157415   407 EEFLEPLEVCYRSLCACGDRPIADGSLLDFLRQISTFGLSLVRLDIRQES 456

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|5157415   457 DRHTDVMDAITKHLEIGSYLEWSEEKRQEWLLSELSGKRPLFGPDLPKTE 506
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                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
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  gi|5157415   507 EIRDVLDTFHVLAELPPDNFGAYIISMATAPSDVLAVELLQRECHIKHPL 556

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLe APAa+++LFsiDWYinridGKqevm+GYsDsGKDAG
  gi|5157415   557 RVVPLFEKLADLEVAPAALARLFSIDWYINRIDGKQEVMIGYSDSGKDAG 606

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    R+sAAWqLYkAqEE+iKvAKk+GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|5157415   607 RFSAAWQLYKAQEELIKVAKKFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 656

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGE +LCFr+LqR+tAAtLEHGmnPP+sP
  gi|5157415   657 PPDTIHGSLRVTVQGEVIEQSFGEQHLCFRTLQRYTAATLEHGMNPPISP 706

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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  gi|5157415   707 KPEWRALMDQMAVISTEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 756

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  gi|5157415   757 PAKRRPTGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKQVIEKDVRNL 806

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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  gi|5157415   807 HMLQEMYNQWPFFRVTIDLVEMVFAKGDPGIAALNDRLLVSKDLWPFGEQ 856

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR kY+Etk+lLLk+A HkDlLEGDPYLKqrlRLR sYittLnvfqAYtL
  gi|5157415   857 LRKKYEETKNLLLKVAAHKDLLEGDPYLKQRLRLRHSYITTLNVFQAYTL 906

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP++ v +r h+sKE   E s  a eLv Lnpt+++aPGLED LiL
  gi|5157415   907 KRIRDPNFNVRPRHHISKE-SLEKSTSATELVSLNPTSEYAPGLEDSLIL 955

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  gi|5157415   956 TMKGIAAGMQNTG    968

gi|115577|sp|P29193.1|CAPP1_SACHY: domain 1 of 1, from 11 to 966: score 2524.1, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLRlL+P K s+d+kL+eYDALLlD+FLDiLqDLHGed++E v
  gi|115577|    11    SIDAQLRLLAPQKLSDDDKLVEYDALLLDRFLDILQDLHGEDIRETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYEl+AeYE K D+k L+E+G +LtsLdP+D+i++ k+++HmL LAnL
  gi|115577|    58 QECYELAAEYENKLDPKMLDEIGNVLTSLDPGDSIVITKSFSHMLILANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRRik+kk GDF DE sAttEsDiEEtlK+L+ +l KsP Ev
  gi|115577|   108 AEEVQIAYRRRIKLKK-GDFVDENSATTESDIEETLKRLMHQLKKSPLEV 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|115577|   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLTQLYAKDITPDEKQ 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|115577|   207 ELDEALQREIQAAFRTDEIRRAPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinERlPY++P+i+FssWmGGDRDG nPRvtPE+tRDvCLL
  gi|115577|   257 RVDTALKNIGINERLPYNAPIIQFSSWMGGDRDG-NPRVTPEITRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY  q+EDLmFElsmWRC dELRv+ +El+r +++d  +K+Yi
  gi|115577|   306 ARMMAANLYNAQIEDLMFELSMWRCSDELRVKVDELHRSSKKD-TTKHYI 354

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKqvPP EPYRviL dvRDKLYntRERaRHLLA G+sei+EeA +t+v
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                   E+FLEPLELCY+sLC CGD+ +ADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|115577|   405 EQFLEPLELCYRSLCACGDRSVADGSLLDFLRQVSTFGLSLVRLDIRQES 454

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|115577|   455 DRHTDVMDAITEYLGIGSYRKWTEEKRQEWLLSELNGKRPLFGPDLPKSD 504

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
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  gi|115577|   505 EIADVLDTFHVLAELPSDSFGAYVISMATAPSDVLAVELLQRECHVKKPL 554

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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  gi|115577|   555 RVVPLFEKLADLEAAPAALARLFSVEWYRNRINGKQEVMIGYSDSGKDAG 604

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   R+sAAWqLYkAqEE+i vAK yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|115577|   605 RFSAAWQLYKAQEELINVAKLYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 654

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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  gi|115577|   655 PPETIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 704

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                   kPEWR Lm+emA+vAt EYRs+v+ EPRFvEYFRlAtPE+EYG+mniGsR
  gi|115577|   705 KPEWRALMDEMAIVATKEYRSIVFEEPRFVEYFRLATPEMEYGRMNIGSR 754

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPs GiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh +dKDi+nl
  gi|115577|   755 PSKRKPSAGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLDKDIRNL 804

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                   q L+EmY++WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+ FGk+
  gi|115577|   805 QTLQEMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWSFGKR 854

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Etk+lLL++AGHkDlLEGDPYLKqrlR+RdsYit Lnv+qAY L
  gi|115577|   855 LRANYEETKQLLLQVAGHKDLLEGDPYLKQRLRIRDSYITALNVCQAYML 904

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP ++v + PhlsK+  d   k+a eLvkLn t+++aPGLEDtLiL
  gi|115577|   905 KRIRDPGFQVNPGPHLSKDIMDMG-KPASELVKLNTTSEYAPGLEDTLIL 953

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|115577|   954 TMKGIAAGMQNTG    966

gi|23503556|dbj|BAC20364.1|: domain 1 of 1, from 11 to 961: score 2520.1, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      siDAqLR L+P Kvsed+kLieYDALLlD+FLDiLqDLHGedLkE v
  gi|2350355    11    SIDAQLRQLAPAKVSEDDKLIEYDALLLDRFLDILQDLHGEDLKETV 57

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qE YElsAeYE K+D +KLeELG ++tsLd +D+i+vAk+++HmLnLAnL
  gi|2350355    58 QEVYELSAEYERKHDHEKLEELGKVITSLDAGDSIVVAKSFSHMLNLANL 107

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++  RRR+k+kk GDFaDE +AttEsDiEEtlKkLv kl KsP+Ev
  gi|2350355   108 AEEVQISRRRRNKLKK-GDFADENNATTESDIEETLKKLVFKLKKSPQEV 156

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|2350355   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHARIRNSLSQLYAKDITPDDKQ 206

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|2350355   207 ELDEALQREIQAAFRTDEIKRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256
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                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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  gi|2350355   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|2350355   306 ARMMASNLYYSQIEDLMFELSMWRCNDELRVHADELHRNSNKDEVAKHYI 355

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  gi|2350355   356 EFWKKVPPNEPYRVVLGEVRDRLYKTREHSRILLAQGYSDIPEEATFTNV 405

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFLEPLELCY+sLC+CGD++iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|2350355   406 EEFLEPLELCYRSLCDCGDRAIADGSLLDFLRQVSTFGLSLVRLDIRQES 455

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDv+DAit+HLeiGsY eWsEeKRqEWLl EL+GKRPL+g+DLP+tE
  gi|2350355   456 DRHTDVMDAITKHLEIGSYQEWSEEKRQEWLLGELSGKRPLFGPDLPQTE 505

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+f+v+AELP+D FGaYiisma aPsDvLAvELLqRE ++k++L
  gi|2350355   506 EIRDVLDTFHVIAELPSDNFGAYIISMAIAPSDVLAVELLQRESHIKNPL 555

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                    rvvPLFEkL DLeAAPAa+++LFsi+WY+nri+GKqevm+GYsDsGKDAG
  gi|2350355   556 RVVPLFEKLDDLEAAPAALARLFSIEWYRNRINGKQEVMIGYSDSGKDAG 605

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    R+sAAWqLYkAqE++iKvAKk+GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2350355   606 RFSAAWQLYKAQEDLIKVAKKFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 655

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGmnPP sP
  gi|2350355   656 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMNPPFSP 705

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                    kPEWR Lm+++Av+AtEEYRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|2350355   706 KPEWRALMDQLAVIATEEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 755

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+P GGie+LRAiPWiFaWtqtRFHLPvWLG+GAAF+  i+KD++nl
  gi|2350355   756 PAKRRPTGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFRQLIEKDVRNL 805

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY++WPFFRvt+DL+EmvFAKGDPGiAaL+D+LLv+E+L+PFG++
  gi|2350355   806 HTLQEMYNQWPFFRVTIDLVEMVFAKGDPGIAALNDRLLVSEDLWPFGEQ 855

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR+kY+Etk+lLL++AGHk++LEGDPYLKqrlRLRdsYitt+nvfqAYtL
  gi|2350355   856 LRNKYEETKKLLLQVAGHKEVLEGDPYLKQRLRLRDSYITTMNVFQAYTL 905

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y v    h+sK    E sk+adeLv+Lnpt+++aPGLEDtLiL
  gi|2350355   906 KRIRDPNYDVK---HISK----EKSKPADELVRLNPTSEYAPGLEDTLIL 948

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|2350355   949 TMKGIAAGMQNTG    961

gi|27657589|emb|CAC83482.1|: domain 1 of 1, from 11 to 965: score 2517.5, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLRlL+P Kvsed+kL+eYDALLlD+FLDiLq++HGed++E v
  gi|2765758    11    SIDAQLRLLAPRKVSEDDKLVEYDALLLDRFLDILQEIHGEDIRETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYElsAeYE  +D+kKLeELG +LtsLdP+D+i+vAk+++ mLnLAnL
  gi|2765758    58 QECYELSAEYEATHDSKKLEELGHVLTSLDPGDSIVVAKSFSNMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A+RRRik+kk GDF DE sA tEsDiEEtl++Lv  l KsPeEv
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  gi|2765758   157 FDALKNQTIDLVFTAHPTQSVRRSLLQKHGRIRNWLLQLYAKDITPDDEQ 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDE   REiqAAFRtDEiRR+ PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|2765758   207 ELDETXQREIQAAFRTDEIRRTAPTPQDEMRAGMSYFHETIWKGVPKFLR 256

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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  gi|2765758   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|2765758   306 ARMMAANLYFSQIEDLMFELSMWRCSDELRVRADELHRASKKD--AKHYI 353

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKqvPP+EPYRv+L dvRDKLYntRER+RHLL  G s+i+Ee   t+v
  gi|2765758   354 EFWKQVPPNEPYRVVLADVRDKLYNTRERSRHLLSSGSSDIPEETTLTNV 403

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY sLC CGD+ iADGsLLD++RqvstFGLsLv+LDiRqEs
  gi|2765758   404 EQFLEPLELCYSSLCTCGDRPIADGSLLDFMRQVSTFGLSLVRLDIRQES 453

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlDAittHL+iGsYR+WsEe+RqEWLl+EL+GKRPL+g+DLPktE
  gi|2765758   454 DRHTDVLDAITTHLGIGSYRDWSEEQRQEWLLSELSGKRPLFGPDLPKTE 503

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
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  gi|2765758   504 EIADVLDTLRVIAELPHDSFGAYIISMATAASDVLAVELLQRECQVKKPL 553

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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  gi|2765758   554 RVVPLFEKLADLEAAPAALSRLFSINWYRNRIDGKQEVMIGYSDSGKDAG 603

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
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  gi|2765758   604 RLSAAWQLYKAQEDLIKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 653

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2765758   654 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 703

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emAvvAt EYRs+v++EPRF EYFRlAtPE+EYG+mniGsR
  gi|2765758   704 KPEWRALLDEMAVVATKEYRSIVFQEPRFAEYFRLATPETEYGRMNIGSR 753

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtq RFHLPvWLG G AFKh + KDiKnl
  gi|2765758   754 PSKRKPSGGIESLRAIPWIFAWTQARFHLPVWLGSGTAFKHVVAKDIKNL 803

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+++L+ FG++
  gi|2765758   804 YMLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSDDLWSFGER 853

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++++Etk lLL++AGH+DlLEGDPYLKqrlRLRd+YittLnv+qA+tL
  gi|2765758   854 LRANFEETKTLLLQVAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAFTL 903

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPs++v lr hls+E  + n k+a+eLvkLnpt+++aPGLEDtLiL
  gi|2765758   904 KRIRDPSFHVNLRSHLSREIMNSN-KPAAELVKLNPTSEYAPGLEDTLIL 952

                    tmKGiAAGmqntG<-*
                     mKGiAAGmqntG
  gi|2765758   953 AMKGIAAGMQNTG    965

gi|5616255|gb|AAD45696.1|AF159051_1: domain 1 of 1, from 3 to 955: score 2515.3, E = 0
```

```
                *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                   siDAq+RlLvPGKvsed+kLieYDALLlD+FLDiLqDLHGed++E+v
gi|5616255     3    SIDAQMRLLVPGKVSEDDKLIEYDALLLDRFLDILQDLHGEDIREMV 49

                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                qECYE s eYEGK D++KLeELG +LtsLdP+D+i+vA++++HmLnLAnL
gi|5616255    50 QECYERSGEYEGKNDPHKLEELGNVLTSLDPGDSIVVASSFSHMLNLANL 99

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AEEv++AyRRR+k k+ G FaDE++AttEsDiEEt+K+Lv +l KsP+Ev
gi|5616255   100 AEEVQIAYRRRNKIKR-GGFADESNATTESDIEETFKRLVNQLGKSPAEV 148

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                F+ALKnq+vDLvltAHPtqsvRRsLLqK+aRiRnCL+qL+ KD+t+++K+
gi|5616255   149 FDALKNQTVDLVLTAHPTQSVRRSLLQKHARIRNCLSQLYGKDITPDEKQ 198

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
gi|5616255   199 ELDEALLREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 248

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                R+DtALK iGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
gi|5616255   249 RIDTALKSIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 297

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                aRmmAanlY+sq+EDLmFElsmWRC dELR+RA  l++ +++d   K+Yi
gi|5616255   298 ARMMAANLYYSQIEDLMFELSMWRCSDELRARALQLHSASKKD--AKHYI 345

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                EFWKq+PP+EP+RviLGdvRDKLYntRER+R LL  Gis+i+Ee  +t++
gi|5616255   346 EFWKQIPPNEPFRVILGDVRDKLYNTRERTRQLLSNGISDIPEEVTFTNI 395

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                +eFLEPLELCY+sLC  GD+ iADGsLLD++RqvstFGLs vKLDiRqEs
gi|5616255   396 DEFLEPLELCYRSLCSTGDQPIADGSLLDFMRQVSTFGLSFVKLDIRQES 445

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                +R+ Dv DAit+HL+iGsY+eWsEe+Rq WLl+EL+GKRPL+g+DLPkt+
gi|5616255   446 DRHSDVADAITRHLGIGSYKEWSEEQRQAWLLSELQGKRPLFGPDLPKTD 495

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                Ev+Dvld+f+v+ ELP D FGaYiismata sDvL vELLqREC+vk++L
gi|5616255   496 EVRDVLDTFHVISELPADNFGAYIISMATAASDVLVVELLQRECHVKKPL 545

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                rvvPLFEkLADLeAAPAa+++LFsi WY+nridGKqevm+GYsDsGKDAG
gi|5616255   546 RVVPLFEKLADLEAAPAALARLFSINWYRNRIDGKQEVMIGYSDSGKDAG 595

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsA W LYkAqE++iKvAK++G+KL++FHGRGGtvGRGGGPtHLAiLsq
gi|5616255   596 RLSAGWALYKAQEDLIKVAKEFGIKLTMFHGRGGTVGRGGGPTHLAILSQ 645

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PPDti+Gs RvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PPv+P
gi|5616255   646 PPDTIHGSFRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPVAP 695

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                kPEWR+Lm+emAvvAt EYRs+v+++PRFvEYFR+AtPElEYG+mniGsR
gi|5616255   696 KPEWRELMDEMAVVATKEYRSIVFQDPRFVEYFRSATPELEYGRMNIGSR 745

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
gi|5616255   746 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVMEKDIRNL 795

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                 +L+ mY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+++L+  G++
gi|5616255   796 HMLQQMYNEWPFFRVTIDLIEMVFAKGDPGIAALYDKLLVSDDLWAIGEK 845

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR++Y EtkdlLL++AGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
gi|5616255   846 LRANYGETKDLLLQVAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 895
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                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+v lrPhlsKE    +   a+eLvkLnpt+++aPGLEDtLiL
  gi|5616255   896 KRIRDPNYHVNLRPHLSKESSTKP---AAELVKLNPTSEYAPGLEDTLIL 942

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|5616255   943 TMKGIAAGMQNTG    955

gi|148908467|gb|ABR17346.1|: domain 1 of 1, from 11 to 963: score 2515.3, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAq+RlLvPGKvsed+kLieYDALLlD+FLDiLqDLHGed++E+v
  gi|1489084    11    SIDAQMRLLVPGKVSEDDKLIEYDALLLDRFLDILQDLHGEDIREMV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE s eYEGK D++KLeELG +LtsLdP+D+i+vA++++HmLnLAnL
  gi|1489084    58 QECYERSGEYEGKNDPHKLEELGNVLTSLDPGDSIVVASSFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRR+k k+ G FaDE++AttEsDiEEt+K+Lv +l KsP+Ev
  gi|1489084   108 AEEVQIAYRRRRNKIKR-GGFADESNATTESDIEETFKRLVNQLGKSPAEV 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+vDLvltAHPtqsvRRsLLqK+aRiRnCL+qL+ KD+t+++K+
  gi|1489084   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHARIRNCLSQLYGKDITPDEKQ 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|1489084   207 ELDEALLREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R+DtALK iGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1489084   257 RIDTALKSIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq+EDLmFElsmWRC dELR+RA  l++ +++d   K+Yi
  gi|1489084   306 ARMMAANLYYSQIEDLMFELSMWRCSDELRARALQLHSASKKD--AKHYI 353

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP+EP+RviLGdvRDKLYntRER+R LL  Gis+i+Ee  +t++
  gi|1489084   354 EFWKQIPPNEPFRVILGDVRDKLYNTRERTRQLLSNGISDIPEEVTFTNI 403

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    +eFLEPLELCY+sLC  GD+ iADGsLLD++RqvstFGLs vKLDiRqEs
  gi|1489084   404 DEFLEPLELCYRSLCSTGDQPIADGSLLDFMRQVSTFGLSFVKLDIRQES 453

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+ Dv DAit+HL+iGsY+eWsEe+Rq WLl+EL+GKRPL+g+DLPkt+
  gi|1489084   454 DRHSDVADAITRHLGIGSYKEWSEEQRQAWLLSELQGKRPLFGPDLPKTD 503

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvld+f+v+ ELP D FGaYiismata sDvL vELLqREC+vk++L
  gi|1489084   504 EVRDVLDTFHVISELPADNFGAYIISMATAASDVLVVELLQRECHVKKPL 553

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAa+++LFsi WY+nridGKqevm+GYsDsGKDAG
  gi|1489084   554 RVVPLFEKLADLEAAPAALARLFSINWYRNRIDGKQEVMIGYSDSGKDAG 603

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsA W LYkAqE++iKvAK++G+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1489084   604 RLSAGWALYKAQEDLIKVAKEFGIKLTMFHGRGGTVGRGGGPTHLAILSQ 653

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+Gs RvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PPv+P
  gi|1489084   654 PPDTIHGSFRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPVAP 703

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR+Lm+emAvvAt EYRs+v+++PRFvEYFR+AtPElEYG+mniGsR
  gi|1489084   704 KPEWRELMDEMAVVATKEYRSIVFQDPRFVEYFRSATPELEYGRMNIGSR 753

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
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                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|1489084   754 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVMEKDIRNL 803

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+ mY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+++L+  G++
  gi|1489084   804 HMLQQMYNEWPFFRVTIDLIEMVFAKGDPGIAALYDKLLVSDDLWAIGEK 853

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y EtkdlLL++AGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|1489084   854 LRANYGETKDLLLQVAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 903

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+v lrPhlsKE    +   a+eLvkLnpt+++aPGLEDtLiL
  gi|1489084   904 KRIRDPNYHVNLRPHLSKESSTKP---AAELVKLNPTSEYAPGLEDTLIL 950

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|1489084   951 TMKGIAAGMQNTG    963

gi|125563186|gb|EAZ08566.1|: domain 1 of 1, from 17 to 971: score 2515.1, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLR LvP K sed+kLieYDALLlD+FLD+L  LHG+dLk+ v
  gi|1255631    17    SIDAQLRQLVPAKLSEDDKLIEYDALLLDRFLDVLHGLHGDDLKDLV 63

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE++AeYE K+D +KL+ELG  +tsLdP+D+i++Aka++HmLnLAnL
  gi|1255631    64 QECYEVAAEYETKHDVQKLDELGNMITSLDPGDSIVIAKAFSHMLNLANL 113

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRRik+kk GDFaDE sA tEsDiEEtlK+Lv  l KsP+Ev
  gi|1255631   114 AEEVQIAYRRRIKLKK-GDFADENSAMTESDIEETLKRLVFDLKKSPAEV 162

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALK q+vDLvltAHPtqsvRRsLLqK++RiRnCL qL+ KD+t++DK+
  gi|1255631   163 FDALKSQTVDLVLTAHPTQSVRRSLLQKHSRIRNCLVQLYSKDITPDDKQ 212

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR+qPtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|1255631   213 ELDEALQREIQAAFRTDEIRRTQPTPQDEMRAGMSYFHETIWKGVPKFLR 262

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1255631   263 RVDTALKNIGIDERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 311

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY sq+EDLmFElsmWRCn+ELR RA++l+r +++d   K+Yi
  gi|1255631   312 ARMMAANLYCSQIEDLMFELSMWRCNEELRSRADDLHRSSKKD--AKHYI 359

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK+vPP+EPYRviL dvRDKLYntRER+R LL  G+ +i+Ee   t+v
  gi|1255631   360 EFWKKVPPNEPYRVILSDVRDKLYNTRERSRELLSSGYCDIPEETTLTNV 409

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+ LEPLELCY+sLC CGD++iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|1255631   410 EQLLEPLELCYRSLCACGDRAIADGSLLDFLRQVSTFGLSLVRLDIRQES 459

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlDAitt L+iGsYReWsEe+RqEWLl+EL GKRPL+g+DLP+t+
  gi|1255631   460 DRHTDVLDAITTYLGIGSYREWSEERRQEWLLSELNGKRPLFGPDLPRTD 509

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvld+f+v+AELP DsFGaY+ismataPsDvLAvELLqREC+vk +L
  gi|1255631   510 EVADVLDTFHVIAELPADSFGAYVISMATAPSDVLAVELLQRECHVKTPL 559

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLe APAa+ +LFsi WY+ ri+GKqevm+GYsDsGKDAG
  gi|1255631   560 RVVPLFEKLADLESAPAALTRLFSISWYRQRINGKQEVMIGYSDSGKDAG 609

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWq+YkAqE ++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1255631   610 RLSAAWQMYKAQEQLVKVAKDFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 659
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                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP +P
  gi|1255631   660 PPDTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPSAP 709

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emAvvAt EYRsvv++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|1255631   710 KPEWRALLDEMAVVATKEYRSVVFQEPRFVEYFRLATPETEYGRMNIGSR 759

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+nl
  gi|1255631   760 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHALQKDIRNL 809

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+eWPFFRvtlDL+EmvFAKG PGiAaLyDkLLv+E+L+P G++
  gi|1255631   810 HMLQEMYNEWPFFRVTLDLIEMVFAKGNPGIAALYDKLLVSEDLQPLGEK 859

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++YvEt++lLL++AGH+DlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|1255631   860 LRANYVETQKLLLQVAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 909

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+vtlrPhlsKE  d   k+a+eLvkLnp++++aPGLEDtLiL
  gi|1255631   910 KRIRDPDYHVTLRPHLSKEVMDGS-KPAAELVKLNPGSEYAPGLEDTLIL 958

                    tmKGiAAGmqntG<-*
                    tmKGiAAG+qntG
  gi|1255631   959 TMKGIAAGLQNTG    971

gi|27657587|emb|CAC83481.1|: domain 1 of 1, from 11 to 965: score 2514.0, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLRlL+P Kvsed+kL+eYDALLlD+FLDiLq++HGed++E v
  gi|2765758    11    SIDAQLRLLAPRKVSEDDKLVEYDALLLDRFLDILQEIHGEDIRETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYElsAeYE  +D+kKLeELG +LtsLdP+D+i+vAk+++ mLnLAnL
  gi|2765758    58 QECYELSAEYEATHDSKKLEELGHVLTSLDPGDSIVVAKSFSNMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A+RRRik+kk GDF DE sA tEsDiEEtl++Lv  l KsPeEv
  gi|2765758   108 AEEVQIAFRRRIKLKK-GDFVDENSAATESDIEETLRRLVHELKKSPEEV 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq++DLv+tAHPtqsvRRsLLqK++RiRn L qL+AKD+t++D +
  gi|2765758   157 FDALKNQTIDLVFTAHPTQSVRRSLLQKHGRIRNWLLQLYAKDITPDDEQ 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDE   REiqAAFRtDEiRR+ PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|2765758   207 ELDETXQREIQAAFRTDEIRRTAPTPQDEMRAGMSYFHETIWKGVPKFLR 256

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2765758   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq+EDLmFElsmWRC dELRvRA+El+r +++d   K+Yi
  gi|2765758   306 ARMMAANLYFSQIEDLMFELSMWRCSDELRVRADELHRASKKD--AKHYI 353

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKqvPP+EPYRv+L dvRDKLYntRER+RHLL  G s+i+Ee   t+v
  gi|2765758   354 EFWKQVPPNEPYRVVLADVRDKLYNTRERSRHLLSSGSSDIPEETTLTNV 403

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY sLC CGD+ iADGsLLD++RqvstFGLsLv+LDiRqEs
  gi|2765758   404 EQFLEPLELCYSSLCTCGDRPIADGSLLDFMRQVSTFGLSLVRLDIRQES 453

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlDAittHL+iGsYR+WsEe+RqEWLl+EL+GKRPL+g+DLPktE
  gi|2765758   454 DRHTDVLDAITTHLGIGSYRDWSEEQRQEWLLSELSGKRPLFGPDLPKTE 503

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
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                    E++Dvld++rv+AELP DsFGaYiismata sDvLAvELLqREC+vk++L
  gi|2765758   504 EIADVLDTLRVIAELPHDSFGAYIISMATAASDVLAVELLQRECQVKKPL 553

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAa+ +LFsi WY+nridGKqevm+GYsDsGKDAG
  gi|2765758   554 RVVPLFEKLADLEAAPAALSRLFSINWYRNRIDGKQEVMIGYSDSGKDAG 603

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqE++iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2765758   604 RLSAAWQLYKAQEDLIKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 653

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2765758   654 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 703

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emAvvAt EYRs+v++EPRF EYFRlAtPE+EYG+mniGsR
  gi|2765758   704 KPEWRALLDEMAVVATKEYRSIVFQEPRFAEYFRLATPETEYGRMNIGSR 753

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtq RFHLPvWLG G AFKh + KDiKnl
  gi|2765758   754 PSKRKPSGGIESLRAIPWIFAWTQARFHLPVWLGSGTAFKHVVAKDIKNL 803

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+++L+ FG++
  gi|2765758   804 YMLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSDDLWSFGER 853

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++++Etk lLL++AGH+DlLEGDPYLKqrlRLRd+YittLnv+qA+tL
  gi|2765758   854 LRANFEETKTLLLQVAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAFTL 903

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPs++v lr hls+E  + n k+a+eLvkLnpt+++aPGLEDtLiL
  gi|2765758   904 KRIRDPSFHVNLRSHLSREIMNSN-KPAAELVKLNPTSEYAPGLEDTLIL 952

                    tmKGiAAGmqntG<-*
                     mKGiAAG+qntG
  gi|2765758   953 AMKGIAAGLQNTG    965

gi|27948554|gb|AAO25631.1|: domain 1 of 1, from 10 to 964: score 2512.6, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLR+L+P   sed+kL+eYDALLlD+FLDiLqDLHG+dL+E+v
  gi|2794855    10    SIDAQLRMLAPAHRSEDDKLVEYDALLLDRFLDILQDLHGDDLREMV 56

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE++AeYEGK+D++KL+ELG  LtsLdP+D+i++Aka++HmLnLAnL
  gi|2794855    57 QECYEIAAEYEGKHDSQKLDELGNMLTSLDPGDSIVMAKAFSHMLNLANL 106

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRRik+kk GDFaDE sA tEsDiEEt+K+Lv+ l KsP+Ev
  gi|2794855   107 AEEVQIAYRRRIKLKK-GDFADENSALTESDIEETFKRLVVDLKKSPAEV 155

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALK q+vDLvltAHPtqsvRRsLLqK++RiRnCL qL+ KD+t++DK+
  gi|2794855   156 FDALKSQTVDLVLTAHPTQSVRRSLLQKHSRIRNCLVQLYSKDITPDDKQ 205

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR+qPtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|2794855   206 ELDEALQREIQAAFRTDEIRRTQPTPQDEMRAGMSYFHETIWKGVPKFLR 255

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R DtALKniGi ER+PY++PLi+FssWmGGDRDG nPRvtPE tR vCLL
  gi|2794855   256 RLDTALKNIGIDERVPYNAPLIQFSSWMGGDRDG-NPRVTPEATRGVCLL 304

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmA+nlY sq+EDLmFElsmWRCndELR+RA+El+  +++d   K+Yi
  gi|2794855   305 ARMMASNLYCSQIEDLMFELSMWRCNDELRARADELHLSSKKD--AKHYI 352

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK+vPP EPYRv+LGdvRDKLYntRERaR LL  G+s+i+Ee   t v
  gi|2794855   353 EFWKKVPPSEPYRVVLGDVRDKLYNTRERARQLLSSGYSDIPEETTLTSV 402
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                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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  gi|2794855   403 EQFLEPLELCYRSLCDCGDRVIADGTLLDFLRQVSTFGLCLVRLDIRQES 452

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlDAitt L+iGsYReWsEe+Rq+WLl+EL GKRPL+g+DLPkt+
  gi|2794855   453 DRHTDVLDAITTYLGIGSYREWSEERRQDWLLSELNGKRPLFGPDLPKTD 502

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                    E++Dvld+frv+AELP D FGaYiismataPsDvLAvELLqREC+vk +L
  gi|2794855   503 EIADVLDTFRVIAELPADNFGAYIISMATAPSDVLAVELLQRECHVKTPL 552

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                    rvvPLFEkLADLe APAav++LFsiDWY+ ri+GKqevm+GYsDsGKDAG
  gi|2794855   553 RVVPLFEKLADLESAPAAVARLFSIDWYRERINGKQEVMIGYSDSGKDAG 602

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYk qEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2794855   603 RLSAAWQLYKSQEELINVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 652

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+Gs RvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP++P
  gi|2794855   653 PPDTIHGSPRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPIAP 702

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emAvvA   YRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|2794855   703 KPEWRALLDEMAVVAAKGYRSIVFQEPRFVEYFRLATPEMEYGRMNIGSR 752

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++KDi+nl
  gi|2794855   753 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGSAFKHILEKDIRNL 802

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+EeL+P G++
  gi|2794855   803 HMLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEELWPLGEK 852

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++ +Etk+lLL++AGHkDlLEGD YLKqrlRLR++YittLnv+qAYt+
  gi|2794855   853 LRANCEETKQLLLQVAGHKDLLEGDLYLKQRLRLRNAYITTLNVCQAYTM 902

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+vtlrPh+sKE  d   k+a+eLvkLnpt+++aPGLEDtLiL
  gi|2794855   903 KRIRDPDYHVTLRPHMSKEIMDWS-KPAAELVKLNPTSEYAPGLEDTLIL 951

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                    tmKGiAAGmqntG
  gi|2794855   952 TMKGIAAGMQNTG    964

gi|3341490|emb|CAA07610.1|: domain 1 of 1, from 18 to 972: score 2512.6, E = 0
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                       siDAqLRlLvP Kvsed+kLieYDALLlD+FLD+Lq LHG+dL+E+v
  gi|3341490    18    SIDAQLRLLVPAKVSEDDKLIEYDALLLDRFLDVLQGLHGDDLREMV 64

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE++AeYE K+D +KL+ELG  +tsLdP+D+i++Aka++HmLnLAnL
  gi|3341490    65 QECYEVAAEYETKHDLEKLDELGEMITSLDPGDSIVIAKAFSHMLNLANL 114

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRR+k+kk GDFaDE sA tEsDiEEtlK+Lv    KsP+Ev
  gi|3341490   115 AEEVQIAYRRRVKLKK-GDFADENSAITESDIEETLKRLVFDMKKSPAEV 163

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|3341490   164 FDALKNQTVDLVLTAHPTQSVRRSLLQKHSRIRNCLVQLYSKDITPDDKQ 213

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR  PtPqD mRaGms +HEt+WkGvPKFLR
  gi|3341490   214 ELDEALQREIQAAFRTDEIRRLSPTPQDHMRAGMSDFHETIWKGVPKFLR 263

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                    aRmmAanlY  q+EDLmFElsmWRCndELR RA+El+r +++d   K+Yi
  gi|3341490   313 ARMMAANLYCAQIEDLMFELSMWRCNDELRSRADELHRSSKKD--AKHYI 360

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK+vPP+EPYRviLGdvRD LYntRER+R LL  G s+i+EeA  t++
  gi|3341490   361 EFWKKVPPNEPYRVILGDVRDNLYNTRERSRELLSSGHSDIPEEATLTNL 410

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+ LEPLELCY+sLC CGD+viADG LLD+LRqvstFGLsLvKLDiRqEs
  gi|3341490   411 EQLLEPLELCYRSLCACGDRVIADGTLLDFLRQVSTFGLSLVKLDIRQES 460

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tD lDAit  L+iGsYReWsEe RqEWLl+EL GKRPL+g+DLP+tE
  gi|3341490   461 DRHTDALDAITSYLGIGSYREWSEEHRQEWLLSELNGKRPLFGADLPMTE 510

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  gi|3341490   511 EVADVMGAFQVIAELPGDNFGAYVISMATSPSDVLAVELLQRECHIKTPL 560

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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  gi|3341490   561 RVVPLFEKLADLEAAPAALARLFSIDWYRERINGKQEVMIGYSDSGKDAG 610

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                    RlsAAWq+YkAqE+++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|3341490   611 RLSAAWQMYKAQEDLVKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 660

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PP+sP
  gi|3341490   661 PPDTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPISP 710

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emAvvAtEEYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|3341490   711 KPEWRALLDEMAVVATEEYRSIVFQEPRFVEYFRLATPETEYGRMNIGSR 760

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++KDi+n+
  gi|3341490   761 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHILKKDIRNF 810

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+eWPFFRvt+DL+EmvFAKG PGiAaLyD+LLv+E L+P G++
  gi|3341490   811 HMLQEMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDRLLVSEGLQPLGEK 860

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Et++lLL++AGHkDlLEGDPYLKqrlRLRd+Yitt+nv+qAYtL
  gi|3341490   861 LRANYEETQKLLLQVAGHKDLLEGDPYLKQRLRLRDAYITTMNVCQAYTL 910

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+v lrPhlsKE  d   k+a+eLv Lnp++++aPGLEDtLiL
  gi|3341490   911 KRIRDPDYHVALRPHLSKEVMDTS-KPAAELVTLNPASEYAPGLEDTLIL 959

                    tmKGiAAGmqntG<-*
                    tmKGiAAG+qntG
  gi|3341490   960 TMKGIAAGLQNTG    972

gi|222619275|gb|EEE55407.1|: domain 1 of 1, from 11 to 966: score 2512.3, E = 0
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  gi|2226192    11    SIDAQLRILAPKKLSEDDKLVEYDALLLDRFLDILQDLHGEDIRETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYEl+AeYE K D+k+L+ +G +Lt LdP+D+i++ k+++HmL LAnL
  gi|2226192    58 QECYELAAEYESKVDPKQLDAIGNVLTRLDPGDSIVMTKSFSHMLILANL 107

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                    AEEv++AyRRRik+kk GDFaDE sAttEs  EEtlK+Lv  l KsP Ev
  gi|2226192   108 AEEVQIAYRRRRIKLKK-GDFADENSATTESNFEETLKRLVGELKKSPHEV 156
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  gi|2226192   157 FDALKNQTIDLVLTAHPTQSVRRSLLQKHGRIRSCLTKLYAKDITPDEKQ 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRRa+PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|2226192   207 ELDEALKREIQAAFRTDEIRRAPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

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                    RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2226192   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+ q+EDLmFElsmWRC dELRv+A+ l+r a+++  +K+Yi
  gi|2226192   306 ARMMAANLYYAQIEDLMFELSMWRCSDELRVKADQLHRCAKKN-TTKHYI 354

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKqvPP EPYRviL +vRDKLYntRERaRHLLA G+sei++eA +t+v
  gi|2226192   355 EFWKQVPPSEPYRVILSNVRDKLYNTRERARHLLASGFSEIPDEATFTDV 404

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC CGD  iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|2226192   405 EQFLEPLELCYRSLCACGDNSIADGSLLDFLRQVSTFGLSLVRLDIRQES 454

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDv+DAit+ L+iGsYReWsEeKRqEWLl+EL GKRPL+g+DLP+t+
  gi|2226192   455 DRHTDVMDAITQYLGIGSYREWSEEKRQEWLLSELNGKRPLFGPDLPQTD 504

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
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  gi|2226192   505 EIADALDTFHVIAELPYDSFGAYVISMATAPSDVLAVELLQRECHVKKPL 554

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  gi|2226192   555 RVVPLFEKLADLEAAPAALARLFSVDWYRNRIDGKQEVMIGYSDSGKDAG 604

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    R+sAAW LYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2226192   605 RFSAAWELYKAQEELIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 654

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFt AtLEHGm+PP+sP
  gi|2226192   655 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTSATLEHGMHPPISP 704

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emA vAt EYRs+v++E RFvEYFRlAtPElEYG+mniGsR
  gi|2226192   705 KPEWRALMDEMAAVATKEYRSIVFQEARFVEYFRLATPELEYGRMNIGSR 754

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                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|2226192   755 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLQKDIRNL 804

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+PFG +
  gi|2226192   805 QILQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWPFGAR 854

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Etk+lLL++AGHkDlLEGDPYL+qrlR+RdsYit Lnv+qA tL
  gi|2226192   855 LRANYEETKQLLLQVAGHKDLLEGDPYLRQRLRIRDSYITALNVCQACTL 904

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP ++v +r hlsK+  d   k+a+eLvkLn t+++ PGLEDtLiL
  gi|2226192   905 KRIRDPGFHVSPRAHLSKDIMDSG-KPAAELVKLNTTSEYGPGLEDTLIL 953

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                    tmKGiAAGmqntG
  gi|2226192   954 TMKGIAAGMQNTG    966

gi|3649776|emb|CAA09588.1|: domain 1 of 1, from 10 to 966: score 2512.2, E = 0
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gi|3649776    10  SIDAQLRQLAPAKVSEDDKLIEYDALLLDRFLDILQDLHGEDLKDSV 56

                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                qE YElsAeYE K+D+kKLeELG  +t+Ld +D+i+vAk+++HmLnLAnL
gi|3649776    57 QEVYELSAEYERKHDPKKLEELGKLITGLDAGDSIVVAKSFSHMLNLANL 106

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gi|3649776   107 AEEVQIAHRRRNKLKK-GDFRDESNATTESNIEETLKRLVFNMKKSPQEV 155

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gi|3649776   156 FDALKNQTVDLVLTAHPTQSVRRSLLQKHARIRNCLSHLYAKDITPDDKQ 205

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                ELDE L REiqAAFRtDEi+R++PtPqDEmRaGmsY+HEt+WkGvPKFLR
gi|3649776   206 ELDESLQREIQAAFRTDEIKRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 255

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                RvDtALKn+GinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
gi|3649776   256 RVDTALKNVGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 304

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                aRmmAanlY+sq+EDLmFElsmWRCndELR RAEEl+r +++d v K+Yi
gi|3649776   305 ARMMAANLYYSQIEDLMFELSMWRCNDELRDRAEELHRNSKKDEVAKHYI 354

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                EFWK+vP +EPYRv+LGd+RDKLY tRER+R LLA+G+s+i+EeA +t+v
gi|3649776   355 EFWKKVPLNEPYRVVLGDIRDKLYRTRERSRYLLAHGYSDIPEEATFTNV 404

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                +eFLEPLELCY+sLC CGD++iADGsLLD+LRqvstFGLsLv+LDiRqEs
gi|3649776   405 DEFLEPLELCYRSLCACGDRAIADGSLLDFLRQVSTFGLSLVRLDIRQES 454

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                +R+tDv+DAit+HLeiGsY eWsEeKRqEWLl+EL GKRPL+g+DLPkt+
gi|3649776   455 DRHTDVMDAITKHLEIGSYQEWSEEKRQEWLLSELIGKRPLFGPDLPKTD 504

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                E++Dvld+f+v+AELP+D FGaYiismataPsDvLAvELLqREC++k++L
gi|3649776   505 EIRDVLDTFHVIAELPSDNFGAYIISMATAPSDVLAVELLQRECKIKNPL 554

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                rvvPLFEkL DLeAAPAa+++LFsiDWY+nridGKqevm+GYsDsGKDAG
gi|3649776   555 RVVPLFEKLDDLEAAPAALARLFSIDWYRNRIDGKQEVMIGYSDSGKDAG 604

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                R+sAAWqLYkAqEE+i vA+k+ vKL++FHGRGGtvGRGGGPtHLAiLsq
gi|3649776   605 RFSAAWQLYKAQEELINVAQKFSVKLTMFHGRGGTVGRGGGPTHLAILSQ 654

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PP+ti+G lRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PP sP
gi|3649776   655 PPETIHGILRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPSSP 704

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                kPEWR Lm+++A++AtEEYRs+v+KEPRFvEYFRlAtPE+EYG+mniGsR
gi|3649776   705 KPEWRILMDQLAIIATEEYRSIVFKEPRFVEYFRLATPEMEYGRMNIGSR 754

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                PaKR+PsGGie+LRAiPWiFaWtqtRFHLPvWLG+GAAFK  i+KD+Knl
gi|3649776   755 PAKRRPSGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKQVIEKDVKNL 804

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                 +L++mY++WPFFRvt+DL+EmvFAKGDPGiAaL+D+LLv+E+L+PFG++
gi|3649776   805 HMLQDMYNQWPFFRVTIDLVEMVFAKGDPGIAALNDRLLVSEDLWPFGEQ 854

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR+kY+Etk+lLL++A Hk++LEGDPYLKqrlRLRdsYittLnvfqAYtL
gi|3649776   855 LRNKYEETKELLLQVATHKEVLEGDPYLKQRLRLRDSYITTLNVFQAYTL 904
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                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP      rP+lsK+   E +k+adeLv Lnpt+++aPGLEDtLiL
  gi|3649776   905 KRIRDPKSSANGRPPLSKD-SPEATKPADELVTLNPTSEYAPGLEDTLIL 953

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|3649776   954 TMKGIAAGMQNTG    966

gi|51091643|dbj|BAD36412.1|: domain 1 of 1, from 18 to 972: score 2511.8, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLR LvP K sed+kLieYDALLlD+FLD+L  LHG+dLk+ v
  gi|5109164    18    SIDAQLRQLVPAKLSEDDKLIEYDALLLDRFLDVLHGLHGDDLKDLV 64

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE++AeYE K+D +KL+ELG  +tsLdP+D+i++Aka++HmLnLAnL
  gi|5109164    65 QECYEVAAEYETKHDVQKLDELGNMITSLDPGDSIVIAKAFSHMLNLANL 114

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRRik+kk GDFaDE sA tEsDiEEtlK+Lv  l KsP+Ev
  gi|5109164   115 AEEVQIAYRRRIKLKK-GDFADENSAMTESDIEETLKRLVFDLKKSPAEV 163

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALK q+vDLvltAHPtqsvRRsLLqK++RiRnCL qL+ KD+t++DK+
  gi|5109164   164 FDALKSQTVDLVLTAHPTQSVRRSLLQKHSRIRNCLVQLYSKDITPDDKQ 213

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR+qPtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|5109164   214 ELDEALQREIQAAFRTDEIRRTQPTPQDEMRAGMSYFHETIWKGVPKFLR 263

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|5109164   264 RVDTALKNIGIDERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 312

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY sq+EDLmFElsmWRCn+ELR RA++l+r +++d   K+Yi
  gi|5109164   313 ARMMAANLYCSQIEDLMFELSMWRCNEELRSRADDLHRSSKKD--AKHYI 360

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK+vP +EPYRviL dvRDKLYntRER+R LL  G+ +i+EeA  t+v
  gi|5109164   361 EFWKKVPLNEPYRVILSDVRDKLYNTRERSRELLSSGYCDIPEEATLTNV 410

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+ LEPLELCY+sLC CGD++iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|5109164   411 EQLLEPLELCYRSLCACGDRAIADGSLLDFLRQVSTFGLSLVRLDIRQES 460

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlDAitt L+iGsYReWsEe+RqEWLl+EL GKRPL+g+DLP+t+
  gi|5109164   461 DRHTDVLDAITTYLGIGSYREWSEERRQEWLLSELNGKRPLFGPDLPRTD 510

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvld+f+v+AELP DsFGaY+ismataPsDvLAvELLqREC+vk +L
  gi|5109164   511 EVADVLDTFHVIAELPADSFGAYVISMATAPSDVLAVELLQRECHVKTPL 560

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLe APAa+ +LFsi WY+ ri+GKqevm+GYsDsGKDAG
  gi|5109164   561 RVVPLFEKLADLESAPAALTRLFSISWYRQRINGKQEVMIGYSDSGKDAG 610

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWq+YkAqE ++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|5109164   611 RLSAAWQMYKAQEQLVKVAKDFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 660

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP +P
  gi|5109164   661 PPDTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPSAP 710

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emAvvAt EYRsvv++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|5109164   711 KPEWRALLDEMAVVATKEYRSVVFQEPRFVEYFRLATPETEYGRMNIGSR 760

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+nl
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  gi|5109164   761 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHALQKDIRNL 810

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY+eWPFFRvtlDL+EmvFAKG PGiAaLyDkLLv+E+L+P G++
  gi|5109164   811 HMLQEMYNEWPFFRVTLDLIEMVFAKGNPGIAALYDKLLVSEDLQPLGEK 860

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++YvEt++lLL++AGH+DlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|5109164   861 LRANYVETQKLLLQVAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 910

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y+vtlrPhlsKE  d   k+a+eLvkLnp++++aPGLEDtLiL
  gi|5109164   911 KRIRDPDYHVTLRPHLSKEVMDGS-KPAAELVKLNPGSEYAPGLEDTLIL 959

                   tmKGiAAGmqntG<-*
                   tmKGiAAG+qntG
  gi|5109164   960 TMKGIAAGLQNTG    972

gi|115478504|ref|NP_001062847.1|: domain 1 of 1, from 21 to 975: score 2511.8, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      siDAqLR LvP K sed+kLieYDALLlD+FLD+L  LHG+dLk+ v
  gi|1154785    21    SIDAQLRQLVPAKLSEDDKLIEYDALLLDRFLDVLHGLHGDDLKDLV 67

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qECYE++AeYE K+D +KL+ELG  +tsLdP+D+i++Aka++HmLnLAnL
  gi|1154785    68 QECYEVAAEYETKHDVQKLDELGNMITSLDPGDSIVIAKAFSHMLNLANL 117

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++AyRRRik+kk GDFaDE sA tEsDiEEtlK+Lv  l KsP+Ev
  gi|1154785   118 AEEVQIAYRRRIKLKK-GDFADENSAMTESDIEETLKRLVFDLKKSPAEV 166

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   F+ALK q+vDLvltAHPtqsvRRsLLqK++RiRnCL qL+ KD+t++DK+
  gi|1154785   167 FDALKSQTVDLVLTAHPTQSVRRSLLQKHSRIRNCLVQLYSKDITPDDKQ 216

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL REiqAAFRtDEiRR+qPtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|1154785   217 ELDEALQREIQAAFRTDEIRRTQPTPQDEMRAGMSYFHETIWKGVPKFLR 266

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALKniGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1154785   267 RVDTALKNIGIDERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 315

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmAanlY sq+EDLmFElsmWRCn+ELR RA++l+r +++d   K+Yi
  gi|1154785   316 ARMMAANLYCSQIEDLMFELSMWRCNEELRSRADDLHRSSKKD--AKHYI 363

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWK+vP +EPYRviL dvRDKLYntRER+R LL  G+ +i+EeA  t+v
  gi|1154785   364 EFWKKVPLNEPYRVILSDVRDKLYNTRERSRELLSSGYCDIPEEATLTNV 413

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   E+ LEPLELCY+sLC CGD++iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|1154785   414 EQLLEPLELCYRSLCACGDRAIADGSLLDFLRQVSTFGLSLVRLDIRQES 463

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +R+tDvlDAitt L+iGsYReWsEe+RqEWLl+EL GKRPL+g+DLP+t+
  gi|1154785   464 DRHTDVLDAITTYLGIGSYREWSEERRQEWLLSELNGKRPLFGPDLPRTD 513

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvld+f+v+AELP DsFGaY+ismataPsDvLAvELLqREC+vk +L
  gi|1154785   514 EVADVLDTFHVIAELPADSFGAYVISMATAPSDVLAVELLQRECHVKTPL 563

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLe APAa+ +LFsi WY+ ri+GKqevm+GYsDsGKDAG
  gi|1154785   564 RVVPLFEKLADLESAPAALTRLFSISWYRQRINGKQEVMIGYSDSGKDAG 613

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWq+YkAqE ++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1154785   614 RLSAAWQMYKAQEQLVKVAKDFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 663
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                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP +P
  gi|1154785   664 PPDTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPSAP 713

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emAvvAt EYRsvv++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|1154785   714 KPEWRALLDEMAVVATKEYRSVVFQEPRFVEYFRLATPETEYGRMNIGSR 763

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+nl
  gi|1154785   764 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHALQKDIRNL 813

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+eWPFFRvtlDL+EmvFAKG PGiAaLyDkLLv+E+L+P G++
  gi|1154785   814 HMLQEMYNEWPFFRVTLDLIEMVFAKGNPGIAALYDKLLVSEDLQPLGEK 863

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++YvEt++lLL++AGH+DlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|1154785   864 LRANYVETQKLLLQVAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 913

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+vtlrPhlsKE  d   k+a+eLvkLnp++++aPGLEDtLiL
  gi|1154785   914 KRIRDPDYHVTLRPHLSKEVMDGS-KPAAELVKLNPGSEYAPGLEDTLIL 962

                    tmKGiAAGmqntG<-*
                    tmKGiAAG+qntG
  gi|1154785   963 TMKGIAAGLQNTG    975

gi|157279525|dbj|BAF80187.1|: domain 1 of 1, from 10 to 964: score 2511.5, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLR+L+P Kvsed+kL+eYDALLlD+FL+iL DLHGed++E v
  gi|1572795    10    SIDAQLRALAPKKVSEDDKLVEYDALLLDRFLEILEDLHGEDIRETV 56

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    q CYElsAeYE K+D+kKL+ELG +LtsLdP+D+i+vA++++HmLnLAnL
  gi|1572795    57 QACYELSAEYEAKHDPKKLDELGNVLTSLDPGDSIVVASSFSHMLNLANL 106

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv+ AyRR+ik+ k+GDF DEa AttEsDiEEtlKkL l   Ks eE+
  gi|1572795   107 AEEVQTAYRRKIKLNKKGDFLDEACATTESDIEETLKKLLLMK-KSKEEI 155

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+vDLv+tAHPtqsvRRsLLqK++RiRnCLaqL+A D+t++DK+
  gi|1572795   156 FDALKNQTVDLVFTAHPTQSVRRSLLQKHGRIRNCLAQLYAHDITPDDKQ 205

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR++P PqDEmRaGmsY+HEt+WkGvPKFLR
  gi|1572795   206 ELDEALQREIQAAFRTDEIRRTPPAPQDEMRAGMSYFHETIWKGVPKFLR 255

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinER PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1572795   256 RVDTALKNIGINERFPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 304

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq++DLmFElsmWRC dELRvRA+ l+r  ++d   K+Yi
  gi|1572795   305 ARMMAANLYFSQIDDLMFELSMWRCSDELRVRADILHRSLKKD--AKHYI 352

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP EPYRviL dvRDKLY tRERaRHLL  G+s+i+EeA +t++
  gi|1572795   353 EFWKQIPPSEPYRVILSDVRDKLYYTRERARHLLSNGYSDIPEEAAFTNI 402

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC+CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|1572795   403 EQFLEPLELCYRSLCDCGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 452

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+tDv+DAit+HLe+GsYReWsEe+RqEWLl+EL+GKRPL+g+DLPktE
  gi|1572795   453 ERHTDVMDAITRHLELGSYREWSEERRQEWLLSELSGKRPLFGPDLPKTE 502

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvl+af+v+ ELP D+FGaYiismat+ sDvLAvELLqR Cgvk++L
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  gi|1572795   503 EIADVLGAFHVISELPYDCFGAYIISMATSSSDVLAVELLQRACGVKKPL 552

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rv PLFEkLADLeAAPAa+e+LFsiDWY+ ri+GKqevm+GYsDsGKDAG
  gi|1572795   553 RVAPLFEKLADLEAAPAAMERLFSIDWYRDRINGKQEVMIGYSDSGKDAG 602

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqE+++KvAK+yGvKL++FHGRGGtvGRGGGPtHLA+Lsq
  gi|1572795   603 RLSAAWQLYKAQEDMVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLALLSQ 652

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGs+RvtvqGEviE+sFGEE LCFr+LqR+tAAtLEHGmnPP+sP
  gi|1572795   653 PPDTINGSIRVTVQGEVIEQSFGEERLCFRTLQRYTAATLEHGMNPPISP 702

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L++emAvvAt EYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|1572795   703 KPEWRALLDEMAVVATKEYRSIVFQEPRFVEYFRLATPETEYGRMNIGSR 752

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KD Kn+
  gi|1572795   753 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIMEKDKKNF 802

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q L+EmY+ WPFFRvt+DLlEmvFAKGDPGiAaLyDkLLv+E+L PFG++
  gi|1572795   803 QTLREMYNVWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVSEDLLPFGER 852

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++YvEtk lLL++AGH+DlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|1572795   853 LRNNYVETKRLLLQVAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 902

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRi+DP y v lrP lsK+  +   k+a+e + Lnpt+++aPGLEDtLiL
  gi|1572795   903 KRIKDPTYNVNLRPRLSKDVTQPR-KPAAEFLTLNPTSEYAPGLEDTLIL 951

                   tmKGiAAGmqntG<-*
                   tmKGiAAG+qntG
  gi|1572795   952 TMKGIAAGLQNTG    964

gi|1705590|sp|P51063.1|CAPP_PICAB: domain 1 of 1, from 11 to 963: score 2511.4, E = 0
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                      siDAq+RlLvPGKvsed+kLieYDALLlD+FLDiLqDLHGed++ +v
  gi|1705590    11    SIDAQMRLLVPGKVSEDDKLIEYDALLLDRFLDILQDLHGEDIRAMV 57

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qECYE s eYEGK D++KLeELG +LtsLdP+D+i+vA++++HmLnLAnL
  gi|1705590    58 QECYERSGEYEGKNDPHKLEELGNVLTSLDPGDSIVVASSFSHMLNLANL 107

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++AyRRR+k k+ G FaDE++AttEsDiEEt+K+Lv +l KsP+Ev
  gi|1705590   108 AEEVQIAYRRRRNKIKR-GGFADESNATTESDIEETFKRLVNQLGKSPAEV 156

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|1705590   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHARIRNCLSQLYGKDITPDEKQ 206

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|1705590   207 ELDEALLREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   R+DtALK iGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1705590   257 RIDTALKSIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmAanlY+sq+EDLmFElsmWRC dELR+RA  l++ +++d   K+Yi
  gi|1705590   306 ARMMAANLYYSQIEDLMFELSMWRCSDELRARALQLHSASKKD--AKHYI 353

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWKq+PP+EP+RviLGdvRDKLYntRER+R LL  Gis+i+Ee  +t++
  gi|1705590   354 EFWKQIPPNEPFRVILGDVRDKLYNTRERTRQLLSNGISDIPEEVTFTNI 403
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                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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  gi|1705590   404 DEFLEPLELCYRSLCSTGDQPIADGSLLDFMRQVSTFGLSFVKLDIRQES 453

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+ Dv DAit+HL+iGsY+eWsEe+Rq WLl+EL+GKRPL+g+DLPkt+
  gi|1705590   454 DRHSDVADAITRHLGIGSYKEWSEEQRQAWLLSELQGKRPLFGPDLPKTD 503

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                    Ev+Dvld+f+v+ ELP D FGaYiismata sDvL vELLqREC+vk++L
  gi|1705590   504 EVRDVLDTFHVISELPADNFGAYIISMATAASDVLVVELLQRECHVKKPL 553

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAa+++LFsi WY+nridGKqevm+GYsDsGKDAG
  gi|1705590   554 RVVPLFEKLADLEAAPAALARLFSINWYRNRIDGKQEVMIGYSDSGKDAG 603

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsA W LYkAqE++iKvAK++G+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1705590   604 RLSAGWALYKAQEDLIKVAKEFGIKLTMFHGRGGTVGRGGGPTHLAILSQ 653

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                    PPDti+Gs RvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PPv+P
  gi|1705590   654 PPDTIHGSFRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPVAP 703

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  gi|1705590   804 HMLQQMYNEWPFFRVTIDLIEMVFAKGDPGIAALYDKLLVSDDLWAIGEK 853

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  gi|1705590   854 LRANYGETKDLLLQVAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 903

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                    KRiRDP+y+v lrPhlsKE    +   a+eLvkLnpt+++aPGLEDtLiL
  gi|1705590   904 KRIRDPNYHVNLRPHLSKESSTKP---AAELVKLNPTSEYAPGLEDTLIL 950

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  gi|1705590   951 TMKGIAAGMQNTG    963

gi|63053872|gb|AAY28731.1|: domain 1 of 1, from 11 to 966: score 2510.9, E = 0
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  gi|6305387    11    SIDAQLRLLAPRKVSEDDKLVEYDALLLDRFLDILDSLHGSDIRETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YE +AeYE  +DtkKLeELG  +t+Ld +D+i+v k+++HmLnL nL
  gi|6305387    58 QELYEHAAEYERTRDTKKLEELGNMITGLDAGDSIVVTKSFSHMLNLSNL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRR kk k+GDFaDE+sA tEsDiEEtl++Lv+ lnKsPeEv
  gi|6305387   108 AEEVQIAYRRRTKKTKKGDFADESSAITESDIEETLRRLVVDLNKSPEEV 157

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|6305387   158 FATLKNQTVDLVLTAHPTQSVRRSLLQKHGRIRDCLTQLYAKDITPDDKQ 207

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|6305387   208 ELDEALQREIQAAFRTDEIRRTQPTPQDEMRAGMSYFHETIWKGVPKFLR 257

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                   aRmmAan+Y+sq+EDLmFElsmWRCndELR+RA E+++ +++d   K+Yi
  gi|6305387   307 ARMMAANMYFSQIEDLMFELSMWRCNDELRARAHEIHQYSKSD--AKHYI 354

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWK +PP+EPYRviLG+vRDKLY tRE aR LL  G s+++EeA +t+v
  gi|6305387   355 EFWKRIPPNEPYRVILGEVRDKLYSTREHARQLLSNGASDVPEEATFTHV 404

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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  gi|6305387   405 DQFLEPLELCYRSLCACGDRPIADGSLLDFMRQVSTFGLSLVRLDIRQES 454

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  gi|6305387   455 DRHTDVLDAITKHLGIGSYRDWSEEKRQEWLLSELRGKRPLFGPDLPKTE 504

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  gi|6305387   505 EIADVLDTFHVISELPSDSFGAYIISMATAPSDVLAVELLQRECRVKDPL 554

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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  gi|6305387   555 RVVPLFEKLADLEAAPASLTRLFSIDWYKNRINGKQEVMIGYSDSGKDAG 604

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  gi|6305387   605 RLSAAWQLYKVQEELIKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILAQ 654

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  gi|6305387   655 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHGMHPPSSP 704

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  gi|6305387   705 KPEWRALLDEMAVVATKEYRSVVFHEPRFVEYFRLATPELEYGRMNIGSR 754

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  gi|6305387   755 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIEKDIRNL 804

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  gi|6305387   805 TMLKEMYNQWSFFRVTIDLLEMVFAKGDPGIAALYDNLLVSEELKPFGEH 854

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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  gi|6305387   855 LRKSYEETKQFLLEVAGHRDLLDADPYLKQRLRLRDPYITTLNVCQAYTL 904

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  gi|6305387   905 KRIRDPNFHVTVRPPLSKDIMDPD-SPAAELVKLNPTSEYPPGLEDTLIL 953

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  gi|6305387   954 TMKGIAAGMQNTG    966

gi|63053870|gb|AAY28730.1|: domain 1 of 1, from 11 to 966: score 2510.6, E = 0
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  gi|6305387    11    SIDAQLRLLAPRKVSEDDKLVEYDALLLDRFLDILDSLHGPDIRETV 57

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qE YE +AeYE  +DtkKLeELG  +t+Ld +D+i+v k+++HmLnL nL
  gi|6305387    58 QELYEHAAEYERTRDTKKLEELGNMITGLDAGDSIVVTKSFSHMLNLSNL 107

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  gi|6305387   108 AEEVQIAYRRRTKKTKKGDFADESSAITESDIEETFRRLVVDLNKSPEEV 157
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  gi|6305387   158 FDTLKNQTVDLVLTAHPTQSVRRSLLQKHGRIRDCLTQLYAKDITPDDKQ 207

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  gi|6305387   208 ELDEALQREIQAAFRTDEIRRTQPTPQDEMRAGMSYFHETIWKGVPKFLR 257

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  gi|6305387   258 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 306

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  gi|6305387   307 ARMMAANMYFSQIEDLMFELSMWRCNDELRARAHEIHQYSKTD--AKHYI 354

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  gi|6305387   355 EFWKRIPPNEPYRVILGEVRDKLYSTREHACQLLSNGVSDVPEEATFTHV 404

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  gi|6305387   405 DQFLEPLELCYRSLCACGDRPIADGSLLDFMRQVSTFGLSLVRLDIRQES 454

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  gi|6305387   555 RVVPLFEKLADLESAPAALTRLFSIDWYRNRIDGKQEVMIGYSDSGKDAG 604

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  gi|6305387   605 RLSAAWQLYKVQEELIKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILAQ 654

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  gi|6305387   655 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHGMHPPSSP 704

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  gi|6305387   705 KPEWRALLDEMAVVATKEYRSVVFHEPRFVEYFRLATPELEYGRMNIGSR 754

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  gi|6305387   755 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLEKDIRNL 804

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  gi|6305387   805 TMLKEMYNQWSFFRVTIDLLEMVFAKGDPGIAALYDNLLVSEELKPFGEH 854

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  gi|6305387   855 LRKSYEETKQLLLEVAGHKDLLDADPYLKQRLRLRDPYITTLNVCQAYTL 904

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  gi|6305387   905 KRIRDPNFHVTERPHLSKEIMDSN-SPAAELVKLNPTSEYPPGLEDTIIL 953

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  gi|6305387   954 TMKGIAAGMQNTG    966

gi|1705589|sp|P51062.1|CAPP_PEA: domain 1 of 1, from 10 to 967: score 2509.4, E = 0
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gi|1705589    57 QEVYELSAEYERKHDPKKLEELGKLITGLDAGDSIVVAKSFSHMLNLANL 106

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gi|1705589   107 AEEVQIAHRRRNKLKK-GDFRDESNATTESDIEETLKKLVFNMKKSPQEV 155

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gi|1705589   156 FDALKNQTVDLVLTAHPTQSVRRSLLQKHARVRNCLSQLYAKDITPDDKQ 205

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gi|1705589   206 ELDESLQREIQAAFRTDEIKRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 255

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gi|1705589   305 ARMMAANLYYSQIEDLMFELSMWRCNDELRDRAEELHRNSKKDEVAKHYI 354

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gi|1705589   355 EFWKKVPLNEPYRVILGHVRDKLYRTRERSRYLLAHGYSDIPEEDTFTNF 404

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gi|1705589   405 DEFLEPLELCYRSLCFCGDRAIADGSLLDFLRQVSTFGLSLVRLDIRQES 454

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gi|1705589   455 DRHTDVMDAITKHLEIGSYQEWSEEKRQEWLLSELVGKRPLFGPDLPTTD 504

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gi|1705589   505 EIRDVLDTFHVIAELPSDNFGAYIISMATAPSDVLAVELLQRECKIKNPL 554

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gi|1705589   555 RVVPLFEKLADLEAAPAALARLFSIDWYRNRIDGKQEVMIGYSDSGKDAG 604

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gi|1705589   605 RFSAAWQLYKAQEELINVAQKFSVKLTMFHGRGGTVGRGGGPTHLAILSQ 654

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gi|1705589   655 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPSSP 704

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gi|1705589   705 KPEWRALMDQMAIIATEEYRSIVFKEPRFVEYFRLATPEMEYGRMNIGSR 754

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gi|1705589   805 HMLQDMYNQWPFFRVTIDLVEMVFAKGDPGIAALNDRLLVSQNLWPFGEQ 854

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  gi|1705589   954 LTMKGIAAGMQNTG    967

gi|89363537|emb|CAJ84247.1|: domain 1 of 1, from 11 to 967: score 2508.7, E = 0
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  gi|8936353    11    SIDAQLRQLVPAKVSEDDKLVEYDALLLDRFLDILQDLHGEDLRETV 57

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                    qE YElsAeYE K++++KLe LG  +tsLd +D+i+ Aka++HmLnLAnL
  gi|8936353    58 QEVYELSAEYEEKHEPEKLEKLGNIITSLDAGDSIVFAKAFSHMLNLANL 107

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  gi|8936353   108 AEEVQIAHRRRNKLKK-GDFADENNATTESDIEETFKRLVGELKKSPQQV 156

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  gi|8936353   157 FDALKNQTVDLVLTAHPTQSIRRSLLQKHGRIRNNLTQLYAKDITPDDKQ 206

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  gi|8936353   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPQFLR 256

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  gi|8936353   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|8936353   306 ARMMASNLYYSMIDDLMFELSMWRCNDELRVRADEISRSSKKDAVAKHYI 355

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  gi|8936353   356 EFWKIIPSSEPYRVVLGEVRDRLYRTRERSRHLLSQGSSDIPEEETFTNV 405

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  gi|8936353   406 EEFLEPLELCYRSLCVCGDRAIADGTLLDFLRQVSTFGLSLVRLDIRQES 455

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  gi|8936353   556 RVVPLFEKLADLESAPAALARLFSIDWYRNRINGKQEVMIGYSDSGKDAG 605

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  gi|8936353   606 RFSAAWQLYKAQEELIEVAKKFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 655

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  gi|8936353   656 PPETIHGSLRVTVQGEVIEQSFGEQHLCFRTLQRYTAATLEHGMHPPISP 705

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  gi|8936353   706 KPEWRALMDQMAVIATEEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 755

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                    PaKR+P GGie+LRAiPWiFaWtqtRFHLPvWLG+GAAF+  i KD++nl
  gi|8936353   756 PAKRRPTGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFRQVITKDVRNL 805
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  gi|8936353   806 NMLQEMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDRLLVSEDLWSFGEQ 855

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  gi|8936353   856 LRTKFEETKKLLLQVAAHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 905

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  gi|8936353   906 KRIRDPNYDVKLRPHISKE-CIEISKAADELVTLNPTSEYAPGLEDTLIL 954

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  gi|8936353   955 TMKGIAAGLQNTG    967

gi|51574147|gb|AAU07997.1|: domain 1 of 1, from 11 to 967: score 2504.3, E = 0
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  gi|5157414    11    SIDAQLRQLAPAKVSEDDKLVEYDALLLDRFLDILQDLHGEDMKETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YElsAeYEGK+D+kKLeELG  +tsLd +D+i+ Aka++HmLnLAnL
  gi|5157414    58 QEIYELSAEYEGKHDPKKLEELGNLITSLDAGDSIVFAKAFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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  gi|5157414   108 AEEVQIAHRRRNKLKK-GDFADENNATTESDIEETFKRLVRELKKSPQEV 156

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  gi|5157414   157 FDALKNQTVDLVLTAHPTQSIRRSLLQKHGRIRNNLTELYAKDITPDDKQ 206

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  gi|5157414   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

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  gi|5157414   306 ARMMAANLYYSMIDDLMFELSMWRCNDELRVRADEISRSSKKDAVAKHYI 355

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  gi|5157414   356 EFWKIIPSSEPYRVILGDVRDRLYRTRERSRYLLAQGYSDIPEEETLTSV 405

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  gi|5157414   406 EEFLEPLELCYRSLRVCGDRAIADGTLLDFLRQVSTFGLSLVRLDIRQES 455

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  gi|5157414   456 DRHTDVLDAITQHLGIGSYQEWSEEKRQQWLLSELSGKRPLFGPDLPQTE 505

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  gi|5157414   506 EIKDVLDTLHVIAELPPDNFGAYIISMATAASDVLAVELLQRECRIKHPL 555

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  gi|5157414   606 RFSAAWQLYKAQEELIEVAKKFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 655

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  gi|5157414   806 NMLQEMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDRLLVSEDLWSFGEQ 855

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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  gi|5157414   856 LRTKFEETKKLLLQVAAHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 905

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  gi|5157414   906 KRIRDPNYDVKLRPHISKE-CIEISKAADELITLNPTSEYAPGLEDTLIL 954

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  gi|5157414   955 TVKGIAAGLQNTG    967

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  gi|2420587    11    SIDAQLRLLAPQKLSDDDKLVEYDALLLDRFLDILQDLHGEDIRETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYEl+AeYE K D+k L+E+G +Lt  d +D++++ k+++H L LAnL
  gi|2420587    58 QECYELAAEYENKLDPKMLDEIGNVLTDWDRGDSMVITKSFSHRLILANL 107

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  gi|2420587   108 AEEVQMAYRRRIKLKK-GDFVDENSATTESDIEETLKRLMHQLKKSPLEV 156

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  gi|2420587   157 LDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLTQLYAKDITPDEKQ 206

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  gi|2420587   207 ELDEALQREIQAAFRTDEIRRAPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

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  gi|2420587   257 RVDTALKNIGINERLPYNAPIIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

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  gi|2420587   306 ARMMAANLYNAQIEDLMFELSMWRCSDELRVKVDELQCSSKKD-RTKHYI 354

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  gi|2420587   355 EFWKQVPPSEPYRVILSDVRDKLYNTRERARHLLASGFSEIPEEATFTDV 404

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  gi|2420587   405 EQFLEPLELCYRSLCACGDQSIADGSLLDFLRQVSTFGLSLVRLDIRQES 454

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  gi|2420587   455 DRHTDVMDAITEYLGIGSYRKWTEEKRQEWLLSELNGKRPLFGPDLPKSD 504

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  gi|2420587   505 EIADVLDTFHVLAELPSDSFGAYVISMATAPSDVLAVELLQRECHVKKPL 554
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  gi|2420587   605 RFSAAWQLYKAQEELINVAKMYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 654

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  gi|2420587   705 KPEWRALMDEMAIVATKEYRSIVFEEPRFVEYFRLATPEMEYGRMNIGSR 754

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  gi|2420587   855 LRANYEETKQLLLQVAGHKDLLEGDPYLKQRLRIRDSYITALNVCQAYTL 904

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  gi|2420587   905 KRIRDPGFQVNPGPHLSKDVMDIG-KPASELVKLNTTSEYAPGLEDTLIL 953

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  gi|2420587   954 TMKGIAAGMQNTG    966

gi|270232663|emb|CBI21984.1|: domain 1 of 1, from 11 to 944: score 2495.8, E = 0
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  gi|2702326    11    SIDAQLRLLAPAKVSEDDKLVEYDALLLDRFLDILQEIHGEDLKETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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  gi|2702326    58 QECYELSAEYEGKHDPQKLEELGRVITSLDAGDSIVVAKSFSNMLTLANL 107

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  gi|2702326   108 AEEVQIAFRRRIKLKK-GDFHDESSATTESDIEETIKRLVVQLKKSPEEV 156

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  gi|2702326   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHARIRNCLAQLYAKDITPDDKQ 206

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  gi|2702326   257 RVDTALKNIGIDERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

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  gi|2702326   306 ARMMAANLYYSQIEDLMFELSMWRCNEELRARADELHRSSRRD--AKHYI 353

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                    EFWKqvPP EPYRviLGdvRDKLY tRER+R LL  Gisei+EeA +t+v
  gi|2702326   354 EFWKQVPPSEPYRVILGDVRDKLYSTRERSRQLLSSGISEIPEEAAFTNV 403

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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                    E+FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|2702326   404 EQFLEPLELCYRSLCACGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 453

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDv+DAit+HLeiGsYReWsEe+RqEWLlaEL+GKRPL+g+DLPktE
  gi|2702326   454 DRHTDVMDAITKHLEIGSYREWSEERRQEWLLAELRGKRPLFGPDLPKTE 503

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+f+v+ ELP+D FGaYiismataPsDvLAvELLqREC+vk++L
  gi|2702326   504 EIADVLDTFHVISELPSDNFGAYIISMATAPSDVLAVELLQRECHVKKPL 553

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAav++LFsiDWY+nridGKqevm+GYsDsGKDAG
  gi|2702326   554 RVVPLFEKLADLEAAPAAVARLFSIDWYRNRIDGKQEVMIGYSDSGKDAG 603

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    R+sAAWqLYkAqE ++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2702326   604 RFSAAWQLYKAQEALVKVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 653

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|2702326   654 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 703

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAv+At EYRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|2702326   704 KPEWRALMDEMAVIATKEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 753

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh i +D +nl
  gi|2702326   754 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHVIGRDPRNL 803

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+ mY+eWPFFRvt+DL+EmvFAKGDPGiAaLyD+LLv+EeL+ FGk+
  gi|2702326   804 PMLQQMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDRLLVSEELWLFGKR 853

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Etk lLL+iAGH+DlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|2702326   854 LRTNYEETKRLLLQIAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 903

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+v  rPhl                      ++aPG+EDtLiL
  gi|2702326   904 KRIRDPNYHVMERPHL----------------------EYAPGMEDTLIL 931

                    tmKGiAAGmqntG<-*
                    tmKGiAAG+qntG
  gi|2702326   932 TMKGIAAGLQNTG    944

gi|270230868|emb|CBI20195.1|: domain 1 of 1, from 11 to 930: score 2493.6, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLRlLvP Kvsed+kL+eYDALLlD+FLDiLqDLHGedLkE v
  gi|2702308    11    SIDAQLRLLVPAKVSEDDKLVEYDALLLDRFLDILQDLHGEDLKETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYElsAeYEGK+D+kKLeELG +LtsLd +D+i++Ak+++HmLnLAnL
  gi|2702308    58 QECYELSAEYEGKHDPKKLEELGNVLTSLDAGDSIVIAKSFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRR+k+kk GDFaDE +AttEsDiEEtlKkLv++l KsPeEv
  gi|2702308   108 AEEVQIAYRRRRNKLKK-GDFADENNATTESDIEETLKKLVVQLKKSPEEV 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+vDLvltAHPtqsvRRsLLqK++RiRnCLaqL+AKD+t++DK+
  gi|2702308   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLAQLYAKDITPDDKQ 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|2702308   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2702308   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305
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                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq+EDLmFElsmWRCndELRvRA+El r +++d   K+Yi
  gi|2702308   306 ARMMAANLYYSQIEDLMFELSMWRCNDELRVRADELLRSSKKD--AKHYI 353

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP EPYRviLG+vRDKLY tRER+RHLLA+Gis+i+ eA yt++
  gi|2702308   354 EFWKQIPPSEPYRVILGEVRDKLYQTRERSRHLLAHGISDIPGEATYTNL 403

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|2702308   404 EQFLEPLELCYRSLCACGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 453

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDv+DAit+HLeiGsYReWsEe+RqEWLl+EL+GKRPL+g+DLPktE
  gi|2702308   454 DRHTDVIDAITRHLEIGSYREWSEERRQEWLLSELSGKRPLFGPDLPKTE 503

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+f+v+AELP D FGaYiismataPsDvLAvELLqREC+vkq+L
  gi|2702308   504 EIADVLDTFHVIAELPADNFGAYIISMATAPSDVLAVELLQRECHVKQPL 553

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAav++LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|2702308   554 RVVPLFEKLADLEAAPAAVARLFSIDWYKNRINGKQEVMIGYSDSGKDAG 603

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAW LYkAqEE+iKvAK+yG+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2702308   604 RLSAAWALYKAQEELIKVAKQYGIKLTMFHGRGGTVGRGGGPTHLAILSQ 653

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2702308   654 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 703

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|2702308   704 KPEWRALMDEMAVVATENYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 753

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFK+Ai+KDi+nl
  gi|2702308   754 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKYAIEKDIRNL 803

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+ +L+ FG++
  gi|2702308   804 HLLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSKDLWSFGER 853

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+ tk lLL+iAGHkDlLEGDPYLKqrlRLRdsYittLnv+qA tL
  gi|2702308   854 LRSNYEQTKSLLLQIAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQACTL 903

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPsy                                    +DtLiL
  gi|2702308   904 KRIRDPSY-----------------------------------DDTLIL 917

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|2702308   918 TMKGIAAGMQNTG    930

gi|3777449|emb|CAA09807.1|: domain 1 of 1, from 11 to 964: score 2490.3, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLRlLvP Kvsed+kL+eYDALLlD+FLDiL  LHGe +kE v
  gi|3777449    11    SIDAQLRLLVPTKVSEDDKLVEYDALLLDRFLDILEGLHGEGIKETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYElsAeYE  +D kKLeELG++LtsLdP+D+i+vAk+i+HmLn+AnL
  gi|3777449    58 QECYELSAEYENTRDKKKLEELGSVLTSLDPGDSIVVAKSISHMLNMANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A   R k kk GDF+DE++  tEsDiEEtlK+Lv+ l KsP Ev
  gi|3777449   108 AEEVQIANSGREKSKK-GDFSDESNLMTESDIEETLKRLVVDLKKSPREV 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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                    FeALKnq+vDLv+tAHPtq+ RRsLLqK+aRiRnCLaqL+AKD+t++DK+
  gi|3777449   157 FEALKNQTVDLVFTAHPTQATRRSLLQKHARIRNCLAQLYAKDITPDDKE 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGm Y+HEt+W+GvPKFLR
  gi|3777449   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMNYFHETIWNGVPKFLR 256

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|3777449   257 RVDTALKNIGINERIPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq++DLmFElsmWRCndELR RA+E +r  +rd   K+Yi
  gi|3777449   306 ARMMAANLYYSQIDDLMFELSMWRCNDELRDRADEQHRSLKRD--EKHYI 353

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKqvPP EPYRvi+GdvRDKLY tRER+R LL  G+sei+EeA yt++
  gi|3777449   354 EFWKQVPPSEPYRVIIGDVRDKLYHTRERTRQLLSNGFSEIPEEATYTNI 403

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|3777449   404 EQFLEPLELCYRSLCACGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 453

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlDAit+HLeiGsYR+WsEe+RqEWLl+EL+GKRPL+g+DLPktE
  gi|3777449   454 DRHTDVLDAITQHLEIGSYRQWSEERRQEWLLSELSGKRPLFGPDLPKTE 503

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvl++f+v+ ELP+D+FGaYiismataPsDvLAvELLqREC+vkq+L
  gi|3777449   504 EIADVLNTFHVISELPSDCFGAYIISMATAPSDVLAVELLQRECHVKQPL 553

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkL DLeAAPAa+++LFsi+WY+nri+GKqevm+GYsDsGKDAG
  gi|3777449   554 RVVPLFEKLDDLEAAPAAIARLFSIEWYKNRINGKQEVMIGYSDSGKDAG 603

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+iKv K+yGvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|3777449   604 RLSAAWQLYKAQEELIKVSKQYGVKLIMFHGRGGTVGRGGGPSHLAILSQ 653

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFt AtLEHGm PP  P
  gi|3777449   654 PPDTIQGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTSATLEHGMYPPFPP 703

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++e+ vvAtE YRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|3777449   704 KPEWRALLDEISVVATEKYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 753

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGie+LRAiPWiFaWtqtRFHLPvWLG+GAAFK+A++KD Knl
  gi|3777449   754 PSKRKPSGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKYALNKDKKNL 803

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L++m k+WPFFRvt DL+EmvFAKGDPGiAaLyDkLLv+E+L+ FG+
  gi|3777449   804 NMLQDMHKKWPFFRVTADLIEMVFAKGDPGIAALYDKLLVSEDLWSFGEL 853

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Etk lLL++AGHk+lLEGDP LKqrlRLRdsYittLnv+qAYtL
  gi|3777449   854 LRSDYEETKSLLLQVAGHKELLEGDPCLKQRLRLRDSYITTLNVCQAYTL 903

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP y vtlrPh+ KEy +    +a+eLv Lnp +++aPGLEDtLiL
  gi|3777449   904 KRIRDPTYNVTLRPHITKEYIESK--PAAELVCLNPESEYAPGLEDTLIL 951

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|3777449   952 TMKGIAAGMQNTG    964

gi|20257597|gb|AAM15963.1|AF495586_1: domain 1 of 1, from 11 to 964: score 2489.3, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLRlL+PGKvsed+kL+eYDALL+D+FLDi qDLHG++++E+v
  gi|2025759    11    SIDAQLRLLAPGKVSEDDKLVEYDALLIDRFLDIFQDLHGPNIREFV 57
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                qECYE++AeYE  +D+ KL ELG++Lt L P Dai+vA+++ mLnL nL
gi|2025759    58 QECYEVAAEYERDRDAAKLSELGSRLTKLSPNDAIVVASSFSNMLNLTNL 107

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AEEv+lA+ RR+k+k+ GDFaDE+ A tEsDiEEtlK+Lv  l Ks eEv
gi|2025759   108 AEEVQLAHLRRNKLKR-GDFADEGFAATESDIEETLKRLVTELGKSKEEV 156

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                F+ALKnq+vDLv+tAHPtqsvRRsLLqK+aRiRnCL+qL+AKD t +DK+
gi|2025759   157 FDALKNQTVDLVFTAHPTQSVRRSLLQKHARIRNCLTQLYAKDNTEDDKQ 206

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                ELDEAL REiqA FRtDEiRRaqPtPqDEmR+GmsY+HEt+WkGvPKFLR
gi|2025759   207 ELDEALQREIQACFRTDEIRRAQPTPQDEMRYGMSYFHETIWKGVPKFLR 256

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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gi|2025759   257 RVDTALKNIGIDERLPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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gi|2025759   306 ARMMASNLYFSRIEELMFELSMWRCNDELRARAEELHASSQRI--SKHYI 353

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                EFW+q+P +EPYRv+LG vRD LY tRER+RHLL  G+s+i+E+  + +v
gi|2025759   354 EFWRQLPANEPYRVVLGYVRDELYSTRERSRHLLTSGFSDIPEDSAFKNV 403

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                EeFLEPLELCYksLC+CGDk iADGsLLD++RqvstFGLs+vKLDiRqEs
gi|2025759   404 EEFLEPLELCYKSLCDCGDKTIADGSLLDFMRQVSTFGLSMVKLDIRQES 453

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                eR+tDv+DAittHL+iGsYReWsEeKRqEWLl+EL+GKRPLl  D+P+tE
gi|2025759   454 ERHTDVIDAITTHLGIGSYREWSEEKRQEWLLSELRGKRPLLSKDMPQTE 503

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                E++Dvl+ f+vLAELP DsFG+YiismataPsDvLAvELLqREC+vkq+L
gi|2025759   504 EIADVLGCFHVLAELPRDSFGPYIISMATAPSDVLAVELLQRECHVKQPL 553

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                +vvPLFEkLADL+ APA++e+LFs+DWY+nri GKq+vmvGYsDsGKDAG
gi|2025759   554 PVVPLFEKLADLQSAPASIERLFSLDWYMNRIGGKQQVMVGYSDSGKDAG 603

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAW LYkAqE ++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|2025759   604 RLSAAWHLYKAQEAMAKVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 653

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PPDtinGslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
gi|2025759   654 PPDTINGSLRVTVQGEVIETSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 703

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                kPEWR Lm+e+A vAt+EYRsvv++EPRFvEYFR+AtPE+EYG++niGsR
gi|2025759   704 KPEWRALMDEIAAVATDEYRSVVMREPRFVEYFRSATPETEYGRLNIGSR 753

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                PaKRkP GGiesLRAiPWiF+WtqtRFHLPvWLG+GAAF hA++KDiKn+
gi|2025759   754 PAKRKPKGGIESLRAIPWIFSWTQTRFHLPVWLGFGAAFEHAMKKDIKNF 803

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                 +LkEmY+eWPFFRvtlDLlEmv AKGDP iA+LyD+LLva+eLkPFG++
gi|2025759   804 RMLKEMYNEWPFFRVTLDLLEMVLAKGDPTIAGLYDQLLVADELKPFGEQ 853

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR++YvEt++l+L++AGHk++LE DP LKq+lRLRd+Yit Lnv qAYtL
gi|2025759   854 LRNNYVETEKLILQVAGHKEILESDPGLKQQLRLRDPYITILNVWQAYTL 903

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                KRiRDP++kvt++P+lsKE+AdEn  ++ ++vkLnp++++ PGLEDtLiL
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  gi|2025759   904 KRIRDPNFKVTPQPPLSKEFADEN--QPRGIVKLNPASEYGPGLEDTLIL 951

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                   tmKGiAAGmqntG
  gi|2025759   952 TMKGIAAGMQNTG    964

gi|108742705|gb|ABG01962.1|: domain 1 of 1, from 11 to 966: score 2480.0, E = 0
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                      siDAqLRlL+P Kvsed+kL+eYDALLlD+FLDiLq LHGe+++E v
  gi|1087427    11    SIDAQLRLLAPRKVSEDDKLVEYDALLLDRFLDILQSLHGEEIRETV 57

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qE YE +AeYE  +D+kK+eELG  +tsLd +D+i+v k++ HmLnLAnL
  gi|1087427    58 QELYEHAAEYERTRDPKKMEELGNMVTSLDAGDSIVVTKSFAHMLNLANL 107

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  gi|1087427   108 AEEVQIAHRRRIKKSKKGDFADESSAITESDIEETLRRLVVDLKKSPQEV 157

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                   R DtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1087427   258 RLDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 306

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmAan+Y+sq+EDLmFE+smWRCndELR RAEEl++ ++rd   K+Yi
  gi|1087427   307 ARMMAANMYFSQIEDLMFEMSMWRCNDELRGRAEELHKYSKRD--AKHYI 354

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                   EFWKq+PP+EPYRv+L dvRDKLYntRERaR +LA G+s+i+EeA +t+v
  gi|1087427   355 EFWKQIPPNEPYRVVLADVRDKLYNTRERARQVLANGYSDIPEEATFTHV 404

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  gi|1087427   505 EIADVLDTFHVISELPSDSFGAYIISMATAPSDVLAVGLLQRECQIKNPL 554

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  gi|1087427   555 RVVPLFEKLADLESAPASVARLFSIDWYKDRINGKQEVMIGYSDSGKDAG 604

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  gi|1087427   655 PPDTVHGSLRVTIQGEVIEQSFGEEHLCFRTLQRYTAATLEHGMHPPITP 704

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  gi|1087427   755 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAVRHVMEKDIRNF 804
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                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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  gi|1087427   805 NMLKEMYNLWPFFRVTIDLLEMVFAKGNPEIAALYDKLLVSEDLQPFGEH 854

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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  gi|1087427   855 LRENYEETKHYLLEVAGHKDLLEADPYLKQRLRLRVPYITTLNVSQAYTL 904

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                    KRiRDP+++vt rPh+sKE  + n   a+eLvkLnpt+++aPGLEDtLiL
  gi|1087427   905 KRIRDPNFQVTERPHISKEIMESN-TAAAELVKLNPTSEYAPGLEDTLIL 953

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  gi|1087427   954 TMKGIAAGMQNTG    966

gi|507808|dbj|BAA03094.1|: domain 1 of 1, from 11 to 964: score 2469.1, E = 0
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                       siDAqLRl++P Kvsed+kL+eYDALLlD+F         +  +E+v
  gi|507808|    11    SIDAQLRLIAPAKVSEDDKLLEYDALLLDRFSIFSRTCMAKKSREFV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE++A+Y+G + t KLeELG  LtsLdP+D+i+v k+++ mL LAnL
  gi|507808|    58 QECYEVAADYDGNRNTAKLEELGNMLTSLDPGDSIVVTKSFSNMLSLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyR Rikk+k+GDFaDEasAttEsDiEEtlK+L  +  K+PeEv
  gi|507808|   108 AEEVQIAYRARIKKLKKGDFADEASATTESDIEETLKRLLQLN-KTPEEV 156

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  gi|507808|   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKFGRIRDCLTQLYAKDITPDDKQ 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|507808|   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

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  gi|507808|   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|507808|   306 ARMMAANLYFSQIEDLMFEMSMWRCNEELRVRA-EVQRCAKRD--AKHYI 352

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  gi|507808|   353 EFWKQIPSNEPYRAILGDVRDKLYNTRERARQLLSSGVSDIPEDSVFASV 402

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  gi|507808|   403 DQFLEPLELCYRSLCDCGDRPTADGSLLDFLRQASAFGLALVKLDIRQES 452

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  gi|507808|   453 DRHTDVLDAITQHLGIGSYKEWSEDKRQEWLLSELSGKRPLFGHDLPKTE 502

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  gi|507808|   503 EIADVLDTFKVISELPHDSFGAYIISMATAPSDVLAVELLQRECGIIHPL 552

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  gi|507808|   553 RVVPLFEKLADLENAPASVARLFSIEWYRNRINGKQEVMIGYSDSGKDAG 602

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                    RlsAAWqLYk qEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|507808|   603 RLSAAWQLYKTQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 652

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                   kPEWR Lm+emAv+AtEEYRsvv+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|507808|   703 KPEWRVLMDEMAVIATEEYRSVVFKEPRFVEYFRLATPELEYGRMNIGSR 752

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  gi|507808|   753 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGSAFKRVIQKDAKNL 802

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  gi|507808|   803 NMLKEMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDRLLVSEELQPFGEQ 852

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR +Y+Et+ lLL++AGHkD+LEGDPYL+qrl LRd+YittLnv+qAYtL
  gi|507808|   853 LRVNYQETRRLLLQVAGHKDILEGDPYLRQRLQLRDPYITTLNVCQAYTL 902

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  gi|507808|   903 KQIRDPSFHVKVRPHLSKDYM-ESSKPAAELVKLNPKSEYAPGLEDTVIL 951

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  gi|507808|   952 TMKGIAAGMQNTG    964

gi|6688533|emb|CAB65171.1|: domain 1 of 1, from 11 to 964: score 2466.8, E = 0
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  gi|6688533    11    SIDAQMRLLVPTKVSEDDMLVEYDALLLDRFLDILEDLHGEGIKTTV 57

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qECYElsAeYE  +D kKLeELG++Lt LdP+D+i+vAk+i+HmLn+AnL
  gi|6688533    58 QECYELSAEYENTHDKKKLEELGSVLTTLDPGDSIVVAKSISHMLNMANL 107

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  gi|6688533   108 AEEVQIANSGRAKSKK-GELSDESNLMTESDIEETLKRLVVNLNKSPREV 156

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  gi|6688533   157 FNALKNQTVDLVFTAHPTQAIRRSLLQKHARIRNCLSQLYAKDITPDDKE 206

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  gi|6688533   207 ELDEALEREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWNGVPKFLR 256

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  gi|6688533   257 RVDTALKNIGIDERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

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  gi|6688533   306 ARMMAANLYYSQIDDLMFELSMWRCNDELRDRADELHRSLKRD--EKHYI 353

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  gi|6688533   354 EFWKQVPPSEPYRVIIGDVRDKLYHTRERTRQLLSHGFSEIPEEATYTNI 403

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  gi|6688533   404 KQFLEPLELCYRSLCACGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 453

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  gi|6688533   454 DRHTDVLDAITQHLEIGSYREWSEERKQEWLLSELSGKRPLFGPDLPKTE 503

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  gi|6688533   504 EIDDVLNTFHVISELPSDCFGAYIISMATAPSDVLAVELLQRECHVKQPL 553
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  gi|6688533   604 RLSAAWQLYKAQEELIKVAKQYDVKLIMFHGRGGTVGRGGGPSHLAILSQ 653

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  gi|6688533   654 PPDTIQGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTSATLEHGMYPPFPP 703

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  gi|6688533   704 KPEWRALLDEISVVATEKYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 753

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  gi|6688533   754 PSKRKRNGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKYALNKDKKNL 803

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                     +L++m k+WPFFRvt DL+EmvFAKGDPGiAaLyDkLLv+E+L+ FG+
  gi|6688533   804 NMLRDMHKKWPFFRVTADLIEMVFAKGDPGIAALYDKLLVSEDLWSFGEL 853

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  gi|6688533   854 LRSDYEETKSLLLKVAGHKELLENDPSLKQRLRLRDSYITTLNVCQAYTL 903

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  gi|6688533   904 KRIRDPTYKVTPRPHITKEYIESK--PAAELVSLNPQSEYAPGLEDTLIL 951

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  gi|6688533   952 TMKGIAAGMQNTG    964

gi|27462753|gb|AAO15570.1|AF459644_1: domain 1 of 1, from 11 to 967: score 2466.2, E = 0
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                       siDAqLR L+P Kvsed+kL+eYDALLlD+FLDiLqDLHGed+kE v
  gi|2746275    11    SIDAQLRQLAPAKVSEDDKLVEYDALLLDRFLDILQDLHGEDMKETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YElsAeYEGK+D+kKLeELG  +tsLd +D+i+ Aka++HmLnLAnL
  gi|2746275    58 QEIYELSAEYEGKHDPKKLEELGNLITSLDAGDSIVFAKAFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A+RRR+ +kk GDFaDE +AttEsDiEEt+K+Lv  l KsP+Ev
  gi|2746275   108 AEEVQIAHRRRNNLKK-GDFADENNATTESDIEETFKRLVRELKKSPQEV 156

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  gi|2746275   157 FDALKNQTVDLVLTAHPTQSIRRSLLQKHGRIRNNLTELYAKDITPDDKQ 206

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  gi|2746275   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

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  gi|2746275   306 ARMMAANLYYSMIDDLMFELSMWRCNDELRVRADEISRSSKKDAVAKHYI 355

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK +P  EPYRviLGdvRDKLY     + HLLA+G+sei+ e + t v
  gi|2746275   356 EFWKIIPSSEPYRVILGDVRDKLYRKSRGSCHLLAQGYSEIPGEEILTSV 405

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  gi|2746275   456 DRHTDVLDAITQHLGIGSYQEWSEEKRQQWLLSELSGKRPLFGPDLPQTE 505

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  gi|2746275   506 EIKDVLDTLHVIAELPPDNFGAYIISMATAASDVLAVELLQRECRIKHPL 555

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  gi|2746275   556 RVVPLFEKLADLESAPAALARLFSIDWYRNRINGKQEVMIGYSDSGKDAG 605

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  gi|2746275   606 RFSAAWQLYKAQEELIEVAKKFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 655

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  gi|2746275   656 PPETIHGSLRVTVQGEVIEQSFGEQHLCFRTLQRYTAATLEHGMHPPISP 705

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  gi|2746275   706 KPEWRALMDQMAVIATEEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 755

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  gi|2746275   756 PAKRRPTGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFRQVVPKDVRNL 805

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY++W FFRvt+DL+EmvFAKGDPGiAaLyD+LLv+ +L+ FG++
  gi|2746275   806 NMLQEMYNQWKFFRVTIDLVEMVFAKGDPGIAALYDRLLVSKNLWSFGEQ 855

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR +++Etk+lLL++A HkDlLEGDPYLKq+lRLRdsYi tLnv+qAYtL
  gi|2746275   856 LRTNFEETKKLLLQVAAHKDLLEGDPYLKQKLRLRDSYISTLNVCQAYTL 905

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y v lrPh+sKE   E sk adeL+ Lnpt+++aPGLEDt iL
  gi|2746275   906 KRIRDPNYDVKLRPHISKE-CIEISKVADELITLNPTSEYAPGLEDTFIL 954

                   tmKGiAAGmqntG<-*
                   tmKGiAAG+qntG
  gi|2746275   955 TMKGIAAGLQNTG    967

gi|90652448|emb|CAJ86550.1|: domain 1 of 1, from 12 to 968: score 2464.6, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      siDAqLR L+P Kvsed+kLieYDALLlD+FLDiLqDLHGe Lk+ v
  gi|9065244    12    SIDAQLRQLAPAKVSEDDKLIEYDALLLDRFLDILQDLHGEGLKDTV 58

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qE YEls eYEGK+D+kKLeE+G ++tsLd +D+i+vAk+++HmLnLAnL
  gi|9065244    59 QEVYELSSEYEGKHDPKKLEEIGNVITSLDAGDSIVVAKSFSHMLNLANL 108

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++ +RRR+k+kk G FaDE++AttEsDiEEtlK+Lv  l KsP+Ev
  gi|9065244   109 AEEVQISHRRRNKLKK-GNFADETNATTESDIEETLKRLVFDLKKSPQEV 157

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   F+ALK q+vDLvltAHPtqs+RRsLLq              K      K+
  gi|9065244   158 FDALKSQTVDLVLTAHPTQSIRRSLLQSMLGYEIAYLICMPKISLLMMKE 207

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL REiqAAFRtDEi+R++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|9065244   208 ELDEALQREIQAAFRTDEIKRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 257

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALKniGinE +P ++P+i+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|9065244   258 RVDTALKNIGINECIPHNAPVIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 306
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                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|9065244   307 ARMMAANMYYSQIEDLMFELSMWRCSDELRNRAEELHRSSNKDEVAKHYI 356

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK++PP+EPYRv+LG+vRD+LY tRER+RHLLA+G+s+i+EeA +t+v
  gi|9065244   357 EFWKKIPPNEPYRVVLGEVRDRLYQTRERSRHLLAHGYSDIPEEATFTNV 406

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    +eFLEPLE+CY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|9065244   407 DEFLEPLEVCYRSLCACGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 456

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDv+DAit+HLeiGsY eWsEeKRqEWLl+EL+GKRPL+g+DLPktE
  gi|9065244   457 DRHTDVMDAITKHLEIGSYLEWSEEKRQEWLLSELSGKRPLFGPDLPKTE 506

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+f+vLAELP+D FGaYiismataPsDvLAvELLqREC++k++L
  gi|9065244   507 EIRDVLDTFHVLAELPSDNFGAYIISMATAPSDVLAVELLQRECHIKHPL 556

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADL+AAPAa+++LFsiDWY+nridGKqevm+GYsDsGKDAG
  gi|9065244   557 RVVPLFEKLADLDAAPAALARLFSIDWYRNRIDGKQEVMIGYSDSGKDAG 606

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    R+sAAWqLYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|9065244   607 RFSAAWQLYKAQEELIKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 656

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGE +LCFr+LqR+tAAtLEHGmnPP+sP
  gi|9065244   657 PPDTIHGSLRVTVQGEVIEQSFGEQHLCFRTLQRYTAATLEHGMNPPISP 706

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm++mAv+AtEEYRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|9065244   707 KPEWRALMDQMAVIATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 756

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+P GGie+LRAiPWiFaWtqtRFHLPvWLG+GAAFK  i+KD++nl
  gi|9065244   757 PAKRRPTGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKQVIEKDVRNL 806

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY++WPFFRvt+DL+EmvFAKGDPGiAaL+D+LLv+ +L+PFG++
  gi|9065244   807 HMLQEMYNQWPFFRVTIDLVEMVFAKGDPGIAALNDRLLVSKDLWPFGEQ 856

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR kY+Etk+lLL++A HkDlLEGDPYLKqrlRLR sYittLnvfqAYtL
  gi|9065244   857 LRKKYEETKNLLLQVATHKDLLEGDPYLKQRLRLRHSYITTLNVFQAYTL 906

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP++ v +rPh+sK+   E s  a eLv Lnpt+++aPGLED LiL
  gi|9065244   907 KRIRDPNFNVPPRPHISKD-SLEKSTSATELVSLNPTSEYAPGLEDSLIL 955

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|9065244   956 TMKGIAAGMQNTG    968

gi|63053868|gb|AAY28729.1|: domain 1 of 1, from 11 to 966: score 2460.0, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLRlL+PGKvsed+kL+eYDALLlD+FL+ L  LHG+ ++E v
  gi|6305386    11    SIDAQLRLLAPGKVSEDDKLVEYDALLLDRFLESLDSLHGPGIRETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YE +AeYE  +DtkKLeELG  +tsLd +D+i+v k+++HmLnL nL
  gi|6305386    58 QELYEHAAEYERTRDTKKLEELGNMITSLDAGDSIVVTKSFSHMLNLSNL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyR+R kk k+GDFaDE+sA tEsDiEEt+++Lv+ l KsP+E+
  gi|6305386   108 AEEVQIAYRKRTKKTKKGDFADESSAITESDIEETFRRLVVDLKKSPQEI 157

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ LKnq+vDLvltAHPtqsvRRsLLqK++RiR CL+qL+AKD+t++DK+
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                    ELDEAL REiqAAFRtDEiRRaqPtPqDEmRaGmsYi Et+WkGvPKFLR
  gi|6305386   208 ELDEALQREIQAAFRTDEIRRAQPTPQDEMRAGMSYIIETIWKGVPKFLR 257

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|6305386   258 RVDTALKNIGINERVPYNAPLIRFSSWMGGDRDG-NPRVTPEVTRDVCLL 306

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAan+Y+sq+ DLmFElsmWRCndELR+RA E+++ ++ d   K+Yi
  gi|6305386   307 ARMMAANMYFSQIQDLMFELSMWRCNDELRARAHEIHQHSKTD--AKHYI 354

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK +PP EPYRviLG+vRDKLY tRE a  LL  G+s+i+EeA +t+v
  gi|6305386   355 EFWKRIPPSEPYRVILGEVRDKLYSTREHALQLLSNGVSNIPEEATFTHV 404

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    ++FLEPLELCY+sLC CGD+ iADGsLLD++RqvstFGLsLv+LDiRqEs
  gi|6305386   405 DQFLEPLELCYRSLCACGDRPIADGSLLDFMRQVSTFGLSLVRLDIRQES 454

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|6305386   455 DRHTDVMDAITKHLGIGSYRAWSEEKRQEWLLSELRGKRPLFGPDLPKTE 504

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvl+af+v+AE+P+DsFGaYiismataPsDvLAvELLqRECgvk +L
  gi|6305386   505 EIADVLGAFHVIAEIPSDSFGAYIISMATAPSDVLAVELLQRECGVKDPL 554

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLe APA+v +LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|6305386   555 RVVPLFEKLADLENAPASVTRLFSIDWYRNRINGKQEVMIGYSDSGKDAG 604

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+iK+AK++GvKL++FHGRGGtvGRGGGPtHLAiL+q
  gi|6305386   605 RLSAAWQLYKAQEELIKIAKEFGVKLTMFHGRGGTVGRGGGPTHLAILAQ 654

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP tinGslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEHGm+PP sP
  gi|6305386   655 PPGTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHGMHPPSSP 704

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emA vAt EYRsvv++EPRFvEYFR AtPElEYG+mniGsR
  gi|6305386   705 KPEWRALLDEMAAVATKEYRSVVFREPRFVEYFRRATPELEYGRMNIGSR 754

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkPsGGiesLRAiPWiF+WtqtRFHLPvWLG+G AFKh i+KD  nl
  gi|6305386   755 PAKRKPSGGIESLRAIPWIFSWTQTRFHLPVWLGFGPAFKHVIEKDKGNL 804

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +LkEmY++W FFRvt+DLlEmvFAKGDP iAaLyDkLLv+E+LkPFG+
  gi|6305386   805 TMLKEMYNQWSFFRVTIDLLEMVFAKGDPKIAALYDKLLVSEDLKPFGEH 854

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR  Y+Et++lLL++AGHkD+L+ DPYLKqrlRLRd+YittLnvfqAYtL
  gi|6305386   855 LRKSYEETQQLLLEVAGHKDILDADPYLKQRLRLRDPYITTLNVFQAYTL 904

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+++vt  PhlsKE  d n  +a+eLvkLn t++++PGLEDtLiL
  gi|6305386   905 KRIRDPNFHVTAGPHLSKEIMDSN-SPAAELVKLNLTSEYPPGLEDTLIL 953

                    tmKGiAAGmqntG<-*
                    tmKGiAAG+qntG
  gi|6305386   954 TMKGIAAGLQNTG    966

gi|18073908|emb|CAC86034.1|: domain 1 of 1, from 11 to 964: score 2459.1, E = 0
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                       siDAq+RlLvP Kvsed+ L+eYDALLlD+FLDiL DLHGe +k  v
  gi|1807390    11    SIDAQMRLLVPTKVSEDDMLVEYDALLLDRFLDILEDLHGEGIKTTV 57
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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gi|1807390    58 QECYELSAEYENTHDKKKLEELGSVLTTLDPGDSIVVAKSISHMLNMANL 107

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AEEv++A   R k kk G+ +DE++  tEsDiEEtlK+Lv+ lnKsP Ev
gi|1807390   108 AEEVQIANSGRAKSKK-GELSDESNLMTESDIEETLKRLVVNLNKSPREV 156

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gi|1807390   157 FNALKNQTVDLVFTAHPTQAIRRSLLQKHARIRNCLSQLYAKDITPDDKE 206

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+W+GvPKFLR
gi|1807390   207 ELDEALEREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWNGVPKFLR 256

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                RvDtALKniGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
gi|1807390   257 RVDTALKNIGIDERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

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                aRmmAanlY+sq++DLmFElsmWRCndELR RA+El+r  +rd   K+Yi
gi|1807390   306 ARMMAANLYYSQIDDLMFELSMWRCNDELRDRADELHRSLKRD--EKHYI 353

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                EFWKqvPP EPYRvi+GdvRDKLY tRER+R LL +G+sei+EeA yt++
gi|1807390   354 EFWKQVPPSEPYRVIIGDVRDKLYHTRERTRQLLSHGFSEIPEEATYTNI 403

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                 +FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
gi|1807390   404 KQFLEPLELCYRSLCACGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 453

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                +R+tDvlDAit  LeiGsYReWsEe++qEWLl+EL+GKRPL+g+DLPktE
gi|1807390   454 DRHTDVLDAITHDLEIGSYREWSEERKQEWLLSELSGKRPLFGPDLPKTE 503

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                E+ Dvl++f+v+ ELP+D+FGaYiismataPsDvLAvELLqREC+vkq+L
gi|1807390   504 EIDDVLNTFHVISELPSDCFGAYIISMATAPSDVLAVELLQRECHVKQPL 553

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                rvvPLFEkL DL+AAPAa+++LFsi+WY+nri+GKqevm+GYsDsGKDAG
gi|1807390   554 RVVPLFEKLDDLDAAPAAIARLFSIEWYKNRINGKQEVMIGYSDSGKDAG 603

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLYkAqEE+iKvAK+y vKL++FHGRGGtvGRGGGP HLAiLsq
gi|1807390   604 RLSAAWQLYKAQEELIKVAKQYDVKLIMFHGRGGTVGRGGGPSHLAILSQ 653

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFt AtLEHGm PP  P
gi|1807390   654 PPDTIQGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTSATLEHGMYPPFPP 703

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                kPEWR L++e+ vvAtE YRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
gi|1807390   704 KPEWRALLDEISVVATEKYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 753

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                P+KRk  GGie+LRAiPWiFaWtqtRFHLPvWLG+GAAFK+A++KD Knl
gi|1807390   754 PSKRKRNGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKYALNKDKKNL 803

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                 +L++m k+WPFFRvt DL+EmvFAKGDPGiAaLyDkLLv+E+L+ FG+
gi|1807390   804 NMLRDMHKKWPFFRVTADLIEMVFAKGDPGIAALYDKLLVSEDLWSFGEL 853

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR +Y+Etk lLLk+AGHk+lLE DP LKqrlRLRdsYittLnv+qAYtL
gi|1807390   854 LRSDYEETKSLLLKVAGHKELLENDPSLKQRLRLRDSYITTLNVCQAYTL 903

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                KRiRDP ykvt+rPh+ KEy +    +a+eLv Lnp +++aPGLEDtLiL
gi|1807390   904 KRIRDPTYKVTPRPHITKEYIESK--PAAELVSLNPQSEYAPGLEDTLIL 951
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                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|1807390   952 TMKGIAAGMQNTG    964

gi|23491823|dbj|BAC19851.1|: domain 1 of 1, from 11 to 968: score 2433.1, E = 0
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                       siDA LRlL+P Kvsed+kL+eYDALLlD+FLDiLq LHGedLkE v
  gi|2349182    11    SIDAHLRLLAPKKVSEDDKLVEYDALLLDRFLDILQALHGEDLKETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYEl+AeYE   D  KL+ELG +L sLd +D+i++Ak+++HmLnLAnL
  gi|2349182    58 QECYELAAEYEKNLDQAKLDELGNVLMSLDAGDSIVLAKSFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRRikk+k+GDF DE sAttEsD++Etl +Lv+ lnKsP+E+
  gi|2349182   108 AEEVQIAYRRRIKKLKKGDFGDENSATTESDLDETLMRLVSDLNKSPAEI 157

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|2349182   158 FEALKNQTVDLVLTAHPTQSVRRSLLQKHARVRDCLAQLNEKDITPDDKQ 207

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|2349182   208 EIDEALQGAIQAAFRTDEIRRAPPTPQDEMRAGMSYFHETIWKGVPKFLR 257

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  gi|2349182   258 RVDTALKDIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 306

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  gi|2349182   307 ARLMAANMYYSQIEDLMFELSMWRCSEELRQRVELLHSSIKKD--NKHYI 354

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                    EFWK+vPP+EPYRviLGdvR KLYntRERaRHLL +G s+i EeA +t++
  gi|2349182   355 EFWKKVPPNEPYRVILGDVRNKLYNTRERARHLLSQGQSDINEEATFTNL 404

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFLEPLELCY+sLC CGD+viA+GsLLD+LRqv+tFGLsLv+LDiRqEs
  gi|2349182   405 EEFLEPLELCYRSLCACGDRVIAEGSLLDFLRQVFTFGLSLVRLDIRQES 454

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+tDvlDAitt L+iGsYReWsEeKRqEWL++EL GKRPL++ D P+tE
  gi|2349182   455 ERHTDVLDAITTYLGIGSYREWSEEKRQEWLISELTGKRPLIPHDFPQTE 504

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  gi|2349182   505 EVKDVLDALHVISEFPSENFGPYIISMATSTSDVLAVELLQRECHVKKPL 554

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  gi|2349182   555 RVVPLFERLADLKAAPAVMTRLFSMDWYRNRINGKQEVMIGYSNSGKDAG 604

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  gi|2349182   605 RLSADWKLYKFQAELAKIAKQFGVKLTLFHGRGGTIGRGGGPSHLAILSQ 654

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  gi|2349182   655 PPNTINGSLRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 704

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  gi|2349182   755 PSKRKPSGGIVSLRAIPWIFSWTQTRFHLPVWLGFGTAFKHVIEKDVRNF 804

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                    LR++Y+Etk+lLL++AGHkDlLEGDPYLKqrlRLRd+YittLn +qAYtL
  gi|2349182   855 LRANYEETKNLLLQVAGHKDLLEGDPYLKQRLRLRDAYITTLNLLQAYTL 904

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  gi|2349182   905 KRIRDPNYNVKFRPHLSKEIMESKTdKPADELVKLNPASEYAPGLEDTLI 954

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  gi|2349182   955 LTMKGIAAGFQNTG    968

gi|115575|sp|P10490.1|CAPP1_MESCR: domain 1 of 1, from 11 to 966: score 2430.6, E = 0
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  gi|115575|    11    SIDAQLRLLAPKKVSEDDKLIEYDALLLDRFLDILQNLHGEDIKETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YE sAeYE  +D+kKLeELG+ +tsLd +D+i+vAk+++HmLnLAnL
  gi|115575|    58 QELYEQSAEYERTHDPKKLEELGSMVTSLDAGDSIVVAKSFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++  R+R+kk k+GDF DE  A tEsD+EEtl++L++ l KsP+E+
  gi|115575|   108 AEEVQISRRKRVKKVKKGDFMDENTAMTESDMEETLRRLIVDLKKSPQEI 157

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    Fe LKnq+vDLv+tAHPtqsvRRsLLqK++RiR CLaqL+AKD+t++DK+
  gi|115575|   158 FETLKNQTVDLVFTAHPTQSVRRSLLQKHGRIRDCLAQLYAKDITPDDKQ 207

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR+qPtPqDEmRaGmsY+HEt+W+GvPKFLR
  gi|115575|   208 ELDEALQREIQAAFRTDEIRRTQPTPQDEMRAGMSYFHETIWNGVPKFLR 257

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  gi|115575|   258 RLDTALKNIGITERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 306

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  gi|115575|   307 ARMMAANMYFSQIDELMFELSMWRCTDELRERAEELHKYSKRD--SKHYI 354

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  gi|115575|   355 EFWKQIPSSEPYRVILADVRDKLYYTRERSRQLLASEVSEIPVEATFTEI 404

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  gi|115575|   405 DQFLEPLELCYRSLCACGDRPVADGSLLDFMRQVATFGLCLVKLDIRQES 454

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  gi|115575|   455 ERHTDVMDAITTHLGIGSYRDWTEEKRQDWLLSELRGKRPLFGPDLPRTD 504

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  gi|115575|   505 EIADVLDTINVIAELPSDSFGAYVISMATAPSDVLAVELLQRECKVKKPL 554

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  gi|115575|   555 RVVPLFEKLADLEAAPASMTRLFSVDWYKNRIDGKQEVMIGYSDSGKDAG 604

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  gi|115575|   605 RLSAAWQMYKVQEELLKVSKKFGVKLTMFHGRGGTVGRGGGPTHLAILAQ 654

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  gi|115575|   655 PAETIGGSLRVTIQGEVIEQSFGEQHLCFRTLQRYTAATLEHGMNPPKSP 704
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  gi|115575|   705 KPEWRALLDQMAVVATEEYRSIVFKEPRFVEYFRLATPETEYGRMNIGSR 754

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  gi|115575|   755 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGVGGALKHVLEKDIRNH 804

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  gi|115575|   805 NMLRDMYNNFPFFRVTIDLLEMVFAKGDPEIAALYDKLLVSEELQSFGER 854

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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  gi|115575|   855 LRANYEDTKRRLLEVAGHKDLLEGDPYLKQRLRLRDPYITTLNVCQAYTL 904

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  gi|115575|   905 KRIRDPDFKVTERPHLSKEIMDAH-KAAAELVKLNPTSEYAPGLEDTLIL 953

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  gi|115575|   954 TMKGVAAGLQNTG    966

gi|4877832|gb|AAD31452.1|AF135371_1: domain 1 of 1, from 11 to 957: score 2430.1, E = 0
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  gi|4877832    11    SIDAQLRQLAPAKVSEDDKLIEYDALLLDRFLDILQDLHGEDLKETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YElsAeYE K+D +KLeELG ++tsLd +D+i+vAk+++HmLnLAnL
  gi|4877832    58 QEVYELSAEYERKHDHEKLEELGKVITSLDAGDSIVVAKSFSHMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++  RRR+k+kk GDFaDE +AttEsDiEEtlKkLv kl KsP+Ev
  gi|4877832   108 AEEVQISRRRRNKLKK-GDFADENNATTESDIEETLKKLVFKLKKSPQEV 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|4877832   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKHARIRNSLSQLYAKDITPDDKQ 206

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  gi|4877832   207 ELDEALQREIQAAFRTDEIKRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

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                    RvDtALKniGinER+PY++PLi+FssWmGGDRDG    vtPEvtRDvCLL
  gi|4877832   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG--NQVTPEVTRDVCLL 304

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  gi|4877832   305 ARMMASNLYYSQIEDLMFELSMWRCNDELRVHADELHRNSKKDEVAKHYI 354

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  gi|4877832   355 EFWKKVPPNEPYRVVLGEVRDRLYKTRERSRYLLAQGYSEIPEEATFTHV 404

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  gi|4877832   405 EEFLEPLELCYRSLCDCGDRAIA-GSLLDFLRQVSTFGLSLVRLDIRQES 453

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  gi|4877832   454 DRHTDVMDAITKHLEIGSYQEWSEEKRQEWLLGELSGKRPLFGPDLPQTE 503

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  gi|4877832   504 EIRDVLDTFHVIAELPSDNFGAYIISMATAPSDVLAVELLQRESH---AL 550

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                    R+sAAWqLYkAqE++iKvAKk+GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|4877832   601 RFSAAWQLYKAQEDLIKVAKKFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 650

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  gi|4877832   651 PPDTIHGSLRVTVQGEVIEQSFGEEHLSFRTLQRFTAATLEHGMNPPFSR 700

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  gi|4877832   701 KPEWRALMDQLAVIATeeEEYRSIVFKEPRFVEY-SLATPELEYGRMNIG 749

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  gi|4877832   750 SRPAKRRPTGGIE-IRAIPWIFAWTQTRFHLPVWLGFGAAFRQLIEKDVR 798

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  gi|4877832   799 NLHTLQEmMYNQWPFFRVTIDLVEMVFLKGDPGIAALNDRLLVSEDLWPF 848

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  gi|4877832   849 GEQLRNKYEETKKLLLQVAGHKEVLEGDPYLKQRLRLRDSYITTMNVFQA 898

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                    YtLKRiRDP+y v    h+sK    E sk+adeLv+Lnpt+++aPGLEDt
  gi|4877832   899 YTLKRIRDPNYDVK---HISK----EKSKPADELVRLNPTSEYAPGLEDT 941

                    LiLtmKGiAAGmqntG<-*
                    LiLtmKGiAAGmqntG
  gi|4877832   942 LILTMKGIAAGMQNTG    957

gi|11991545|gb|AAG42288.1|: domain 1 of 1, from 10 to 955: score 2427.4, E = 0
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  gi|1199154    10    SIDAQLRLLAPGKVSEDDKLVEYDALLIDRFLDILQNLHGSALRELV 56

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                    qECYE+sAeY+ K+D  +L+ELGakL +LdPaDai vA++++HmLnLAnL
  gi|1199154    57 QECYEMSAEYDVKRDETRLDELGAKLSGLDPADAITVASSFSHMLNLANL 106

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                    AEEv++A RRR +k+khGDF+DE+sAttEsDiEEtlK+Lv+   KsP+Ev
  gi|1199154   107 AEEVQIAQRRR-SKLKHGDFSDEGSATTESDIEETLKRLVSEIGKSPQEV 155

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  gi|1199154   156 FDALKNQTVELVLTAHPTQSLRRSLLQKHTKIRNCLTQLYAKDITEDEKK 205

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  gi|1199154   206 ELDEALQAEIQAAFRTDEIRRSQPTPQDEMRYGMSYFHETIWKGVPKFLR 255

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  gi|1199154   256 RVDTALKSIGINERLPYDAPVIKFSSWMGGDRDG-NPRVTPEVTRDVCLL 304

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                    aRmmAanlY+s +EDLmFElsmWRCndELR+RA+E       +   K+Yi
  gi|1199154   305 ARMMAANLYVSSIEDLMFELSMWRCNDELRARADEHLASRETK---KHYI 351

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  gi|1199154   352 EFWRAIPESEPYRVLLGYVRDKLYNTRERALHMLTKGYSEIKEEATITSV 401

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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  gi|1199154   402 EEFMEPLEVCYKSLCDCGDKTIADGLLLDFMRQVNTFGLSLAKLDIRQES 451
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  gi|1199154   452 ERHTDAVDAITTHLGIGSYKEWPEEKRQEWLLSELQGKRPLLVPDLPVTE 501

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  gi|1199154   502 EVEAVLGCFKVLAELPRDSFGPYIISMATAPSDVLAVELLQRECGVRQPL 551

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  gi|1199154   552 PVVPLFERLADLQNAPASVERLFSIDWYLNRIGGKQQIMVGYSDSGKDAG 601

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                    RlsAAWqLY+AqE +++vAKky vK++ FHGRGGtvGRGGGPtHLAiLsq
  gi|1199154   602 RLSAAWQLYQAQELVAQVAKKYDVKVTFFHGRGGTVGRGGGPTHLAILSQ 651

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  gi|1199154   652 PPETINGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPISP 701

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  gi|1199154   702 KPEWRKLMDEMAVVATDAYRSVVVKEPRFVEYFRSATPETEYGRMNIGSR 751

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  gi|1199154   752 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGSAFKSAIDKDIKNF 801

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  gi|1199154   802 QLLKDMYREWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVTDELKPFGEQ 851

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  gi|1199154   852 LRSKYAETEQLLLQIAGHKEILEADPYLKQRLRLRDPYITTLNVFQAYTL 901

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  gi|1199154   902 KQIRDPNFKVKTQPPLNKE---------QDLVKLNPASEYAPGLEDTLII 942

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  gi|1199154   943 TMKGIAAGMQNTG    955

gi|219944332|gb|AAX98688.3|: domain 1 of 1, from 8 to 964: score 2427.2, E = 0
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  gi|2199443     8    SIDAQLRLLAPGKVSEDDKLVEYDALLLDRFLDILQDLHGPNLREFV 54

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  gi|2199443   105 AEEVQIAQRRRNKLKR-GDFTDEGSALTESDIEETLKRLVTDLGKTKEEV 153

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  gi|2199443   154 FDALKNQIVELVMTAHPTQSVRRSLLQKYSRIRNCLTELYAKDISADDKK 203

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  gi|2199443   204 ELDEALQREIQAAFRTDEIRRAQPTPQDEMRYGMSYFHETIWKGVPKFLR 253

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGi ERlPY+vPLikFssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2199443   254 RVDTALKNIGIDERLPYNVPLIKFSSWMGGDRDG-NPRVTPEVTRDVCLL 302

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                    aRmmAanlY+sq+EDLmFElsmWRCndELR+RA+El   a ++   K+Yi
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                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFW+ +PP+EPYRv+LG vRDKLYntRER+RHLL  G+sei E+ v+t++
  gi|2199443   353 EFWRGIPPNEPYRVVLGYVRDKLYNTRERSRHLLTSGFSEITEDLVFTNI 402

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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  gi|2199443   403 EEFLEPLELCYKSLCECGDKIVADGSLLDFLRQVSTFGLSFVKLDIRQES 452

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+tD +DAittHL+iGsY++W+EeKRqEWLl+EL+GKRPLl +D P  +
  gi|2199443   453 ERHTDAIDAITTHLGIGSYKSWPEEKRQEWLLSELQGKRPLLTPDPPTSD 502

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl+ frvLAELP DsFG+YiismataPsDv AvELLqREC++k +L
  gi|2199443   503 EVADVLGCFRVLAELPRDSFGPYIISMATAPSDVPAVELLQRECQIKDPL 552

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFE+LADL+A PA+ve+LFs++WY  ri+GKq+vmvGYsDsGKDAG
  gi|2199443   553 PVVPLFERLADLRAGPASVERLFSTEWYLKRINGKQQVMVGYSDSGKDAG 602

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAW LY+AqE ++ vAKkyGv+++ FHGRGGtvGRGGGPtHLAiLsq
  gi|2199443   603 RLSAAWALYRAQEGMAEVAKKYGVQITFFHGRGGTVGRGGGPTHLAILSQ 652

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  gi|2199443   653 PPNTINGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPASP 702

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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  gi|2199443   703 KPEWRALMDEVTAVATEEYRSYVFKEPRFVEYFRSATPETEYGRLNIGSR 752

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  gi|2199443   753 PAKRKPGGGTESLRAIPWIFSWTQTRFHLPVWLGFGAAFNLRHQEgTSGN 802

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
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  gi|2199443   803 IQTLKEMYNEWPFFRVTLDLVEMVFAKGDPGIVGFYNDLLVADELKPFGE 852

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
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  gi|2199443   853 QLRKNYIDTCSFSCRLLGTRKSLEGDPYLKQRLHLRDPYITTLNVFQAYT 902

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                    LKRiRDP++kvtl P+ls E+AdEn  k+++LvkLnp++++ PGLEDtLi
  gi|2199443   903 LKRIRDPNFKVTLNPPLSNEFADEN--KPAGLVKLNPASEYGPGLEDTLI 950

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  gi|2199443   951 LTMKGIAAGMQNTG    964

gi|225461662|ref|XP_002285442.1|: domain 1 of 1, from 11 to 921: score 2424.8, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLRlLvP Kvsed+kL+eYDALLlD+FLDiLqDLHGedLkE v
  gi|2254616    11    SIDAQLRLLVPAKVSEDDKLVEYDALLLDRFLDILQDLHGEDLKETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYElsAeYEGK
  gi|2254616    58 QECYELSAEYEGK---------------------------------- 70

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                         +AyRRR+k+kk GDFaDE +AttEsDiEEtlKkLv++l KsPeEv
  gi|2254616    71 -----IAYRRRNKLKK-GDFADENNATTESDIEETLKKLVVQLKKSPEEV 114

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+vDLvltAHPtqsvRRsLLqK++RiRnCLaqL+AKD+t++DK+
  gi|2254616   115 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLAQLYAKDITPDDKQ 164
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  gi|2254616   165 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 214

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2254616   215 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 263

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq+EDLmFElsmWRCndELRvRA+El r +++d   K+Yi
  gi|2254616   264 ARMMAANLYYSQIEDLMFELSMWRCNDELRVRADELLRSSKKD--AKHYI 311

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP EPYRviLG+vRDKLY tRER+RHLLA+Gis+i+ eA yt++
  gi|2254616   312 EFWKQIPPSEPYRVILGEVRDKLYQTRERSRHLLAHGISDIPGEATYTNL 361

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|2254616   362 EQFLEPLELCYRSLCACGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 411

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDv+DAit+HLeiGsYReWsEe+RqEWLl+EL+GKRPL+g+DLPktE
  gi|2254616   412 DRHTDVIDAITRHLEIGSYREWSEERRQEWLLSELSGKRPLFGPDLPKTE 461

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+f+v+AELP D FGaYiismataPsDvLAvELLqREC+vkq+L
  gi|2254616   462 EIADVLDTFHVIAELPADNFGAYIISMATAPSDVLAVELLQRECHVKQPL 511

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAav++LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|2254616   512 RVVPLFEKLADLEAAPAAVARLFSIDWYKNRINGKQEVMIGYSDSGKDAG 561

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAW LYkAqEE+iKvAK+yG+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2254616   562 RLSAAWALYKAQEELIKVAKQYGIKLTMFHGRGGTVGRGGGPTHLAILSQ 611

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2254616   612 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 661

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|2254616   662 KPEWRALMDEMAVVATENYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 711

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
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  gi|2254616   712 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKYAIEKDIRNL 761

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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  gi|2254616   762 HLLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSKDLWSFGER 811

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+ tk lLL+iAGHkDlLEGDPYLKqrlRLRdsYittLnv+qA tL
  gi|2254616   812 LRSNYEQTKSLLLQIAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQACTL 861

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPsy v +rPh+ K+  +     a+eLv Lnpt+ + PGLEDtLiL
  gi|2254616   862 KRIRDPSYDVKVRPHICKDIMESA---AQELVNLNPTSDYGPGLEDTLIL 908

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|2254616   909 TMKGIAAGMQNTG    921

gi|1870188|emb|CAA60627.1|: domain 1 of 1, from 4 to 956: score 2416.6, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLRlL+P Kvsed+kL+eY  LLlD+FLDiLqDLHGe ++E v
  gi|1870188     4    SIDAQLRLLAPAKVSEDDKLVEYVRLLLDRFLDILQDLHGEVVRETV 50

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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                qE YElsAeYE K+D+kKL+ELG  L sLdP+ +i++A++++HmLnLAnL
gi|1870188    51 QELYELSAEYESKHDPKKLDELGNLLISLDPGNSIVIASSFSHMLNLANL 100

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AEEv++A+RRRik+kk GDF DE sAttEsDiEEtlK+Lv  l KsPeEv
gi|1870188   101 AEEVQIAHRRRIKLKK-GDFVDENSATTESDIEETLKRLVHDLKKSPEEV 149

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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gi|1870188   150 FDALKNQTVDLVLTAHPTQSVRRSLLQKHARIRNCLAQLYAKDITPDDKQ 199

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                ELDEAL +   AAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
gi|1870188   200 ELDEAL-KGGSAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 248

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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gi|1870188   249 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 297

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                aRmmAanlY+sq+EDLmFElsmWRC dELR+RA+El+r ++rd   K++i
gi|1870188   298 ARMMAANLYFSQIEDLMFELSMWRCSDELRIRADELHRSSKRD--AKHFI 345

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                EFWKqvPP+EPYRv+L dvRDKLYntRER+RHLL  Gis+++Ee   t+v
gi|1870188   346 EFWKQVPPNEPYRVVLADVRDKLYNTRERSRHLLSSGISDVPEESSMTNV 395

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                E+ LEPLELCY+sLC CGD+ iADGsLLD++RqvstFGL+LvKLDiRqEs
gi|1870188   396 EQLLEPLELCYRSLCSCGDRPIADGSLLDFMRQVSTFGLALVKLDIRQES 445

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaEL.kGKRPL.lgsDLPk
                +R+tDv+DAittHL+iGsYReWsE+ RqEWLl+EL +GK  L++gsDLP
gi|1870188   446 DRHTDVIDAITTHLGIGSYREWSED-RQEWLLSELaSGKGDLqIGSDLPA 494

                tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
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gi|1870188   495 TCSV-DVIDTFLVIAELPPDNFGAYIISMATAPSDVLAVELLQRECHVRQ 543

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gi|1870188   544 PLRVVPLFEKLADLEAAPAALARLFSIEWYRNRIDGKQEVMIGYSDSGKD 593

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gi|1870188   594 AGRLSAAWQLYKGQEDLIKVAKKYGVKLTMFHGRGGTVGRGGGPTHLAIL 643

                sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
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gi|1870188   644 SQPPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPI 693

                sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                sPkPEWR L++emAvvAtEEYRs+v++EPRFvEY RlAtPElEYG+mniG
gi|1870188   694 SPKPEWRTLLDEMAVVATEEYRSIVFQEPRFVEYGRLATPELEYGRMNIG 743

                sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                sRP+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh   KDiK
gi|1870188   744 SRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGTAFKHVSPKDIK 793

                nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                nl  L+EmY+eWPFFRvt+DL+EmvFAKG PGiA+Ly kLLv+ eL+ FG
gi|1870188   794 NLRILQEMYNEWPFFRVTIDLVEMVFAKGNPGIASLYGKLLVSSELWSFG 843

                ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                ++LR++Y+EtkdlLL++AGHk  L  +      + LRdsYittLnv+qAY
gi|1870188   844 ERLRANYQETKDLLLQVAGHKVFLK-ESLSEAEVGLRDSYITTLNVCQAY 892

                tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                tLKRiRDP+++v +rPh+sKE  d   k+a+eLvkLnpt+++aPGLEDtL
gi|1870188   893 TLKRIRDPNFHVKVRPHISKEISDAS-KPAAELVKLNPTSEYAPGLEDTL 941
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                  iLtmKGiAAGmqntG<-*
                  iLtmKGiAAGmqntG
  gi|1870188   942 ILTMKGIAAGMQNTG    956

gi|164449187|gb|ABY56044.1|: domain 1 of 1, from 11 to 965: score 2414.4, E = 0
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD....iLqDLHGedL
                     siDAq+RlLvPGKvsed+kLieYDALLl   L + +  +  + G+
  gi|1644491    11    SIDAQMRLLVPGKVSEDDKLIEYDALLLTGSLTsckiYMERISGKRF 57

                  kEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLn
                  k ++     +      K   +    LG +LtsLdP+D+i+vAk++ HmL
  gi|1644491    58 KHVMSFLLSMKESMTRKSYQS----LGDVLTSLDPGDSIVVAKSFAHMLS 103

                  LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                  LAnLAEEv++AyRRR+k+kk GDFaDE sAttEsDiEEtlK+Lv  l Ks
  gi|1644491   104 LANLAEEVQIAYRRRNKLKK-GDFADENSATTESDIEETLKRLVGDLKKS 152

                  PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
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  gi|1644491   153 PQEVFDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLTQLYAKDITP 202

                  eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
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  gi|1644491   203 DDKQELDEALQREIQAAFRTDEIRRTAPTPQDEMRAGMSYFHETIWKGVP 252

                  KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
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  gi|1644491   253 KFLRRVDTALKNIGVNERVPHNAPLIQFSSWMGGDRGG-NPRVTPEVTRD 301

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  gi|1644491   302 VCLLARMMAANLYYSQIEDLMFELSMWRCNDELRVRADVLHRSTRRD--A 349

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  gi|1644491   350 KHYIEFWKQVPPNEPYRVILGDLRDKLYHTRERSRQLLASGHSDIPEEAT 399

                  ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                     vE+FLEPLELCY+sLC CGD++iADGsLLD+LRqvstFGLsLvKLDi
  gi|1644491   400 LISVEQFLEPLELCYRSLCSCGDRAIADGSLLDFLRQVSTFGLSLVKLDI 449

                  RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                  RqEs+R+tDv+DAit+HLeiGsYReWsEe+RqEWLl+EL GKRPL+g+DL
  gi|1644491   450 RQESDRHTDVIDAITKHLEIGSYREWSEERRQEWLLSELCGKRPLFGPDL 499

                  PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                  PktEE+ Dvld+++v+ ELP+D FGaYiismataPsDvLAvEL+qREC v
  gi|1644491   500 PKTEEISDVLDTLHVISELPSDNFGAYIISMATAPSDVLAVELMQRECRV 549

                  kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsG
                  k++LrvvPLFEkLADLeAAPAa+ +LFsi WY+ ri+G qevm+GYsDsG
  gi|1644491   550 KKPLRVVPLFEKLADLEAAPAALSRLFSINWYRERINGTQEVMIGYSDSG 599

                  KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
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  gi|1644491   600 KDAGRFSAAWQLYKAQEELINVAKKFGVKLTMFHGRGGTVGRGGGPTHLA 649

                  iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP
                  iLsqPPDti+GslRvtvqGEviE+sFGEE LCFr+LqRFtAAtLEHGm+
  gi|1644491   650 ILSQPPDTIHGSLRVTVQGEVIEQSFGEELLCFRTLQRFTAATLEHGMHM 699

                  PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmn
                  PvsPkPE R Lm+emAvv tE+YRs+v++EPRFvEYFRlAtPElEYG+mn
  gi|1644491   700 PVSPKPERRALMDEMAVVSTEDYRSIVFQEPRFVEYFRLATPELEYGRMN 749

                  iGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                  iGsRP+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+h i+KD
  gi|1644491   750 IGSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHVIKKD 799

                  iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP
                  iKnl +L+EmY++WPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+E+L+
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  gi|1644491   800 IKNLHMLQEMYNQWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEDLWS 849

                   FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfq
                   FG+ LR +Y+Etk++LL+iAGHkDlLEGDP LKqrlRLRdsYittLnv+q
  gi|1644491   850 FGELLRSNYEETKNFLLQIAGHKDLLEGDPHLKQRLRLRDSYITTLNVCQ 899

                   AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                   AYtLKRiRDP+++vtlrPh+sKE  + n k+a+eLvkLnpt+++aPGLED
  gi|1644491   900 AYTLKRIRDPNFHVTLRPHISKEINETN-KPANELVKLNPTSEYAPGLED 948

                   tLiLtmKGiAAGmqntG<-*
                   tLiLtmKGiAAG+qntG
  gi|1644491   949 TLILTMKGIAAGLQNTG    965

gi|225446611|ref|XP_002280580.1|: domain 1 of 1, from 11 to 923: score 2412.2, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      siDAqLRlL+P Kvsed+kL+eYDALLlD+FLDiLq++HGedLkE v
  gi|2254466    11    SIDAQLRLLAPAKVSEDDKLVEYDALLLDRFLDILQEIHGEDLKETV 57

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qECYElsAeYEGK
  gi|2254466    58 QECYELSAEYEGK----------------------------------- 70

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                        +A+RRRik+kk GDF DE+sAttEsDiEEt+K+Lv++l KsPeEv
  gi|2254466    71 -----IAFRRRIKLKK-GDFHDESSATTESDIEETIKRLVVQLKKSPEEV 114

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   F+ALKnq+vDLvltAHPtqsvRRsLLqK+aRiRnCLaqL+AKD+t++DK+
  gi|2254466   115 FDALKNQTVDLVLTAHPTQSVRRSLLQKHARIRNCLAQLYAKDITPDDKQ 164

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL REiqAAFRtDEiRR+ PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|2254466   165 ELDEALQREIQAAFRTDEIRRTAPTPQDEMRAGMSYFHETIWKGVPKFLR 214

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALKniGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2254466   215 RVDTALKNIGIDERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 263

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmAanlY+sq+EDLmFElsmWRCn+ELR+RA+El+r ++rd   K+Yi
  gi|2254466   264 ARMMAANLYYSQIEDLMFELSMWRCNEELRARADELHRSSRRD--AKHYI 311

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWKqvPP EPYRviLGdvRDKLY tRER+R LL  Gisei+EeA +t+v
  gi|2254466   312 EFWKQVPPSEPYRVILGDVRDKLYSTRERSRQLLSSGISEIPEEAAFTNV 361

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   E+FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|2254466   362 EQFLEPLELCYRSLCACGDRPIADGSLLDFLRQVSTFGLSLVRLDIRQES 411

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +R+tDv+DAit+HLeiGsYReWsEe+RqEWLlaEL+GKRPL+g+DLPktE
  gi|2254466   412 DRHTDVMDAITKHLEIGSYREWSEERRQEWLLAELRGKRPLFGPDLPKTE 461

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dvld+f+v+ ELP+D FGaYiismataPsDvLAvELLqREC+vk++L
  gi|2254466   462 EIADVLDTFHVISELPSDNFGAYIISMATAPSDVLAVELLQRECHVKKPL 511

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAav++LFsiDWY+nridGKqevm+GYsDsGKDAG
  gi|2254466   512 RVVPLFEKLADLEAAPAAVARLFSIDWYRNRIDGKQEVMIGYSDSGKDAG 561

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   R+sAAWqLYkAqE ++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2254466   562 RFSAAWQLYKAQEALVKVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 611

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|2254466   612 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 661
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                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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  gi|2254466   662 KPEWRALMDEMAVIATKEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 711

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh i +D +nl
  gi|2254466   712 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHVIGRDPRNL 761

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+ mY+eWPFFRvt+DL+EmvFAKGDPGiAaLyD+LLv+EeL+ FGk+
  gi|2254466   762 PMLQQMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDRLLVSEELWLFGKR 811

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Etk lLL+iAGH+DlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|2254466   812 LRTNYEETKRLLLQIAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 861

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                    KRiRDP+y+v  rPhlsKE   E sk+a+eLvkLnpt+++aPG+EDtLiL
  gi|2254466   862 KRIRDPNYHVMERPHLSKEIM-ESSKPAAELVKLNPTSEYAPGMEDTLIL 910

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                    tmKGiAAG+qntG
  gi|2254466   911 TMKGIAAGLQNTG    923

gi|2499465|sp|Q43299.1|CAPP_AMAHP: domain 1 of 1, from 11 to 964: score 2408.9, E = 0
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                       siDAqLRlL+P Kvsed+kL+eYDALLlD+FLDiL  LHG  ++E v
  gi|2499465    11    SIDAQLRLLAPKKVSEDDKLVEYDALLLDRFLDILESLHGSGIRETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YE +AeYE  +DtkKLeELG  +tsLd +D+i++Ak+++ mLnLAnL
  gi|2499465    58 QELYEHAAEYERTHDTKKLEELGNLITSLDAGDSIVIAKSFSQMLNLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv+lAyRRRikk k+GDFaDE+sA tEsD EEtl++Lv +  KsPeE+
  gi|2499465   108 AEEVQLAYRRRIKKTKKGDFADESSAITESDFEETLRRLVDLK-KSPEEI 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F  LKnq+vDLvltAHPtqsvRRsLLqK++RiR CL+qL+AKD+ ++DK+
  gi|2499465   157 FATLKNQTVDLVLTAHPTQSVRRSLLQKHGRIRDCLSQLYAKDISPDDKQ 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL R iqAAFRtDEiRR qPtPqDEmR+GmsY+HEt+WkGvPKFLR
  gi|2499465   207 ELDEALQRAIQAAFRTDEIRRVQPTPQDEMRMGMSYFHETIWKGVPKFLR 256

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinER+PY+vPLi+FssWmGGDRDG nPRvtPEvtRDv LL
  gi|2499465   257 RVDTALKNIGINERVPYNVPLIQFSSWMGGDRDG-NPRVTPEVTRDVVLL 305

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                    aRmmAan+Y+ q+ DLmFElsmWRCndE+R+RA El++ +++d   K+Yi
  gi|2499465   306 ARMMAANMYFTQITDLMFELSMWRCNDEVRARAQELHSQSKSD--AKHYI 353

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+P  EPYRviLGdvRDKLYntRE a  LLA G s+++Ee  +t++
  gi|2499465   354 EFWKQIPLSEPYRVILGDVRDKLYNTREHAHKLLANGSSDVPEESTFTHI 403

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    ++FLEPLELCYksLC  GD+ iADGsLLD++RqvstFGLsLvKLDiRqEs
  gi|2499465   404 DQFLEPLELCYKSLCASGDQPIADGSLLDFMRQVSTFGLSLVKLDIRQES 453

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|2499465   454 DRHTEVMDAITTHLGIGSYRSWSEEKRQEWLLSELRGKRPLFGSDLPMSY 503

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+D +++frvLAELP DsFGaYiismataPsDvLAvELLqRECg+k++L
  gi|2499465   504 EVADAIGTFRVLAELPNDSFGAYIISMATAPSDVLAVELLQRECGIKKPL 553

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                   RlsAAWqLYk qE +i+vAK+yGvKL++FHGRGGtvGRGGGPtHLA+Lsq
  gi|2499465   604 RLSAAWQLYKVQEQLIQVAKEYGVKLTMFHGRGGTVGRGGGPTHLALLSQ 653

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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  gi|2499465   654 PPDTIHGSLRVTIQGEVIEQSFGEEHLCFRTLERYTAATLEHGIDPPTSP 703

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                   kPEWR Lm+emAv+ t EYRsvv++EPRFvEYFR+AtPElEYG+mniGsR
  gi|2499465   704 KPEWRALMDEMAVITTKEYRSVVLQEPRFVEYFRSATPELEYGRMNIGSR 753

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKRkP+GGie+LRAiPWiF+WtqtRFHLPvWLG GAAFKh i+KDiKnl
  gi|2499465   754 PAKRKPGGGIETLRAIPWIFSWTQTRFHLPVWLGCGAAFKHVIEKDIKNL 803

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                    +Lk+mY++W FFRvt+DLlEmvFAKGDPGiAaLyDkLLv +eLkPFG++
  gi|2499465   804 AMLKDMYNQWSFFRVTIDLLEMVFAKGDPGIAALYDKLLVKDELKPFGEN 853

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR  Y E +++LL+iAGHkD L+ DPYLKq lRLRd+Y ttLnvfq YtL
  gi|2499465   854 LRKSYLEAQKFLLEIAGHKDPLDADPYLKQILRLRDPYTTTLNVFQVYTL 903

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPs++vt+rPhlsKE  +     a++LvkLnpt++++PGLEDtLiL
  gi|2499465   904 KRIRDPSFHVTVRPHLSKEMDANS--LAADLVKLNPTSEYPPGLEDTLIL 951

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                   tmKGiAAGmqntG
  gi|2499465   952 TMKGIAAGMQNTG    964

gi|22347639|gb|AAM95946.1|: domain 1 of 1, from 11 to 954: score 2399.6, E = 0
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                      s+DA LRlL+PGKvs+d+kL+eYDA+LlD+FL+i+qDLHGe ++E v
  gi|2234763    11    SMDAHLRLLAPGKVSDDDKLVEYDAMLLDRFLEIVQDLHGEGIRETV 57

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qECYElsAeYE  +D+kKL+ELG +LtsL+P+D+i+vA++++HmLnLAnL
  gi|2234763    58 QECYELSAEYERTHDSKKLDELGNVLTSLEPGDSIVVASSFSHMLNLANL 107

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++A RRR k kk G F        Es +EEt+K+L+  l K+PeE+
  gi|2234763   108 AEEVQIAQRRRTKPKK-GYF--------ESNLEETFKRLIGELKKTPEEI 148

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  gi|2234763   149 FDALKNQTVDLVFTAHPTQSIRRSLLQKHGRIRNSLTQLCAKDITPDEKQ 198

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                   ELDEAL REiqAAFRtDEiRR+qP PqDEmRaGmsY+HEt+WkGvPKFLR
  gi|2234763   199 ELDEALQREIQAAFRTDEIRRTQPQPQDEMRAGMSYFHETIWKGVPKFLR 248

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                   RvDtA K iGinERlPY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2234763   249 RVDTAPKSIGINERLPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 297

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|2234763   298 ARLMAANLYFSQIEDLMFELSMWRCSDELRLRADELHRSSKKD--AKHYI 345

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWK+vPP EPYRviLGdvRDKLYntRERaR LL  Gis+i+EeA  t+v
  gi|2234763   346 EFWKKVPPSEPYRVILGDVRDKLYNTRERARQLLSSGISDIPEEATLTNV 395

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   E+FLEPLELCY+sLC CGD  iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|2234763   396 EQFLEPLELCYRSLCACGDSPIADGSLLDFLRQVSTFGLSLVRLDIRQES 445
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                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|2234763   446 DRHTDVLDAITRHLQIGSYREWPEEKRQEWLLSELRGKRPLFGSDLPKTE 495

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvl+af v+AELP+D FGaYiismata sDvLAvELLqRE  vk++L
  gi|2234763   496 EIADVLGAFDVIAELPSDGFGAYIISMATATSDVLAVELLQRESRVKKPL 545

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAave+LFsiDWY+nri+GKqevm+GYsDsGK AG
  gi|2234763   546 RVVPLFEKLADLEAAPAAVERLFSIDWYRNRINGKQEVMIGYSDSGKGAG 595

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2234763   596 RLSAAWQLYKAQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 645

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti GslRvtvqGEviE+sFGEEnLCF++LqR+t  tLEHGm+ P+sP
  gi|2234763   646 PPDTILGSLRVTVQGEVIEQSFGEENLCFKTLQRYTVGTLEHGMQLPISP 695

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emA+vAtEEYRsvv+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|2234763   696 KPEWRALMDEMAIVATEEYRSVVFKEPRFVEYFRLATPELEYGRMNIGSR 745

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                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD Knl
  gi|2234763   746 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIKKDPKNL 795

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                      L+Em ++WPFFRvt+DL+EmvF KG  GiAaLyDkLLv+ +L PFG++
  gi|2234763   796 LILREMHNDWPFFRVTIDLIEMVFSKGNSGIAALYDKLLVSPDLLPFGEQ 845

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+EtkdlLL++A Hk lLEGDPYLKqrlRLR +YittLnv+qAYtL
  gi|2234763   846 LRANYEETKDLLLQVADHKTLLEGDPYLKQRLRLRVPYITTLNVYQAYTL 895

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiR+P+y v   Ph+s +  + n k a+eLvkLnpt+++aPGLEDtLiL
  gi|2234763   896 KRIREPDYAV---PHISNDKLNSN-KTAAELVKLNPTSEYAPGLEDTLIL 941

                    tmKGiAAGmqntG<-*
                    tmKGiAAG+qntG
  gi|2234763   942 TMKGIAAGLQNTG    954

gi|149364113|gb|ABR24265.1|: domain 1 of 1, from 11 to 964: score 2397.4, E = 0
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                       siDAqLRlL+P Kvsed+kL+eYDALLlD+FLDiL  LHG  ++E v
  gi|1493641    11    SIDAQLRLLAPKKVSEDDKLVEYDALLLDRFLDILESLHGSGIRETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YE +AeYE  +DtkKLeELG  +tsLd +D+i++Ak+++ mLnLAnL
  gi|1493641    58 QELYEHAAEYERTHDTKKLEELGNLITSLDAGDSIVIAKSFSQMLNLANL 107

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  gi|1493641   108 AEEVQLAYRRRIKKTKKGDFADESSAITESDFEETLRRLVDLK-KSPEEI 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|1493641   157 FATLKNQTVDLVLTAHLTQSVRRSLLQKHGRIRDCLPQLYAKDITPDDKQ 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|1493641   207 ELDEALQREIQAAFRTGEIRRVQPTPQDEMRMGMSYFHETIWKGVPKFLR 256

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                    RvDtALKniGinER+PY+vPLi+FssWmGGDRDG nPRvtPEvtRDv LL
  gi|1493641   257 RVDTALKNIGINERVPYNVPLIQFSSWMGGDRDG-NPRVTPEVTRDVVLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWKq+P  EPYRviLGdvRDKLYntRE a  LLA G s+++Ee  +t++
  gi|1493641   354 EFWKQIPLSEPYRVILGDVRDKLYNTREHAHQLLANGASDVPEESTFTHI 403

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   ++FLEPLELCYksLC  GD+ iADGsLLD++RqvstFGLsLvKLDiRqEs
  gi|1493641   404 DQFLEPLELCYKSLCASGDQPIADGSLLDFMRQVSTFGLSLVKLDIRQES 453

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +R+t+v+DAittHL+iGsYR+WsEeKRqEWLl+EL+GKRPL+gsDLP+
  gi|1493641   454 DRHTEVMDAITTHLGIGSYRSWSEEKRQEWLLSELRGKRPLFGSDLPMSY 503

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+D +++frvLAELP DsFGaYiismataPsDvLAvELLqRECg+k++L
  gi|1493641   504 EVADAIGTFRVLAELPNDSFGAYIISMATAPSDVLAVELLQRECGIKKPL 553

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  gi|1493641   554 RVVPLFEKLADLQSAAASMTRLFSIDWYKNRINGTQEVMIGYSDSGKDAG 603

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
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  gi|1493641   604 RLSAAWQLYKVQEQLIQVAKEYGVKLTMFHGRGGTVGRGGGPTQLALLSQ 653

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvt+qGEviE+sFGEE+LCFr+L R+tAAtLEHGm+PP sP
  gi|1493641   654 PPDTIHGSLRVTIQGEVIEQSFGEEHLCFRTLERYTAATLEHGMHPPTSP 703

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emAv+ t EYRsvv++EPRFvEYFR+AtPEl YG+mniGsR
  gi|1493641   704 KPEWRALMDEMAVITTKEYRSVVLQEPRFVEYFRSATPELGYGRMNIGSR 753

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKRkP+GGie+LRAiPWiF+WtqtRF LPvWLG GAAFKh i+KDiKnl
  gi|1493641   754 PAKRKPGGGIETLRAIPWIFSWTQTRFQLPVWLGCGAAFKHVIEKDIKNL 803

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +Lk+mY++W FFRvt+DLlEmvFAKGDPGiAaLyDkLLv +eLkPFG++
  gi|1493641   804 AMLKDMYNQWSFFRVTIDLLEMVFAKGDPGIAALYDKLLVKDELKPFGEN 853

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR  Y E +++LL+iAGHkD L+ DPYLKq lRLRd+Y ttLnvfq YtL
  gi|1493641   854 LRKSYLEAQKFLLEIAGHKDPLDADPYLKQILRLRDPYTTTLNVFQVYTL 903

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPs++vt+rPhlsKE  +     a+eLvkLnpt++++PGLEDtLiL
  gi|1493641   904 KRIRDPSFHVTVRPHLSKEMDANS--LAAELVKLNPTSEYPPGLEDTLIL 951

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|1493641   952 TMKGIAAGMQNTG    964

gi|2145481|emb|CAA62747.1|: domain 1 of 1, from 1 to 944: score 2396.7, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      siDAqLRlLvP Kvsed+kLieYDALL+D+FLDiLqDLHGe+++E v
  gi|2145481     1    SIDAQLRLLVPTKVSEDDKLIEYDALLMDRFLDILQDLHGEEIRETV 47

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qECYEls eYEGK Dt KLeELG +LtsLd +D+i+vA a++HmLnLAnL
  gi|2145481    48 QECYELSGEYEGKFDTAKLEELGGVLTSLDAGDSIVVA-ALSHMLNLANL 96

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++AyRRRik kk+GDFaDE sAttEsDiEEt+K+Lv +l +sP+Ev
  gi|2145481    97 AEEVQIAYRRRIKHKKKGDFADENSATTESDIEETFKRLVNQLGRSPQEV 146

                   FeALKnqsvDLvltAHPt.qsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   F+ALKnq++DLvltAHPt+qsv  sLLqK++RiRnCL+qL+AKD+t+++K
  gi|2145481   147 FDALKNQTIDLVLTAHPThQSV--SLLQKHGRIRNCLSQLYAKDITPDEK 194
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                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFL
  gi|2145481   195 QELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFL 244

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    RRvDtALK iGinERlPY++PLi+FssWmGGDRDG nPRvtPEvtRDvCL
  gi|2145481   245 RRVDTALKSIGINERLPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCL 293

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    LaRmmA+nlY+sq+EDLmFElsmWRC dELR RA  l+  a+rd   K+Y
  gi|2145481   294 LARMMATNLYYSQIEDLMFELSMWRCSDELRQRALQLHNSAKRD--AKHY 341

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                    iEFWKqvPP+EP+RviLGdvRDKLYntRER+R LLA G+s+++EeA  t
  gi|2145481   342 IEFWKQVPPNEPFRVILGDVRDKLYNTRERTRQLLANGFSDVPEEAL-TS 390

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    v++ LEPLELCY+sLC  GD+ iADGsLLD++RqvstFGL LvKLDiRqE
  gi|2145481   391 VDQLLEPLELCYRSLCSTGDQPIADGSLLDFMRQVSTFGLTLVKLDIRQE 440

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s+R+tDv+DAit+HL++GsY+eW+E+KRqEWLlaEL+GKRPL+g+DLP t
  gi|2145481   441 SDRHTDVIDAITRHLGLGSYKEWPEDKRQEWLLAELRGKRPLFGPDLPTT 490

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    +E+++vld+f+v+AELP D FGaYiismataPsDvL vELLqREC vk++
  gi|2145481   491 DEIREVLDTFHVVAELPPDNFGAYIISMATAPSDVLVVELLQRECRVKKP 540

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    LrvvPLFEkLADLe  PAa+++LFsiDWY+nridGKqevm GYsDsGKDA
  gi|2145481   541 LRVVPLFEKLADLENRPAALARLFSIDWYRNRIDGKQEVMXGYSDSGKDA 590

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    GRlsAAWqLYkAqEE+iKvAK++G+KL++FHGRGGtvGRGGGPtHLAiLs
  gi|2145481   591 GRLSAAWQLYKAQEELIKVAKQFGIKLTMFHGRGGTVGRGGGPTHLAILS 640

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPPDti+GslRvtvqGEviE+ FGEE+LCFr+LqRFtAAtLEHGm+PP++
  gi|2145481   641 QPPDTIHGSLRVTVQGEVIEQCFGEEHLCFRTLQRFTAATLEHGMHPPIA 690

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    PkPEWR+Lm+emAvvAt EYRs v+   RFvEYFR+AtPElEYG+mniGs
  gi|2145481   691 PKPEWRQLMDEMAVVATQEYRSYVFHNKRFVEYFRSATPELEYGRMNIGS 740

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RP+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFK  i+KDi+n
  gi|2145481   741 RPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKSVIEKDIRN 790

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l  L+ mY+eWPFFRvt+DL+EmvFAK  P iAaLyDkLLv+  L+ FG+
  gi|2145481   791 LHTLQQMYNEWPFFRVTIDLVEMVFAK-HPEIAALYDKLLVSSVLWAFGE 839

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR +YvEtk lLL++AGHk++LEGDPYLKqrlRLRdsYittLn +qAYt
  gi|2145481   840 QLRKNYVETKTLLLQVAGHKEVLEGDPYLKQRLRLRDSYITTLNALQAYT 889

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    LKRiRDPsy+vtlrPhlsKE    +   a+eLvkLnpt+++aPGLEDtLi
  gi|2145481   890 LKRIRDPSYHVTLRPHLSKESSTKP---AAELVKLNPTSEYAPGLEDTLI 936

                    LtmKGiAAGmqntG<-*
                    LtmKGiAA
  gi|2145481   937 LTMKGIAA------    944

gi|222622510|gb|EEE56642.1|: domain 1 of 1, from 15 to 937: score 2384.8, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLRlL+PGKvsed+kL+eYDALL+D+FLDiLqDLHG+ L+E+v
  gi|2226225    15    SIDAQLRLLAPGKVSEDDKLVEYDALLVDRFLDILQDLHGPHLREFV 61

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYElsAeYE  +D  +L+ELG kLt  + +D+i++
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gi|2226225    62 QECYELSAEYENDRDEARLDELGRKLTKPAAGDSIVI------------ 98

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                       A+RRRik+k+ GDFaDEas  tEsDiEEtlK+Lv +l Ks eEv
gi|2226225    99 ------AHRRRIKLKR-GDFADEASGPTESDIEETLKRLVTQLGKSREEV 141

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                 F+ALKnq+vDLv+t  PtqsvRRsLLqK++RiRnCL qL+AKD+t +DK+
gi|2226225   142 FDALKNQTVDLVFTGNPTQSVRRSLLQKHGRIRNCLRQLYAKDITADDKQ 191

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                 ELDEAL RE            ++PtPqDEmRa msY+HEt+WkGvPKFLR
gi|2226225   192 ELDEALQRE------------TPPTPQDEMRARMSYFHETIWKGVPKFLR 229

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                 R+DtALKniGinERlPY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
gi|2226225   230 RIDTALKNIGINERLPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 278

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                 aRmmAanlY+sq+EDLmFElsmWRC dELR+RA++l+  +++    K+Yi
gi|2226225   279 ARMMAANLYFSQIEDLMFELSMWRCSDELRIRADDLHCSSRKA--AKHYI 326

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                 EFWKq+PP+EPYRviLG vRDKLY tRER+RHLL tG+sei+EeA +t+v
gi|2226225   327 EFWKQIPPNEPYRVILGGVRDKLYYTRERTRHLLTTGVSEIPEEATFTNV 376

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                 EeFLEPLELCY+sLC CGDk iADGsLLD+LRqvstFGL+LvKLDiRqEs
gi|2226225   377 EEFLEPLELCYRSLCACGDKPIADGSLLDFLRQVSTFGLALVKLDIRQES 426

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                 +R+tDvlDAitt L+iGsY eWsEeKRq+WLl+EL+GKRPL+g+DLP+tE
gi|2226225   427 DRHTDVLDAITTYLGIGSYAEWSEEKRQDWLLSELRGKRPLFGPDLPQTE 476

                 EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                 E++Dvl++f+vLAELP D+FGaYiismataPsDvLAvELLqREC++kq+L
gi|2226225   477 EIADVLGTFHVLAELPADCFGAYIISMATAPSDVLAVELLQRECHIKQPL 526

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                 rvvPLFEkLADLeAAPAav++LFsiDWY+nri+GKqevm+GYsDsGKDAG
gi|2226225   527 RVVPLFEKLADLEAAPAAVARLFSIDWYMNRINGKQEVMIGYSDSGKDAG 576

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 RlsAAWq+YkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGP HLAiLsq
gi|2226225   577 RLSAAWQMYKAQEELVKVAKHYGVKLTMFHGRGGTVGRGGGPSHLAILSQ 626

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                 PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
gi|2226225   627 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPISP 676

                 kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                 kPEWR Lm+emAvvAt EYRs+v+KEPRFvEYFR+AtPE+EYG+mniGsR
gi|2226225   677 KPEWRALMDEMAVVATKEYRSIVFKEPRFVEYFRSATPETEYGRMNIGSR 726

                 PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                 P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++KDi+n+
gi|2226225   727 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHIMQKDIRNI 776

                 qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva +L+ FG++
gi|2226225   777 HTLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVAGDLQSFGEQ 826

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                 LR++++Etk+lLL++AGHkD+LEGDPYLKqrlRLR+sYittLnv+qAYtL
gi|2226225   827 LRNNFEETKQLLLQVAGHKDILEGDPYLKQRLRLRESYITTLNVCQAYTL 876

                 KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                 KRiRDPs++v  +P lsKE+ d n  +++eLv+Ln ++++aPGLEDtLiL
gi|2226225   877 KRIRDPSFEVMSQPALSKEFVDSN--QPAELVQLNAASEYAPGLEDTLIL 924

                 tmKGiAAGmqntG<-*
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                  tmKGiAAGmqntG
  gi|2226225   925 TMKGIAAGMQNTG    937

gi|108782494|gb|ABG20459.1|: domain 1 of 1, from 11 to 968: score 2382.3, E = 0
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                     siDAqLR+L+PGKvsed+kL+eYDALLlD+FLD +q LHGe+++E v
  gi|1087824    11    SIDAQLRALAPGKVSEDDKLVEYDALLLDRFLDSVQALHGEEIRETV 57

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                  q  YE +AeYE  +DtkKLeELG  L  Ld +D+i+vAk+++HmL LAnL
  gi|1087824    58 QGLYEHAAEYERTRDTKKLEELGDMLIRLDAGDSIVVAKSFSHMLILANL 107

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AEEv++AyRRRik +k+GDFaDE+sA tEsD+EEtl++Lv+ l KsPeE+
  gi|1087824   108 AEEVQIAYRRRIKNLKKGDFADESSAITESDLEETLRRLVVDLKKSPEEI 157

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                  Fe LKnq+v+LvltAHPtqsvRRsLLqK++RiR CL+qL+AKD+t++DK+
  gi|1087824   158 FETLKNQTVELVLTAHPTQSVRRSLLQKHGRIRDCLTQLYAKDITPDDKQ 207

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                  ELDEAL REiqAAFRtDEiRR qPtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|1087824   208 ELDEALQREIQAAFRTDEIRRMQPTPQDEMRAGMSYFHETIWKGVPKFLR 257

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                  R DtALKniGinER+PY++PLi+Fss mGGDRDG nPRvtPEvtRDv LL
  gi|1087824   258 RLDTALKNIGINERVPYNAPLIQFSSSMGGDRDG-NPRVTPEVTRDVVLL 306

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                  aRmmAan+Y+sq+ DLmFElsmWRCndEL +RA E+++ +++d   K+Yi
  gi|1087824   307 ARMMAANMYFSQIQDLMFELSMWRCNDELNARAHEIHKLSKSD--AKHYI 354

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                  EFWK +PP EPYRv+L dvRDKLY tRE aR LL  G s+++ e  +t+v
  gi|1087824   355 EFWKPIPPSEPYRVVLADVRDKLYHTREHARQLLSNGTSDVPLESTFTHV 404

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                  ++FLEPLELCYksLC+CGD+ iADGsLLD++RqvstFGL LvKLDiRqEs
  gi|1087824   405 DQFLEPLELCYKSLCDCGDRPIADGSLLDFMRQVSTFGLCLVKLDIRQES 454

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  eR+tDv+DAit+HL++GsYReWsEeKRqEWLl+EL+G RPL+gsDLPktE
  gi|1087824   455 ERHTDVMDAITKHLGVGSYREWSEEKRQEWLLSELRGTRPLFGSDLPKTE 504

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++ vld+f+v+ ELP+D FGaYiismataPsDvLAvELLqREC+++++L
  gi|1087824   505 EIAAVLDTFHVISELPSDGFGAYIISMATAPSDVLAVELLQRECHIQNPL 554

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLe APA++ +LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|1087824   555 RVVPLFEKLADLENAPASITRLFSIDWYRNRINGKQEVMIGYSDSGKDAG 604

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+iK+AK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1087824   605 RLSAAWQLYKAQEELIKIAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 654

                  PPDtinGslRvtv...qGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                  PP+  + s+   v + +   iE+sFGEE+LCFr+LqRFtAAtLEHGm+PP
  gi|1087824   655 PPE--HDSMDHFVlpfKVKCIEQSFGEEHLCFRTLQRFTAATLEHGMHPP 702

                  vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                  +sPkPEWR L++emAv At EYRs+v+K PRFvEYFRlAtPElEYG+mni
  gi|1087824   703 ISPKPEWRTLLDEMAVAATKEYRSIVLKKPRFVEYFRLATPELEYGRMNI 752

                  GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                  GsRP+KRkP+GGiesLRAiPWiF+WtqtRFHLP  LG GAAFKh i+KDi
  gi|1087824   753 GSRPSKRKPGGGIESLRAIPWIFSWTQTRFHLPGGLGCGAAFKHVIEKDI 802

                  KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                  Knl +L+ mY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+EeL PF
  gi|1087824   803 KNLAMLEQMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEELCPF 852
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                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G++LR +Y+Etk++  +iAGHk++LEGDP L+qrlRLRd+YittLnv+qA
  gi|1087824   853 GEQLRSDYEETKNFFFQIAGHKEILEGDPHLRQRLRLRDPYITTLNVCQA 902

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                    YtLKRiRDP+y+vt+rPh+sK+y d   k+a+eLvkLnp++++aPGLEDt
  gi|1087824   903 YTLKRIRDPNYHVTVRPHISKDYMDSTDKPAAELVKLNPSSEYAPGLEDT 952

                    LiLtmKGiAAGmqntG<-*
                    LiLtmKGiAAGmqntG
  gi|1087824   953 LILTMKGIAAGMQNTG    968

gi|1870190|emb|CAA60626.1|: domain 1 of 1, from 4 to 958: score 2377.7, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLRlL+P Kvsed+kL+eY  LLlD+FLDiLqDLHGe L+E v
  gi|1870190     4    SIDAQLRLLAPAKVSEDDKLLEYVSLLLDRFLDILQDLHGEVLRETV 50

                    qECYElsAeYEGKkDtkKLe.ELGakLtsLdPaDailvAkailHmLnLAn
                    qE YEls eYE K+D+kK +  LG  L  LdP+ +i++A++++HmLnLAn
  gi|1870190    51 QELYELSSEYESKHDPKKFGmNLGILLITLDPGNSIVIASSFSHMLNLAN 100

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAEEv++A+RRRik+kk GDFaDEasAttEsD EEtlK+Lv kl K+P+E
  gi|1870190   101 LAEEVQIAFRRRIKLKK-GDFADEASATTESDFEETLKRLVGKLKKTPQE 149

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +F+ALK q+vDLvltAHPtqsvRRsLLqK++RiRnCL+qL+AKD+t++DK
  gi|1870190   150 IFDALKSQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLTQLYAKDITPDDK 199

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +ELDEALHREiqAAFRtDEiRR +PtPqDEmRaGmsY+HEt+WkGvP+FL
  gi|1870190   200 QELDEALHREIQAAFRTDEIRRIPPTPQDEMRAGMSYFHETIWKGVPQFL 249

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    RRvDtALKn+GinERlPY++PLi+Fs WmGGDRDG nPRvtPEvtRDvCL
  gi|1870190   250 RRVDTALKNLGINERLPYNAPLIQFSPWMGGDRDG-NPRVTPEVTRDVCL 298

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    LaRmmAanlY+sq+EDLmFElsmW C dELR RA+El   +++d   K+Y
  gi|1870190   299 LARMMAANLYFSQIEDLMFELSMWPCSDELRLRADELNVSSKKD--AKHY 346

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                    iEFWK+vPP+EPYRviLGdvRDKLY tRERaR +L +G+s+i+E A +t+
  gi|1870190   347 IEFWKKVPPNEPYRVILGDVRDKLYHTRERARQILSHGVSDIPE-ATFTN 395

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    vE+FLEPLELCY+sLC C  + iADGsLLD+LRqvstFGLsLvKLDiRqE
  gi|1870190   396 VEQFLEPLELCYRSLCACAHRPIADGSLLDFLRQVSTFGLSLVKLDIRQE 445

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    seR+tDv+DAit+H+eiGsYReWsEe+Rq WLl+EL  KRPL+g+DLP+t
  gi|1870190   446 SERHTDVMDAITRHIEIGSYREWSEEQRQQWLLSELAEKRPLFGPDLPRT 495

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    EE++Dvld+f+v+AELP+D FGaYiismat+ sDvLAvELLqRE  v ++
  gi|1870190   496 EEIADVLDTFQVIAELPSDGFGAYIISMATSSSDVLAVELLQREFRVPKP 545

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    LrvvPLFEkLADLeAAPAav +LFsiDWY+ ri+GKqevm+GYsDsGKDA
  gi|1870190   546 LRVVPLFEKLADLEAAPAAVSRLFSIDWYRDRINGKQEVMIGYSDSGKDA 595

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    GR      +Yk qEE+++vAK++GvKL++FHGRGGtvGRGGGPtHLAiLs
  gi|1870190   596 GRTFCCLAVYKTQEELVQVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILS 645

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPPDtinGslRvtvqGEviE+ FGEE LCFr+LqR+tAAtLEHGmnP  s
  gi|1870190   646 QPPDTINGSLRVTVQGEVIEQCFGEERLCFRTLQRYTAATLEHGMNPYFS 695

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
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                     kPEWR L++emAv+At EYR +v++EPRFvEYFRlAtPElEYG+mniGs
  gi|1870190   696 -KPEWRSLLDEMAVIATNEYRWIVFQEPRFVEYFRLATPELEYGRMNIGS 744

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RP+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i KD Kn
  gi|1870190   745 RPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVISKDNKN 794

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l  L+EmY+ WPFFRvt+DL+EmvF KG PGiA+LyDkLLv+ eL PFG
  gi|1870190   795 LHTLREMYNGWPFFRVTIDLIEMVFTKGNPGIASLYDKLLVSSELLPFGA 844

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLK.qrlRLRdsYittLnvfqAY
                    +LR++Y Etk lLL +AGHkDlLEGDPYLK+qrlRLRd+YittLnv+qAY
  gi|1870190   845 QLRENYGETKRLLLLVAGHKDLLEGDPYLKdQRLRLRDPYITTLNVCQAY 894

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    tLKRiR+P y+vt rPhl KE  dE  k a+eLvkLnpt+++ PGLEDtL
  gi|1870190   895 TLKRIREPGYHVTARPHLLKE-TDESIKSAAELVKLNPTSEYGPGLEDTL 943

                    iLtmKGiAAGmqntG<-*
                    i+tmKGiAAG+qntG
  gi|1870190   944 IITMKGIAAGLQNTG    958

gi|4559332|gb|AAD22994.1|: domain 1 of 1, from 11 to 941: score 2371.1, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLRlL+PGKvsed+kLieYDALLlD+FLDiLqDLHGed++E+v
  gi|4559332    11    SIDAQLRLLAPGKVSEDDKLIEYDALLLDRFLDILQDLHGEDVREFV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYE++A+Y+G + t+KLeELG  LtsLdP+D+i+v k+++ mL LAnL
  gi|4559332    58 QECYEVAADYDGNRNTEKLEELGNMLTSLDPGDSIVVTKSFSNMLSLANL 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++AyRRRikk+k+GDFaDEasAttEsDiEEtlK+L  +  K+PeEv
  gi|4559332   108 AEEVQIAYRRRIKKLKKGDFADEASATTESDIEETLKRLLQLN-KTPEEV 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+vDLvltAHPtqsvRRsLLqK +RiR CL+qL+AKD+t++DK+
  gi|4559332   157 FDALKNQTVDLVLTAHPTQSVRRSLLQKFGRIRDCLTQLYAKDITPDDKQ 206

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|4559332   207 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 256

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|4559332   257 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 305

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq+EDLmFE+smWRCn+ELRvRAE  +r a+rd   K+Yi
  gi|4559332   306 ARMMAANLYFSQIEDLMFEMSMWRCNEELRVRAER-QRCAKRD--AKHYI 352

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+P +EPYR iLGdvRDKLYntRERaR LL  G+s+++E+Av+t v
  gi|4559332   353 EFWKQIPANEPYRAILGDVRDKLYNTRERARQLLSSGVSDVPEDAVFTSV 402

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    ++FLEPLELCY+sLC+CGD+ iADGsLLD+LRqvstFGL+LvKLDiRqEs
  gi|4559332   403 DQFLEPLELCYRSLCDCGDRPIADGSLLDFLRQVSTFGLALVKLDIRQES 452

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+ DvlDAittHL+iGsY+eWsE+KRqEWLl+EL+GKRPL+g+DLPktE
  gi|4559332   453 ERHSDVLDAITTHLGIGSYKEWSEDKRQEWLLSELSGKRPLFGPDLPKTE 502

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvld+f+v+ ELP+DsFGaYiismataPsDvLAvELLqRECg+  +L
  gi|4559332   503 EVADVLDTFKVISELPSDSFGAYIISMATAPSDVLAVELLQRECGITDPL 552

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLe APAav++LFsi+WY+nri+GKqevm+GYsDsGKDAG
  gi|4559332   553 RVVPLFEKLADLESAPAAVARLFSIEWYRNRINGKQEVMIGYSDSGKDAG 602
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                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYk qEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|4559332   603 RLSAAWQLYKTQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 652

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+G lRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|4559332   653 PPDTIHGQLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 702

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emA++AtEEYRsvv+KEPRFvEYFRl        + n   R
  gi|4559332   703 KPEWRVLMDEMAIIATEEYRSVVFKEPRFVEYFRL--------RRN---R 741

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                     a   P                     HLPvWLG+G AFK  i+KD+Knl
  gi|4559332   742 VAACNPVD-----------LCVDSDEVHLPVWLGFGGAFKRVIQKDSKNL 780

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +LkEmY++WPFFRvt+DL+EmvFAKGDPGiAaLyD+LLv+EeL+PFG++
  gi|4559332   781 NMLKEMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDRLLVSEELQPFGEQ 830

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Et+ lLL++AGHkD+LEGDPYL+qrl LRd+YittLnv+qAYtL
  gi|4559332   831 LRVNYQETRRLLLQVAGHKDILEGDPYLRQRLQLRDPYITTLNVCQAYTL 880

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    K iRDPs++v +rPhlsK+y +    +a+eLvkLnp +++aPGLEDt+iL
  gi|4559332   881 KQIRDPSFHVKVRPHLSKDYMESS--PAAELVKLNPKSEYAPGLEDTVIL 928

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|4559332   929 TMKGIAAGMQNTG    941

gi|115440043|ref|NP_001044301.1|: domain 1 of 1, from 11 to 924: score 2368.5, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLR+L+P K sed+kL+eYDALLlD+FLDiLqDLHGed++E v
  gi|1154400    11    SIDAQLRILAPKKLSEDDKLVEYDALLLDRFLDILQDLHGEDIRETV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qECYEl+AeYE K
  gi|1154400    58 QECYELAAEYESK----------------------------------- 70

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                         +AyRRRik+kk GDFaDE sAttEs  EEtlK+Lv  l KsP Ev
  gi|1154400    71 -----IAYRRRIKLKK-GDFADENSATTESNFEETLKRLVGELKKSPHEV 114

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq++DLvltAHPtqsvRRsLLqK++RiR CL++L+AKD+t+++K+
  gi|1154400   115 FDALKNQTIDLVLTAHPTQSVRRSLLQKHGRIRSCLTKLYAKDITPDEKQ 164

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRRa+PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|1154400   165 ELDEALKREIQAAFRTDEIRRAPPTPQDEMRAGMSYFHETIWKGVPKFLR 214

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1154400   215 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 263

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+ q+EDLmFElsmWRC dELRv+A+ l+r a+++  +K+Yi
  gi|1154400   264 ARMMAANLYYAQIEDLMFELSMWRCSDELRVKADQLHRCAKKN-TTKHYI 312

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKqvPP EPYRviL +vRDKLYntRERaRHLLA G+sei++eA +t+v
  gi|1154400   313 EFWKQVPPSEPYRVILSNVRDKLYNTRERARHLLASGFSEIPDEATFTDV 362

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC CGD  iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|1154400   363 EQFLEPLELCYRSLCACGDNSIADGSLLDFLRQVSTFGLSLVRLDIRQES 412

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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                    +R+tDv+DAit+ L+iGsYReWsEeKRqEWLl+EL GKRPL+g+DLP+t+
  gi|1154400   413 DRHTDVMDAITQYLGIGSYREWSEEKRQEWLLSELNGKRPLFGPDLPQTD 462

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++D ld+f+v+AELP DsFGaY+ismataPsDvLAvELLqREC+vk++L
  gi|1154400   463 EIADALDTFHVIAELPYDSFGAYVISMATAPSDVLAVELLQRECHVKKPL 512

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAa+++LFs+DWY+nridGKqevm+GYsDsGKDAG
  gi|1154400   513 RVVPLFEKLADLEAAPAALARLFSVDWYRNRIDGKQEVMIGYSDSGKDAG 562

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    R+sAAW LYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1154400   563 RFSAAWELYKAQEELIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 612

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFt AtLEHGm+PP+sP
  gi|1154400   613 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTSATLEHGMHPPISP 662

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emA vAt EYRs+v++E RFvEYFRlAtPElEYG+mniGsR
  gi|1154400   663 KPEWRALMDEMAAVATKEYRSIVFQEARFVEYFRLATPELEYGRMNIGSR 712

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|1154400   713 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLQKDIRNL 762

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+PFG +
  gi|1154400   763 QILQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWPFGAR 812

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Etk+lLL++AGHkDlLEGDPYL+qrlR+RdsYit Lnv+qA tL
  gi|1154400   813 LRANYEETKQLLLQVAGHKDLLEGDPYLRQRLRIRDSYITALNVCQACTL 862

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP ++v +r hlsK+  d   k+a+eLvkLn t+++ PGLEDtLiL
  gi|1154400   863 KRIRDPGFHVSPRAHLSKDIMDSG-KPAAELVKLNTTSEYGPGLEDTLIL 911

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|1154400   912 TMKGIAAGMQNTG    924

gi|115435200|ref|NP_001042358.1|: domain 1 of 1, from 56 to 1014: score 2286.8, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDA LR L+P Kvs d++L++Y+ LL+ +FLDiL DLHG d + +v
  gi|1154352    56    SIDARLRQLAPEKVSADDRLVDYETLLVARFLDILEDLHGGDFRQVV 102

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     +C  ls eY    D+ +L+ELG  LtsLd +Dai+vA++++HmLnLAnL
  gi|1154352   103 EDCLRLSGEYQSEGDPARLGELGGLLTSLDVGDAIMVASSFSHMLNLANL 152

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEE+++ yR++ +  + GDF DEasA tEsDi+Et+++Lv  l KsP Ev
  gi|1154352   153 AEEIQMVYRKKAEASRRGDFVDEASAPTESDIDETFQRLVRGLGKSPREV 202

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+AL+ q++DLvltAHPtqsvRRsLLqK+a iR CL+qL    +  ++ +
  gi|1154352   203 FDALRSQTIDLVLTAHPTQSVRRSLLQKHASIRSCLTQLCGEGISDNEEQ 252

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    E+DEAL REi AAF+tDEiRR++PtPqDEmRaGmsY+H+t+W+GvPKFLR
  gi|1154352   253 EIDEALQREILAAFKTDEIRRTPPTPQDEMRAGMSYFHDTIWNGVPKFLR 302

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGi ERlPY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1154352   303 RVDTALKNIGIDERLPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 351

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAan+Y+s++ DLmFElsmWRCndELR+RA El+r + r+   KyYi
  gi|1154352   352 ARMMAANMYFSKMADLMFELSMWRCNDELRARANELHRKSSRK-YAKYYI 400
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                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK++ P EPYR+iLGdvRDKLYnt ERaR +L +Gis i+E+  yt+v
  gi|1154352   401 EFWKKISPGEPYRIILGDVRDKLYNTCERARQILSKGISSIPEDQTYTNV 450

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC+CGDk iADG LLDl+RqvstFGLsLvKLDiRqEs
  gi|1154352   451 EQFLEPLELCYRSLCDCGDKLIADGRLLDLMRQVSTFGLSLVKLDIRQES 500

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+tD +DAittHL+iGsYReW+Ee+RqEWL++EL+G+RPL+g+DLP+ E
  gi|1154352   501 ERHTDAMDAITTHLGIGSYREWPEERRQEWLVSELRGRRPLFGPDLPQSE 550

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl+afrv+AELP DsFGaYiismataPsDvLAvELLqRECgvk++L
  gi|1154352   551 EVADVLGAFRVIAELPADSFGAYIISMATAPSDVLAVELLQRECGVKKPL 600

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADL+ A A++e LFs+DWY+ ridGKqe+m+GYsDsGKDAG
  gi|1154352   601 RVVPLFEKLADLQQARATMELLFSVDWYKERIDGKQEIMIGYSDSGKDAG 650

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEEi+ vA ++GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1154352   651 RLSAAWQLYKAQEEIVGVAERHGVKLTIFHGRGGTVGRGGGPSHLAILSQ 700

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP t+nGslRvtvqGEviE sFGEEnLCFr+LqRFtAAtLEHGmnPPvsP
  gi|1154352   701 PPNTVNGSLRVTVQGEVIEKSFGEENLCFRTLQRFTAATLEHGMNPPVSP 750

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR+L+++mA vAt+EYRs+v++EPRFvEYFR AtPE+EYG+mniGsR
  gi|1154352   751 KPEWRRLLDDMATVATDEYRSIVFQEPRFVEYFRAATPETEYGRMNIGSR 800

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK..
                    P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+hA+++   ++
  gi|1154352   801 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHAMQQSDAgg 850

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     l  L+EmY+eWPFFRvt+DLlEmvFAKGDPGiAaLyD+LLv ++L+PFG
  gi|1154352   851 GLATLREMYDEWPFFRVTIDLLEMVFAKGDPGIAALYDELLVPDDLRPFG 900

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    ++LR++YvEt+ lLL++AGHkDlLE DPYL+qrl LRdsYit Lnv+qAY
  gi|1154352   901 EQLRANYVETQRLLLQVAGHKDLLESDPYLRQRLMLRDSYITALNVCQAY 950

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    tLKRiRD  ++   rP+lsKE        a+ LvkLnp +++ PGLEDtL
  gi|1154352   951 TLKRIRDGGFRPETRPPLSKELLGSS-AVAEKLVKLNPNSEYDPGLEDTL 999

                    iLtmKGiAAGmqntG<-*
                    iLtmKGiAAGmqntG
  gi|1154352  1000 ILTMKGIAAGMQNTG    1014

gi|168027443|ref|XP_001766239.1|: domain 1 of 1, from 8 to 969: score 2225.4, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAq+RlLvP +vs+d+kLieYDALLlD+FLDiL +LHG++Lk+ v
  gi|1680274     8    SIDAQMRLLVPKRVSDDDKLIEYDALLLDRFLDILEELHGKELKDTV 54

                    qECYElsAeY...EGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    q+ YEls  Y++++G  D +KL  L   L  LdP+  i+vA++++HmLnL
  gi|1680274    55 QDLYELSGLYsktDGHGDVEKLRQLAEMLNNLDPGVNIVVASSFSHMLNL 104

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                     nLAEEv++A RRR++  k+GD  DE sA tEsD+EEtl +Lv +l KsP
  gi|1680274   105 GNLAEEVQIALRRRVSNAKKGDIGDENSALTESDMEETLHRLVKQLKKSP 154

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    eE+FeALK q+vDLvltAHPtq+vRRsLLqK++RiRnCL+q++ KD+t +
  gi|1680274   155 EEIFEALKDQTVDLVLTAHPTQAVRRSLLQKHSRIRNCLSQMYQKDITAD 204

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
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                    +KkELDEAL REiqAAFRtDEiRR+qPtPqDEmRaGmsY+HEt+W+G PK
  gi|1680274   205 EKKELDEALQREIQAAFRTDEIRRSQPTPQDEMRAGMSYFHETIWNGLPK 254

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    FLRRvDtALK iG+ ERlPY+v Li+FssWmGGDRDG nPRvtPEvtRDv
  gi|1680274   255 FLRRVDTALKSIGVKERLPYNVKLIQFSSWMGGDRDG-NPRVTPEVTRDV 303

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                    CLLaR+mAanlY+sq+E+LmFElsmWRC dEL++R   + +  +++   K
  gi|1680274   304 CLLARLMAANLYFSQIEELMFELSMWRCSDELKARVLKIESLQRKE--AK 351

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                    +YiEFWK +PP EP+Rv+LGd+RDKLYntRER R LL  G s+i+ e  y
  gi|1680274   352 HYIEFWKHIPPSEPFRVLLGDMRDKLYNTRERMRLLLQNGKSDIPIEDTY 401

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                    t+  + LEPLELCY+sLCe GDk iADGsLLD++Rqvs FGLsLvKLDiR
  gi|1680274   402 TDASQILEPLELCYRSLCETGDKPIADGSLLDFMRQVSCFGLSLVKLDIR 451

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  gi|1680274   452 QESDRHTDVIDAITNHLGIGSYRNWTEEQRQEWLLSELRGKRPLFGADLP 501

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  gi|1680274   502 TTEEIKDVLDTMKVVAELPQDCFGAYVISMATAPSDVLAVELLQRECRIK 551

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                    ++LrvvPLFEkLADLeAAPAa+ +LFsiDWY nri+GKqevm+GYsDsGK
  gi|1680274   552 KPLRVVPLFEKLADLEAAPAALSRLFSIDWYLNRINGKQEVMIGYSDSGK 601

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
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  gi|1680274   602 DAGRLSAAWQMFKAQEDLVKVAKQYGVRLTMFHGRGGTVGRGGGPTHLAI 651

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  gi|1680274   652 LSQPPDTINGSLRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPP 701

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  gi|1680274   702 IAPKPEWRELMDAMAVASTKEYRSIVFQNPSFVEYFRAATPELEYGRMNI 751

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
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  gi|1680274   752 GSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGLGSALKQALQSDP 801

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    +n+   + mY++WPFFRvt+DL+EmvFAKGDP iAaLyD+LLv++eLkP
  gi|1680274   802 RNIATFRRMYNQWPFFRVTIDLVEMVFAKGDPRIAALYDDLLVSDELKPL 851

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
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  gi|1680274   852 GEELRQKYNETRDLLLKITFHDEILQGNPSLKQRLRLREPYITALNVQQA 901

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                      LK++RD   +       sK+  d ++++k+a+eLv+Lnpt +++PGLE
  gi|1680274   902 LVLKKMRDQGLQFCALQNSSKDQSDIPTtpKRAAELVELNPTTEFPPGLE 951

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                    DtLiLtmKGiAAG+qntG
  gi|1680274   952 DTLILTMKGIAAGIQNTG    969

gi|168061648|ref|XP_001782799.1|: domain 1 of 1, from 9 to 961: score 2221.4, E = 0
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                       siDAq+RlLvP +vs+d+kLieYDALLlD+FLDiLqDLHG+++kEav
  gi|1680616     9    SIDAQMRLLVPKRVSDDDKLIEYDALLLDRFLDILQDLHGKEIKEAV 55

                    qECYElsAeYEGK..kDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    q CYEls  +   ++kD  KL+ L + L  Ld +D+i+vA++++HmLnL
  gi|1680616    56 QNCYELSGAFCKTdgKDEAKLQQLSSLLNNLDAGDSIVVASSFSHMLNLG 105
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gi|1680616   106 NLAEEVQIAYRRPGSRK--GDLGDESSALTESDLDQTFQRLVKQLKKTPE 153

                EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                E+FeALK q+vDLvltAHPtqsvRRsLLqK++RiR CL+q++ KD+t e+
gi|1680616   154 EIFEALKDQTVDLVLTAHPTQSVRRSLLQKHSRIRDCLSQMYGKDITAEE 203

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                K+ELDEAL REiqAAFRtDEiRR+qPtPqDEmRaGmsY+HEt+W+G PKF
gi|1680616   204 KQELDEALQREIQAAFRTDEIRRSQPTPQDEMRAGMSYFHETIWNGLPKF 253

                LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                LRRvDtALK iG+ ERlP +vPLi+FssWmGGDRDG nPRvtP+vtRDvC
gi|1680616   254 LRRVDTALKTIGVKERLPHNVPLIQFSSWMGGDRDG-NPRVTPDVTRDVC 302

                LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                LLaR+mAanlY+ q+EDLmFElsmWRC dEL+ R   l   a+++   K+
gi|1680616   303 LLARLMAANLYFAQIEDLMFELSMWRCSDELKQRVATLEAHAKKE--AKH 350

                YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                YiEFWK +PP+EP+Rv+LGd+RDKLYntRER R LLA G s+i  e  +t
gi|1680616   351 YIEFWKHIPPNEPFRVLLGDMRDKLYNTRERMRQLLASGKSDINIEDTFT 400

                kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                +  + LEPLELC +sLCe GDk iADGsLLD++Rqvs FGLsLvKLDiRq
gi|1680616   401 DASQILEPLELCHRSLCETGDKPIADGSLLDFMRQVSCFGLSLVKLDIRQ 450

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gi|1680616   451 ESERHTDVLDTITNYLGIGSYRDWSEEQRQEWLLSELRGKRPLFGDDLPT 500

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gi|1680616   501 TEEVQDVLDTFRVIAELPTDSFGAYIISMATSPSDVLAVELLQRECRVPK 550

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gi|1680616   551 PLRVVPLFEKLADLESAPAALSRLFSIDWYLNHIKGKQEVMIGYSDSGKD 600

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gi|1680616   601 AGRLSAAWAMYKAQEDLVKVAKQYGIRLTMFHGRGGTVGRGGGPTHLAIL 650

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gi|1680616   651 SQPPDTINGSLRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPI 700

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gi|1680616   701 APKPEWRNLMDSMAVTATEEYRSIVFQNPRFVEYFRTATPELEYGRMNIG 750

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                sRP+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAA + A++ +
gi|1680616   751 SRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGLGAALRQALEAEPN 800

                nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                n+  L  mY++WPFFRvt+DL+EmvFAKGDP iA LyD LLv+EeL+P G
gi|1680616   801 NMTVLSRMYDQWPFFRVTIDLVEMVFAKGDPRIAELYDSLLVSEELRPLG 850

                ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
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gi|1680616   851 DELREKYEETKAHLLKIARHKDILQGNPTLKQRLRLREPYITALNIQQAF 900

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gi|1680616   901 TLKKMRDRSaYYATLQPE-----SPRPTKAAAELVTLNPTTEFAPGLEDT 945

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  gi|1680616   946 LILTMKGIAAGIQNTG    961

gi|125524860|gb|EAY72974.1|: domain 1 of 1, from 56 to 1069: score 2208.1, E = 0
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                     siDA LR L+P Kvs d++L++Y+ LL+ +FLDiL DLHG d + +v
  gi|1255248    56    SIDARLRQLAPEKVSADDRLVDYETLLVARFLDILEDLHGGDFRQVV 102

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   +C  ls eY    D+ +L+ELG  LtsLd +Dai+vA++++HmLnLAnL
  gi|1255248   103 EDCLRLSGEYQSEGDPARLGELGGLLTSLDVGDAIMVASSFSHMLNLANL 152

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AEE+++ yR++ +  + GDF DEasA tEsDi+Et+++Lv  l KsP Ev
  gi|1255248   153 AEEIQMVYRKKAEASRRGDFVDEASAPTESDIDETFQRLVRGLGKSPREV 202

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                  F+AL+ q++DLvltAHPtqsvRRsLLqK+a iR CL+qL    +  ++ +
  gi|1255248   203 FDALRSQTIDLVLTAHPTQSVRRSLLQKHASIRSCLTQLCGEGISDNEEQ 252

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                  E+DEAL REi AAF+tDEiRR++PtPqDEmRaGmsY+H+t+W+GvPKFLR
  gi|1255248   253 EIDEALQREILAAFKTDEIRRTPPTPQDEMRAGMSYFHDTIWNGVPKFLR 302

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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  gi|1255248   303 RVDTALKNIGIDERLPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 351

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                  aRmmAan+Y+s++ DLmFElsmWRCndELR+RA El+r + r+k+++ +
  gi|1255248   352 ARMMAANMYFSKMADLMFELSMWRCNDELRARANELHRKSSRNKrpplta 401

                  .............vvKy.........Yi.......................
                  +  ++  + + +++ K++++ + +++++   ++    ++   +++  ++
  gi|1255248   402 slctpaatvsvsdLHKHqeparftsFLnaaiedaalvsdiaarpealrrl 451

                  ....EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                   +++EFWK++ P EPYR+iLGdvRDKLYnt ERaR +L +Gis i+E+
  gi|1255248   452 lsppEFWKKISPGEPYRIILGDVRDKLYNTCERARQILSKGISSIPEDQT 501

                  ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                  yt+vE+FLEPLELCY+sLC+CGDk iADG LLDl+RqvstFGLsLvKLDi
  gi|1255248   502 YTNVEQFLEPLELCYRSLCDCGDKLIADGRLLDLMRQVSTFGLSLVKLDI 551

                  RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                  RqEseR+tD +DAittHL+iGsYReW+Ee+RqEWL++EL+G+RPL+g+DL
  gi|1255248   552 RQESERHTDAMDAITTHLGIGSYREWPEERRQEWLVSELRGRRPLFGPDL 601

                  PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv
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  gi|1255248   602 PQSEEVADVLGAFRVIAELPADSFGAYIISMATAPSDVLAVELLQRECGV 651

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  gi|1255248   652 KKPLRVVPLFEKLADLQQARATMELLFSVDWYKERIDGKQEIMIGYSDSG 701

                  KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                  KDAGRlsAAWqLYkAqEEi+ vA ++GvKL++FHGRGGtvGRGGGP HLA
  gi|1255248   702 KDAGRLSAAWQLYKAQEEIVGVAERHGVKLTIFHGRGGTVGRGGGPSHLA 751

                  iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP
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  gi|1255248   752 ILSQPPNTVNGSLRVTVQGEVIEKSFGEENLCFRTLQRFTAATLEHGMNP 801

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  gi|1255248   802 PVSPKPEWRRLLDDMATVATDEYRSIVFQEPRFVEYFRAATPETEYGRMN 851

                  iGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                  iGsRP+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+hA+++
  gi|1255248   852 IGSRPSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHAMQQS 901
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  gi|1255248   902 DAggGLATLREMYDEWPFFRVTIDLLEMVFAKGDPGIAALYDELLVPDDL 951

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                    +PFG++LR++YvEt+ lLL++AGHkDlLE DPYL+qrl LRdsYit Lnv
  gi|1255248   952 RPFGEQLRANYVETQRLLLQVAGHKDLLESDPYLRQRLMLRDSYITALNV 1001

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                    +qAYtLKRiRD  ++   rP+lsKE        a+ LvkLnp +++ PGL
  gi|1255248  1002 CQAYTLKRIRDGGFRPETRPPLSKELLGSS-AVAEKLVKLNPNSEYDPGL 1050

                    EDtLiLtmKGiAAGmqntG<-*
                    EDtLiLtmKGiAAGmqntG
  gi|1255248  1051 EDTLILTMKGIAAGMQNTG    1069

gi|168010333|ref|XP_001757859.1|: domain 1 of 1, from 7 to 969: score 2189.0, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAq+RlLvP +vsed+kLieYDALLlD+FLDiL +LHG++Lk+ v
  gi|1680103     7    SIDAQMRLLVPKRVSEDDKLIEYDALLLDRFLDILEELHGKELKDKV 53

                    qECYElsAeY...EGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    q+ YEls  Y++++G  D +KL+ L  +L  LdP+D i+vA++++HmLnL
  gi|1680103    54 QDLYELSGLYsktDGAGDVQKLQQLADVLNNLDPGDDIVVASSFSHMLNL 103

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                     nLAEEv++A RRR++  k+GD  DE sA tEsD+EEtl +Lv +l KsP
  gi|1680103   104 GNLAEEVQIALRRRVSNAKKGDIGDENSALTESDMEETLHRLVKQLKKSP 153

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    +E FeALK q+vDLv+tAHPtq+vRRsLLqK++RiRnCL+q++ KD+t +
  gi|1680103   154 QELFEALKEQTVDLVFTAHPTQAVRRSLLQKHSRIRNCLSQMYQKDITAD 203

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
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  gi|1680103   204 EKKEWDEALQREIQAAFRTDEIRRSQPTPQDEMRAGMSYFHETIWNGLPK 253

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
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  gi|1680103   254 FLRRVDTALKSIGVKERLPHNVKLIHFSSWMGGDRDG-NPRVTPEVTRDV 302

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                    CLLaR+mAanlY+ q+EDLmFElsmWRC dELR R   + +  +++   K
  gi|1680103   303 CLLARLMAANLYFAQIEDLMFELSMWRCSDELRERVSKIESLHRKE--AK 350

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLL.AtGiseisEeAv
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  gi|1680103   351 HYIEFWKHIPPNEPFRVLLGDMRDKLYSTRERMRQLLqMNGKSDIPVEET 400

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                    yt+  + LEPLELC +sLCe GDk iADGsLLD++Rqvs FGLsLv+LDi
  gi|1680103   401 YTDASQILEPLELCHRSLCETGDKPIADGSLLDFMRQVSCFGLSLVRLDI 450

                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    RqEs+R+tD +DAit  L+iGsYR+WsEe RqEWLl+EL+GKRPL+gsDL
  gi|1680103   451 RQESDRHTDAIDAITNYLGIGSYRNWSEEERQEWLLSELRGKRPLFGSDL 500

                    PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv
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  gi|1680103   501 PVTDEVKDVLDTLKVVAELPPDCFGAYVISMATAPSDVLAVELLQRESRI 550

                    kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsG
                    kq+LrvvPLFEkLADLeAAPAa+ +LFsiDWY n+i+GKqevm+GYsDsG
  gi|1680103   551 KQPLRVVPLFEKLADLEAAPAALSRLFSIDWYLNHINGKQEVMIGYSDSG 600

                    KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                    KDAGRlsAAWq++kAqE+++KvAK+y v+L++FHGRGGtvGRGGGPtHLA
  gi|1680103   601 KDAGRLSAAWQMFKAQEDLVKVAKQYDVRLTMFHGRGGTVGRGGGPTHLA 650

                    iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP
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  gi|1680103   701 PIAPKPEWRQLMDVMAVASTNEYRSIVFQNPSFVEYFRAATPELEYGRMN 750

                   iGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                   iGsRP+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G A + A+  D
  gi|1680103   751 IGSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGLGSALRDALRTD 800

                   iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP
                    +n+  L+ mY++WPFFRvt+DL+EmvFAKGDP iAaLyD LLv++eLkP
  gi|1680103   801 PRNIATLRRMYNQWPFFRVTIDLVEMVFAKGDPRIAALYDALLVSDELKP 850

                   FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfq
                    G++LR kY Et+dlLLki  H ++L G P LKqrlRLR++Yit Lnv q
  gi|1680103   851 LGEELRRKYSETRDLLLKITFHDEILQGNPSLKQRLRLREPYITALNVQQ 900

                   AYtLKRiRDPsykvtlrPhlsKEyAdEns..kkadeLvkLnptervaPGL
                   A  LK++RD + +   +   sK+  d ++++++a+eLvkLnpt ++aPGL
  gi|1680103   901 ALVLKKMRDQNSQFCSQQNGSKDQSDVPTtpRRAAELVKLNPTTEFAPGL 950

                   EDtLiLtmKGiAAGmqntG<-*
                   EDtLiLtmKGiAAG+qntG
  gi|1680103   951 EDTLILTMKGIAAGIQNTG    969

gi|168016115|ref|XP_001760595.1|: domain 1 of 1, from 6 to 965: score 2182.3, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      si Aq+RlL P Kvs+d++L+eYD +LlD+FL +LqDLHG d+kE v
  gi|1680161     6    SINAQMRLLLPKKVSDDDQLVEYDSILLDRFLNVLQDLHGSDVKETV 52

                   qECYElsAeY...EGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                     CYEls  Y++ EG+ D +KLe LG  L  Ld +D+i+vA++++HmLnL
  gi|1680161    53 EKCYELSGMYsrvEGQGDLEKLERLGELLNNLDAGDSIVVASSFSHMLNL 102

                   AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                    nLAEEv++AyRRR+k  k+GD  DE sA tEsD+EEt+++Lv +  K+P
  gi|1680161   103 GNLAEEVQIAYRRRVKMAKKGDLGDENSALTESDLEETFRRLVNQIGKTP 152

                   eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                   +E+FeALK q+vDLvltAHPtqsvRRsLLqK++RiR CL+qL   D+t +
  gi|1680161   153 AEIFEALKHQTVDLVLTAHPTQSVRRSLLQKHTRIRSCLSQLNQVDITSD 202

                   DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                   +++ELDEALHREiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+W+G P
  gi|1680161   203 ERQELDEALHREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWNGLPI 252

                   FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                   FLRRvDtALK iG+ ERlPYdvPLi+FssWmGGDRDG nPRvtPEvtRDv
  gi|1680161   253 FLRRVDTALKAIGVEERLPYDVPLIQFSSWMGGDRDG-NPRVTPEVTRDV 301

                   CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                   CLLaR+mAanlY+ q+EDLmFElsmWRC dELR R   ++ t a +k  K
  gi|1680161   302 CLLARLMAANLYFAQIEDLMFELSMWRCSDELRNRV--VQLTGATKKEAK 349

                   yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                   +YiEFWK +P tEP+Rv+LGdvRDKLY tRER R  L  G sei+ +  +
  gi|1680161   350 HYIEFWKTIPSTEPFRVVLGDVRDKLYQTRERMRQQLSSGKSEIALDETF 399

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                   t+  + +EPL+LCY+sLCe GDk +ADGsLLD++Rqvs FGLsLvKLDiR
  gi|1680161   400 TDKSQIIEPLDLCYRSLCETGDKPVADGSLLDFMRQVSCFGLSLVKLDIR 449

                   qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                   qEseR+ Dv+DAit HL++GsY++WsEe+RqEWL++EL+GKRPL+gsDLP
  gi|1680161   450 QESERHADVMDAITLHLGMGSYKDWSEEQRQEWLISELRGKRPLFGSDLP 499

                   ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                   +tEEvkDvl+++rv+A+LP+D+FGaYiismataPsDvLAvELLqREC+v
  gi|1680161   500 MTEEVKDVLETLRVVADLPSDCFGAYIISMATAPSDVLAVELLQRECQVP 549
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                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                    ++LrvvPLFEkLADL+ A A++ +LFsiDWY n+i+GKqevm+GYsDsGK
  gi|1680161   550 KPLRVVPLFEKLADLQLAAATLSRLFSIDWYLNHINGKQEVMIGYSDSGK 599

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAGRlsAAWq++ AqEE++KvAK+yG+KL++FHGRGGtvGRGGGPtHLAi
  gi|1680161   600 DAGRLSAAWQMFTAQEELVKVAKQYGIKLTMFHGRGGTVGRGGGPTHLAI 649

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPPDt+nGslRvt+qGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PP
  gi|1680161   650 LSQPPDTVNGSLRVTIQGEVIEKSFGEEELCFRTLQRFTAATLEHGMHPP 699

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                     +PkP WR+Lm++mA v tEEYRsvv+K P Fv YFR AtPE EYG+mni
  gi|1680161   700 FAPKPAWRNLMDDMAGVSTEEYRSVVMKNPTFVPYFRAATPEQEYGRMNI 749

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvG A K+ ++ D
  gi|1680161   750 GSRPAKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGVGGALKYVLQVDP 799

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    Kn+  L+ mY++WPFFRvtlDL+EmvFAKGDP iAaLyD+LLv ++ k F
  gi|1680161   800 KNMGILRKMYDQWPFFRVTLDLIEMVFAKGDPRIAALYDRLLVKDDHKSF 849

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G++LR++Y Et++l+Lk+AGH D+LEG P LKqrlRLR+ Yit Lnv qA
  gi|1680161   850 GEKLRNNYNETRELVLKVAGHEDVLEGNPTLKQRLRLREQYITPLNVQQA 899

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                    YtLK++RD   +  ++ + +      n k + eLv Ln t +++PGLEDt
  gi|1680161   900 YTLKKMRDFRAQLGVHEENANQEELHNGKVSSELVMLNTTTQYPPGLEDT 949

                    LiLtmKGiAAGmqntG<-*
                    LiLtmKGiAAGmqntG
  gi|1680161   950 LILTMKGIAAGMQNTG    965

gi|168042979|ref|XP_001773964.1|: domain 1 of 1, from 9 to 958: score 2153.6, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDA +RlLvP Kvsed+ L++Y A L+D+ L iL  LHG+++k+ v
  gi|1680429     9    SIDASMRLLVPKKVSEDDMLVDYGAKLVDRSLAILENLHGKEMKDTV 55

                    qECYElsAeYEGK.kDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                     ECYEl+  +   ++  +KL+ L + L  Ld +D+i+vA++++HmLnL n
  gi|1680429    56 LECYELAGAFCADsRNEEKLQQLSSLLNNLDAGDSIVVASSFSHMLNLEN 105

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAEEv++A+RR   kk  G   DE sA tEsD++ t+++Lv kl KsPeE
  gi|1680429   106 LAEEVQIAHRRPANKK--GNIGDENSALTESDLDQTFQRLVKKLKKSPEE 153

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +FeALKnq+vDLv+tAHPtqsvRRsLLqK++RiRnCL+q++ KD+t e+K
  gi|1680429   154 IFEALKNQTVDLVFTAHPTQSVRRSLLQKHSRIRNCLSQMYQKDITAEEK 203

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +ELDEAL REiqAAFRtDEiRR+qPtPqDEmRaGmsY+HEt+W+G PKFL
  gi|1680429   204 QELDEALQREIQAAFRTDEIRRSQPTPQDEMRAGMSYFHETIWNGLPKFL 253

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    RRvDtALK iG+n RlP +vPLi+FssWmGGDRDG nPRvtP++tRDvCL
  gi|1680429   254 RRVDTALKAIGVNKRLPHNVPLIQFSSWMGGDRDG-NPRVTPDMTRDVCL 302

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    LaR+mAanlY+sq+EDLmFElsmWRC dELR R   l   ++++   K+Y
  gi|1680429   303 LARLMAANLYYSQIEDLMFELSMWRCSDELRQRVAVLEAQPKKE--SKHY 350

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                    iEFWKq+PP EP+Rv+LGd+RDKLYntRE  R LLA G s++  +  +t+
  gi|1680429   351 IEFWKQIPPSEPFRVLLGDMRDKLYNTREWMRQLLANGKSDVNRDNTFTE 400

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      + LEPLELCY+sLCe GDk iADGsLLD++R vs FGLsLv+LDiRqE
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  gi|1680429   401 KSQILEPLELCYRSLCETGDKPIADGSLLDFMRRVSCFGLSLVRLDIRQE 450

                   seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                   s+R+tDv+D it  L+iGsYR+WsEe+Rq+WLl+EL+GKRPL+g+ +P
  gi|1680429   451 SDRHTDVMDTITNYLGIGSYRDWSEEQRQDWLLSELRGKRPLFGPGMPTS 500

                   EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                   EEvkDvld+frv+AELP D+FGaY+ismataPsDvLAvELLqREC +  +
  gi|1680429   501 EEVKDVLDTFRVVAELPADCFGAYVISMATAPSDVLAVELLQRECRIPTP 550

                   LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                   LrvvPLFEkLADLe APA++ +LFsiDWY nri+GKqevm+GYsDsGKDA
  gi|1680429   551 LRVVPLFEKLADLESAPASLSRLFSIDWYLNRINGKQEVMIGYSDSGKDA 600

                   GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                   GRlsAAWq++kAqE + KvAK+yGv+L++FHGRGGtvGRGGGPtHLAiLs
  gi|1680429   601 GRLSAAWQMFKAQENLLKVAKHYGVRLTMFHGRGGTVGRGGGPTHLAILS 650

                   qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                   qPPDtinGslRvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP++
  gi|1680429   651 QPPDTINGSLRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPIA 700

                   PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                   PkPEWR+Lm+ mAvvAt+EYRsvv+K PRFvEYFR+AtPElEYG+mniGs
  gi|1680429   701 PKPEWRDLMDSMAVVATDEYRSVVFKNPRFVEYFRMATPELEYGRMNIGS 750

                   RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                   RP++RkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAA K A++    n
  gi|1680429   751 RPSRRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGLGAALKRALEDNPSN 800

                   lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                   +  L  mY++WPFFRvt+DL+EmvFAKGDP iA LyD+LLva+eLk  G
  gi|1680429   801 FNTLYRMYDQWPFFRVTIDLMEMVFAKGDPRIAQLYDDLLVADELKSLGI 850

                   sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                   +LR+kY Etk+ LLk+A H ++L G P LKqrlRLR++Yit Lnv qA+t
  gi|1680429   851 ELRQKYNETKEHLLKVARHTEILQGNPTLKQRLRLREPYITALNVQQAFT 900

                   LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                   LK++R+   + t +P   K     ++k+a+eLv Lnpt ++aPGLEDt+i
  gi|1680429   901 LKKMREQHSQLT-QPDSPK-----PTKPAAELVTLNPTTEFAPGLEDTMI 944

                   LtmKGiAAGmqntG<-*
                   LtmKGiAAG+qntG
  gi|1680429   945 LTMKGIAAGIQNTG    958

gi|168044057|ref|XP_001774499.1|: domain 1 of 1, from 9 to 959: score 2109.2, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      siDA +RlLvP Kvsed+ L++Y   L  +FLDiL  LHG++++E v
  gi|1680440     9    SIDAPMRLLVPKKVSEDDMLVDYGSQLGNRFLDILESLHGKSMRETV 55

                   qECYElsAeYEGKk..DtkKLeELGakLtsLdPaDailvAkailHmLnLA
                     CYEl+  +   ++++ +KL+ L + L  L+P+D+i+vA++++HmLnL
  gi|1680440    56 MNCYELAGAFANSHsrEEEKLQQLSSLLNNLNPTDSIVVASSFSHMLNLG 105

                   nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                   nLAEE+++AyRR   kk  G   DE sA tEsD++ t+++L   l KsP+
  gi|1680440   106 NLAEEIQIAYRRPTNKK--GNIGDENSALTESDLDQTFQRLKDELHKSPD 153

                   EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                   E+FeALK q+vDLv+tAHPtqsvRRsLLqK++RiR CL+q++ KDvt e+
  gi|1680440   154 EIFEALKKQTVDLVFTAHPTQSVRRSLLQKHSRIRDCLSQMYQKDVTAEE 203

                   KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                   K+ELDEAL REiqAAFRtDEiRR+qP PqDEmRaGmsY+HEt+W+G PKF
  gi|1680440   204 KQELDEALQREIQAAFRTDEIRRSQPAPQDEMRAGMSYFHETIWNGLPKF 253

                   LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   LRRvDtALK iG+ ERlP dvPLi+FssWmGGDRDG nPRvtP+vtRDvC
  gi|1680440   254 LRRVDTALKGIGVKERLPHDVPLIQFSSWMGGDRDG-NPRVTPDVTRDVC 302
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                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LLaR+mAanlY+sq+EDLmFElsmWRC dEL+ R   l    +++   K+
  gi|1680440   303 LLARLMAANLYYSQIEDLMFELSMWRCSDELKQRVAILEAQTKKE--SKH 350

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                    Y EFWK +PP+EP+Rv+LG++RDKLYntRER R LLA G s+i  e  +t
  gi|1680440   351 YTEFWKHIPPNEPFRVLLGNMRDKLYNTRERMRQLLANGKSDINLEDTFT 400

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  + LEPLELC +sLCe GDk iADGsLLD++Rqvs FGLsLvKLDiRq
  gi|1680440   401 EKSQILEPLELCHRSLCETGDKPIADGSLLDFMRQVSCFGLSLVKLDIRQ 450

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es+R+tDvlD it  L+iGsYR+WsEe+Rq+WLl+EL+G+RPL+g+D+P
  gi|1680440   451 ESDRHTDVLDTITNYLGIGSYRDWSEEQRQDWLLSELRGRRPLFGPDMPT 500

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                    tEEvkDvld+f+v+AELP D+FGaYiismataPsDvLAvELLqRE ++
  gi|1680440   501 TEEVKDVLDTFKVIAELPEDCFGAYIISMATAPSDVLAVELLQRESHIPT 550

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    +LrvvPLFEkLADLe APA++ +LFsiDWY  ri+GKqevm+GYsDsGKD
  gi|1680440   551 PLRVVPLFEKLADLESAPATLSRLFSIDWYLSRINGKQEVMIGYSDSGKD 600

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AGRlsAAWq++kAqE+++KvAK+y v+L++FHGRGGtvGRGGGPtHLAiL
  gi|1680440   601 AGRLSAAWQMFKAQEDLVKVAKQYEVRLTMFHGRGGTVGRGGGPTHLAIL 650

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPPDtinGslRvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGmnPP+
  gi|1680440   651 SQPPDTINGSLRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMNPPI 700

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                    +P PEWR+Lm+ mAv+At+EYRs+v+K PRFvEYFR AtPElEYG+mniG
  gi|1680440   701 APEPEWRDLMDFMAVIATDEYRSIVFKNPRFVEYFRTATPELEYGRMNIG 750

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRP+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAA K A++
  gi|1680440   751 SRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGLGAALKQALEAGPG 800

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                    n+  L  mY+ WPFFRvt+DL+EmvFAKGDP iA LyD+LLv EeLkP G
  gi|1680440   801 NFDTLSRMYDLWPFFRVTIDLVEMVFAKGDPRIAELYDNLLVPEELKPLG 850

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    ++LR+kY Etk  LLkiA H D+L G P LKqrlRLR++ it Lnv qA+
  gi|1680440   851 EELREKYNETKSHLLKIARHTDILQGNPTLKQRLRLREPVITALNVQQAF 900

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    tLK++R+   + t       E      k+a + v Lnpt ++aPGLEDt+
  gi|1680440   901 TLKKMREQTGQGTQS-----ESPKST-KPASDPVTLNPTTEFAPGLEDTM 944

                    iLtmKGiAAGmqntG<-*
                    i+tmKGiAAG+qntG
  gi|1680440   945 IITMKGIAAGIQNTG    959

gi|108782496|gb|ABG20460.1|: domain 1 of 1, from 1 to 851: score 2073.5, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1087824     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1087824     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                             RRik  k+GDFaDE+sA tEsD EEtl++Lv+ l KsP+E+
  gi|1087824     1 ---------RRIKTPKKGDFADESSAMTESDFEETLRRLVVDLKKSPQEI 41

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    Fe LKnq+v+LvltAHPtqs+RRsLLqK++RiR CL+qL+AKD+t++DK+
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  gi|1087824    42 FETLKNQTVELVLTAHPTQSIRRSLLQKHGRIRDCLTQLYAKDITPDDKQ 91

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                   ELDEAL REiqAAFRtDEiRR+qPtPqDEmRaGmsYiHEt+WkGvPKFLR
  gi|1087824    92 ELDEALQREIQAAFRTDEIRRTQPTPQDEMRAGMSYIHETIWKGVPKFLR 141

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALKn+GinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDv LL
  gi|1087824   142 RVDTALKNLGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVVLL 190

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmAan+Y+sq+ DLmFElsmWRCndEL +RA E+++ +++d   K+Yi
  gi|1087824   191 ARMMAANMYFSQIQDLMFELSMWRCNDELNARAHEIHKLSKSD--AKHYI 238

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWK +PP EPYRv+L dvRDKLY tRE aR LL  G s+++ e  +t+v
  gi|1087824   239 EFWKPIPPSEPYRVVLADVRDKLYHTREHARQLLSNGTSDVPLESTFTHV 288

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   ++FLEPLELCYksLC+CGD+ iADGsLLD++RqvstFGL LvKLDiRqEs
  gi|1087824   289 DQFLEPLELCYKSLCDCGDRPIADGSLLDFMRQVSTFGLCLVKLDIRQES 338

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   eR+tDv+DAit+HL++GsYReWsEeKRqEWLl+EL+G RPL+gsDLPktE
  gi|1087824   339 ERHTDVMDAITKHLGVGSYREWSEEKRQEWLLSELRGTRPLFGSDLPKTE 388

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++ vld+f+v+ ELP+D FGaYiismataPsDvLAvELLqREC++k++L
  gi|1087824   389 EIAAVLDTFHVISELPSDGFGAYIISMATAPSDVLAVELLQRECHIKNPL 438

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLe APA+v +LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|1087824   439 RVVPLFEKLADLESAPASVTRLFSIDWYRNRINGKQEVMIGYSDSGKDAG 488

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYk qEE++K+AK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1087824   489 RLSAAWQLYKVQEELVKIAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 538

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEHGm+PP sP
  gi|1087824   539 PPDTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHGMHPPSSP 588

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emA vAt EYRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|1087824   589 KPEWRALMDEMAAVATKEYRSMVLQEPRFVEYFRLATPELEYGRMNIGSR 638

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkP+GGiesLRAiPWiF+WtqtRFHLP  LG GAAFKh i+KDiKnl
  gi|1087824   639 PSKRKPGGGIESLRAIPWIFSWTQTRFHLPGGLGCGAAFKHVIEKDIKNL 688

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+ mY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+EeL PFG++
  gi|1087824   689 AMLEQMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEELCPFGEQ 738

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR +Y+Etk++  +iAGHk++LEGDP L+qrlRLRd+YittLnv+qAYtL
  gi|1087824   739 LRSDYEETKNFFFQIAGHKEILEGDPHLRQRLRLRDPYITTLNVCQAYTL 788

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y+vt+rPh+sK+y d    +a+eLvkLnp++++aPGLEDtLiL
  gi|1087824   789 KRIRDPNYHVTVRPHISKDYMDSTDNPAAELVKLNPSSEYAPGLEDTLIL 838

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|1087824   839 TMKGIAAGMQNTG    851

gi|290350842|dbj|BAI78342.1|: domain 1 of 1, from 11 to 969: score 1988.5, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      siDAqLRlL+P Kvsed+kLieYDALL+ +FLDiLqDLHGe L+E+v
  gi|2903508    11    SIDAQLRLLAPAKVSEDDKLIEYDALLVGRFLDILQDLHGEALREFV 57
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                qECYElsA YE   D  KL+ELG  LtsL P+D+i+vA +++HmLnLAnL
gi|2903508    58 QECYELSATYESASDFAKLDELGKMLTSLSPGDSIVVAGSFSHMLNLANL 107

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AEEv++A+RRR+k+k  GD  DEa A tEsDiEEtlK+Lv   nKsPeEv
gi|2903508   108 AEEVQIAFRRRRNKQKERGDLGDEALAITESDIEETLKRLVQDYNKSPEEV 157

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                F+ALKnq+vDLv+tAHPtqsvRRs+LqK+aRiRnCL+qL AKD+t ++K
gi|2903508   158 FDALKNQTVDLVFTAHPTQSVRRSVLQKHARIRNCLTQLCAKDITADEKY 207

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                ELDEAL REiqAAFRtDEiRR qP PqDEmRaGmsY+HEt+WkGvPKFLR
gi|2903508   208 ELDEALQREIQAAFRTDEIRRIQPAPQDEMRAGMSYFHETIWKGVPKFLR 257

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                RvDtALKniGinERlPY+vPLi+FssWmGGDRDG nPRvtPEvtRDvCLL
gi|2903508   258 RVDTALKNIGINERLPYNVPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 306

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                aRmmAanlY+sq+EDLmFElsmWRC dE        y+ ++ +   K+Yi
gi|2903508   307 ARMMAANLYYSQIEDLMFELSMWRCSDETPWFVLMSYSDPQGK-DAKHYI 355

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                EFWKqvP +EPYRviL dvR KLYntRER+R +L  G s+i+ eA +t+v
gi|2903508   356 EFWKQVPANEPYRVILDDVRSKLYNTRERSRNILSNGSSDIPLEATFTNV 405

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFG.LsLvKLDiRqE
                E+FL+PL   Y+sLC CGD+viADGsLLD++Rq     +Ls       +
gi|2903508   406 EQFLDPLSSVYRSLCSCGDRVIADGSLLDFMRQSIDLRpLSCEAGTSGKK 455

                seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                s+R+tDvlDAittHL+iGsYR+WsEeKRqEWLl+E + + P +   LPkt
gi|2903508   456 SDRHTDVLDAITTHLGIGSYRDWSEEKRQEWLLSETSRQAPPFRTRLPKT 505

                EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                EE++Dvld+f+v+AELP D FG          sDvL    L REC vkq+
gi|2903508   506 EEIADVLDTFHVIAELPADNFGGLYNLNGNCTSDVLRSSFLRRECNVKQP 555

                LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                LrvvPLFEkLADLeA PAa+++LFsiDWY nri+ Kqevm+GYsDsGKDA
gi|2903508   556 LRVVPLFEKLADLEAGPAAMARLFSIDWYLNRINRKQEVMIGYSDSGKDA 605

                GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                GRlsAAWqLYkAqEE+++vAK+yGvKL++FHG+GGtvGRGGGPtHLAiLs
gi|2903508   606 GRLSAAWQLYKAQEELVQVAKQYGVKLTMFHGKGGTVGRGGGPTHLAILS 655

                qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                qPP+tinGslRvtvqGEviE+sFGEE LCF++LqR+tAAtLEHGm PP s
gi|2903508   656 QPPETINGSLRVTVQGEVIEQSFGEERLCFKTLQRYTAATLEHGMRPPTS 705

                PkPEWRkLmeemAvvA.tEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                PkPEWR +++e+Av  +tEEYRsvv+KEPRFvEYFRlAtPElEYG+
gi|2903508   706 PKPEWRAILDEIAVCGpTEEYRSVVFKEPRFVEYFRLATPELEYGRSE-H 754

                sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG.vGAAFKhAidKDi
                  P+ +k +     +     +     t    P  +  +GAAFKh + KD
gi|2903508   755 WQPTIKKEAQRRHRIPPCNPMDICVDTDKVSPSRVAwFGAAFKHILRKDR 804

                KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                +nl  LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLv++eLkPF
gi|2903508   805 RNLRILKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVSDELKPF 854

                GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                G++LR++Y+Etk+lLLk+   +      P L     LR++YittLnv+qA
gi|2903508   855 GEQLRANYEETKQLLLKVCRPHGSSRRGPLLETEDTLREAYITTLNVCQA 904

                YtLKRiRDPsykvtlr.PhlsKEyAdEnskkadeLvkLnptervaPGLED
                YtLKRiRDP++kv +r+P+lsKE  d n  k +eLvkLnp++++aPGLED
gi|2903508   905 YTLKRIRDPNFKVDVRpPPLSKEILDSN--KQAELVKLNPASEYAPGLED 952
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                  tLiLtmKGiAAGmqntG<-*
                  tLi    G    +
  gi|2903508   953 TLIFDHEGYRCRIEEHW    969

gi|20152211|dbj|BAB89367.1|: domain 1 of 1, from 1 to 820: score 1987.4, E = 0
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2015221     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2015221     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                                                +Lv+ l KsP+Ev
  gi|2015221     1 -----------------------------------RLVVALKKSPQEV 13

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                  F+ALKnq+vDLv+tAHPtqs+RRsLLqK+aRiRnCLaqL+AKD+t++DK+
  gi|2015221    14 FDALKNQTVDLVFTAHPTQSIRRSLLQKHARIRNCLAQLYAKDITPDDKQ 63

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                  ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|2015221    64 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 113

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                  RvDtALKniGinER+PY +PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2015221   114 RVDTALKNIGINERVPYSAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 162

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                  aRmmAanlY+sq++DLmFE+smWRCndELRvRA+El++ ++rd   K+Yi
  gi|2015221   163 ARMMAANLYYSQIDDLMFEMSMWRCNDELRVRADELHSSSKRD--EKHYI 210

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                  EFWKq+PP EPYRviLGdvRDKLY t ER+R LL  G+s+i+EeA yt++
  gi|2015221   211 EFWKQIPPSEPYRVILGDVRDKLYHTCERTRQLLSNGFSDIPEEATYTNI 260

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                  E+FLEPLELCY+sLC  G   +   + L +LRqvstFGLsLv+LDiRqEs
  gi|2015221   261 EQFLEPLELCYRSLCLVGIDPLLMEAFLHFLRQVSTFGLSLVRLDIRQES 310

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  +R+tDvlDAit+HLeiGsYReWsEe+RqEWLl+EL+GKRPL+g+DLPktE
  gi|2015221   311 DRHTDVLDAITQHLEIGSYREWSEERRQEWLLSELSGKRPLFGPDLPKTE 360

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E+++vld+f+v+ ELP+D+FGaYiismataPsDvLAvELLqREC+vk++L
  gi|2015221   361 EIAEVLDTFHVISELPSDCFGAYIISMATAPSDVLAVELLQRECHVKRPL 410

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkL DLeAAPAav++LFsi+WY+nri+GKqevm+GYsDsGKDAG
  gi|2015221   411 RVVPLFEKLDDLEAAPAAVARLFSIEWYKNRINGKQEVMIGYSDSGKDAG 460

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  R+sAAWqLYkAqEE+iKv K+yGvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|2015221   461 RMSAAWQLYKAQEELIKVSKQYGVKLTMFHGRGGTVGRGGGPSHLAILSQ 510

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+L  Ft AtLEHGmnPP+sP
  gi|2015221   511 PPDTIQGSLRVTVQGEVIEQSFGEEHLCFRTLHGFTSATLEHGMNPPLSP 560

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++e+Av+AtE YRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|2015221   561 KPEWRALLDEIAVIATEKYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 610

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFK+A++KD+Knl
  gi|2015221   611 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKYALNKDVKNL 660

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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                     L++mY++WPFFRvt+DL+EmvF KGDPGiAaLyDkLLv+E+L+ FG+
  gi|2015221   661 HILQDMYNKWPFFRVTIDLVEMVFGKGDPGIAALYDKLLVSEDLWSFGEL 710

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Etk lLL+iAGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|2015221   711 LRANYEETKSLLLQIAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 760

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KR+RDP+y vtlrPh+ KEy +    +a+eLvkLn    +aPGLEDtLiL
  gi|2015221   761 KRVRDPNYLVTLRPHITKEYMESK--PAAELVKLN-PRSYAPGLEDTLIL 807

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|2015221   808 TMKGIAAGMQNTG    820

gi|108782498|gb|ABG20461.1|: domain 1 of 1, from 1 to 830: score 1987.3, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1087824     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1087824     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                                           sD  EtlK+Lv+ l KsP+E+
  gi|1087824     1 ----------------------------SDFGETLKRLVVDLKKSPQEI 21

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ LKnq+v+LvltAHPtqsvRRsLLqK++RiR CL+qL+AKD+t++DK+
  gi|1087824    22 FDTLKNQTVELVLTAHPTQSVRRSLLQKHGRIRDCLTQLYAKDITPDDKQ 71

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDE L REiqAAFRtDEiRR+qPtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|1087824    72 ELDESLQREIQAAFRTDEIRRTQPTPQDEMRAGMSYFHETIWKGVPKFLR 121

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDt LKn+GinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDv LL
  gi|1087824   122 RVDTTLKNLGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVVLL 170

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAan+Y+ q+EDLmFElsmWRCndEL +RA E+ + +++d   K+Yi
  gi|1087824   171 ARMMAANMYFTQIEDLMFELSMWRCNDELSARAHEILKLSKSD--AKHYI 218

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP EPYRv+L dvRDKLYntRE aR LL  G s+++Ee  +t++
  gi|1087824   219 EFWKQLPPSEPYRVVLADVRDKLYNTREHARQLLSNGASDVPEETTFTHI 268

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    ++FLEPLELCY+sLC CGD+ iADGsLLD++RqvstFGLsLvKLDiRqEs
  gi|1087824   269 DQFLEPLELCYRSLCACGDQPIADGSLLDFMRQVSTFGLSLVKLDIRQES 318

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     R+ Dv+DAit+HL++G YR+WsEeKRqEWLl+EL+GKRPL+gsDLP+
  gi|1087824   319 GRHADVMDAITKHLGVGPYRSWSEEKRQEWLLSELRGKRPLFGSDLPMSY 368

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+D +++frvLAELP DsFGaYiismataPsDvLAvELLqRECg+k++L
  gi|1087824   369 EVADAIGTFRVLAELPNDSFGAYIISMATAPSDVLAVELLQRECGIKKPL 418

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADL+ A A+v +LFsiDWY+ ri+GKqevm+GYsDsGKDAG
  gi|1087824   419 RVVPLFEKLADLKSAAASVTRLFSIDWYKDRINGKQEVMIGYSDSGKDAG 468

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYk qEE+iKvA+k+GvKL++FHGRGGtvGRGG PtHLAiLsq
  gi|1087824   469 RLSAAWQLYKVQEELIKVAQKFGVKLTMFHGRGGTVGRGGAPTHLAILSQ 518

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEHGm+PP+sP
  gi|1087824   519 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHGMHPPISP 568
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                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emAv AtE YRs+v+KEPRFvEYFRlAtPE+ YG++niGsR
  gi|1087824   569 KPEWRTLLDEMAVAATEKYRSIVFKEPRFVEYFRLATPETAYGRLNIGSR 618

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkPsGGiesLRAiPWiF+WtqtRFHLPvWLG+GAAFKhAi+     l
  gi|1087824   619 PAKRKPSGGIESLRAIPWIFSWTQTRFHLPVWLGFGAAFKHAIQEGQPKL 668

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+ mY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+EeL PFG++
  gi|1087824   669 VMLEQMYNEWPFFRVTIDLIEMVFAKGDPGIAALYDKLLVSEELCPFGEQ 718

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Etk+lLL++AGHk++L GDP L+qrlRLRd+YittLnv+qAYtL
  gi|1087824   719 LRSDYEETKKLLLQVAGHKEILQGDPHLRQRLRLRDPYITTLNVCQAYTL 768

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+vt+rPh+sK+y d n   a+eLvkLnp++++aPGLEDtLiL
  gi|1087824   769 KRIRDPNYHVTMRPHISKDYMDSN-SLAAELVKLNPSSEYAPGLEDTLIL 817

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|1087824   818 TMKGIAAGMQNTG    830

gi|20152209|dbj|BAB89366.1|: domain 1 of 1, from 1 to 750: score 1782.0, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2015220     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2015220     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2015220     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2015220     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                             iqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|2015220     1 ---------IQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 41

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2015220    42 RVDTALKNIGIDERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 90

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEEl.yrtaardkvvKyY
                    aRmmAanlY+sq+EDLmF lsmWRCnd+ RvR +E+ ++ ++rd   K+Y
  gi|2015220    91 ARMMAANLYYSQIEDLMFALSMWRCNDDCRVRSDEVlHSSSRRD--AKHY 138

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                    iEFWKqvPP+EPYRviLGdvRDKLY t ERaR LLA+G+sei+EeA yt+
  gi|2015220   139 IEFWKQVPPNEPYRVILGDVRDKLYQTPERARQLLAHGYSEIPEEATYTN 188

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    +E+FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLv+LDiRqE
  gi|2015220   189 IEQFLEPLELCYRSLCACGDRSIADGSLLDFLRQVSTFGLSLVRLDIRQE 238

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s+R+tDvlDAit+HLeiGsYReWsEe++qEWLl+EL+GKRPL+g+DLPkt
  gi|2015220   239 SDRHTDVLDAITQHLEIGSYREWSEERKQEWLLSELSGKRPLFGPDLPKT 288

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    EE++Dvld+f+v+AELP D+FGaYiismataPsDvLAvELLqREC vkq+
  gi|2015220   289 EEIADVLDTFHVIAELPADCFGAYIISMATAPSDVLAVELLQRECRVKQP 338

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
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                    LrvvPLFEkLADL+AAPAav++LFs++WY+nri+GKqevm+GYsDsGKDA
  gi|2015220   339 LRVVPLFEKLADLDAAPAAVARLFSVEWYRNRINGKQEVMIGYSDSGKDA 388

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    GRlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLs
  gi|2015220   389 GRLSAAWQLYKAQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILS 438

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPPDti+G lRvtvqGEviE+ FGEE+LCFr+LqRFtAAtLEHGm+PPvs
  gi|2015220   439 QPPDTIHGNLRVTVQGEVIEQCFGEEHLCFRTLQRFTAATLEHGMHPPVS 488

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    PkPEWR Lm+e+AvvAtE YRs+v+KEPRFvEYFRlAtPElEYG+mniGs
  gi|2015220   489 PKPEWRALMDEIAVVATEKYRSIVFKEPRFVEYFRLATPELEYGRMNIGS 538

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RP+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFK+Ai+KDiKn
  gi|2015220   539 RPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKYAINKDIKN 588

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l +L+EmY+ WPFFRvt+DL+EmvFAKG P iAaLyDkLLv+E+L+ FG+
  gi|2015220   589 LRMLQEMYNAWPFFRVTIDLVEMVFAKGNPSIAALYDKLLVSEDLWSFGE 638

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR +Y+Etk lLL+iAGHkDlLEGDPYL+qrlRLRdsYittLnv+qAYt
  gi|2015220   639 QLRSNYEETKSLLLQIAGHKDLLEGDPYLRQRLRLRDSYITTLNVCQAYT 688

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    LKRiRDP+y vt+rPh+sKEy +    +a+eLvkLnpt+++aPGLEDtLi
  gi|2015220   689 LKRIRDPNYSVTPRPHISKEYMESK--PAAELVKLNPTSEYAPGLEDTLI 736

                    LtmKGiAAGmqntG<-*
                    LtmKGiAAGmqntG
  gi|2015220   737 LTMKGIAAGMQNTG    750

gi|125527770|gb|EAY75884.1|: domain 1 of 1, from 11 to 748: score 1605.5, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLR+L+P K sed+kL+eYDALLlD+FLDiLqDLHGed++E
  gi|1255277    11    SIDAQLRILAPKKLSEDDKLVEYDALLLDRFLDILQDLHGEDIRETL 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                      C E+
  gi|1255277    58 INC-EI---------------------------------------------- 62

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                                                          +vl l
  gi|1255277    63 -------------------------------------MVLIL------- 67

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1255277     - -------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                                                            +W
  gi|1255277    68 -------------------------------------MWTT------ 71

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                                                  G nPRvtPEvtRDvCLL
  gi|1255277    72 --------------------------------G-NPRVTPEVTRDVCLL 87

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+ q+EDLmFElsmWRC dELRv+A+ l+r  +++  +K+Yi
  gi|1255277    88 ARMMAANLYYAQIEDLMFELSMWRCSDELRVKADQLHRCTKKN-TTKHYI 136

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKqvPP EPYRviL +vRDKLYntRERaRHLLA G+sei++eA +t+v
  gi|1255277   137 EFWKQVPPSEPYRVILSNVRDKLYNTRERARHLLASGFSEIPDEATFTDV 186

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC CGD  iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|1255277   187 EQFLEPLELCYRSLCACGDNSIADGSLLDFLRQVSTFGLSLVRLDIRQES 236
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                    eRqtDvlDAitthLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDv+DAit+ L+iGsYReWsEeKRqEWLl+EL GKRPL+g+DLP+t+
  gi|1255277   237 DRHTDVMDAITQYLGIGSYREWSEEKRQEWLLSELNGKRPLFGPDLPQTD 286

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++D ld+f+v+AELP DsFGaY+ismataPsDvLAvELLqREC+vk++L
  gi|1255277   287 EIADALDTFHVIAELPYDSFGAYVISMATAPSDVLAVELLQRECHVKKPL 336

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAa+++LFs+DWY+nridGKqevm+GYsDsGKDAG
  gi|1255277   337 RVVPLFEKLADLEAAPAALARLFSVDWYRNRIDGKQEVMIGYSDSGKDAG 386

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    R+sAAW LYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1255277   387 RFSAAWELYKAQEELIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 436

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFt AtLEHGm+PP+sP
  gi|1255277   437 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTSATLEHGMHPPISP 486

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emA vAt EYRs+v++E RFvEYFRlAtPElEYG+mniGsR
  gi|1255277   487 KPEWRALMDEMAAVATKEYRSIVFQEARFVEYFRLATPELEYGRMNIGSR 536

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|1255277   537 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLQKDIRNL 586

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+PFG +
  gi|1255277   587 QILQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWPFGAR 636

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Etk+lLL++AGHkDlLEGDPYL+qrlR+RdsYit Lnv+qA tL
  gi|1255277   637 LRANYEETKQLLLQVAGHKDLLEGDPYLRQRLRIRDSYITALNVCQACTL 686

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP ++v +r hlsK+  d   k+a+eLvkLn t+++ PGLEDtLiL
  gi|1255277   687 KRIRDPGFHVSPRAHLSKDIMDSG-KPAAELVKLNTTSEYGPGLEDTLIL 735

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|1255277   736 TMKGIAAGMQNTG    748

gi|3649778|emb|CAA09589.1|: domain 1 of 1, from 1 to 704: score 1566.1, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|3649778     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|3649778     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|3649778     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|3649778     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|3649778     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                           niGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|3649778     1 -------NIGIDERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 42

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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                    aRmmAanlY+sq+EDLmFElsmWRCndELRvRAEEl r +++d v K+Yi
  gi|3649778     43 ARMMAANLYYSQIEDLMFELSMWRCNDELRVRAEELNRSSKKDAVAKHYI 92

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK +PP+EPYRv+LG+vRD+LY tRE +RHLLA+G+s+i+Ee  +t+v
  gi|3649778     93 EFWKNIPPNEPYRVLLGEVRDRLYQTREASRHLLAHGYSDIPEEHTFTNV 142

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    +eFLEPLELCY+sLC CGD++iADGsLLD+LRqvstFGLsLv+LDiRqEs
  gi|3649778    143 DEFLEPLELCYRSLCACGDRAIADGSLLDFLRQVSTFGLSLVRLDIRQES 192

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlDAit+HLeiGsY eWsEeKRq WLl+EL+GKRPL+g DLP+tE
  gi|3649778    193 DRHTDVLDAITKHLEIGSYQEWSEEKRQQWLLSELSGKRPLFGTDLPQTE 242

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E+kDvld+f+v+AELP+D FGaYiismata sDvLAvELLqREC+vkq+L
  gi|3649778    243 EIKDVLDTFHVIAELPSDNFGAYIISMATAASDVLAVELLQRECHVKQPL 292

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAa+++LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|3649778    293 RVVPLFEKLADLEAAPAALARLFSIDWYRNRINGKQEVMIGYSDSGKDAG 342

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    R+sAAWqLYkAqEE+iKvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|3649778    343 RFSAAWQLYKAQEELIKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 392

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGE +LCFr+LqRFtAAtLEHGm+PP+sP
  gi|3649778    393 PPDTIHGSLRVTVQGEVIEQSFGEQHLCFRTLQRFTAATLEHGMHPPISP 442

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm++mAv+AtEEYRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|3649778    443 KPEWRALMDQMAVIATEEYRSMVFQEPRFVEYFRLATPELEYGRMNIGSR 492

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkPsGGie+LRAiPWiFaWtqtRFHLPvWLG+GAAFKh idKDi+nl
  gi|3649778    493 PAKRKPSGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIDKDIRNL 542

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+L+EmY++WPFFRvt+DL+EmvFAKGDPGiAaLyD+LLv+++L+ FG+
  gi|3649778    543 QMLQEMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDRLLVSDDLWSFGEL 592

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR k++Etk+lLL++A HkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|3649778    593 LRTKFEETKQLLLQVAAHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 642

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y v lrPh+sKE+  E sk adeLv Lnpt+++aPGLEDtLiL
  gi|3649778    643 KRIRDPNYNVKLRPHISKEFI-EISKAADELVTLNPTSEYAPGLEDTLIL 691

                    tmKGiAAGmqntG<-*
                    tmKGiAAG+qntG
  gi|3649778    692 TMKGIAAGLQNTG    704

gi|219884355|gb|ACL52552.1|: domain 1 of 1, from 1 to 658: score 1415.5, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2198843      -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2198843      - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2198843      - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2198843      - ------------------------------------------------- -
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                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2198843     - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2198843     - ------------------------------------------------ -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    mmAanlYi+q+E+LmFElsmWRCndELRvRAEEl++ + ++ v+KyYi
  gi|2198843     1 --MMAANLYIDQIEELMFELSMWRCNDELRVRAEELHSSSGSK-VTKYYI 47

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                  EFWKq+PP+EPYRviLG vRDKLYntRERaRHLLA G+s is e  +t +
  gi|2198843    48 EFWKQIPPNEPYRVILGHVRDKLYNTRERARHLLASGVSKISAESSFTSI 97

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                  EeFLEPLELCYksLC+CGDk+iADGsLLDlLRqv+tFGLsLvKLDiRqEs
  gi|2198843    98 EEFLEPLELCYKSLCDCGDKAIADGSLLDLLRQVFTFGLSLVKLDIRQES 147

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  eR+tDv+DAittHL+iGsYReW+E+KRqEWLl+EL+GKRPLl++DLP+t+
  gi|2198843   148 ERHTDVIDAITTHLGIGSYREWPEDKRQEWLLSELRGKRPLLPPDLPQTD 197

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++Dv++af+vLAELP DsFG+YiismataPsDvLAvELLqRECgv+q+L
  gi|2198843   198 EIADVIGAFHVLAELPPDSFGPYIISMATAPSDVLAVELLQRECGVRQPL 247

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +vvPLFE+LADL+ APA+ve+LFs+DWY+ ri GKq+vmvGYsDsGKDAG
  gi|2198843   248 PVVPLFERLADLQSAPASVERLFSVDWYMDRIKGKQQVMVGYSDSGKDAG 297

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLY+AqEE+++vAK+yGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|2198843   298 RLSAAWQLYRAQEEMAQVAKRYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 347

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGs+RvtvqGEviEf FGEE+LCF++LqRFtAAtLEHGm+PPvsP
  gi|2198843   348 PPDTINGSIRVTVQGEVIEFCFGEEHLCFQTLQRFTAATLEHGMHPPVSP 397

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWRkLm+emAvvAtEEYRsvvvKE RFvEYFR+AtPE+EYG+mniGsR
  gi|2198843   398 KPEWRKLMDEMAVVATEEYRSVVVKEARFVEYFRSATPETEYGRMNIGSR 447

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+AidKD++n+
  gi|2198843   448 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKFAIDKDVRNF 497

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q LkEmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLvaEeLkPFGk+
  gi|2198843   498 QVLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVAEELKPFGKQ 547

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LRdkYvEt++lLL+iAGHkD+LEGDP+LKq+l LR++YittLnvfqAYtL
  gi|2198843   548 LRDKYVETQQLLLQIAGHKDILEGDPFLKQGLVLRNPYITTLNVFQAYTL 597

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDP++kvt++P+lsKE+AdEn  k+++LvkLnp+++++PGLEDtLiL
  gi|2198843   598 KRIRDPNFKVTPQPPLSKEFADEN--KPAGLVKLNPASEYPPGLEDTLIL 645

                  tmKGiAAGmqntG<-*
                  tmKGiAAGmqntG
  gi|2198843   646 TMKGIAAGMQNTG    658

gi|38044102|dbj|BAB89368.2|: domain 1 of 1, from 1 to 657: score 1363.6, E = 0
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|3804410     -    ------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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gi|3804410     - ------------------------------------------------- -

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|3804410     - ------------------------------------------------- -

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|3804410     - ------------------------------------------------- -

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|3804410     - ------------------------------------------------- -

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|3804410     - ------------------------------------------------- -

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   mmAanlY+sq+E+LmFElsmWRCnd+LRvRA Elyr ++rd  +K+Yi
gi|3804410     1 --MMAANLYYSQIEELMFELSMWRCNDDLRVRAAELYRSSRRD--TKHYI 46

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                 EFWK +PP EPYRviLGdvRDKLY tRER+R +LA+Gis+i+E+A y +v
gi|3804410    47 EFWKTIPPSEPYRVILGDVRDKLYQTRERTRQMLAHGISDIPEDATYNNV 96

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                 E+FLEPLELCY+sLCeCGD+ iADGsLLD+LRqvstFGLs v+LDiRqEs
gi|3804410    97 EQFLEPLELCYRSLCECGDRPIADGSLLDFLRQVSTFGLSFVRLDIRQES 146

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                 +R+tDvlDAit+HLeiGsYReWsEe+RqEWLl+EL+GKRPL+g+DLP+tE
gi|3804410   147 DRHTDVLDAITQHLEIGSYREWSEERRQEWLLSELSGKRPLFGPDLPRTE 196

                 EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                 E++Dvld+++v+AELP+D+FGaYiismataPsDvLAvELLqREC+vkq+L
gi|3804410   197 EIADVLDTLHVIAELPSDCFGAYIISMATAPSDVLAVELLQRECHVKQPL 246

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                 rvvPLFEkL DLe APAav++LFsi+WY+nri+GKqevmvGYsDsGKDAG
gi|3804410   247 RVVPLFEKLDDLESAPAAVARLFSIEWYRNRINGKQEVMVGYSDSGKDAG 296

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 R+sAAWqLYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|3804410   297 RFSAAWQLYKAQEELIKVAKEHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 346

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                 PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
gi|3804410   347 PPDTIQGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 396

                 kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                 kPEWR Lm+e+Av+AtE YRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
gi|3804410   397 KPEWRALMDEIAVIATEKYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 446

                 PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                 P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFK+Ai+KDiKnl
gi|3804410   447 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKYAIEKDIKNL 496

                 qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  + +EmY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+E+L PFG+
gi|3804410   497 RMFHEMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEDLLPFGEL 546

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                 LR +Y+Et+ lLL+iAGHkDlLEGDPYLKqrlRLRdsYittLn +qAYtL
gi|3804410   547 LRSNYEETRSLLLQIAGHKDLLEGDPYLKQRLRLRDSYITTLNLLQAYTL 596

                 KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                 KRiRDP+y+vtlrPh+sK+y +     a+eL++Lnpt+++aPGLEDtLiL
gi|3804410   597 KRIRDPNYHVTLRPHISKDYMESK--SAAELLQLNPTSEYAPGLEDTLIL 644
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                  tmKGiAAGmqntG<-*
                  tmKGiAAG+qntG
  gi|3804410   645 TMKGIAAGLQNTG    657

gi|2145477|emb|CAA62749.1|: domain 1 of 1, from 1 to 676: score 1342.0, E = 0
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2145477     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2145477     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2145477     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2145477     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2145477     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                                          WmGGDRDG nPRvtPEvtRDvCLL
  gi|2145477     1 -------------------------WMGGDRDG-NPRVTPEVTRDVCLL 23

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                  aRmmAanlY+sq++DLmFElsmWRC dELR+RA+ l +  ++d   K+Yi
  gi|2145477    24 ARMMAANLYYSQIDDLMFELSMWRCSDELRARADALLQSTRKD--EKHYI 71

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                  EFWKqvP +EPYRviL dvR KLY tRER+RH+L  G s+i+Ee  +t+v
  gi|2145477    72 EFWKQVPANEPYRVILDDVRNKLYKTRERSRHMLSNGSSDIPEETTFTNV 121

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                  E+FLEPLELCY+sL  CGD  iADGsLLD+LRqvstFGLsLvKLDiRqEs
  gi|2145477   122 EQFLEPLELCYRSLFLCGDLTIADGSLLDFLRQVSTFGLSLVKLDIRQES 171

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  eR+tD +DAit+HL+iGsYReWsEeKRq WLl+EL+GKRPL+g+DLP+tE
  gi|2145477   172 ERHTDAIDAITKHLGIGSYREWSEEKRQAWLLSELRGKRPLFGPDLPRTE 221

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E+ Dvld+f+v+AELP D FGaYiismata sDvLAvELLqR C+vk++L
  gi|2145477   222 EIVDVLDTFHVIAELPADNFGAYIISMATAASDVLAVELLQRACQVKKPL 271

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADL+ APA++++LFsiDWY nri+GKqevm+GYsDsGKDAG
  gi|2145477   272 RVVPLFEKLADLQSAPASMDRLFSIDWYSNRINGKQEVMIGYSDSGKDAG 321

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   lsAAW LYkAqE+++KvAKkyGvKL++FHGRGGtvGRGGGPtH+AiLsq
  gi|2145477   322 ALSAAWELYKAQEDLVKVAKKYGVKLTMFHGRGGTVGRGGGPTHVAILSQ 371

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGslRvtvqGEviE+sFGEE LCFr+LqRFtAAtLEHGmnPP+sP
  gi|2145477   372 PPDTINGSLRVTVQGEVIEQSFGEERLCFRTLQRFTAATLEHGMNPPISP 421

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR  ++e+AvvAtEEYRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|2145477   422 KPEWRGNLDEIAVVATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 471

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|2145477   472 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHILQKDIRNL 521

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLv+++LkPFG++
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  gi|2145477   522 HLLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVSDDLKPFGEQ 571

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Etk+lLL++ GHkDlLEGDPYL+q      +YittLnv+qAYt
  gi|2145477   572 LRANYEETKQLLLQVTGHKDLLEGDPYLRQTYACVSPYITTLNVCQAYTP 621

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+++v +r +lsKE  d n  k++e +kLn t+++aPGLEDtLiL
  gi|2145477   622 KRIRDPNFQVDMRAPLSKEISDSN--KPAEQLKLNLTSEYAPGLEDTLIL 669

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|2145477   670 TMKGIAA------    676

gi|108782500|gb|ABG20462.1|: domain 1 of 1, from 1 to 671: score 1341.1, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1087825     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1087825     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1087825     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1087825     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1087825     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                                                       PEvt DvCLL
  gi|1087825     1 ----------------------------------------PEVTGDVCLL 10

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmAan+Y+sq+EDLmFElsmWRCndEL +RA E+++ ++ d   K+Yi
  gi|1087825    11 ARMMAANMYFSQIEDLMFELSMWRCNDELSARAHEIHKLSKTD--AKHYI 58

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWK +PP+EPYRv+L dvRDKLY tRE aR LL  G s+++Ee  +t++
  gi|1087825    59 EFWKRIPPNEPYRVVLADVRDKLYYTREHARQLLSNGTSDVPEESTFTHI 108

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   ++FLEPLELCY+sLC CGD+ +ADGsLLD+L qv tFGL LvKLDiRqEs
  gi|1087825   109 DQFLEPLELCYRSLCTCGDRPVADGSLLDFLPQVPTFGLCLVKLDIRQES 158

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +R+tDv+DAit+HL++GsYR WsEeKRqEWLl+EL+GKRPL+g+DLPk
  gi|1087825   159 DRHTDVMDAITKHLGVGSYRPWSEEKRQEWLLSELRGKRPLFGADLPKSY 208

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++D  ++f+v+ ELP+D FGaYiismataPsDvLAvELLqREC++k +L
  gi|1087825   209 EIADAFGTFHVISELPSDGFGAYIISMATAPSDVLAVELLQRECHIKSPL 258

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLe APA++ +LFsiDWY+nridGKqevm+GYsDsGKDAG
  gi|1087825   259 RVVPLFEKLADLESAPASLTRLFSIDWYRNRIDGKQEVMIGYSDSGKDAG 308

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYk qEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1087825   309 RLSAAWQLYKVQEELIKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 358

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEHGm+PP+sP
  gi|1087825   359 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHGMHPPISP 408
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                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAv At EYRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|1087825   409 KPEWRALMDEMAVAATKEYRSIVLQEPRFVEYFRLATPELEYGRMNIGSR 458

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhAi+KDiK l
  gi|1087825   459 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAIEKDIKKL 508

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+ mY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+EeL PFG++
  gi|1087825   509 VMLEQMYNEWPFFRVTIDLIEMVFAKGDPGIAALYDKLLVSEELCPFGEK 558

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Et+d+  ++AGHk++LEGDP L+qrlRLRd+YittLnv+qAYtL
  gi|1087825   559 LRSDYEETQDFFFQVAGHKEILEGDPHLRQRLRLRDPYITTLNVCQAYTL 608

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+v +rPh+sK+y +     a+eLvkLnp++++aPGLEDtLiL
  gi|1087825   609 KRIRDPNYHVKVRPHISKDYMESSDNLAAELVKLNPSSEYAPGLEDTLIL 658

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|1087825   659 TMKGIAAGMQNTG    671

gi|283896826|emb|CAX65714.1|: domain 1 of 1, from 1 to 658: score 1305.7, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838968     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838968     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838968     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838968     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838968     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                                                        tPEvtRDvCLL
  gi|2838968     1 ------------------------------------TPEVTRDVCLL 11

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY sq+EDLm ElsmWRCndELRvR +El+r +++d   K+Yi
  gi|2838968    12 ARMMAANLYCSQIEDLMIELSMWRCNDELRVRVDELHRSSKKD--AKHYI 59

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK++PP+ PYRviLGdvRDKLYntRERaR +L  G+s+i+Ee   t+v
  gi|2838968    60 EFWKKIPPNQPYRVILGDVRDKLYNTRERARQILSSGYSDIPEESTLTNV 109

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC CGD+viADGsLLD+LRqvstFGL Lv+LDiRqEs
  gi|2838968   110 EQFLEPLELCYRSLCACGDRVIADGSLLDFLRQVSTFGLCLVRLDIRQES 159

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+tDvlDAitt L+iGsYReWsEe+RqEWLl+EL GKRPLlg+DLP+t+
  gi|2838968   160 ERHTDVLDAITTYLGIGSYREWSEERRQEWLLSELNGKRPLLGPDLPMTD 209

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dv++afrv+AELP D FG+YiismataPsDvLAvELLqREC+vk +L
  gi|2838968   210 EVADVIGAFRVIAELPADNFGPYIISMATAPSDVLAVELLQRECHVKTPL 259

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADL+ APAav +LFs+DWY+ ri+GKqevm+GYsDsGKDAG
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  gi|2838968   260 RVVPLFEKLADLQGAPAAVTRLFSVDWYRERINGKQEVMIGYSDSGKDAG 309

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+  vAK++GvKL++FHGRGGtvGRGGGPtHLAiL+q
  gi|2838968   310 RLSAAWQLYKAQEELTNVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILAQ 359

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP tinGslRvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2838968   360 PPNTINGSLRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPMSP 409

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L++emAvvAt EYRs+v++EPRFvEYFRlAtPE+EYGkmniGsR
  gi|2838968   410 KPEWRALLDEMAVVATKEYRSIVLQEPRFVEYFRLATPETEYGKMNIGSR 459

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGi+sLRAiPWiF+WtqtR HLPvWLG+GAAFKh ++KD +n+
  gi|2838968   460 PSKRKPSGGITSLRAIPWIFSWTQTRLHLPVWLGFGAAFKHVLEKDNRNM 509

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+EmY eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+ eL+PFG++
  gi|2838968   510 HVLQEMYSEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSPELWPFGEK 559

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR +Y+Etk lLL++AGHkDlLEGD YLKqrlRLR++YittLnv+qAYt+
  gi|2838968   560 LRTNYEETKRLLLQVAGHKDLLEGDLYLKQRLRLRQAYITTLNVCQAYTM 609

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y+vtlrPhlsKE  d n k+a+eLvkLnpt+++aPGLEDtLiL
  gi|2838968   610 KRIRDPDYHVTLRPHLSKEIMDWN-KPAAELVKLNPTSEYAPGLEDTLIL 658

                   tmKGiAAGmqntG<-*

  gi|2838968     - -------------    -

gi|254587351|emb|CAR63824.1|: domain 1 of 1, from 1 to 650: score 1298.7, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2545873     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2545873     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2545873     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2545873     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2545873     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                                                      vtPEvtRDvCLL
  gi|2545873     1 -------------------------------------VTPEVTRDVCLL 12

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aR+mAan+Y+sq+EDLmFEls WRC +E+  RAE l++  ++d   K+Yi
  gi|2545873    13 ARLMAANMYYSQIEDLMFELSTWRCTEEVSQRAELLHSSTKKD--NKHYI 60

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWK+vPP EPYRviLGdvRDKLYntRERaRHLL +G s+i+E+A +t+v
  gi|2545873    61 EFWKKVPPSEPYRVILGDVRDKLYNTRERARHLLSQGHSDIPEDATFTNV 110

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   EeFLEPLELCY+sLC CGD+ iA+GsLLD+LRqvstFGLsLv+LDiRqEs
  gi|2545873   111 EEFLEPLELCYRSLCTCGDRTIAEGSLLDFLRQVSTFGLSLVRLDIRQES 160
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                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlDAitt LeiGsYReWsEeKRqEWLl+EL GKRPL++ D P+tE
  gi|2545873   161 DRHTDVLDAITTYLEIGSYREWSEEKRQEWLLSELTGKRPLIPHDFPQTE 210

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E+kDvld+++v+AELP+D FGaYiismat+PsDvLAvELLqREC+vk++L
  gi|2545873   211 EIKDVLDTLHVIAELPSDNFGAYIISMATSPSDVLAVELLQRECHVKNPL 260

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAav++LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|2545873   261 RVVPLFEKLADLEAAPAAVARLFSIDWYRNRINGKQEVMIGYSDSGKDAG 310

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    R+sAAWqLYk q E+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2545873   311 RFSAAWQLYKSQAELIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 360

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PP+sP
  gi|2545873   361 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPISP 410

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEW  Lm+emA+vAtEEYRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|2545873   411 KPEWAALMDEMAIVATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 460

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i KD++n+
  gi|2545873   461 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIAKDVRNI 510

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+EeL+PFG++
  gi|2545873   511 HMLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEELWPFGEK 560

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++++Etk+lLL++AGHkDlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|2545873   561 LRANFEETKNLLLQVAGHKDLLEGDPYLKQRLRLRDAYITTLNVLQAYTL 610

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y v  rPhlsKE  +    +a+eLvkLnpt+++aP
  gi|2545873   611 KRIRDPNYNVKCRPHLSKEIMESK--PANELVKLNPTSEYAP-------- 650

                    tmKGiAAGmqntG<-*

  gi|2545873     - -------------    -

gi|283898028|emb|CAX65715.1|: domain 1 of 1, from 1 to 641: score 1277.0, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838980     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838980     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838980     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838980     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838980     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838980     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                         anlY+sq+EDLmFElsmWRC dELRvRA+El+r +++    K+Yi
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  gi|2838980     1 -----ANLYFSQIEDLMFELSMWRCSDELRVRADELHRSSKKA--AKHYI 43

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWKqvPP+EPYRviLGdvRDKLY tRER+RHLL  Gisei+EeA +t+v
  gi|2838980    44 EFWKQVPPNEPYRVILGDVRDKLYYTRERSRHLLTSGISEIPEEATFTNV 93

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   E+FLEPLELCY+sLC CGDk iADGsLLD+LRqvstFGL+LvKLDiRqEs
  gi|2838980    94 EQFLEPLELCYRSLCACGDKPIADGSLLDFLRQVSTFGLALVKLDIRQES 143

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +R+tDvlD it+HL+iGsY eWsEeKRqEWLl+EL+GKRPL+gsDLP+tE
  gi|2838980   144 DRHTDVLDSITKHLGIGSYAEWSEEKRQEWLLSELRGKRPLFGSDLPQTE 193

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E +Dvl+af+vLAELP D+FGaY+ismataPsDvLAvELLqREC+vkq+L
  gi|2838980   194 ETADVLGAFHVLAELPADCFGAYVISMATAPSDVLAVELLQRECHVKQPL 243

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAav++LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|2838980   244 RVVPLFEKLADLEAAPAAVARLFSIDWYMNRINGKQEVMIGYSDSGKDAG 293

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   R sAAWq+YkAqEE+iKvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838980   294 RPSAAWQMYKAQEELIKVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 343

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE sFGEE+LCFr+LqR+tAAtLEHGm+PP+sP
  gi|2838980   344 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRYTAATLEHGMHPPISP 393

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emAvvAt EYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|2838980   394 KPEWRALMDEMAVVATKEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 443

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAA Kh ++KDi+n+
  gi|2838980   444 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAIKHIMQKDIRNI 493

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     LkEmY+eWPF RvtlDLlEmvFAKGDPGiAa+yDkLLvaE+L+PFG++
  gi|2838980   494 HTLKEMYNEWPFLRVTLDLLEMVFAKGDPGIAAVYDKLLVAEDLQPFGEQ 543

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR +Y+Etk+lLL++AGHkD+LEGDPYLKqrlRLR+sYittLnv+qAYtL
  gi|2838980   544 LRKNYEETKELLLQVAGHKDVLEGDPYLKQRLRLRESYITTLNVCQAYTL 593

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPs+kv ++P lsKE+ dE    ++eLv+Lnp++++aPGLEDtLiL
  gi|2838980   594 KRIRDPSFKVKPQPALSKEFTDES--LPAELVQLNPASEYAPGLEDTLIL 641

                   tmKGiAAGmqntG<-*

  gi|2838980     - -------------    -

gi|218201055|gb|EEC83482.1|: domain 1 of 1, from 10 to 683: score 1259.9, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      siDAqLR+L+P K sed+kL+eYDALLlD+FLDiLqDLHG+dL+E+v
  gi|2182010    10    SIDAQLRMLAPAKLSEDDKLVEYDALLLDRFLDILQDLHGDDLREMV 56

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   qECYE++AeYEGK+D++KL+ELG  LtsLdP+D+i++Aka++HmLnLAnL
  gi|2182010    57 QECYEIAAEYEGKHDSQKLDELGNMLTSLDPGDSIVMAKAFSHMLNLANL 106

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEEv++AyRRRik+kk GDFaDE sA tEsDiEEt+K+Lv+ l KsP+Ev
  gi|2182010   107 AEEVQIAYRRRIKLKK-GDFADENSALTESDIEETFKRLVVDLKKSPAEV 155

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   F+ALK q+vDLvltAHPtqsvRRsLLqK++RiRnCL qL+ KD+t++DK+
  gi|2182010   156 FDALKSQTVDLVLTAHPTQSVRRSLLQKHSRIRNCLVQLYSKDITPDDKQ 205
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                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRR+qPtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|2182010   206 ELDEALQREIQAAFRTDEIRRTQPTPQDEMRAGMSYFHETIWKGVPKFLR 255

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R DtALKniGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2182010   256 RLDTALKNIGIDERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 304

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmA+nlY sq+EDLmFElsmWRCndELR+RA+El+  +++d   K+Yi
  gi|2182010   305 ARMMASNLYCSQIEDLMFELSMWRCNDELRARADELHLSSKKD--AKHYI 352

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWK+vPP EPYRv+LGdvRDKLYntRERaR LL  G+s+i+Ee   t v
  gi|2182010   353 EFWKKVPPSEPYRVVLGDVRDKLYNTRERARQLLSSGYSDIPEETTLTSV 402

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC+CGD+viADG LLD+LRqvstFGL Lv+LDiRqEs
  gi|2182010   403 EQFLEPLELCYRSLCDCGDRVIADGTLLDFLRQVSTFGLCLVRLDIRQES 452

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlDAitt L+iGsYReWsEe+Rq+WLl+EL GKRPL+g+DLPkt+
  gi|2182010   453 DRHTDVLDAITTYLGIGSYREWSEERRQDWLLSELNGKRPLFGPDLPKTD 502

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+frv+AELP D FGaYiismataPsDvLAvELLqREC+vk +L
  gi|2182010   503 EIADVLDTFRVIAELPADNFGAYIISMATAPSDVLAVELLQRECHVKTPL 552

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLe APAav++LFsiDWY+ ri+GKqevm+GYsDsGKDAG
  gi|2182010   553 RVVPLFEKLADLESAPAAVARLFSIDWYRERINGKQEVMIGYSDSGKDAG 602

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYk qEE+i vAK++GvKL++FHGRGGtvGR
  gi|2182010   603 RLSAAWQLYKSQEELINVAKEFGVKLTMFHGRGGTVGR------------ 640

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                                                          HG++
  gi|2182010   641 ----------------------------------------VHGVD----- 645

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|2182010     - ------------------------------------------------- -

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                          sGG    R +    a t t   L +  G+GAA
  gi|2182010   646 ------SGGAHGERDM----AKTVTTLPLSIHHGLGAA------------ 673

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                                                + +L
  gi|2182010   674 ------------------------------LSGL---------------- 677

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|2182010     - ------------------------------------------------- -

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                                 ++s  +
  gi|2182010   678 --------------PISAVW----------------------------- 683

                    tmKGiAAGmqntG<-*

  gi|2182010     - -------------    -

gi|254587353|emb|CAR63825.1|: domain 1 of 1, from 1 to 640: score 1255.8, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2545873     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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gi|2545873     - ------------------------------------------------ -

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|2545873     - ------------------------------------------------ -

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|2545873     - ------------------------------------------------ -

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|2545873     - ------------------------------------------------ -

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|2545873     - ------------------------------------------------ -

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    mAan+Y+sq+EDLmFElsmWRC dEL  RAE l++  ++d   K+Yi
gi|2545873     1 ---MAANMYYSQIEDLMFELSMWRCTDELSQRAELLHSSTKKD--NKHYI 45

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                 EFWK+vPP EPYRviLGdvRDKLYntRERaRHLL +G s+i+E+A +t+v
gi|2545873    46 EFWKKVPPSEPYRVILGDVRDKLYNTRERARHLLSQGHSDIPEDATFTNV 95

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                 EeFLEPLELCY+sLC CGD+ iA+GsLLD+LRqvstFGLsLv+LDiRqEs
gi|2545873    96 EEFLEPLELCYRSLCACGDRTIAEGSLLDFLRQVSTFGLSLVRLDIRQES 145

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                 +R+t vlDAitt LeiGsYReWsEeKRqEWLl+EL GKRPL++ D P+tE
gi|2545873   146 DRHTGVLDAITTYLEIGSYREWSEEKRQEWLLSELTGKRPLIPHDFPQTE 195

                 EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                 E+kDvld+++v+AELP+D FGaYiismat+PsDvLAvELLqREC+vk++L
gi|2545873   196 EIKDVLDTLHVIAELPSDNFGAYIISMATSPSDVLAVELLQRECHVKNPL 245

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                 rvvPLFEkL DLeAAPAav++LFsiDWY+nri+GKqevm+GYsDsGKDAG
gi|2545873   246 RVVPLFEKLVDLEAAPAAVARLFSIDWYRNRINGKQEVMIGYSDSGKDAG 295

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 R+sAAWqL+k q E+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|2545873   296 RFSAAWQLFKSQAELIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 345

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                 PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
gi|2545873   346 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 395

                 kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                 kPEW  Lm+emA+vAtEEYRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
gi|2545873   396 KPEWAALMDEMAIVATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 445

                 PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                 P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i KD++n+
gi|2545873   446 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIAKDVRNI 495

                 qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  +L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+EeL+PFG++
gi|2545873   496 HMLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEELWPFGER 545

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                 LR++++Etk+lLL++AGH DlLEGDPYLKqrlRLRd+YittLnv+qAYtL
gi|2545873   546 LRANFEETKNLLLQVAGHNDLLEGDPYLKQRLRLRDAYITTLNVLQAYTL 595

                 KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                 KRiRDP+y v  rPhlsKE  +    +adeLvkLnpt+++aPGLEDt
gi|2545873   596 KRIRDPNYNVKCRPHLSKEIMETK--PADELVKLNPTSEYAPGLEDT--- 640

                 tmKGiAAGmqntG<-*
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  gi|2545873     - -------------    -

gi|154146668|emb|CAM83969.1|: domain 1 of 1, from 1 to 628: score 1241.8, E = 0
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541466     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541466     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541466     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541466     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541466     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541466     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                                          CndELR+RAEEl+  +++    K+Yi
  gi|1541466     1 ----------------------CNDELRIRAEELHGASRKA--AKHYI 24

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP+EPYRv+LG vRDKLY tRER+RHLL tG+sei+E+  +t+v
  gi|1541466    25 EFWKQIPPNEPYRVVLGYVRDKLYYTRERSRHLLTTGFSEIPEDSAFTNV 74

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFLEPLELCY+sLC CGDk +ADGsLLD+LRq stFGLsLvKLDiRqEs
  gi|1541466    75 EEFLEPLELCYRSLCACGDKTVADGSLLDFLRQASTFGLSLVKLDIRQES 124

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+ DvlDA+ttHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
  gi|1541466   125 ERHNDVLDAVTTHLGIGSYREWPEEKRQEWLLSELRGKRPLLGPDLPQTE 174

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541466   175 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECHVRHPL 224

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAav++LFs+DWY+ ridGKqevm+GYsDsGKDAG
  gi|1541466   225 RVVPLFEKLADLEAAPAAVARLFSVDWYMDRIDGKQEVMIGYSDSGKDAG 274

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541466   275 RLSAAWQLYKAQEELVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 324

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541466   325 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 374

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+e+AvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541466   375 KPEWRALMDELAVVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 424

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD++n+
  gi|1541466   425 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHTIKKDVRNI 474

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva++LkPFG++
  gi|1541466   475 QTLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADDLKPFGEQ 524
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                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y +t++lLL++AGHk++LEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|1541466   525 LRNNYLDTQQLLLQVAGHKEILEGDPYLKQRLRLRDPYITTLNVCQAYTL 574

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPs++vt +P+lsKE+AdEn  ++++LvkL p++++aPGLEDtLiL
  gi|1541466   575 KRIRDPSFQVTAQPPLSKEFADEN--QPAGLVKLDPASEYAPGLEDTLIL 622

                    tmKGiAAGmqntG<-*
                    tmKGiA
  gi|1541466   623 TMKGIA-------    628

gi|154146674|emb|CAM83972.1|: domain 1 of 1, from 1 to 628: score 1240.3, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541466     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541466     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541466     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541466     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541466     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541466     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                                        CndELRvRAEElyr +++    K+Yi
  gi|1541466     1 ------------------------CNDELRVRAEELYRASRKA--AKHYI 24

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP+EPYRviLG vRDKLY tRER+RHLL tG+sei+E+  +t+v
  gi|1541466    25 EFWKQIPPNEPYRVILGYVRDKLYCTRERSRHLLTTGFSEIPEDSTFTNV 74

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFLEPLELCY+sLC CGDk iADG LLD+LRqvstFGL+LvKLDiRqEs
  gi|1541466    75 EEFLEPLELCYRSLCACGDKTIADGNLLDFLRQVSTFGLALVKLDIRQES 124

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDvlDAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg DLP+ E
  gi|1541466   125 DRHTDVLDAITTHLGIGSYREWPEEKRQEWLLSELRGKRPLLGTDLPQNE 174

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541466   175 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECHVRHPL 224

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAav++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|1541466   225 RVVPLFEKLADLEAAPAAVARLFSVDWYMDRINGKQEVMIGYSDSGKDAG 274

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541466   275 RLSAAWQLYKAQEELVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 324

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541466   325 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 374

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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                    kPEWR Lm+emAvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541466   375 KPEWRALMDEMAVVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 424

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF h ++ Di+n+
  gi|1541466   425 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFEHVMKEDIRNI 474

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLv++++kPFG++
  gi|1541466   475 HMLREMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDELLVTDDIKPFGEQ 524

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR+ Y +t++lLL++AGHkD+LEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|1541466   525 LRNTYLDTQQLLLQVAGHKDILEGDPYLKQRLRLRDPYITTLNVCQAYTL 574

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPs++vt++ +lsKE+AdEn  ++++LvkLnp++++aPGLEDtLiL
  gi|1541466   575 KRIRDPSFQVTPQRPLSKEFADEN--QPAGLVKLNPASEYAPGLEDTLIL 622

                    tmKGiAAGmqntG<-*
                    tmKGiA
  gi|1541466   623 TMKGIA-------    628

gi|255071487|ref|XP_002499417.1|: domain 1 of 1, from 15 to 982: score 1222.3, E = 0
                    *->siDAqLRlLvPGKvsedek..LieYDALLlDkFLDiLqDLHGedLkE
                        +  q  +        d ++ L e D L+   F  i+++  G +
  gi|2550714    15    VVGSQYLAGTGESTQFDHHqvLQESDDLIRALFFSIVKETTGTEFFQ 61

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                      ++ Y+ls  +   +  +  + L +kL sL   +++++A+a++ +LnL
  gi|2550714    62 SLKDVYDLSEKFHETQAQSDFDALTTKLGSLTNEETMMLASAFSNVLNLH 111

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+ E v  A   R  ++   D       tt   i    K Lv k+  s e
  gi|2550714   112 NVSEHVASAMEERHARLD--DIPRGPAKTTNGAI----KGLVAKG-ISKE 154

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                     ++ A+  q vDLvltAHPtq+ RRs+L+  + +R  L  L    +   +
  gi|2550714   155 AIYKAITEQEVDLVLTAHPTQALRRSMLKNFGTVRQKLLDLQRARLSGYE 204

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    + EL + +   iq A+RtDEiRR++P PqDEmRaG+sY+ Etv++G PKF
  gi|2550714   205 RAELLDSMASAIQSAWRTDEIRRTPPKPQDEMRAGLSYFNETVFEGLPKF 254

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                     RR+D AL n G+  R+P +  +++FssWmGGDRDG nP vt   tRDv
  gi|2550714   255 CRRIDSALINQGLP-RIPMEHSIMRFSSWMGGDRDG-NPFVTATCTRDVV 302

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv...
                     LaR+ A nlY+  + DL+F lsmWRC d  R RA  l+     ++v +
  gi|2550714   303 YLARITAVNLYFKAIQDLIFSLSMWRCTDAFRERARLLHERESAEHVyem 352

                    ..vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLA..tGisei
                    ++ + Y +FW+ +P +EPYRv+L +vRDKLYntRE    ++ ++    +
  gi|2550714   353 rkQRNYADFWRSLPMEEPYRVVLAEVRDKLYNTREALQAVIMgkAEALDP 402

                    sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                    +++ ++ +  + LEPL  C +sL e GD  +ADGsLLDl+Rqv  FGLsL
  gi|2550714   403 ADDSIFRDKNQLLEPLMACHQSLIEVGDGTVADGSLLDLIRQVNCFGLSL 452

                    vKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPL
                    vKLDiRqEs+R+ D +DAit+H+++GsY +W EeK+ EWL++ELk KRPL
  gi|2550714   453 VKLDIRQESDRHADAVDAITRHIGLGSYNDWDEEKKTEWLVSELKSKRPL 502

                    lgsDLPktEEvkDvldafrvLAELPiDs...FGaYiismataPsDvLAvE
                    + sDL  t++v++vld+f+++A L   ++++ G Y+ismat  sDvLAv
  gi|2550714   503 VASDLECTDDVREVLDTFKMIAHLQEVCpgsLGTYVISMATVASDVLAVV 552

                    LLqRECg..vkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKq
                    LLqRE g+++ q Lrv PLFE+L DL+  P  + +LFsi WY   idG q
  gi|2550714   553 LLQREMGgkMDQLLRVAPLFERLDDLNEGPNQLRRLFSIPWYHELIDGHQ 602
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```
                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                    evm+GYsDsGKDAGR++AAW LY  qE   KvA ++GvKL+lFHGRGGtv
  gi|2550714   603 EVMIGYSDSGKDAGRMAAAWALYEGQENATKVADEFGVKLTLFHGRGGTV 652

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                    GRGGGP HLAiLsqPP tinG lRvtvqGEviE+ FGE + CF++L  +t
  gi|2550714   653 GRGGGPSHLAILSQPPATINGRLRVTVQGEVIEQNFGEHENCFHTLDLYT 702

                    AAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlA
                    AAtLEH + PP++P  EWR  m  m  v  E YR +v+K P F  YF  A
  gi|2550714   703 AATLEHSLAPPLAPSDEWRGAMATMSEVSCERYREIVFKTPEFNPYFLQA 752

                    tPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvG
                    tP  E G +niGsRPaKRk   G+++LRAiPWiFaWtq RFHLPvWLG+
  gi|2550714   753 TPGQELGALNIGSRPAKRKSNAGVTALRAIPWIFAWTQSRFHLPVWLGIA 802

                    AAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyD
                      F+    K+   l  L+EmY++WPFFRvt+DL+Emv AK DP +A Ly+
  gi|2550714   803 EGFQRV--KEQGKLETLREMYRTWPFFRVTMDLIEMVLAKADPTVARLYE 850

                    kLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDP.........Y
                    k Lv E+ + FG++LR     t d++L++  H DlL    +++++++ +
  gi|2550714   851 KELVEEQYHAFGEQLRKALRSTVDIVLEVTEHPDLLTSQTtnggqgsinT 900

                    LKqrlRLRdsYittLnvfqAYtLKRiRDPsy.kvtlrPhlsKEyAdEnsk
                    LK +l +R  Y+t Ln++q   LKR+RD + +kv  +  +     + +
  gi|2550714   901 LKDKLAMRSIYLTPLNIIQVENLKRLRDIEDgKVDTKGYVPVMPWAKQ-- 948

                    kadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                         +++   + +   + DtLi+tmKGiAAGmqntG
  gi|2550714   949 --MLSLHVS-KDYYHAAVSDTLIITMKGIAAGMQNTG    982

gi|226463760|gb|EEH61038.1|: domain 1 of 1, from 10 to 991: score 1207.4, E = 0
                    *->siDAqLRlLvPG...........KvsedekLieYDALLlDkFLDiLq
                         DA+ + Lv  ++  +++++++     e L e + L+   F  i+
  gi|2264637    10    --DAKFKELVADshylsgsgethDFDHHEVLQESEDLMRALFFSIVR 54

                    DLHGedLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAk
                    +  G +  +     Y ls ++    D+     L +kL sL   +++++A+
  gi|2264637    55 ETTGTEFDDSLEAVYALSEQFHKSNDPADFAALTTKLGSLSDEETVMLAS 104

                    ailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkL
                    a++ +LnL n+ E v  A   R  ++   D       tt   i    K L
  gi|2264637   105 AFSNVLNLHNVSEHVAAAMEERHARLD--DIPRGPAKTTNGAI----KGL 148

                    vlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL
                    +  +  s e ++eAL  q vDLv+tAHPtq+ RRs+L+  aRiR CL  L
  gi|2264637   149 IANG-VSKETIYEALAEQEVDLVFTAHPTQALRRSMLKNFARIRQCLLDL 197

                    sAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHE
                     A+ +   ++ E+   +   iqAA+RtDEiRR +P PqDEmRaG+sY+ +
  gi|2264637   198 QARRLSGYERAEILASMSSAIQAAWRTDEIRRNPPKPQDEMRAGLSYFND 247

                    tvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRv
                    t+++G PKF+RR+DtAL n G+  R+P d  ++kFssWmGGDRDG nP v
  gi|2264637   248 TLFEGLPKFVRRIDTALINQGLP-RIPLDKSIMKFSSWMGGDRDG-NPNV 295

                    tPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrt
                        t+D   LaR  Aa lY++ +  L+F lsmWRC +  ++RA   +
  gi|2264637   296 DSHCTKDAVYLARSKAADLYFDAIQNLIFSLSMWRCSESFKARAAARHAF 345

                    ...........aardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRE
                      ++++++   a r+   + Y++FW  +P   PYRv+L +vRD+LYnt+E
  gi|2264637   346 vlsqqddgalyAERK--RRNYVDFWHALPLSQPYRVVLSEVRDRLYNTKE 393

                    RaRHLLAtGisei.sEeA.vytkvEeFLEPLELCYksLCeCGDkviADGs
                      + ++A  +  +++++A+++t  E+ LEPL  CY sL + GDk +ADG
  gi|2264637   394 AIKDVIAGRVDALnPDDAsIFTSKEQLLEPLLACYNSLIDVGDKSVADGY 443

                    LLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeK
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                    LLDl+Rqv  FGLsLv+LDiRqEs+R+ D +DAit+H+++GsY eW EeK
  gi|2264637   444 LLDLIRQVNCFGLSLVRLDIRQESDRHADAMDAITKHIGLGSYNEWDEEK 493

                    RqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDs...FGaY
                    +  +L+aEL+GKRPL++ DL  t Ev++v+d+f++   L   ++++ G Y
  gi|2264637   494 KCAFLVAELEGKRPLVPRDLECTAEVQEVIDTFHMAGHLQRVCpgsLGTY 543

                    iismataPsDvLAvELLqREC..gvkqtLrvvPLFEkLADLeAAPAavek
                    +ismat  sDvLAv LLqREC+++  + Lrv PLFE+L DL+  PA + +
  gi|2264637   544 VISMATVASDVLAVVLLQRECggHEDRLLRVAPLFERLDDLRDGPAQLRR 593

                    LFsiDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKk
                    LFs+ WY  +idG qevm+GYsDsGKDAGR++AAW LY  qE    v  +
  gi|2264637   594 LFSVPWYHKHIDGFQEVMIGYSDSGKDAGRMAAAWALYEGQENATHVGNE 643

                    yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                    +GvKL+lFHGRGGtvGRGGGP HLAi+sqPP tinG lRvtvqGEviE+
  gi|2264637   644 FGVKLTLFHGRGGTVGRGGGPSHLAIMSQPPATINGRLRVTVQGEVIEQN 693

                    FGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRs
                    FGE + CF++L  +tAAtLEH ++PP sP+ EWR++m+ m     E YR
  gi|2264637   694 FGEHENCFHTLDLYTAATLEHSLKPPTSPQTEWRDVMNVMSEESCEKYRK 743

                    vvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFa
                    vv+  P F+ YF  AtP  E G +niGsRPaKRk    +++LRAiPWiFa
  gi|2264637   744 VVFETPEFIRYFAQATPAQELGSLNIGSRPAKRKANPTVTALRAIPWIFA 793

                    WtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlE
                    Wtq RFHLPvWLG+   F+    KD   l +L+ mYk+WPFFRvt+DL+E
  gi|2264637   794 WTQSRFHLPVWLGMAEGFQKL--KDDGKLPMLRAMYKDWPFFRVTMDLIE 841

                    mvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDl
                    mv AK D  +A  y+k+Lv   L+ FG  LR++ v t +++L+i  H Dl
  gi|2264637   842 MVLAKADFNVAEYYEKVLVEPGLHAFGATLRQQLVNTVKIVLEITEHPDL 891

                    LEGD.........PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtl
                    L   +++++++++ +L  +l +R  Yit Ln++q   LKR+R  +
  gi|2264637   892 LTPQsdskgqsssTFLAEKLSMRSTYITPLNIIQVENLKRLRAIESGEVS 941

                    rPhlsKEyAdEnskkadeLvkLnpter..vaPGLEDtLiLtmKGiAAGmq
                       ++K     +   + e++ L  ++++ +   + DtLi+tmKGiAAGmq
  gi|2264637   942 EEFMAKYAPSMP--WSKEMLSLH-GKNnwYHATVSDTLIITMKGIAAGMQ 988

                    ntG<-*
                    ntG
  gi|2264637   989 NTG    991

gi|2145463|emb|CAA62748.1|: domain 1 of 1, from 1 to 669: score 1179.5, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2145463     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2145463     - ---------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2145463     - ---------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2145463     - ---------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2145463     - ---------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                                        WmGGDRDG nPRvtPEvtRDvCLL
  gi|2145463     1 -------------------------WMGGDRDG-NPRVTPEVTRDVCLL 23
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                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aR++A+nlY+s +EDLmFElsmWRC dELR+R  El   +++d   KyY+
  gi|2145463    24 ARLIASNLYFSRIEDLMFELSMWRCSDELRARVNELVFSSRKD--AKYYM 71

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP+EP+Rv+LG vRD+LYnt E +R LLA G se +Ee  +t v
  gi|2145463    72 EFWKQIPPNEPFRVVLGHVRDRLYNTYELSRQLLAXGXSEXPEET-FTSV 120

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    +e LEPLELCY sLC  GDk+iADGsLLD++Rqvs FGLsLvKLDiRqEs
  gi|2145463   121 DEILEPLELCYASLCSTGDKAIADGSLLDFMRQVSCFGLSLVKLDIRQES 170

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+ Dv+DAit  L+iGsYReWsEe+Rq WLl+EL+G RPL+g+  P+ E
  gi|2145463   171 DRHSDVMDAITNYLGIGSYREWSEEQRQKWLLSELRGNRPLYGPGXPRXE 220

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++D l++++v+ ELP DsFGaYiismataPsDvLAvELLqREC v ++L
  gi|2145463   221 EIRDCLETIHVISELPPDSFGAYIISMATAPSDVLAVELLQRECRVTHPL 270

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLe APAa+++LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|2145463   271 RVVPLFEKLADLESAPAALARLFSIDWYRNRINGKQEVMIGYSDSGKDAG 320

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqL+kAqEE+i vAK+yG+KL +FHGRGGtvGRGGGPtHLAiLsq
  gi|2145463   321 RLSAAWQLFKAQEELINVAKQYGIKLNMFHGRGGTVGRGGGPTHLAILSQ 370

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+ FGEE+L F++LqRFtAAtLEHGm+PP+sP
  gi|2145463   371 PPDTIHGSLRVTVQGEVIEQLFGEEHLSFQTLQRFTAATLEHGMHPPISP 420

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emA +AtEEYRs+v+KE RF+EYF  AtP lEYG+mniGsR
  gi|2145463   421 KPEWRALMDEMASIATEEYRSLVFKESRFMEYFHAATPVLEYGRMNIGSR 470

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkP  GiesLRAiPWiFaWtqtRFHLPvWLG+GAAFK  +++D  nl
  gi|2145463   471 PSKRKPNSGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKSVMERDPNNL 520

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmYkeWPFFRvt+DL+EmvFAKGDP i aLyDkLLv ++L+ FG+
  gi|2145463   521 IVLQEMYKEWPFFRVTIDLVEMVFAKGDPRITALYDKLLVNDDLQYFGDI 570

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR+kY+Etk+lLLk+AGHk++LEG P LKqrl LR++ ittLnv qA+tL
  gi|2145463   571 LRAKYEETKKLLLKVAGHKEILEGNPTLKQRLLLREPCITTLNVQQAFTL 620

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KR R+ +      P  sK     n   a+eL+ Ln t+++aPGLEDtLiL
  gi|2145463   621 KRXREGNKDL---PVHSK---SRN--SAAELITLNTTSEYAPGLEDTLIL 662

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|2145463   663 TMKGIAA------    669

gi|51701301|sp|P81831.2|CAPP1_CHLRE: domain 1 of 1, from 13 to 974: score 1170.8, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +   LR       s    L + D LL   F  iL   H ++L   v
  gi|5170130    13    RVSQDLRTGPANFLS---GLRDDDSLLRQVFFSILRH-HHPNLAAKV 55

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       Y ls  +   +     e +   +  L P + ilvA++++HmLnL nL
  gi|5170130    56 DVIYALSQAWCTSQSDNDFELMVKYVSDLKPEERILVASSFSHMLNLHNL 105

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     EEv+     R  ++       E +  t  D    l kL      +P+ v
  gi|5170130   106 TEEVNSSQIGRAVRLG------EMDSPTR-DTNHSLLKLTTTNGFTPQQV 148

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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                    ++ L  q+v+LvltAHPtq+ R sLL+K a +R  L  L  K +   +K
  gi|5170130   149 YDTLCSQTVELVLTAHPTQALRASLLKKYAIVRRELDTLHSKRMSEYEKI 198

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    E  EA+   +qAA+RtDEiRR++PtPqDEmR G+sY+   +++ vP F R
  gi|5170130   199 ETLEAIRAAVQAAWRTDEIRRSKPTPQDEMRSGLSYFSTVIFDVVPVFHR 248

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtAL  +G+  RlP d  L kF sWmGGDRDG nP vt E tRDv +L
  gi|5170130   249 RVDTALEKLGLP-RLPLDRALFKFGSWMGGDRDG-NPNVTAETTRDVVVL 296

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv.....
                    aR+ A n+Y+ qvE LmF+ls+WRC  E++  AE l     rd  +  ++
  gi|5170130   297 ARLEAVNVYFRQVEGLMFDLSIWRCSPEMKELAERLAAAESRDAArvaee 346

                    ..vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseis.
                    ++ + Y++FW  +PPtEP+Rv+L  +RD+LYntR      L +    + +
  gi|5170130   347 rkRRNYVDFWAPIPPTEPFRVVLAHMRDRLYNTRQVLHQCLIHTHMSVRg 396

                    ..EeA.vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                      EeA+ y ++E+   PL L Y sL   GD  +A   LLDlLRq+ tFGL
  gi|5170130   397 alEEAgAYVDIEDMARPLKLMYDSLMSTGDESVANARLLDLLRQIRTFGL 446

                    sLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKR
                     ++ LD+RqEs R+t+v+DA+tt L++GsY +W E KR  +Ll EL+GKR
  gi|5170130   447 CMMGLDVRQESTRHTEVMDAVTTYLGLGSYASWDEPKRLAFLLGELQGKR 496

                    PLlgsDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvEL
                    PL+++ + +  Evk+v+ ++r+L ELP Ds GaYiisma + sDvLAv L
  gi|5170130   497 PLMPPGMDMSPEVKEVVRTLRILSELPGDSLGAYIISMAKTASDVLAVVL 546

                    LqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevm
                    LqRE gv+ +LrvvPLFE L DL+ AP ++  L   DWY+ +i+G qe m
  gi|5170130   547 LQRETGVRPALRVVPLFETLDDLHNAPGTMTTLLGNDWYRGHINGVQECM 596

                    vGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRG
                    +GYsDsGKDAGRl+AAW LY  qE ++ vA   Gv+LvlFHGRGGtvGRG
  gi|5170130   597 IGYSDSGKDAGRLAAAWALYETQEKLVEVAAGCGVRLVLFHGRGGTVGRG 646

                    GGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAt
                    GGPtH+Ai sqP  tinG lRvtvqGE+iE+ FGE ++CFr+L  +t A
  gi|5170130   647 GGPTHMAIRSQPSGTINGHLRVTVQGEIIEQQFGEKEVCFRTLDLYTSAV 696

                    LEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPE
                    LE  ++PP +P  EWR+Lm  +A    + YRsvv++ P F +YF   t
  gi|5170130   697 LEAALDPPPAPAQEWRDLMSLLATESCDMYRSVVYRTPEFYDYFMQSTAA 746

                    lEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAF
                     E G++niGsRP+ Rk sGGie+LRAiPWiFaWtq R HLPvWLG+G A
  gi|5170130   747 SELGRLNIGSRPSSRK-SGGIETLRAIPWIFAWTQQRLHLPVWLGIGEAL 795

                    KhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL
                      AidK    +  L++mY +WPFF  tlDL+Emv AK D  + a y++ L
  gi|5170130   796 EAAIDKGYGPV--LQDMYANWPFFTSTLDLVEMVLAKADSRLSAFYERTL 843

                    vaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGD.......PYLKqrl
                    v   L P G++LR+    t++ +L +     lLEG ++++ ++P L  ++
  gi|5170130   844 VDSSLAPLGQRLRELLAKTQQNILIVVRKSVLLEGNtpsqmstPNLDEKI 893

                    RLRdsYittLnvfqAYtLKRiR......DPsykvtlrPhlsKEyAdEnsk
                    RLR +Y+  Lnv+qA  L+ +R+ ++++D +y     P++      ++ k
  gi|5170130   894 RLRSPYVAPLNVLQALSLQGLRkfrdggDTEYN-PSDPEIIDLLSRDPHK 942

                    kadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    k ++  +          ++D L++t+KGiAAGmqntG
  gi|5170130   943 KGEGAQHPF-----VSAMDDCLMITIKGIAAGMQNTG    974

gi|154146672|emb|CAM83971.1|: domain 1 of 1, from 1 to 627: score 1144.6, E = 0
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541466     -    ---------------------------------------------- -
```

```
                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|1541466    - ------------------------------------------------ -

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1541466    - ------------------------------------------------ -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1541466    - ------------------------------------------------ -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1541466    - ------------------------------------------------ -

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1541466    - ------------------------------------------------ -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                                  CndELR+RAEEl++ ++     K+Yi
gi|1541466    1 ------------------------CNDELRARAEELHSGSKTT---KHYI 23

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                EFWKq+P +EPYRv+LG vRDKLYntRERa  LL  G s i+Ee     v
gi|1541466   24 EFWKQIPLNEPYRVVLGSVRDKLYNTRERALQLLTAGTSTIAEESTVRSV 73

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                EeFLEPLELCY+sL  CGDk iADGsLLD+LRqvstFGLsLvKLDiRqEs
gi|1541466   74 EEFLEPLELCYRSLVACGDKTIADGSLLDFLRQVSTFGLSLVKLDIRQES 123

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                +R+t+v+DAittHL+iGsYR+WsEe Rq WL+ EL+GKRPLl +D+P+ E
gi|1541466  124 DRHTEVVDAITTHLGIGSYRSWSEEERQKWLINELRGKRPLLAPDMPMSE 173

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                Ev+D +++f+vLAELP DsFG+Yiism+ta sDvLAv LLqRECg+k++L
gi|1541466  174 EVADAIGTFKVLAELPDDSFGPYIISMCTAASDVLAVYLLQRECGIKNPL 223

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                +vvPLFE+LADL+AAPA++e LFs+DWY   i+GKq+vm+GYsDsGKDAG
gi|1541466  224 PVVPLFERLADLQAAPASMELLFSVDWYAQTINGKQQVMIGYSDSGKDAG 273

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLY+AqE+++K+AKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1541466  274 RLSAAWQLYRAQEDLAKIAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 323

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PPDtinGs+Rvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
gi|1541466  324 PPDTINGSIRVTIQGEVIEYSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 373

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                kPEWR Lm+emAvvAtEEYRsvv++EPRFvEYFR+AtPE+EYGkmniGsR
gi|1541466  374 KPEWRALMDEMAVVATEEYRSVVFREPRFVEYFRSATPETEYGKMNIGSR 423

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                PaKRkP GGiesLRAiPWiF+WtqtRFH+PvWLGvG AF+ Ai+KD Knl
gi|1541466  424 PAKRKPKGGIESLRAIPWIFSWTQTRFHVPVWLGVGSAFQSAIKKDPKNL 473

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  LkEmY+eWPFFRvtlDLlEmvFAKG P iAa+yD+LLvaEeLkP G+
gi|1541466  474 NLLKEMYNEWPFFRVTLDLLEMVFAKGNPNIAAIYDELLVAEELKPLGET 523

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR kYvEt++lLL+iAGHkD+LEGDPYLKqrlRLRd+YittLnv+qAYtL
gi|1541466  524 LRSKYVETQELLLQIAGHKDILEGDPYLKQRLRLRDPYITTLNVLQAYTL 573

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                K+iRDPs++vt++P lsKE+AdE   + ++L kLnp++++aPGLEDtLiL
```

```
  gi|1541466   574 KKIRDPSFQVTPQPLLSKEFADEA--QRADLEKLNPASEYAPGLEDTLIL 621

                    tmKGiAAGmqntG<-*
                    tmKGiA
  gi|1541466   622 TMKGIA-------    627

gi|116060913|emb|CAL57391.1|: domain 1 of 1, from 42 to 1014: score 1123.2, E = 0
                    *->siDAqLRlLvPGKvsedekLi.eYDALLlDkFLDiLqDLHGedLkEa
                            L      K  +  ++i+e DALL   F  ++ +   e+
  gi|1160609    42    TTSSYLSGRGETKDFNAHDVIeECDALLQTIFFSVVRETTSEEFLAK 88

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                     q  Y+ s  +    ++k  e +   L  ++  +++  A+a++ +LnL n
  gi|1160609    89 LQGVYDGSEAFGKTGEPKDFEAMKKLLETMEVDESLQFASAYSNLLNLHN 138

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E v  A   R k++   D        t   i    K L+  + K+ eE
  gi|1160609   139 ISEQVANAMEERHKRLD--DIPRGPAKSTNGAI----KGLIRSG-KTIEE 181

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    ++ AL  q vDLvltAHPtq+ RRs+L+  +++R  L qL    +   ++
  gi|1160609   182 IYAALSRQHVDLVLTAHPTQALRRSMLKAFGKVREKLLQLQRFRLSRFER 231

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     E+ + +   i AA+RtDEiRR++P PqDEmRaG+ Y+  t+W+ vP F+
  gi|1160609   232 AEILDEIRSNIAAAWRTDEIRRTPPKPQDEMRAGLTYFQQTIWDCVPTFM 281

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    RRvDtAL   G   RlP d  ++ F sWmGGDRDG nP vt E tRDv L
  gi|1160609   282 RRVDTALLANGCG-RLPLDRSIVTFGSWMGGDRDG-NPFVTSECTRDVVL 329

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy.
                    LaR+  +n+ +s +  L+FElsmWRCnd ++  A ++  t+  dk   ++
  gi|1160609   330 LARVQGTNFLFSTIQKLLFELSMWRCNDTVKRLANDILATSETDKNAIFe 379

                    .......YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAt.Gis.e
                    ++++++Y +FWK +P  EPYRviL   RDKLYntRE     +  + +s +
  gi|1160609   380 erkrrnYDDFWKAIPEHEPYRVILAMLRDKLYNTREALQKCVTDpNVSiD 429

                    isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                    + ++ +    Ee  EPL  CY sL e  D  iA   LLD++Rqv  FGL
  gi|1160609   430 VNDDSIIRTKEEIYEPLVACYESLIEVKDDQIANSLLLDVIRQVQCFGLG 479

                    LvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRP
                    LvKLDiRqEs+R+ + lDA+t+ +++GsY eWsE+++ EWL +EL  KRP
  gi|1160609   480 LVKLDIRQESDRHAEALDAVTRYIGLGSYIEWSEDQKIEWLTSELMSKRP 529

                    LlgsDLPktEEvkDvldafrvLAELPiDs...FGaYiismataPsDvLAv
                    L++ DL    +v++vld+ +++A L   ++++ G Y+ismat+ sDvLAv
  gi|1160609   530 LIPHDLECSADVREVLDTCKMIAHLQQTCpgsLGTYVISMATSASDVLAV 579

                    ELLqRECgvkq..tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK
                     LLqRECg ++++ Lrv PLFE+L DL+ AP  + +LFs+ WY  +i+G
  gi|1160609   580 VLLQRECGCREkdVLRVAPLFERLDDLNDAPRVLRQLFSVKWYLDHINGF 629

                    qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                    qevm+GYsDsGKDAGR++AAW LY  qE ++    ++ v ++lFHGRGGt
  gi|1160609   630 QEVMIGYSDSGKDAGRMAAAWALYEGQERVVAAGNEFNVAMTLFHGRGGT 679

                    vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                    vGRGGGP H+A+LsqPP t+nGs+RvtvqGEviE  FGE + CF++L  +
  gi|1160609   680 VGRGGGPAHIAMLSQPPGTVNGSIRVTVQGEVIESDFGERENCFHTLDLY 729

                    tAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRl
                    tA  LEH ++PP  P   WR +m++m       YR  v+  P Fv YF
  gi|1160609   730 TASVLEHSLKPPSHPDDKWRAVMDRMSEYSCAHYRKTVFETPEFVQYFAQ 779

                    AtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGv
                    AtP  E G +niGsRPaKRkP  G+++LRAiPWiFaWtq RFHLPvWLG+
  gi|1160609   780 ATPGSELGSLNIGSRPAKRKPNAGVTALRAIPWIFAWTQSRFHLPVWLGI 829
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                    GAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLy
                     A FK  i+     lq L++mYk WPFF vt+DL+Emv AK DP + a y
  gi|1160609   830 SASFKRLIEEG--ELQTLRDMYKRWPFFEVTIDLVEMVLAKADPVVVAYY 877

                    DkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlL.............
                    +k Lv E L+ FG +LR + +   d +L +  H  lL ++++++++ ++
  gi|1160609   878 EKALVDESLHDFGAKLRGELESSIDVILTVSEHIGLLvqpekteenanea 927

                    .EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                    +     LK +l  R+ Yit Lnv+q   LK  R  +++     +ls
  gi|1160609   928 rRMQQKLKHKLEKRNLYITPLNVCQVRFLKQARALEHEEDGE-KLSMRKV 976

                    dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                         +       n    +   + D L +tmKGiAAGmqntG
  gi|1160609   977 KITMLEGYPFQDFN----YKGAVNDVLKITMKGIAAGMQNTG    1014

gi|145353090|ref|XP_001420862.1|: domain 1 of 1, from 31 to 1007: score 1108.1, E = 0
                    *->siDAqLR....lLvPGKvse...dekLieYDALLlDkFLDiLqDLHG
                       ++DA  R+++ l   G   e +  + + e D LL   F  ++ +  G
  gi|1453530    31    ALDALARsssyLSGRGETKEfnaHDVIEECDELLRTIFFAVVRETAG 77

                    edLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailH
                    +      +  YE s  +   +D+k  + + a L  ++  +++  A+a++
  gi|1453530    78 DKFLGQLKSVYEASEKFGSSHDPKDFDAMQAMLETMEVDESLQFASAYSN 127

                    mLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkl
                    +LnL n+ E v  A   R +++   D       tt   i    K L   +
  gi|1453530   128 LLNLHNISEQVANAMEERHRRLD--DIPRGPAKTTNGAI----KGLLRAG 171

                    nKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKD
                     Ks eE++ AL  q vDLvltAHPtq+ RRs+L+  + iR  L qL
  gi|1453530   172 -KSTEEIYSALAVQHVDLVLTAHPTQALRRSMLKSFGIIREKLLQLQRFR 220

                    vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWk
                    +   ++ E+ + +   +  A+RtDEiRR++P PqDEmRaG+ Y+  t+W+
  gi|1453530   221 LSRYERAEVLDEIRSKVASAWRTDEIRRTPPKPQDEMRAGLTYFQQTIWD 270

                    GvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEv
                    G+P F+RRvDt L   G   RlP d  ++ F sWmGGDRDG nP vt
  gi|1453530   271 GIPTFMRRVDTSLLANGCP-RLPLDRSIVTFGSWMGGDRDG-NPYVTASC 318

                    tRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaard
                    tRDv LLaR+   nl +  +  L+F+lsmWRCnd +++ A ++   +  d
  gi|1453530   319 TRDVVLLARVQGVNLLFRAIQRLIFDLSMWRCNDAVKALAKDILENSETD 368

                    kvvKy.......YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAt
                      + ++++++++Y +FWK +P  EPYRviL + RDKLYntRE     +A
  gi|1453530   369 NFTIFeerkkrnYDDFWKAIPEHEPYRVILAELRDKLYNTREALQRCIAD 418

                    Gisei..sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqv
                       +i+  +e +    +e   PL +CY sL e GD  iA   LLD++Rqv
  gi|1453530   419 NDVNIdmNDETIIRSKDELFAPLVVCYESLIEVGDAQIANAYLLDVIRQV 468

                    stFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaE
                      FGL LvKLDiRqEs+R+ + lDA+t+ +++GsY eWsEe++ E+L  E
  gi|1453530   469 QCFGLGLVKLDIRQESDRHAEALDAVTRYIGLGSYLEWSEEQKIEFLTRE 518

                    LkGKRPLlgsDLPktEEvkDvldafrvLAELPiDs...FGaYiismataP
                    L+ KRPLl+sDL   ++v++vld+ +++A L   +++  G Y+ismat+
  gi|1453530   519 LESKRPLLPSDLECSDDVREVLDTCKMIAHLQQTCpgaLGTYVISMATSA 568

                    sDvLAvELLqRECgvkqt..LrvvPLFEkLADLeAAPAavekLFsiDWYi
                    sDvLAv LLqRECg ++ + Lrv PLFE+L DL+ AP  + +LFs+ WY
  gi|1453530   569 SDVLAVVLLQRECGCRKQdlLRVAPLFERLDDLNDAPRVLRQLFSVKWYH 618

                    nridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                     +i G qevm+GYsDsGKDAGR++AAW LY  qE ++   K++ v L+lF
  gi|1453530   619 DHIAGFQEVMIGYSDSGKDAGRMAAAWALYDGQERVVAAGKEFDVALTLF 668

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGGtvGRGGGP H+A+LsqPP t+nGs+RvtvqGEviE  FGE + CF
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  gi|1453530   669 HGRGGTVGRGGGPAHIAMLSQPPGTVNGSIRVTVQGEVIETDFGEKENCF 718

                   rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                   ++L  +tA  LEH ++PP  P+ EWR++m++m       YR  v+  P F
  gi|1453530   719 HTLDLYTASVLEHTLKPPAHPRDEWRRVMDRMSEYSCAHYRKTVFETPDF 768

                   vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                   v YF  AtP  E G +niGsRPaKRkPs G+++LRAiPWiFaWtq RFHL
  gi|1453530   769 VGYFAQATPGAELGSLNIGSRPAKRKPSAGVTALRAIPWIFAWTQSRFHL 818

                   PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                   PvWLG+   F+  i  D   l  L++mYk WPFF vt+DL+Emv AK DP
  gi|1453530   819 PVWLGISTSFRRLI--DEGELETLRDMYKSWPFFEVTIDLVEMVLAKADP 866

                   GiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlL.......
                    + a y++ Lv   L+ FG sLR + +E  d +L +  H  lL ++++ +
  gi|1453530   867 VVVAYYERALVDPKLHDFGASLRGELQESIDCILAVSEHIGLLakpekve 916

                   .....EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                    ++       L  +l  R  Yit Lnv+q           y +  r
  gi|1453530   917 aneavQVHKKLAHKLHKRSLYITPLNVCQV---------RYLIAARALEN 957

                   KEyAdEnskkadeLvkLn....ptervaPGLEDtLiLtmKGiAAGmqntG
                    E  d  s +   +  L + +    ++   + D L +tmKGiAAGmqntG
  gi|1453530   958 EEDGDKLSMQKVKITLLEgypfQDYNYKGAVNDVLKITMKGIAAGMQNTG 1007

                   <-*

  gi|1453530     -     -

gi|154146670|emb|CAM83970.1|: domain 1 of 1, from 1 to 630: score 1051.9, E = 0
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541466     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541466     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541466     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541466     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541466     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541466     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                                       CndELR+RA+El+r + r+   KyYi
  gi|1541466     1 ----------------------CNDELRARADELHRQSSRK-YAKYYI 25

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWKq+ P EPYR++LGdvRDKLYnt ERaR +L +G+s+i+E+  + +v
  gi|1541466    26 EFWKQISPREPYRIVLGDVRDKLYNTCERARQILSHGVSNIPEDQTFINV 75

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    +FLEPLELCY+sLC+CGDk iADG LLD++RqvstFGLsLvKLDiRqEs
  gi|1541466    76 KQFLEPLELCYRSLCDCGDKLIADGNLLDFMRQVSTFGLSLVKLDIRQES 125

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +R+tD +DAittHL+iGsYRe +Ee+RqEWL++EL+GKRPL+g+DLP+ +
  gi|1541466   126 DRHTDAMDAITTHLGIGSYRERPEEQRQEWLVSELRGKRPLFGPDLPQSD 175
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                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl++frv+AELP DsFGaYiismataPsDvLAvELLqRECgvk++L
  gi|1541466   176 EVADVLGTFRVIAELPDDSFGAYIISMATAPSDVLAVELLQRECGVKRPL 225

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADL+  PA+++ LFsiDWY+ ri GKqe+m+GYsDsGKDAG
  gi|1541466   226 RVVPLFEKLADLQQGPATMDLLFSIDWYKQRIGGKQEIMIGYSDSGKDAG 275

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEEi++vA ++GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541466   276 RLSAAWQLYKAQEEIVRVAERHGVKLTIFHGRGGTVGRGGGPNHLAILSQ 325

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP t+nGslRvtvqGEviE sFGEEnLCFr+LqRFtAAtLEHGmnPPvsP
  gi|1541466   326 PPNTVNGSLRVTVQGEVIEKSFGEENLCFRTLQRFTAATLEHGMNPPVSP 375

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR+L+++m  v tEEYRs+v++EPRFvEYFR AtPE+EYG+mniGsR
  gi|1541466   376 KPEWRRLLDDMVAVSTEEYRSIVFQEPRFVEYFRAATPETEYGRMNIGSR 425

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+hA +     l
  gi|1541466   426 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHAAEAPG-GL 474

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvt+DLlEmvFAKGDPGiAaLyDkLLv  eL+PFG++
  gi|1541466   475 ATLREMYDEWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVPGELRPFGEQ 524

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y  t+ lLL++AGH +lLE DPYL+qrl LRdsYit Ln +qAYtL
  gi|1541466   525 LRANYAATQRLLLQVAGHEELLESDPYLRQRLMLRDSYITALNACQAYTL 574

                    KRiRDPsykvtlr.PhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    KRiRD  ++   r  +lsKE        a++LvkLnp++++ PGLEDtLi
  gi|1541466   575 KRIRDGGFRPAARaAPLSKELLGSA-STAEGLVKLNPSSEYDPGLEDTLI 623

                    LtmKGiAAGmqntG<-*
                    LtmKGiA
  gi|1541466   624 LTMKGIA-------    630

gi|88813079|ref|ZP_01128321.1|: domain 1 of 1, from 5 to 880: score 899.6, E = 1.6e-267
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        iDA LR          e++ +   LL     +  qD  Ge L   v
  gi|8881307     5    RIDAPLR----------EDIRQLGGLLGSTLYE--QD--GEPLYNTV 37

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E   ls +      +   e L + L +Ld a  + v +a++  LnLAn+
  gi|8881307    38 EEIRRLSKDARAGV-PGAAEQLSSMLAGLDDAMIMPVVRAFSNFLNLANI 86

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE     +R R ++       D  sA     +EE + +L       P+E
  gi|8881307    87 AEQ---HHRIRRSRAW---LRDPKSAPLRGSLEEAFERLAEAV--EPQEL 128

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    +e +    ++LvltAHPt   RRsLLqK  Ri   L q    D t+e+ +
  gi|8881307   129 YETVCRLEIELVLTAHPTEVTRRSLLQKYNRIAELLDQQDRLDSTPEEIE 178

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    E+  AL REi AA+ tDEiRR +P P DE R G++ i  t+W+ +P+++R
  gi|8881307   179 EVHQALQREIIAAWHTDEIRRRRPSPVDEARWGLAVIEQTLWNVMPRYMR 228

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R D  LK       lP dv  i+F sWmGGDRDG nPRvt  vtR+vCLL
  gi|8881307   229 RLDKILKR-KTGHHLPLDVAPIRFGSWMGGDRDG-NPRVTARVTREVCLL 276

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                     R mA  lY   +  ++ Els+    ++LR      +  + r
  gi|8881307   277 NRWMAVELYERELNPIISELSLQCVDEDLR------KLVPGRW------- 313

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             EPYRv+L   R +L  tR      L       ++  +  +
```

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  gi|8881307   314 ---------EPYRVLLKRLRARLRITRSWIEARLEG--RHPPDGEILLEA 352

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    +    L  CY+sL  CG  v+ADG LLDl+R v  FGL L+++DiRqE+
  gi|8881307   353 SDLKATLLACYHSLQRCGAGVVADGRLLDLIRRVTAFGLTLMRVDIRQEA 402

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    R+tD lDAit+ L++GsY eW E++R  +L+ EL  +RPL++ +    +
  gi|8881307   403 SRHTDALDAITRELGLGSYAEWTEDQREAFLIRELGNRRPLIPREFEPDD 452

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev++vld+f+++AEL  Ds GaY+isma  PsD+LAvELLq E g+++ L
  gi|8881307   453 EVREVLDTFQMIAELGPDSLGAYVISMASQPSDILAVELLQQEAGIRHYL 502

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFE L DL  A A +e+L  i WY+nri+G qevm+GYsDsGKDAG
  gi|8881307   503 RVVPLFETLDDLTGAEACIEHLMQIPWYRNRIQGYQEVMIGYSDSGKDAG 552

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    l AAW LYk qE ++ vA++ G+KL+lFHGRGG +GRGGGPtH AiLsq
  gi|8881307   553 HLTAAWTLYKTQERLVAVARRQGIKLTLFHGRGGSIGRGGGPTHAAILSQ 602

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP  + G lR t qGEvi   FG   +  r L  +t A LE  ++
  gi|8881307   603 PPGSVAGCLRATEQGEVIQAKFGLPGIALRNLEVYTTAVLETTLQAAQPL 652

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   +  WR++m+++A  AtE YR vv   P F+EYFR AtPE E   + iGsR
  gi|8881307   653 QQPWRDIMDRLAQLATETYRGVVRENPDFIEYFRHATPEHEISMLTIGSR 702

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   Pa+R P  G++sLRAiPW+FaWtqtR  LP WLG+G   + A+  D+
  gi|8881307   703 PARRSPTQGVNSLRAIPWVFAWTQTRLLLPAWLGIGESLQRAL--DSGDA 750

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     Lk mY++WPFFR  lD++Emv AKGDP +Aa yD+ Lv  eL+P G++
  gi|8881307   751 ALLKSMYRDWPFFRAFLDMVEMVLAKGDPAVAAWYDNRLVPSELQPLGER 800

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   +R ++  t   +L+i GH   L+  P  +  + +R++Y+  Ln +q   L
  gi|8881307   801 MRGQFDKTLRAVLEITGHEQPLDDFPVTQRSVIVRNPYVDPLNLLQVELL 850

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    R+R               +  E+          n        L   L++
  gi|8881307   851 YRVR---------------HGKEE----------N--------LRKALMV 867

                   tmKGiAAGmqntG<-*
                    + GiAAGm ntG
  gi|8881307   868 CINGIAAGMRNTG    880

gi|281207688|gb|EFA81868.1|: domain 1 of 1, from 3 to 917: score 888.9, E = 2.7e-264
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLH..GedLkE
                           +     G v   ++L +    L    L+ ++ L ++G+ L
  gi|2812076     3    ----DIGPFDFGSVE-PDELDKDTERLRHILLESVKVLEkdGDRLIN 44

                   avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    v     l  +    +D+  +e    k+ sL  aDa+ + + ++  LnLA
  gi|2812076    45 LVESI--LLKDQPSERDPVSMEQYKQKISSLSNADALSISRILSQCLNLA 92

                   nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                   n+AE  +l      + +k    a  a        E tlK L+  +  sP+
  gi|2812076    93 NVAEQHHLV----RSVLK----ANLAGEDLMYSCEHTLKSLIDEG-ISPD 133

                   EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    +++A+  qs++LvltAHPtq  RR L+ Kn  i n L+ L  K +t  +
  gi|2812076   134 TIYNAICEQSIELVLTAHPTQMMRRTLIAKNNAIGNALSELE-KQLTDYE 182

                   KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                   + E +E L RE++A + tDEiRR +PtP +E   G s +   +W+  P+F
  gi|2812076   183 RFEWEEELNREVKATWLTDEIRRKKPTPEEEAQGGWSILEQNLWHTLPRF 232
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                    LRRvD.tALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     R  D+t  K  G    lP     i+F sW GGDRDG n  vt +vtR v
  gi|2812076   233 FRILDrTVEKYTG--RSLPLGFTNIRFGSWCGGDRDG-NDNVTADVTRQV 279

                    CLLaRmmAanlYisqvEDLmFElsmWRCndEL...RvRAEElyrtaardk
                    C  +R +Aa l++  ++ L+FElsm +  d + +    A E  +  + +
  gi|2812076   280 CYFSRWIAATLFYREIDALLFELSMVKKTDSMadaALAANERRQSNKPKS 329

                    vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                    +   Y EF   +P  E YR++L +vRDK+  t+ +   L+  G    +++
  gi|2812076   330 ILTLYKEFREGIPEKEAYRIVLAEVRDKMLLTKKKYEDLIS-GQTPCPDD 378

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y   Ee + PL +CY sL   G k+iADG LLD++R    FGL L KL
  gi|2812076   379 VCYETAEEVIAPLKMCYDSLVAIGGKAIADGRLLDIIRRLNCFGLNLSKL 428

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    DiRqEs R+ + lDAitt L+iGsY  WsEe+R E+Ll EL+ KRPL++
  gi|2812076   429 DIRQESSRHSETLDAITTYLGIGSYNAWSEEQRVEFLLKELESKRPLIPV 478

                    DLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqREC
                    D P    v++v+++fr+ AELP Ds GaY+ism+  PsD+LAvELLq+
  gi|2812076   479 DFPCNPRVQEVINTFRMAAELPKDSLGAYVISMCQKPSDILAVELLQKVV 528

                    gvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsD
                    g k++ rvvPLFE + DL  AP ++e LF i WY+ ri+G qe+m+GYsD
  gi|2812076   529 GNKHPQRVVPLFEMIDDLVRAPTTMESLFNIPWYKKRINGSQEIMLGYSD 578

                    sGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtH
                    s KDAGRl  AW LYkAqE + K   k+GvK  lFHGRGGtvGRGG Pt
  gi|2812076   579 SAKDAGRLCSAWSLYKAQEILTKLSEKHGVKCNLFHGRGGTVGRGGSPTY 628

                    LAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm
                    LAi sqP   inG lRvt qGE+i   +G   +  r++  +t AtL   +
  gi|2812076   629 LAIQSQPGGSINGRLRVTEQGEMITAHYGQPGMALRTIEVYTTATLKQTL 678

                    nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGk
                     PP +P   WR++m+ +A v    YRsvv  +P Fv YFR  tPE E  +
  gi|2812076   679 LPPPAPLDKWREIMDFLADVSSKKYRSVVRDDPNFVRYFRASTPERELTH 728

                    mniGsRPaKRkP.sGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAi
                    +niGsRPaKR      iesLRAiPWiF++tqtR  LP WLGv  AFK Ai
  gi|2812076   729 LNIGSRPAKRNVlNPTIESLRAIPWIFSFTQTRLILPAWLGVCDAFKEAI 778

                    dKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEe
                    +K  +  q L +mYk+WPFF  t+DL+Emv  K DP iA  y +LLv  e
  gi|2812076   779 NKGWQ--QDLVDMYKNWPFFSTTVDLIEMVLMKTDPLIALRYNDLLVPFE 826

                    LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLn
                    L+  Gk+L d   Et + +L +  H  l      L+  + +R +Y+  +n
  gi|2812076   827 LQSKGKELIDLLNETVNSVLSLTSHETLQQENKLLQHFVSIRRAYMDPIN 876

                    vfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPG
                     +qA  L+R+R            s+   + +                 P
  gi|2812076   877 YIQAEILRRLR------------SQHVDAMD-----------------PI 897

                    LEDtLiLtmKGiAAGmqntG<-*
                    L D Li+t+ GiAA +
  gi|2812076   898 LIDILIITINGIAAVVNSVP    917

gi|114319423|ref|YP_741106.1|: domain 1 of 1, from 2 to 882: score 857.8, E = 6e-255
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       si           s  +  ++ D  Ll   L+D L++  G dL +
  gi|1143194     2    SIQD----------S--DAALRDDIRLLGEMLgDTLKEQEGTDLFDT 36

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     l A      D    e L   L sLd    + vA+a++  LnLAn
  gi|1143194    37 VERIRAL-AKQARAGDQGAAEALEQELGSLDEHQIMPVARAFSQFLNLAN 85

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE     +R R ++      + +as    s + E + +L       Pe
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  gi|1143194    86 IAEQ---HHRVRRSREW--ARSPDASPLKGS-LAEAFPRLLQGE-TDPEA 128

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + A     ++LvltAHPt   RR +LqK  Ri   L      D+t+++
  gi|1143194   129 LYHAACELDIELVLTAHPTETQRRTMLQKYNRIARLLDGRDRLDLTPDET 178

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   +E+   L REi  A+  DEiRR +PtP DE R G++ +   +W+ vP++L
  gi|1143194   179 EEVTAGLRREIIGAWQSDEIRRRRPTPVDEARWGLAVMEQVLWDAVPRYL 228

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   R  D  L+       lP d+  i+F sWmGGDRDG nP vt  vtR+vCL
  gi|1143194   229 RNLDRSLRE-HTGRALPLDAAPIRFGSWMGGDRDG-NPNVTARVTREVCL 276

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                     R mAa lY   +  L+  lsm RC + LR    El   a
  gi|1143194   277 AGRWMAATLYEKEIQTLINTLSMTRCDQALR----ELVGDA--------- 313

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                      W      EPYRv+L   R +L  t       LA      +E  v  +
  gi|1143194   314 ---W------EPYRVLLKRLRARLRLTQRWVEARLAG--KRPPEGEVLLD 352

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    E+ L PL  CY+sL  CG   +A+G LLD +R vs FGL L +LDiRq
  gi|1143194   353 KEDLLRPLLTCYHSLHRCGAGQVAEGELLDTIRRVSCFGLTLTRLDIRQH 402

                   seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                   ++R+ D l  it  L++G Y +W Ee Rq WLl+EL  +RPL++ DL
  gi|1143194   403 ADRHADALSEITSALGLGRYDQWDEEARQRWLLSELASRRPLIPDDLEPG 452

                   EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                   EE ++vl++ r LAEL +D  GaYiisma  PsD+LAvELLq+ Cgv q+
  gi|1143194   453 EEAAEVLETCRTLAELGSDGLGAYIISMAEHPSDILAVELLQKACGVTQP 502

                   LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                   Lr vPLFE    L+ A  ++  LF   WY+ ri G qe+m+GYsDsGKDA
  gi|1143194   503 LRSVPLFETRDTLQNAAETMRVLFEQPWYRDRIGGHQEIMIGYSDSGKDA 552

                   GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                   G l AAW LY+AqE ++  A + G++L+lFHGRGG +GRGGGPtH A+Ls
  gi|1143194   553 GHLTAAWTLYQAQEALVALAEENGIQLTLFHGRGGSIGRGGGPTHAAVLS 602

                   qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    PP  ++G lRvt qGEvi   FG   +  r L  +tAA LE  ++PP
  gi|1143194   603 LPPGSVKGTLRVTEQGEVIQSKFGLPGIALRNLEIYTAAVLEATLQPPAE 652

                   PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                   P+PEWR++m+++   A   YR +v   P F+EYF  AtP  E G++ iGs
  gi|1143194   653 PRPEWREVMDRLSDTACGAYRGLVKETPEFIEYFQAATPVREIGQLAIGS 702

                   RPaKR.kPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                   RPaKR++ +  ++ LRAiPWiFaWtqtR  LP WLGvG A   A++ D
  gi|1143194   703 RPAKRnQKALTVDNLRAIPWIFAWTQTRLMLPAWLGVGDALSEALEEDLG 752

                   nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                       L+Em+++WPFF   lD++Emv AKGDPG+A+LyD+ Lv EeL+  G
  gi|1143194   753 D--TLREMFQQWPFFEAFLDMVEMVLAKGDPGVASLYDRRLVPEELHGMG 800

                   ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                   ++LR +Y  t d +L + GH   L   P ++  + +R++Y+  Ln +qA
  gi|1143194   801 EQLRGRYRKTLDAVLSVTGHERPLADFPVVRRAVDVRNPYVDPLNLLQAE 850

                   tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    L R              s+   dE+                   L   L
  gi|1143194   851 LLYR--------------SRLCDDEQ-------------------LRRVL 867

                   iLtmKGiAAGmqntG<-*
                   ++ + GiAAGm ntG
  gi|1143194   868 MVAINGIAAGMRNTG    882

gi|255561196|ref|XP_002521610.1|: domain 1 of 1, from 1 to 607: score 846.2, E = 1.9e-251
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                *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

gi|2555611     -    ---------------------------------------------- -

                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                                                    +A +i
gi|2555611     1 -----------------------------------MALSIY-------- 6

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                                                      ++
gi|2555611     7 ---------------------------------------SQH------- 9

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                            +t   tq v         R+  CL     K
gi|2555611    10 ------------ITTNTTQNV---------RVQSCLCGGVTKNSVF---- 34

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                         +q  F    iR
gi|2555611    35 ---------VQMNF----IR------------------------------ 41

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                                             R Gk P  t
gi|2555611    42 -----------------------------RQGKMPNTT---------- 50

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|2555611     - ---------------------------------------------- -

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                     +PP EPYRviLGdvRDKLYnt ER+R LLA Gis+i+EeA +t+v
gi|2555611    51 ----YIPPSEPYRVILGDVRDKLYNTCERSRQLLANGISDIPEEATFTNV 96

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                E+FLEPLELCY+sLC  GD+ iADGsLLD+LRqvstFGLsLv++DiRqEs
gi|2555611    97 EQFLEPLELCYRSLCAYGDRPIADGSLLDFLRQVSTFGLSLVRIDIRQES 146

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                eR+tDvlDAit+HL+iG YReWsEe RqEWLl+EL+GKRPL+g+DLPk +
gi|2555611   147 ERHTDVLDAITKHLGIGFYREWSEEHRQEWLLTELRGKRPLFGPDLPKID 196

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                E++Dvld+f+v+AEL  D FGaYiismataPsDvLA
gi|2555611   197 EIADVLDTFHVIAELLADNFGAYIISMATAPSDVLA-------------- 232

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                        LADLeAAP av++LFsiDWY+nri+GKqevm+GYsDsGKDAG
gi|2555611   233 --------LADLEAAPTAVARLFSIDWYRNRINGKQEVMIGYSDSGKDAG 274

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRG tvGRGGGPtHLAiLsq
gi|2555611   275 RLSAAWQLYKAQEELVKVAKQYGVKLTMFHGRGRTVGRGGGPTHLAILSQ 324

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                P Dti+GslRvtvq EviE+sF EE+LC r+LqRFtAAtLEHGm+P vsP
gi|2555611   325 PADTIHGSLRVTVQSEVIEQSFREEHLCVRTLQRFTAATLEHGMHPLVSP 374

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRl.............
                kPEWR Lm+emAv+At EYRs+v++EPRFvEYFRl +  +    ++
gi|2555611   375 KPEWRTLMDEMAVIATKEYRSIVFQEPRFVEYFRLisfctiivygplivl 424

                ......AtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                +    +AtPElEYG+mniGsRP+KRkPsGGiesLRAiPWiFaW qt
gi|2555611   425 salivqATPELEYGRMNIGSRPSKRKPSGGIESLRAIPWIFAWIQT---- 470

                PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                                                  Rvt+DL+EmvFAKGDP
gi|2555611   471 ---------------------------------RVTIDLVEMVFAKGDP 486

                GiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLK
                GiAaLyDkLLv+ eL+PFG++LR            +AGHkDlLEGDPYLK
gi|2555611   487 GIAALYDKLLVSKELWPFGERLR------------VAGHKDLLEGDPYLK 524
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                  qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                  qrlRLRd+YittLnv+qA tLKRiRDP+y+vtlrPhlsKE+  E sk+a+
  gi|2555611   525 QRLRLRDAYITTLNVCQANTLKRIRDPDYHVTLRPHLSKEHM-ELSKPAA 573

                  eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                  eLvkLnp +++aPGLEDtLiLtmKGiAAGmqntG
  gi|2555611   574 ELVKLNPRSEYAPGLEDTLILTMKGIAAGMQNTG    607

gi|70671531|gb|AAZ06136.1|: domain 1 of 1, from 1 to 526: score 825.6, E = 3e-245
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                    s
  gi|7067153     1    --------------S------------------------------- 1

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7067153     - ------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                                    asAttEsDiEEtlK+L  +  K+PeEv
  gi|7067153     2 ----------------------ASATTESDIEETLKRLLQLN-KTPEEV 27

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                  F+ALKnq+vDLvltAHPtqsvRRsLLqK +RiR CL+qL+AKD+t++DK+
  gi|7067153    28 FDALKNQTVDLVLTAHPTQSVRRSLLQKFGRIRDCLTQLYAKDITPDDKQ 77

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                  ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|7067153    78 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 127

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                  RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|7067153   128 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 176

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                  aRmmAanlY+sq+EDLmFE+smWRCn+ELRvRA E++r a+rd   K+Yi
  gi|7067153   177 ARMMAANLYFSQIEDLMFEMSMWRCNEELRVRA-EVQRCAKRD--AKHYI 223

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                  EF Kq+P +EPYR i  dvRDKLYntRERaR LL  G+s+i+E+ v+t v
  gi|7067153   224 EFLKQIPSNEPYRAIPRDVRDKLYNTRERARQLLSSGVSDIPEDSVFTSV 273

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                  ++FLEPLELCY+sLC+CGD+ iADGsLLD+LRqvstFGL+LvKLDiRqEs
  gi|7067153   274 DQFLEPLELCYRSLCDCGDRPIADGSLLDFLRQVSTFGLALVKLDIRQES 323

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  +R+tDvlDAit+HL+iGsY+eWsE+KRqEWLl+EL+GKRPL+g DLPktE
  gi|7067153   324 DRHTDVLDAITQHLGIGSYKEWSEDKRQEWLLSELSGKRPLFGHDLPKTE 373

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++Dvld+f+v+ ELP DsFGaYiismataPsDvLAvELLqRECg+ ++L
  gi|7067153   374 EIADVLDTFKVISELPHDSFGAYIISMATAPSDVLAVELLQRECGITHPL 423

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLe APA+v++LFsi+WY+nri+GKqevm+GYsDsGKDAG
  gi|7067153   424 RVVPLFEKLADLENAPASVARLFSIEWYRNRINGKQEVMIGYSDSGKDAG 473

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYk qEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7067153   474 RLSAAWQLYKTQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 523

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPD
  gi|7067153   524 PPD---------------------------------------------- 526

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|7067153     - ------------------------------------------------- -

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
```

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  gi|7067153     - ------------------------------------------------ -

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|7067153     - ------------------------------------------------ -

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|7067153     - ------------------------------------------------ -

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|7067153     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|7067153     - -------------    -

gi|152995284|ref|YP_001340119.1|: domain 1 of 1, from 1 to 876: score 817.4, E = 9.2e-243
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                              +   + s    L e   LL D   + +    Ge   E v
  gi|1529952     1    --------MSDSQAS----LRENVRLLGDCLGESMSNHLGEGFLEKV 35

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        ls +     D+  L      L +Ld  + + vA+a+   LnL n+
  gi|1529952    36 ENIRLLSKNGRQSGDSAALIQ---ALEALDDKEIVPVARAFNQFLNLSNI 82

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AE  +  +RRR                    + + l +L  +   + e +
  gi|1529952    83 AEQYHRVHRRRTNESL---------GVYHNPVGDLLTRLSKQS-FTAEQM 122

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      L+ qs++LvltAHPt  vRRsL+ K   i   L  L    + + +
  gi|1529952   123 ISSLQSQSIELVLTAHPTEVVRRSLIRKYDNISSELEALDKDNILPLEET 172

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                        L   i  A+ tDEiR  +PtP DE + G + i   +W+ vP+F R
  gi|1529952   173 KHIRRLKEIITQAWHTDEIREDRPTPVDEAKWGFAVIEQSLWQAVPRFFR 222

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     D         +RlP d   i+F+ WmGGDRDG nP vt  vt++v LL
  gi|1529952   223 QLDEQFSEFSKEDRLPLDLAPIRFATWMGGDRDG-NPNVTHKVTKEVTLL 271

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aR mAa lYi  +  L  E+sm  Cn+ LR+R  +      +
  gi|1529952   272 ARWMAADLYIKDLNVLRSEFSMTQCNEALRARVGD------SA------- 308

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             PYR +L     K+  t+  a+  L       s e ++ ++
  gi|1529952   309 ---------QPYREVLRHLENKMLATKNWAKACLDG--KPTSGEDIFLDI 347

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    e  + L LCY+sL +CG kviA GsLLDl+R   tFG  Lv+LD+Rq++
  gi|1529952   348 QELTDDLILCYQSLLDCGMKVIANGSLLDLIRCAATFGATLVRLDVRQDA 397

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    R+ D l Ait+  ++G Y eW E  Rq +Ll+EL  KRPLl+ +   t
  gi|1529952   398 SRHIDALSAITRFYGLGDYAEWDEASRQAFLLTELNSKRPLLPMEWTPTA 447

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Evk+vld+f ++      sFG+Y+isma aPsDvLAv L+ +E gv  ++
  gi|1529952   448 EVKEVLDTFAMISQGQQNSFGSYVISMASAPSDVLAVALMLKESGVGFPM 497

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   r+vPLFE LADL+ A   +e+LFsi WY+  i+G+qevm+GYsDs KDAG
  gi|1529952   498 RIVPLFETLADLDNAEPIIEQLFSIPWYKSYINGRQEVMIGYSDSAKDAG 547

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    ++A W  Y+AqE + +  Kk+G+ L+lFHGRGGtvGRGGGP H+AiLsq
  gi|1529952   548 QIAATWGQYRAQEALTRLCKKHGIHLTLFHGRGGTVGRGGGPAHVAILSQ 597
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                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  +nG++Rvt qGE+i f FG  ++  rsL  ++ A +E  + P   P
  gi|1529952   598 PPGSVNGAIRVTEQGEMIRFKFGIPDIAVRSLELYCSAVMEASLIPAEPP 647

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    k EWR +m+emA v    YRs++     Fv YFR  tPE E  k+ +GsR
  gi|1529952   648 KEEWRAIMDEMAEVGMNQYRSIIRGHEDFVPYFRATTPEQELAKLPLGSR 697

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    Pa+R+  GG+esLRAiPWiFaW q R  LP WLG   A +  ++  + nl
  gi|1529952   698 PARRRSDGGVESLRAIPWIFAWMQIRLMLPAWLGAESALQQGVE--SGNL 745

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     kL+Em k+WPFF   lD+l+mv AK +P iA  y+k Lv EeL+  G+
  gi|1529952   746 EKLREMHKKWPFFGAYLDMLDMVLAKAEPEIAEYYEKRLVGEELQGLGRL 795

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR k +   +l+  +     l+E    ++q + +R++Yi  L  +qA  L
  gi|1529952   796 LRGKLKQVSELVKMLKKQERLIEDNKTIRQSIDVRNPYIDPLHYLQAELL 845

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     R                      s+k +e  ++n            L++
  gi|1529952   846 YR----------------------SRKDEENAEVN----------KALMI 863

                    tmKGiAAGmqntG<-*
                    tm GiA GmqntG
  gi|1529952   864 TMAGIASGMQNTG    876

gi|226320262|gb|ACO48252.1|: domain 1 of 1, from 16 to 1036: score 811.9, E = 4e-241
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s D   RlL  G   +d    e    ++Dk          e ++
  gi|2263202    16    SFDDDCRLL--GNLLNDILQREVGTTVVDKL---------ERIRVLA 51

                    qECYElsAeYEGKkDtkKLeE..LGakLtsLdPaDailvAkailHmLnLA
                    q    +     G  D   + E++L + L  +   +a+ +A+a++H L L
  gi|2263202    52 QSGCNMRQA--GIVDMAEMLEkqLASELSKMTLEEALTLARAFSHYLTLM 99

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                     +AE     +R R +            A t    ++ + +Lv  +  sP+
  gi|2263202   100 GIAET---HHRVRKRGNN--------IAQTAKSCDDIFNQLVQGG-VSPD 137

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    E ++ +  q v++vltAHPtq  RR L  K+ Ri   L      D+t+eD
  gi|2263202   138 ELYDTVCKQEVEIVLTAHPTQINRRTLQYKHIRIAHLLDYNDRPDLTIED 187

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    ++ + E L REi   + tDE+RR +PtP DE RaG+  +   +Wk vP +
  gi|2263202   188 REMVIEDLVREITSIWQTDELRRQKPTPVDEARAGLNIVEQSLWKAVPHY 237

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    L Rv  ALK       lP     ikF sWmGGDRDG nP vt  vt+Dv
  gi|2263202   238 LHRVSNALKK-HTGKPLPLTCTPIKFGSWMGGDRDG-NPNVTAKVTKDVS 285

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEl.............
                    LL+R mA  lYi  v+ L FElsm  C + L   A E+ ++ + ++++++
  gi|2263202   286 LLSRWMAIDLYIREVDSLRFELSMNQCSESLSRLAHEIleeanlenrhen 335

                    .............yrtaardkv............................
                     +++ +++++ +++ +ar ++++  ++++ ++++ + ++++++++++++
  gi|2263202   336 wnqpvsrsqslpKQLPARAHLpsfaengeaqhprldipgpdhsqhnhkeg 385

                    ....vKyYi.....................................E
                    + +++ + i++++ +++ +    +++++ ++ ++ ++++++ +++ +++
  gi|2263202   386 evssTLFKIgetsansgasaaaispsssfnsiqqlgqrkssagsqigrsS 435

                    FWK.......qvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                    F K  +++ +q+P   PYRv+LG+v+DKL   R R   LL     +
  gi|2263202   436 FQKlmepklpQLPGIAPYRVVLGNVKDKLERSRRRLELLLEDVSCDNDPL 485

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
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                     y   ++ LEPL LCY sL  CG  v+ADG L Dl+R v tFG+ L+KL
  gi|2263202   486 DYYETTDQLLEPLLLCYESLQSCGSGVLADGRLADLIRRVATFGMVLMKL 535

                   DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                   D+RqEs R+ + +DAit+ L++G Y eW EeK+ E+L  ELkGKRPL++
  gi|2263202   536 DLRQESGRHAETIDAITKYLDLGTYSEWDEEKKLEFLTRELKGKRPLVPH 585

                   DLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqREC
                    +    Evk+vld+fr+ AEL +Ds GaY+isma   sDvLAvELLq++
  gi|2263202   586 SIEVPHEVKEVLDTFRIAAELGSDSLGAYVISMASNASDVLAVELLQKDA 635

                   gvkq..........tLrvvPLFEkLADLeAAPAavekLFsiDWYinri.
                    +   ++ +++ +++tLrvvPLFE + DL+ A   + kL siDWY+ ++
  gi|2263202   636 RLSVagdlgrecpggTLRVVPLFETVKDLRGAGSVIRKLLSIDWYREHVi 685

                   ...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                   ++++G qevmvGYsDsGKDAGR+ AAW LYkAqE+++    +yG+K++lF
  gi|2263202   686 knhNGHQEVMVGYSDSGKDAGRFTAAWELYKAQEDVVAACNEYGIKVTLF 735

                   HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                   HGRGG +GRGGGPt LAi sqPP  + G lR t qGE+i+  FG  ++
  gi|2263202   736 HGRGGSIGRGGGPTYLAIQSQPPGSVMGTLRSTEQGEMIDAKFGLPQIAV 785

                   rsLqRFtAAtLEHGmnPPvsPkPE.WRkLmeemAvvAtEEYRsvvvKEPR
                   r L  +t A L   + PP  P+ E+WRk++ee+  +    YRsvv+  P
  gi|2263202   786 RQLEIYTTAVLLATLRPPHPPREEkWRKVIEEISNISCQCYRSVVYENPE 835

                   FvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFH
                   F  YF  AtPE E G +niGsRPa+Rk s Gi  LRAiPW+FaWtqtRF
  gi|2263202   836 FLSYFHEATPEAELGFLNIGSRPARRKSSKGIGHLRAIPWLFAWTQTRFV 885

                   LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                   LP WLGvGA  K A +K       LkEmYkeWPFF  t+DL+Emv  K D
  gi|2263202   886 LPAWLGVGAGLKGACEKGHTE--ELKEMYKEWPFFQSTIDLIEMVLGKAD 933

                   PGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     iA  yD++Lv+ e +  G++LR +    ++++L i GH  l      L
  gi|2263202   934 IPIAKHYDEVLVSKERQELGRELRSELMTAEKFVLVISGHEKLQQNNRSL 983

                   KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                   +  +  R +++  Ln++q   LKR+R                     +
  gi|2263202   984 RRLIENRLPFLNPLNMLQVEILKRLR----------------------RE 1011

                   deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   d+  k+           D L++t+ GiAAGm+ntG
  gi|2263202  1012 DDNRKIR----------DALLITINGIAAGMKNTG    1036

gi|83644641|ref|YP_433076.1|: domain 1 of 1, from 1 to 881: score 808.3, E = 4.9e-240
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           ++ L P       +L e   LL +     +    G+++   +
  gi|8364464     1    ----MMKELHP-------ELRENVRLLGELLGQSIRYHLGDEIFNKI 36

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    E   ++A  +   + ++   L  +L +L+  +   vA+a+   LnL n+
  gi|8364464    37 -EKIRIAAKADRNAEISQRKQLKEVLSGLNDEELAPVARAFNQFLNLTNI 85

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AE  ++  RRR          D    t    iE  + +L+ ++  s +
  gi|8364464    86 AEQYHIV-RRRAPASE---LVDNRLDT----IEVVFDRLIGQG-VSKDKF 126

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   F  L     + vltAHPt   RR L+qK   i  CL  L   D+  e+
  gi|8364464   127 FAQLADLNLEFVLTAHPTEITRRTLIQKYDQISECLESLDRSDLLDEEYA 176

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    + E L R i  A+ tDEiR  +Pt  DE + G + i   +W+ vP F+R
  gi|8364464   177 KIVERLRRLITEAWHTDEIRYERPTAVDEAKWGFAVIENSLWQAVPDFMR 226

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    +D AL      E lP +v  ++F+sWmGGDRDG nP vt EvtR+v LL
  gi|8364464   227 QMDAALLE-RFGEGLPINVNPVRFASWMGGDRDG-NPNVTSEVTREVFLL 274
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                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    +R mAa lY+  +E L  Elsm  Cn EL +RA       ++
  gi|8364464   275 SRWMAADLYLRDIEALRSELSMTACNGEL-ARA-----SGQSR------- 311

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             EPYR iL   R +L  tR  a   L       +E  v  +
  gi|8364464   312 ---------EPYRKILAKLRSRLEATRAWAAEALDSTKKPAAE--VLLNN 350

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                     e +EPL +CY+sL +CG  viA G LLD++R    FGL Lv+LDiRq+s
  gi|8364464   351 AELIEPLMVCYRSLRDCGMEVIANGPLLDVIRRAQCFGLQLVRLDIRQDS 400

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+ Dv+  i   L+iG Y +W Ee +q +L+ EL+G+RPLl+ + P
  gi|8364464   401 ERHSDVMKEICAYLGIGDYSQWTEEEKQAFLIRELEGRRPLLPKEWPASA 450

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E ++vld+ rv+A  P +   +Y+isma  PsDvL v LL RE g+++ +
  gi|8364464   451 EAREVLDTCRVVAMQPPEGLASYVISMASDPSDVLTVILLLRESGMRHHI 500

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    ++ PLFE L DL+ A  ++ +L  + WY+  i GKqevm+GYsDs KDAG
  gi|8364464   501 PIAPLFETLSDLQGAADSIGRLLDLPWYREYIGGKQEVMIGYSDSAKDAG 550

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     ++AAW  Y+AqE ++KvA k+ vKL+lFHGRGGtvGRGGGP   AiLsq
  gi|8364464   551 QMAAAWAQYQAQEALVKVAAKHDVKLTLFHGRGGTVGRGGGPANRAILSQ 600

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  + G  R+t qGE+i f FG  ++  +s   +  A LE  + PP  P
  gi|8364464   601 PPGSVAGNFRITEQGEMIRFKFGQPKVAKQSFNLYLGAVLEASLVPPPEP 650

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                     P WR++m+++   A   YR vv   P FvEYFR+AtPE E Gk+ +GsR
  gi|8364464   651 EPAWREMMDKLSHLAVNSYREVVRERPGFVEYFRSATPEQELGKLALGSR 700

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    Pa+Rk sGG+esLRAiPWiFaWtq R  LP WLG   A + A+  D
  gi|8364464   701 PARRKASGGVESLRAIPWIFAWTQMRLMLPAWLGSDTALQTAV--DDGGA 748

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      Lk m   WPFF   +D+lEmv  K DP iA  y++ Lv  eL+P G++
  gi|8364464   749 DTLKAMLTGWPFFETHVDMLEMVLSKVDPEIARFYEERLVKPELHPLGDE 798

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +      l+ ++ G  +lL   P     l +R++Y   L  +q   L
  gi|8364464   799 LRRRAGCAVRLINELKGQDELLLDNPVFMHSLQVRNPYTDPLHFLQVELL 848

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     R R                +E         + n        +E  L +
  gi|8364464   849 VRDR-----------------AEG--------ETN-----KETVEKALKV 868

                    tmKGiAAGmqntG<-*
                    tm G+AAGm ntG
  gi|8364464   869 TMAGVAAGMRNTG    881

gi|12324139|gb|AAG52040.1|AC011914_10: domain 1 of 1, from 2 to 981: score 807.9, E = 6.5e-240
                    *->siDAqLRlLvPGKvsedekLieYDA.LLlDkFLDiLqDLHGedLkEa
                              +   +s   +  e D +LL   F D+Lq   G+   E
  gi|1232413     2    ---TDTTDDIAEEIS--FQSFEDDCkLLGSLFHDVLQREVGNPFMEK 43

                    vqECYEl..sA...eYEGKkDtkKLeE..LGakLtsLdPaDailvAkail
                    v     l +sA +    G +Dt  L E++L + +  +   +a+ +A+++
  gi|1232413    44 VERIRILaqSAlnlRMAGIEDTANLLEkqLTSEISKMPLEEALTLARTFT 93

                    HmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlk
                    H LnL  +A+                        t  s       +L
  gi|1232413    94 HSLNLMGIAD-----------------------THHS-------QLLQS 112

                    lnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK
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                +  sP+E +  +  q v++vltAHPtq  RR L  K+ Ri   L
gi|1232413   113 G-ISPDELYKTVCKQEVEIVLTAHPTQINRRTLQYKHIRIAHLLEYNTRS 161

                DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvW
                D+ veD++ L E L REi   + tDE+RR +PtP DE RaG+  +   +W
gi|1232413   162 DLSVEDRETLIEDLVREITSLWQTDELRRQKPTPVDEARAGLNIVEQSLW 211

                kGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPE
                k vP++LRRv   LK       lP     +kF sWmGGDRDG nP vt
gi|1232413   212 KAVPQYLRRVSNSLKKF-TGKPLPLTCTPMKFGSWMGGDRDG-NPNVTAK 259

                vtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndEL.RvRAEElyrtaa
                vt++v LL+R mA  lYi  v+ L FEls  RC d  +R     l +
gi|1232413   260 VTKEVSLLSRWMAIDLYIREVDSLRFELSTDRCSDRFsRLADKILEKDFG 309

                rdkvvKyYiEFWKqvPPt.............................
                  + +K+ i     +PP+ +++++++ ++++ ++ +++++++ +++++ +
gi|1232413   310 ESRHTKFEIATTDYMPPNlqkqneqdfsesdwekidngsrsgltsrgsfs 359

                .................................EPYRviLGdvRDKL
                ++++   +++  ++++ ++++ ++  ++++ ++ ++ PYR++LG+v++KL
gi|1232413   360 stsqlllqrklfeesqvgktsfqkllepplkragsAPYRIVLGEVKEKL 409

                YntRERaRHLLAtGi.seisEeAvytkvEeFLEPLELCYksLCeCGDkvi
                  tR R   LL  G++ e      y   ++ LEPL LCY sL   G +v+
gi|1232413   410 VKTR-RLLELLIEGLpCEYDPKNSYETSDQLLEPLLLCYESLQSSGARVL 458

                ADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReW
                ADG L Dl+R vstFG+ LvKLD+RqE+ R+ + lDAitt L++G Y eW
gi|1232413   459 ADGRLADLIRRVSTFGMVLVKLDLRQEAARHSEALDAITTYLDMGTYSEW 508

                sEeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGa
                 EeK+ E+L  ELkGKRPL++  +    +vk+vld+frv AEL ++s Ga
gi|1232413   509 DEEKKLEFLTRELKGKRPLVPQCIKVGPDVKEVLDTFRVAAELGSESLGA 558

                YiismataPsDvLAvELLqRECgvkq...........tLrvvPLFEkLAD
                Y+isma   sDvLAvELLq++  +  +++++++ +++tLrvvPLFE + D
gi|1232413   559 YVISMASNASDVLAVELLQKDARLALtsehgkpcpggTLRVVPLFETVND 608

                LeAAPAavekLFsiDWYinri....dGKqevmvGYsDsGKDAGRlsAAWq
                L+AA  ++ kL siDWY+ +i+++++G qevmvGYsDsGKDAGR+ AAW
gi|1232413   609 LRAAGPSIRKLLSIDWYREHIqknhNGHQEVMVGYSDSGKDAGRFTAAWE 658

                LYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinG
                LYkAqE ++    ++G+K++lFHGRGG +GRGGGPt LAi sqPP  + G
gi|1232413   659 LYKAQENVVAACNEFGIKITLFHGRGGSIGRGGGPTYLAIQSQPPGSVMG 708

                slRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE.WRk
                slR t qGE++   FG  +   r L  +t A L   ++PP  P+ E+WR+
gi|1232413   709 SLRSTEQGEMVQAKFGIPQTAVRQLEVYTTAVLLATLKPPQPPREEkWRN 758

                LmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkP
                Lmee+  +    YRs v+  P F  YF  AtP  E G +niGsRP++Rk
gi|1232413   759 LMEEISGISCQHYRSTVYENPEFLSYFHEATPQAELGFLNIGSRPTRRKS 808

                sGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEm
                s Gi  LRAiPW+FaWtqtRF LP WLGvGA  K   +K       LkEm
gi|1232413   809 SSGIGHLRAIPWVFAWTQTRFVLPAWLGVGAGLKGVSEKGHAD--DLKEM 856

                YkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYv
                YkeWPFF  tl+L+Emv AK D  +   yD+ Lv+E  +  G +LR +
gi|1232413   857 YKEWPFFQSTLELIEMVLAKADIPMTKHYDEQLVSEKRRGLGTELRKELM 906

                EtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDP
                 t++++L i GH  lL     LK+ +  R +Y+  +n++q   LKR+R
gi|1232413   907 TTEKYVLVISGHEKLLQDNKSLKKLIDSRLPYLNAMNMLQVEILKRLR-- 954

                sykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiA
                             dE+          n        L D L++t+ GiA
gi|1232413   955 --------------RDED----------N------NKLRDALLITINGIA 974
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                  AGmqntG<-*
                  AGm ntG
  gi|1232413   975 AGMRNTG    981

gi|87118647|ref|ZP_01074546.1|: domain 1 of 1, from 1 to 854: score 807.1, E = 1.1e-239
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                                    ++  L GedL   v
  gi|8711864     1    ---------------------------------MINHL-GEDLLNQV 13

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   +   ls e     D+  L E    L +L+  + + vA+a+   LnL n+
  gi|8711864    14 EDIRRLSKEGRQAGDSGPLIE---ALEALNDDEIVPVARAFNQFLNLSNI 60

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AE  +  +RRR                    + + l +L  k+  s e +
  gi|8711864    61 AEQYHRVHRRRTNESL---------GVYQNPVGDLLARLHDKG-HSRESI 100

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     LK qs++LvltAHPt  vRRsL+qK   i   L  L    + + +
  gi|8711864   101 LSTLKEQSIELVLTAHPTEVVRRSLIQKYDNISSELEALDKDNILPLEED 150

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                       L   i  A+ tDEiR  +PtP DE + G + i   +W+ +P+F R
  gi|8711864   151 IHVRRLSEIITQAWHTDEIRDQRPTPVDEAKWGFAVIEQSLWQAIPRFYR 200

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    +           lP +   +kF+ WmGGDRDG nP vt  vtR+v LL
  gi|8711864   201 QLEQQFSKHLNDSLLPMELAPVKFATWMGGDRDG-NPNVTAKVTREVSLL 249

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                  aR mAa lYi  +  L  E+sm  Cn+ LR R  E
  gi|8711864   250 ARWMAADLYIKDLNVLRSEFSMSECNQALRDRVGE--------------- 284

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                           t PYR iL +   +L  tR  a   + +G s +s e +  +
  gi|8711864   285 -------STQPYREILRNLENRLIATRHWAQASI-KGES-VSREGILLDS 325

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   +  + L LC +sL +CG kviA G LLDl+R   tFGLsLvKLD+Rq++
  gi|8711864   326 QQLHDDLVLCHQSLIDCGMKVIANGRLLDLIRCAATFGLSLVKLDVRQDA 375

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   R+ D l Ait+  ++G Y eW E  Rq +Ll+EL  KRPLl+ D   t+
  gi|8711864   376 SRHIDALSAITRFYGVGDYAEWDEASRQAFLLTELNSKRPLLPRDWKTTD 425

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Evk+vld+f ++A+    sFG+Y+isma aPsDvLAv LL  E gv + +
  gi|8711864   426 EVKEVLDTFAMIADGDASSFGSYVISMASAPSDVLAVALLLQESGVDHKM 475

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  r+vPLFE LADL+ A  ++e+LFs+ WY+  idG+qevm+GYsDs KDAG
  gi|8711864   476 RIVPLFETLADLDNAQPTIEQLFSMPWYKAYIDGQQEVMIGYSDSAKDAG 525

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   ++A W  Y+AqE +    Kk+Gv+L+lFHGRGGtvGRGGGP H+AiLsq
  gi|8711864   526 QIAATWGQYRAQEALTDLCKKHGVRLTLFHGRGGTVGRGGGPAHVAILSQ 575

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP  +nGs+Rvt qGE+i f FG  ++  rsL  ++ A LE  + P  +P
  gi|8711864   576 PPGSVNGSIRVTEQGEMIRFKFGIPDIAVRSLELYCSAVLEATLMPAQAP 625

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  k EWR +m+emA +    YRs+v     Fv YFR  tPE E   + +GsR
  gi|8711864   626 KEEWRAVMDEMAEIGMNQYRSIVRGHQDFVPYFRAITPEQELAELPLGSR 675

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  Pa+Rk  GG+esLRAiPWiFaW q R  LP WLG   A + A+  D+  l
  gi|8711864   676 PARRKSDGGVESLRAIPWIFAWMQIRLMLPAWLGAESALQQAV--DSGHL 723

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   kL+ m +eWPFF   lD+l+mv AK +P iA  y+k Lv EeLkP G+
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  gi|8711864   724 EKLRQMREEWPFFSAYLDMLDMVLAKAEPEIAEYYEKRLVPEELKPLGRL 773

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR+k +    l++++     l+     ++q + +R++Yi  L  +qA  L
  gi|8711864   774 LRNKLQKVSSLIIELKEQERLIADNQTIRQSIDVRNPYIDPLHYLQAELL 823

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     R R  s              d          k+             L++
  gi|8711864   824 YRSRQTS--------------DNK--------KVS----------KALMI 841

                    tmKGiAAGmqntG<-*
                    tm GiA GmqntG
  gi|8711864   842 TMAGIASGMQNTG    854

gi|89094559|ref|ZP_01167497.1|: domain 1 of 1, from 1 to 869: score 806.6, E = 1.6e-239
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL..DiLqDLHGedLkE
                                    + +  + ++ D  +l   L++ i  DL Ge
  gi|8909455     1    -------------MTDLHEALRDDVRMLGTSLgeTIKSDL-GEAFLS 33

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                     +     l+ e    + ++  e L   L  L   D + +A+a+   LnLA
  gi|8909455    34 KIESVRKLAKEGRTEEQPEH-EQLLQALIDLGDDDVLPLARAFNQFLNLA 82

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AEE    +R R ++         ++  t   +   + +L  k+  +P+
  gi|8909455    83 NIAEE---HHRVRRHLEV-------TDVCTPDSLCTLFAQLRKKG-FTPK 121

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                     v + L    +DLvltAHPt   RR L+qK   i  CL  L   D   e
  gi|8909455   122 QVADTLSETQIDLVLTAHPTEVNRRTLIQKYDDIADCLRRLDRGD--SEA 169

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    +  LDE L R i   + tDEiR+ +PtP DE + G + i   +W  vPKF
  gi|8909455   170 QIRLDE-LIRQI---WHTDEIRKQRPTPVDEAKWGFAVIENSLWTAVPKF 215

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    LRR D  L    + ERlP     i+F+sWmGGDRDG nP v   vt +v
  gi|8909455   216 LRRLDAQLDET-LGERLPLSCSPIRFASWMGGDRDG-NPNVKAKVTEEVL 263

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R mAa lY+  v+ L  Elsm+    ELR    E+
  gi|8909455   264 LLSRWMAADLYLKDVDALRAELSMYQASKELRDHVGEV------------ 301

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRE.RaRHLLAtGiseisEeAvy
                              EPYR +LG+vR+KL  t+   aR L   G  e   + +y
  gi|8909455   302 ----------SEPYRALLGEVREKLLATKNwVARQL--NGQVEQDCD-IY 338

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     + Ee LEPL LCY+sL  CG  +iA+ +L D++R +  FGL LvKLDiR
  gi|8909455   339 VHEEELLEPLQLCYRSLQACGMGIIAESALEDIIRRIACFGLTLVKLDIR 388

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    q s+R+  v + + +  ++GsY  W Ee Rq +Ll EL+ KRPLl+ +
  gi|8909455   389 QSSDRHAQVFEELSQFYGLGSYNGWTEEGRQSFLLKELQSKRPLLPNEWV 438

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                      EEv++vld+ +v+A     + G+Y+isma  PsDvLAv LL RE g+
  gi|8909455   439 PSEEVQEVLDTCEVVAKAEKSALGSYVISMASHPSDVLAVILLLREMGIS 488

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                    + +rv PLFE L DLe A   ++ L s+DWY+   +G qevm+GYsDs K
  gi|8909455   489 HNMRVAPLFETLNDLENARDCIDALLSVDWYKAYTQGHQEVMIGYSDSSK 538

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG l+AAW  YkAqE +    K++ v L+lFHGRGGtvGRGGGP H Ai
  gi|8909455   539 DAGQLAAAWGQYKAQEGLTALCKEHDVHLTLFHGRGGTVGRGGGPSHTAI 588

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    L+qPP  ++ slR t qGE+i f +G  +L  r L   t A LE  ++P
  gi|8909455   589 LAQPPGSVDRSLRLTEQGEMIRFKYGMPDLAVRNLELCTGAVLEATLDPS 638
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                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      P   WR+ me +  v   EYR++v  +P Fv YFR AtPE E  k+ +
  gi|8909455   639 PGPEEAWREQMESITKVSLAEYRAIVREDPMFVPYFRAATPEQELAKLPL 688

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKR+  GG+esLRAiPWiFaWtq R  LP WLG   A   A++  +
  gi|8909455   689 GSRPAKRRQDGGVESLRAIPWIFAWTQIRLMLPAWLGSDKALCSAMEGSS 738

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                      l  +k mY++WPFFR t+D+lEmv AK D  i a yD+ Lv+ eL
  gi|8909455   739 AVL--IKQMYQQWPFFRSTIDMLEMVLAKSDRNISAYYDERLVSQELGIL 786

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G sLR++  +  d +  i     lL G P ++q + +R++Yi  L  +qA
  gi|8909455   787 GSSLRNRLGDIVDVINLIKEQDGLLQGNPVIRQSIDVRNPYIDPLHFLQA 836

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R        +P       d                     LE
  gi|8909455   837 ELLNRDRN-------QP-------DQR-------------------LEQA 853

                    LiLtmKGiAAGmqntG<-*
                    L++tm Gi AGm ntG
  gi|8909455   854 LMVTMAGISAGMRNTG    869

gi|115434082|ref|NP_001041799.1|: domain 1 of 1, from 16 to 1035: score 804.7, E = 6e-239
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       + +   RlL  G    d  L e    L  +F+ +L     e +
  gi|1154340    16    AFEDDCRLL--GSLLHDVLLRE----LGPRFIHLL-----ERITILA 51

                    qECYElsAeYEGKkDtkKLeE..LGakLtsLdPaDailvAkailHmLnLA
                    q    +     G +Dt  + E++LGa L ++   D++ +A+a++H LnL
  gi|1154340    52 QSAVNMRSA--GVEDTAVVVEkqLGAELAAMSLEDSLCLARAFSHHLNLM 99

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                     +A+  +     R++k +   FaD +        ++t+ kL+  +  sPe
  gi|1154340   100 TIADTYH-----RVRKAR--NFADLSKSC-----DDTFAKLIQSG-VSPE 136

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    E ++ +  q v++vltAHPtq  RR L  K+ Ri   L      D+  eD
  gi|1154340   137 ELYDTVCKQEVEIVLTAHPTQINRRTLQYKHLRIAHLLEFNERADLSLED 186

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    K+ L E L REi A + tDE+RR +PtP DE RaG+  +   +Wk +P +
  gi|1154340   187 KEILIEDLVREITAIWQTDELRRHKPTPVDEARAGLHIVEQSLWKAIPHY 236

                    LRRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    LRRv  AL+Kn G    lP     ikF sWmGGDRDG nP vt  vtRDv
  gi|1154340   237 LRRVSNALkKNTG--KPLPLTCTPIKFGSWMGGDRDG-NPNVTAKVTRDV 283

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEly.........
                     +L+  mA  lYi  ++ L FEls+ RC + L   A ++  +++ +++++
  gi|1154340   284 SILSQWMAIDLYIRELDTLSFELSINRCSEKLANLANDILlkesasedqk 333

                    ..................................................
                    +++ ++++++++ + +++   + + +++ + ++ ++ ++++++ + ++ +
  gi|1154340   334 tntwnqtgpqnnlklqhslalpaqlpsgadlpsctecndgesqirmsklp 383

                    ............................rtaardkvvKyYiE.......
                    ++++++   + ++++++++ +++++++ +rt+   ++ K + E++ ++++
  gi|1154340   384 gnpkhklalnitekredsplpspshrpmgRTPSGGQLRKMFTEsqigrss 433

                    FWKqvPP.......tEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                    F K + P+ +++++  PYRv+LGdv++KL ntR R   LL     +
  gi|1154340   434 FRKLLEPsiserpgSTPYRVVLGDVKEKLMNTRRRLELLLEDLPCDRDTS 483

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y   ++ LEPL LCY+sL  CG  v+ADG L Dl+R v tFG+ L+KL
  gi|1154340   484 EYYDTSDKLLEPLLLCYQSLQSCGSSVLADGRLADLIRRVATFGMVLMKL 533

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    D+RqEs R+t+ lDAit  L++G Y eW E+K+ ++L  ELkGKRPL+++
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  gi|1154340   534 DVRQESGRHTETLDAITSYLDLGVYSEWDEQKKLDFLTRELKGKRPLVPP 583

                   DLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqREC
                    +  t +v++vld+frv AEL +D+ GaY+isma   sDvLAvELLq++
  gi|1154340   584 YIQVTADVQEVLDTFRVAAELGSDALGAYVISMASNASDVLAVELLQKDA 633

                   gvkq..........tLrvvPLFEkLADLeAAPAavekLFsiDWYinri.
                    +  +++ +++ +++tLrvvPLFE + DL+ A  a+ kL siDWY+ +i
  gi|1154340   634 RLTVsgdlgrpcpggTLRVVPLFETVNDLREAGPAIRKLLSIDWYRDHIi 683

                   ...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                   ++++G qevmvGYsDsGKDAGR+ AAW LYkAqE+++     +G+K++lF
  gi|1154340   684 knhNGHQEVMVGYSDSGKDAGRFTAAWELYKAQEDVVAACNAFGIKVTLF 733

                   HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                   HGRGG +GRGGGPt LAi sqPP  + G lR t qGE++   FG  +
  gi|1154340   734 HGRGGSIGRGGGPTYLAIQSQPPGSVMGTLRSTEQGEMVQAKFGLPQTSV 783

                   rsLqRFtAAtLEHGmnPPvsPkPE.WRkLmeemAvvAtEEYRsvvvKEPR
                   r L  +t A L   + PP  P+ ++WR +mee+  v    YRs v+  P
  gi|1154340   784 RQLEIYTTAVLLATLRPPQPPRDDkWRGVMEEISRVSCAQYRSTVYENPE 833

                   FvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFH
                   F+ YF  AtP  E G +niGsRPaKR+   Gi  LRAiPW+FaWtqtR
  gi|1154340   834 FIKYFQEATPQAELGYLNIGSRPAKRRTTPGISNLRAIPWVFAWTQTRLV 883

                   LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                   LP WLGvG   + A dK       L+ mY+eWPFF  t+DL+Emv AK D
  gi|1154340   884 LPAWLGVGRGLQDACDKGHT--HELRAMYEEWPFFQSTVDLIEMVVAKAD 931

                   PGiAaLyDkLLvaEe.LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                     +A  yD++Lv + + +  G +LR++   t++ +L + GHk l
  gi|1154340   932 APMAKHYDDVLVHDAgRRTLGAELRQELARTENCVLAVSGHKKLSANNRS 981

                   LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                   L++ +  R  Y+  +n++q   L+R+R                 d+n
  gi|1154340   982 LRKLIDSRLTYLNPMNMLQVEVLRRLRQ---------------DDDN--- 1013

                   adeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        kL           D L++t+ GiAAGm ntG
  gi|1154340  1014 ----RKLR----------DALLITINGIAAGMRNTG    1035

gi|30697740|ref|NP_177043.2|: domain 1 of 1, from 2 to 1032: score 804.2, E = 8.2e-239
                   *->siDAqLRlLvPGKvsedekLieYDA.LLlDkFLDiLqDLHGedLkEa
                              +   +s   +  e D +LL   F D+Lq   G+   E
  gi|3069774     2    ---TDTTDDIAEEIS--FQSFEDDCkLLGSLFHDVLQREVGNPFMEK 43

                   vqECYEl..sA...eYEGKkDtkKLeE..LGakLtsLdPaDailvAkail
                   v     l +sA +    G +Dt  L E++L + +  +   +a+ +A+++
  gi|3069774    44 VERIRILaqSAlnlRMAGIEDTANLLEkqLTSEISKMPLEEALTLARTFT 93

                   HmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlk
                   H LnL  +A+  +  ++  +  +          A    Di   + +L
  gi|3069774    94 HSLNLMGIADTHHRMHKVHNVTQL---------ARSCDDI---FSQLLQS 131

                   lnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK
                   +  sP+E +  +  q v++vltAHPtq  RR L  K+ Ri   L
  gi|3069774   132 G-ISPDELYKTVCKQEVEIVLTAHPTQINRRTLQYKHIRIAHLLEYNTRS 180

                   DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvW
                   D+ veD++ L E L REi   + tDE+RR +PtP DE RaG+  +   +W
  gi|3069774   181 DLSVEDRETLIEDLVREITSLWQTDELRRQKPTPVDEARAGLNIVEQSLW 230

                   kGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPE
                   k vP++LRRv   LK       lP     +kF sWmGGDRDG nP vt
  gi|3069774   231 KAVPQYLRRVSNSLKKF-TGKPLPLTCTPMKFGSWMGGDRDG-NPNVTAK 278

                   vtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEly.....
                   vt++v LL+R mA  lYi  v+ L FEls  RC d     A+ + +++ +
  gi|3069774   279 VTKEVSLLSRWMAIDLYIREVDSLRFELSTDRCSDRFSRLADKILekdyd 328
```

```
                    .................rtaardkv...........vKyYiEFWKqvPPt
                    +++++ +++++++  +++ +ar +++   + ++++++K+ i     +PP+
  gi|3069774   329 rgksnfqkqqsssclptQLPARAHLpacidfgesrhTKFEIATTDYMPPN 378

                    ................................................
                     +++++++ ++++ ++ +++++++ +++++ +++++   +++  ++++ +
  gi|3069774   379 lqkqneqdfsesdwekidngsrsgltsrgsfsstsqlllqrklfeesqvg 428

                    ..................EPYRviLGdvRDKLYntRERaRHLLAtGi.se
                    +++ ++  ++++ ++ ++ PYR++LG+v++KL  tR R   LL  G++ e
  gi|3069774   429 ktsfqkllepplkragsAPYRIVLGEVKEKLVKTR-RLLELLIEGLpCE 477

                    isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                          y   ++ LEPL LCY sL   G +v+ADG L Dl+R vstFG+
  gi|3069774   478 YDPKNSYETSDQLLEPLLLCYESLQSSGARVLADGRLADLIRRVSTFGMV 527

                    LvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRP
                    LvKLD+RqE+ R+ + lDAitt L++G Y eW EeK+ E+L  ELkGKRP
  gi|3069774   528 LVKLDLRQEAARHSEALDAITTYLDMGTYSEWDEEKKLEFLTRELKGKRP 577

                    LlgsDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                    L++  +    +vk+vld+frv AEL ++s GaY+isma   sDvLAvELL
  gi|3069774   578 LVPQCIKVGPDVKEVLDTFRVAAELGSESLGAYVISMASNASDVLAVELL 627

                    qRECgvkq...........tLrvvPLFEkLADLeAAPAavekLFsiDWYi
                    q++  +  +++++++ +++tLrvvPLFE + DL+AA  ++ kL siDWY+
  gi|3069774   628 QKDARLALtsehgkpcpggTLRVVPLFETVNDLRAAGPSIRKLLSIDWYR 677

                    nri....dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvK
                     +i+++++G qevmvGYsDsGKDAGR+ AAW LYkAqE ++    ++G+K
  gi|3069774   678 EHIqknhNGHQEVMVGYSDSGKDAGRFTAAWELYKAQENVVAACNEFGIK 727

                    LvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEE
                    ++lFHGRGG +GRGGGPt LAi sqPP  + GslR t qGE++   FG
  gi|3069774   728 ITLFHGRGGSIGRGGGPTYLAIQSQPPGSVMGSLRSTEQGEMVQAKFGIP 777

                    nLCFrsLqRFtAAtLEHGmnPPvsPkPE.WRkLmeemAvvAtEEYRsvvv
                    +   r L  +t A L   ++PP  P+ E+WR+Lmee+  +    YRs v+
  gi|3069774   778 QTAVRQLEVYTTAVLLATLKPPQPPREEkWRNLMEEISGISCQHYRSTVY 827

                    KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                      P F  YF  AtP  E G +niGsRP++Rk s Gi  LRAiPW+FaWtq
  gi|3069774   828 ENPEFLSYFHEATPQAELGFLNIGSRPTRRKSSSGIGHLRAIPWVFAWTQ 877

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                    tRF LP WLGvGA  K   +K       LkEmYkeWPFF  tl+L+Emv
  gi|3069774   878 TRFVLPAWLGVGAGLKGVSEKGHAD--DLKEMYKEWPFFQSTLELIEMVL 925

                    AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                    AK D  +   yD+ Lv+E  +  G +LR +   t++++L i GH  lL
  gi|3069774   926 AKADIPMTKHYDEQLVSEKRRGLGTELRKELMTTEKYVLVISGHEKLLQD 975

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                       LK+ +  R +Y+  +n++q   LKR+R                dE+
  gi|3069774   976 NKSLKKLIDSRLPYLNAMNMLQVEILKRLR----------------RDED 1009

                    skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                              n        L D L++t+ GiAAGm ntG
  gi|3069774  1010 ----------N------NKLRDALLITINGIAAGMRNTG    1032

gi|119476550|ref|ZP_01616901.1|: domain 1 of 1, from 1 to 884: score 801.7, E = 4.9e-238
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +  q  +     v           LL     D L D   e+L   v
  gi|1194765     1    -MPDQQHAPLRDNVR----------LLGGLLGDTLRDQVDESLLNRV 36

                    qECYEls..AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                     E   l+++A  +G   +     L  ++  L  +D + vA+a+ H Ln A
  gi|1194765    37 EEIRTLAkqARSDGNWQP-----LLDVMSELPDSDLVPVARAFTHFLNYA 81

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE  +   RRR  ++      D  s      + E l +L   +  s e
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  gi|1194765    82 NIAEQHHRVRRRRDNRRE----IDVPSPL--GTMAELLPRLLNNG-HSAE 124

                   EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    +  A+     +LvltAHPt   RR LL K   i   L qL   D+t+ +
  gi|1194765   125 AIVTAISQCRTELVLTAHPTEITRRTLLRKYNDIDVILGQLDRPDLTPKE 174

                   KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                   ++     L R i A + tDEiRR +PtP DE + G + i  t+W+  P F
  gi|1194765   175 QQTQLKRLRRRIIAGWQTDEIRRNRPTPVDEAKWGFATIESTLWHALPEF 224

                   LRRvD.tALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                   LR  D+  L+  G   RlP d   i+ ssWmGGDRDG nP vt  vt +v
  gi|1194765   225 LRDLDeQMLQHTG--KRLPLDKAPIRLSSWMGGDRDG-NPNVTARVTEEV 271

                   CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                    LLaR  Aa l +  + +L  +ls   Cn+ LR         aa d
  gi|1194765   272 LLLARWEAADLLLRDINELREDLSFGTCNSALR--------EAAGD---- 309

                   yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                               EPYR +L  vR  L ntRE a    At   ei E  +y
  gi|1194765   310 ----------HHEPYRELLRKVRQTLTNTREWAE---ATLNGEIFEGHIY 346

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                    + Ee L PL L Y+sL +CG  +iA G L  +LR v  FGL L+KLDiR
  gi|1194765   347 QHDEELLQPLQLIYQSLLDCGMEAIAHGRLETILRRVACFGLTLMKLDIR 396

                   qEseRqtDvlDAittHLeiGs....YReWsEeKRqEWLlaELkGKRPLlg
                   qEs R+ Dv+  +t  L+i  ++++Y +WsE  +q +L+ ELk +RPL++
  gi|1194765   397 QESTRHSDVINEVTHYLGIQInnkpYQDWSETEKQTFLINELKNRRPLIP 446

                   sDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRE
                      P   Ev++vld+f vLA  P  + GaYiismat PsD+LAv LLq E
  gi|1194765   447 KHFPASAEVQEVLDTFAVLARQPASALGAYIISMATYPSDILAVRLLQQE 496

                   CgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYs
                    g   + r+ PLFE L DLe A  ++e+L +i+WY+  i G+qevm+GYs
  gi|1194765   497 AGCLTPQRIAPLFETLDDLEGAADSIEQLLAIEWYRQDIGGQQEVMIGYS 546

                   DsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPt
                   Ds KDAG ++A W  Y+AqE +  v  + Gv L+lFHGRGG v RGGGP
  gi|1194765   547 DSAKDAGFFAASWAQYRAQEALSSVCENAGVHLTLFHGRGGSVSRGGGPA 596

                   HLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHG
                   H A+LsqPP ti+Gs+Rvt qGE+i f FG  +L  + L  +t AtLE
  gi|1194765   597 HEALLSQPPGTIKGSVRVTEQGEMIQFKFGLKELAIHNLELYTTATLEAT 646

                   mnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYG
                   + P   Pk EWR++m+ +A v   EYR +v  +PRFv+YFR  tPE E
  gi|1194765   647 LSPIEKPKQEWREMMQTLADVSVKEYRRIVHHDPRFVDYFRCVTPEQELS 696

                   kmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAi
                   ++ +GsRPaKR+ sGG+esLRAiPW+FaWtq R  LP WLG G A    i
  gi|1194765   697 RLSLGSRPAKRRASGGVESLRAIPWVFAWTQMRLMLPAWLGTGKALAEQI 746

                   dKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDk.LLvaE
                   d+  +nl  L+ m k+W FF + +D+ Emv AK D  +A+ y+++LL
  gi|1194765   747 DQGQQNL--LQVMLKDWNFFSMLVDMQEMVMAKADAKVAGYYEQrLLDNV 794

                   eLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittL
                   + +  G++L + +   ++ +  i GH  lL   P L+  + +R++Yi  L
  gi|1194765   795 NAQSLGQELQAGFHQAHQAIESISGHS-LLANNPMLQFSIAVRNPYIDPL 843

                   nvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaP
                    + q   ++R+R           l     +E+
  gi|1194765   844 HITQVELMRRLR-----------LQDQDNQEQ----------------- 864

                   GLEDtLiLtmKGiAAGmqntG<-*
                    LE  L++ + GiAAG+ ntG
  gi|1194765   865 -LEQALMVSIAGIAAGLRNTG    884

gi|149911768|ref|ZP_01900373.1|: domain 1 of 1, from 6 to 876: score 798.3, E = 4.9e-237
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                 *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       A LR      v           LL       ++D  Ge+  + +
gi|1499117     6    ---AALRS----NVG----------LLGQVLGNTIKDHLGEEFLDKI 35

                 qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                      l+       D  +   L ++L  L   + + vA+a++  LnLAn+
gi|1499117    36 ETIRQLAKSSRAGSDKDR-AQLLTVLRNLSDDELLPVARAFSQFLNLANI 84

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                 AE  +   R                        i+E + kL      s e+v
gi|1499117    85 AEQFHTTSRNCADNVC-----------VPDSIDELFAKLNNSE-ISEEDV 122

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   A+Kn  +DLvltAHPt   RR L+ K++ i  CL+qL   ++  +++
gi|1499117   123 LAAVKNLKIDLVLTAHPTEITRRTLIHKHGAINKCLSQLELTELSSQERD 172

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                      +   +  A+ t EiR  +PtP DE + G + +   +W+ vP FLR
gi|1499117   173 VFMTRIEQLVSQAWHTNEIRTVRPTPVDEAKWGFAVVENSLWDAVPNFLR 222

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   D  L+   +   lP d+  +kF+sWmGGDRDG nP vt  vt +v L
gi|1499117   223 SLDKRLQD-RLDYQLPIDAAPVKFTSWMGGDRDG-NPFVTSTVTEEVLLT 270

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                 +R mA  l++  v  L  Elsm  C d LR+   E      ++
gi|1499117   271 SRWMAIHLFLKDVTHLSSELSMNNCDDRLRALVGE------SH------- 307

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                          EPYRv+L   R  L  t       L +G    s + + t
gi|1499117   308 ---------EPYRVLLKKLRNELTETLASLTAQL-KGEHTQSRD-IITTT 346

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                  +  EPL  CY sL  CG +viA G+LLD +R v  FG+sLvKLDiRq+s
gi|1499117   347 AQLREPLLACYNSLNACGMRVIAKGALLDTIRRVECFGVSLVKLDIRQDS 396

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                 +R+tDv+  +t+ L++G Y +WsE+ +q +Ll EL  KRPL++
gi|1499117   397 DRHTDVIAEVTRYLGLGDYAQWSEQDKQAFLLQELNNKRPLIPQCWQPSA 446

                 EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                 +vk+vld+fr +A    +s G Yiisma   sDvLAv LL +E g    L
gi|1499117   447 DVKEVLDTFRTVAKQDPESLGIYIISMARKASDVLAVQLLLKETGCPFRL 496

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                 +v PLFE L DL+ A    + L +iDWY+n i+G q +m+GYsDs KDAG
gi|1499117   497 PVAPLFETLDDLNNAGTVTASLLAIDWYKNYINGHQYIMIGYSDSAKDAG 546

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  ++A W  Y+ qE ++ +  k  +KL+lFHGRGG +GRGG P H A+Lsq
gi|1499117   547 VIAASWAQYRSQEVLVDICEKEDIKLTLFHGRGGSIGRGGAPAHAALLSQ 596

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                 PP  ++G lRvt qGE+i f FG  n+  +sL  +t A LE  + PP +P
gi|1499117   597 PPGSLKGGLRVTEQGEMIRFKFGLANVAEQSLNLYTSAILEANLLPPPAP 646

                 kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    WR+ m++m     EEYRs +    +Fv YFR+AtPElE Gk+ +GsR
gi|1499117   647 EQSWRDAMDQMSADSCEEYRSYIQGHEKFVPYFRSATPELELGKLPLGSR 696

                 PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                 PaKRkP GG+esLRAiPWiFaWtq R  LP WLG  AAFK  +    +
gi|1499117   697 PAKRKPNGGVESLRAIPWIFAWTQNRLMLPAWLGCTAAFKNMLGSGQRE- 745

                 qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   L+Em ++WPFF   +++ EmvF K D  +A  yD+ Lv+EeL+P Gk+
gi|1499117   746 -TLQEMQQQWPFFNTRIEMFEMVFLKADAWLAEYYDQCLVTEELWPLGKE 794

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                 LR+      +l++ +   k lL+  P++K+ + LR++Y   Ln++qA  L
gi|1499117   795 LRASLALATELIVGLNPNKQLLDAQPWIKKSIELRNPYTDPLNILQAELL 844
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                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   R R            sKE              +n      P +E  L++
  gi|1499117   845 SRARS-----------SKE--------------VN------PDVEQALMV 863

                  tmKGiAAGmqntG<-*
                   + G+AAGm ntG
  gi|1499117   864 SIAGVAAGMRNTG    876

gi|149789412|gb|ABR29877.1|: domain 1 of 1, from 2 to 1052: score 798.2, E = 5.4e-237
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                              +   +s   +  + D  Ll   L+D+Lq   G    E
  gi|1497894     2    ---TDTTDDIAEEIS--FQSFDDDCKLLGNLLnDVLQREVGSKFMEK 43

                  vqECYEls.....AeYEGKkDtkKLeE..LGakLtsLdPaDailvAkail
                        l+++  +    G +Dt  L E++L   +  +   +a+ +A+a++
  gi|1497894    44 LERNRILAqsacnMRLAGIEDTAELLEkqLALEISRMTLEEALTLARAFS 93

                  HmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsD.iEEtlKkLvl
                  H LnL  +AE        R++k +        s t  s + ++ + +L
  gi|1497894    94 HYLNLMGIAET-----HHRVRKAR--------SMTHLSKsCDDIFNQLLQ 130

                  klnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsA
                   +  s eE ++ +  q v++vltAHPtq  RR L  K+ Ri   L
  gi|1497894   131 SG-ISAEELYDTVCKQEVEIVLTAHPTQINRRTLQYKHIRIAHLLDYNDR 179

                  KDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtv
                   D+t eD++ L E L REi   + tDE+RR +PtP DE RaG+  +   +
  gi|1497894   180 PDLTHEDREMLIEDLVREITSIWQTDELRRHKPTPVDEARAGLNIVEQSL 229

                  WkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtP
                  Wk  P +LRRv tALK       lP     i+F sWmGGDRDG nP vt
  gi|1497894   230 WKALPHYLRRVSTALKK-HTGKPLPLTCTPIRFGSWMGGDRDG-NPNVTA 277

                  EvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEl.....
                   vtRDv LL+R mA  lYi  v+ L FElsm  C d L   A ++  +++
  gi|1497894   278 KVTRDVSLLSRWMAVDLYIREVDSLRFELSMVQCSDRLLKVANDIlieet 327

                  ........yrtaardkvvKy.............................
                  ++++++++   +a+   +K+++++ +++ +++ + +  ++ ++++++ ++
  gi|1497894   328 ssedhhesWNQPASRSQTKFprkslptqlppradlpactecndgesqypk 377

                  .......YiEFWK.....................................
                   + ++++Y+ F +++  +++ +++++++ +++ ++++++++  +++++++
  gi|1497894   378 lelpgtdYMPFNRqealgssysesssqdinhglpkttgngsvanssgspr 427

                  ....................................qvPPtEPYRviLGdvR
                   + ++ +   +++   +++ ++++ ++  +++ +q P   PYR++LG+v+
  gi|1497894   428 asfssaqlvaqrklfaeskigrssfqkllepslpQRPGIAPYRIVLGNVK 477

                  DKLYntRERaRHLLAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDk
                  DKL  tR R   LL     e      y   ++ L+PL LCY sL  CG
  gi|1497894   478 DKLMRTRRRLELLLEDLPCEYDQWDYYETTDQLLDPLLLCYESLQSCGAG 527

                  viADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYR
                  v+ADG L Dl+R v tFG+ L+KLD+RqEs R+ D lDAit+ Le+G Y
  gi|1497894   528 VLADGRLADLIRRVATFGMVLMKLDLRQESGRHADTLDAITKYLEMGTYS 577

                  eWsEeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsF
                  eW EeK+ E+L  ELkGKRPL+++ +    +vk+vldafrv AEL +Ds
  gi|1497894   578 EWDEEKKLEFLTRELKGKRPLVPPTIEVAPDVKEVLDAFRVAAELGSDSL 627

                  GaYiismataPsDvLAvELLqRECgvkq...........tLrvvPLFEkL
                  GaY+isma   sDvLAvELLq++  +  +++ +++ +++tLrvvPLFE +
  gi|1497894   628 GAYVISMASNASDVLAVELLQKDARLAVsgelgrpcpggTLRVVPLFETV 677

                  ADLeAAPAavekLFsiDWYinri....dGKqevmvGYsDsGKDAGRlsAA
                   DL+ A   + kL siDWY+ +i ++++G qevmvGYsDsGKDAGR+ AA
  gi|1497894   678 KDLRGAGSVIRKLLSIDWYREHIiknhNGHQEVMVGYSDSGKDAGRFTAA 727

                  WqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDti
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                    W LYkAqE+++    ++G+K++lFHGRGG +GRGGGPt LAi sqPP  +
  gi|1497894   728 WELYKAQEDVVAACNDFGIKVTLFHGRGGSIGRGGGPTYLAIQSQPPGSV 777

                    nGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE.W
                     G lR t qGE++   FG  +   r L  +t A L   + PP  P+ E+W
  gi|1497894   778 MGTLRSTEQGEMVQAKFGLPHTAIRQLEIYTTAVLLATLRPPHPPREEqW 827

                    RkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKR
                    R++mee+  +    YRs v+  P F  YF  AtP  E G +niGsRP++R
  gi|1497894   828 RNVMEEISKISCQNYRSTVYENPEFLAYFHEATPQAELGFLNIGSRPTRR 877

                    kPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLk
                    k s Gi  LRAiPW+FaWtqtRF LP WLGvGA  K A +K       Lk
  gi|1497894   878 KSSTGIGHLRAIPWVFAWTQTRFVLPAWLGVGAGLKGACEKGFTE--DLK 925

                    EmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdk
                     mYkeWPFF  t+DL+Emv  K D  iA  yD++Lv+E  +  G +LR +
  gi|1497894   926 AMYKEWPFFQSTIDLIEMVLGKADIPIAKHYDEVLVSESRRELGAELRSE 975

                    YvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiR
                       t++++L + GH  l      L+  +  R +Y+  +n++q   LKR+R
  gi|1497894   976 LLTTEKYVLVVSGHEKLSQNNRSLRRLIESRLPYLNPMNMLQVEVLKRLR 1025

                    DPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKG
                                   d+n          n        L D L++t+ G
  gi|1497894  1026 R---------------DDDN----------N-------KLRDALLITING 1043

                    iAAGmqntG<-*
                    iAAGm ntG
  gi|1497894  1044 IAAGMRNTG    1052

gi|224284385|gb|ACN39927.1|: domain 1 of 1, from 2 to 1073: score 795.9, E = 2.6e-236
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                               +   +s   +  e D  Ll   L+D+Lq   G++  E
  gi|2242843     2    ---TDTTDDIAEEIS--FQAFEDDCRLLGSLLnDVLQREVGQQFTEK 43

                    vqECYEls.....AeYEGKkDtkKLeE..LGakLtsLdPaDailvAkail
                    v     l+++  +    G +D+  + E++L   L s+   +a  +A+a++
  gi|2242843    44 VERERILAqsacnMRIAGIEDAAEVLEkkLALELSSMTLEEAASLARAFS 93

                    HmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlk
                    H LnL  +AE     + R  + k                  ++ + k++
  gi|2242843    94 HYLNLMGIAE----THHRVRRIKN--------TVQLSKSCDDIFSKMIQS 131

                    lnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK
                    +  sPe+ + A+  q v++vltAHPtq  RR L  K+ Ri   L
  gi|2242843   132 G-TSPEDLYSAVCDQEVEIVLTAHPTQINRRTLQYKHLRIAHLLEYNDRA 180

                    DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvW
                    D+  e+++ L E L RE+   + tDE+RR +PtP DE R G+  +   +W
  gi|2242843   181 DLSHEEREMLIEDLRREVTSLWQTDELRRHKPTPVDEARSGLHIVEQSLW 230

                    kGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPE
                    k vP +LRRv  ALK       lP     i+F sWmGGDRDG nP+vt
  gi|2242843   231 KAVPHYLRRVSAALKK-HTGRPLPLTCTPIRFGSWMGGDRDG-NPKVTAK 278

                    vtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEl......
                    vtRDvC LaR mAa lYi  ++ L FElsm RCndEL   A E+ + +++
  gi|2242843   279 VTRDVCFLARWMAADLYIREIDSLRFELSMNRCNDELAKFAYEIleaenq 328

                    ..........yrtaardkvvKy.........................
                     ++++++++ ++t+ r    K++ ++++  +++ + + + +  ++ ++++
  gi|2242843   329 yeerhqesgfHQTSHRV-HAKHsvshspalptqlpagadmpactecndge 377

                    ....YiEF.......................................
                    ++ + +EF+ ++++++ +++++ +++ +  ++++++++++ ++++ + +
  gi|2242843   378 sqlpILEFpvtdhsdsfesghnaessvtllksspsrtsekyedgkldvdv 427

                    ................................................
                    ++ + +++ ++++++++  + +++ + + +++++++++ + ++++ ++
  gi|2242843   428 rtinistnasstgtgtgiasasstagfgfssprkktsefnvgkssfdkii 477
```

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                    ...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                    +++  q P   PYR++LG vR+KL  tR R   +L     +      y k
  gi|2242843   478 npsIPQRPDIAPYRIVLGHVREKLISTRRRIEEILEGIPWDYDPSQYYEK 527

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      + LEPL LCY s+  CG  ++ADG L Dl+R vstFG+ L+KLD+RqE
  gi|2242843   528 SAQLLEPLMLCYESMQSCGSEILADGRLADLIRRVSTFGMILMKLDLRQE 577

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s ++ + lDAit+ L++G Y eW EeK+ E+L++ELkGKRPL+++ +
  gi|2242843   578 SGKHSETLDAITEYLDMGTYSEWDEEKKLEFLVTELKGKRPLVPPTIEVS 627

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv...
                     Ev++vld+frv AEL ++s GaY+isma   sD+LAvELLq++  +  +
  gi|2242843   628 AEVREVLDTFRVAAELGSESLGAYVISMASKASDILAVELLQKDARLavs 677

                    ........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri....dG
                    ++ +++ ++ tLrvvPLFE + DL+ A   + kL siDWY+n+i ++++G
  gi|2242843   678 gelgrpcpHTTLRVVPLFETVKDLRGAGSVIRKLLSIDWYRNHIiendNG 727

                    KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                     qevmvGYsDsGKD GR+ AAW LYkAqE+++   K++G+K++lFHGRGG
  gi|2242843   728 HQEVMVGYSDSGKDSGRFTAAWELYKAQEDVVAACKEFGIKVTLFHGRGG 777

                    tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                     +GRGGGPt LAi sqPP  + G lR t qGE++   FG  +   r L
  gi|2242843   778 SIGRGGGPTYLAIQSQPPGSLMGTLRSTEQGEMVQAKFGLAQTAVRQLEI 827

                    FtAAtLEHGmnPPvsPk.PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                    +t A L   ++PP  P++  WR++me++  +    YRs v+    F EYF
  gi|2242843   828 YTTAVLLATLHPPDPPRsANWREVMEKISEISRQYYRSTVYENEQFLEYF 877

                    RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                    R AtPE E G +niGsRP++Rk s Gi  LRAiPWiFaWtqtRF LP WL
  gi|2242843   878 REATPEAELGNLNIGSRPTRRKKSSGIGHLRAIPWIFAWTQTRFVLPAWL 927

                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    GvGA    A  K  K    L+ mY+eWPFF  t+DL+Emv AK D  iA
  gi|2242843   928 GVGAGLEAACAKGYKE--ELQAMYREWPFFQCTIDLIEMVLAKSDISIAK 975

                    LyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                     yD++Lv+   +  G +LR+ +  t++++L + GH  l E    LK  +
  gi|2242843   976 HYDEVLVSPCRQKLGGELREAFCMTEKYVLLVSGHEKLTENNKSLKRLIE 1025

                    LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                     R +++  +n++q   L+R+R                 d n
  gi|2242843  1026 SRLPFLNPINMIQVEILRRLR----------------RDVN--------- 1050

                    LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     n      P L D L++t+ GiAAGm ntG
  gi|2242843  1051 -N------PKLRDALLITINGIAAGMRNTG    1073

gi|237806868|ref|YP_002891308.1|: domain 1 of 1, from 3 to 877: score 795.8, E = 2.9e-236
                    *->siDAqLRlLvPGKvsedekLi..eYDALLlDkFLDiLqDLHGedLkE
                        + A LR    G v    +L+++     L D FLD +     e+++
  gi|2378068     3    DMYAALR----GNVGMLGHLLgkTIKEHLGDEFLDKI-----ENIRQ 40

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                      +     s      +D +KL    + L  L   + + vA+a++  LnLA
  gi|2378068    41 LAK-----SSRQGNEEDRQKLI---TTLKNLSDDELLPVARAFSQFLNLA 82

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE  +     R   ++          tt   ++  + kL      s +
  gi|2378068    83 NVAE--QFHSMSRQGELH----------TTLDPLDSLFDKLKNAN-LSEQ 119

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    E+ + +    ++LvltAHPt   RR L+ K+  +  CL  L  +D+t+ +
  gi|2378068   120 EIIDTVCELDIELVLTAHPTEVTRRTLIHKHVQLNECLEELELQDLTPRE 169

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
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                     k +   +   +   + t EiR  +PtP DE + G + i   +W  +P F
  gi|2378068   170 CKFIQHRIEQLVNQSWHTNEIREQRPTPVDEAKWGFAVIENNLWPAIPLF 219

                     LRRvDtALK.niGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     LR  D  L++n Gi  RlP  +  ++ +sWmGGDRDG nP vt  vt +v
  gi|2378068   220 LRQLDDRLQeNFGI--RLPLRAHPVRIASWMGGDRDG-NPFVTAKVTQEV 266

                     CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      LL+R +A nl++  + +L+ Elsm  Cn+ELR R  E
  gi|2378068   267 LLLSRWVAINLFLTDIQELVSELSMTDCNEELRQRVGEC----------- 305

                     yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                                 EPYR iL  vRD L  t       L   + e
  gi|2378068   306 -----------SEPYRAILRVVRDSLRETQQAVTAKLQGQYTE--NRDLI 342

                     tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     t+ E+  EPLELCY+sL  CG  +iADG LLD+LR+   FG+ L KLDiR
  gi|2378068   343 TRTEQLREPLELCYRSLQSCGMSIIADGMLLDVLRKLACFGVNLLKLDIR 392

                     qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                     q+ eR+  vl  +t+ Le+G Y eW E  +qE+Ll EL  +RPLl++
  gi|2378068   393 QDGERHGQVLSELTQYLELGDYAEWRETEKQEFLLKELASRRPLLPANWQ 442

                     ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                        E ++v+d+ rv+A    D+FG Yiisma  PsDvLAv LL +E g k
  gi|2378068   443 PSAESQEVVDTCRVIAQTDPDAFGIYIISMARQPSDVLAVQLLLKEVGCK 492

                     qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                       +++ PLFE   DL+ A A +++L s++WY+n i G+q vm+GYsDs K
  gi|2378068   493 FHMPIAPLFETQNDLQNAAAVLNRLLSVEWYRNYIRGQQYVMIGYSDSAK 542

                     DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                     DAG +sA W  Y+A E+++ +A +   KL+lFHGRGGt+GRGGGP H Ai
  gi|2378068   543 DAGMMSAGWAQYRAMEDLVAIAEREDLKLTLFHGRGGTIGRGGGPAHQAI 592

                     LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                     LsqPP  ++G  Rvt qGE+i f FG  ++  +  + +t A LE  + PP
  gi|2378068   593 LSQPPGSLKGGFRVTEQGEMIRFKFGLPEVAIHNFKLYTSAVLEANLLPP 642

                     vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                       P   W ++m+++  +    YRs+v  EP Fv YFR AtPE+E Gk+ +
  gi|2378068   643 PKPEAAWYDVMDKLSEISCQHYRSIVRDEPDFVPYFRAATPEMELGKLPL 692

                     GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                     GsRP+KRkP GG+esLRAiPWiFaWtq R  LP WLG   A +  +d
  gi|2378068   693 GSRPSKRKPNGGVESLRAIPWIFAWTQNRLMLPSWLGAHVALQAVMDEGK 742

                     KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                       l  LkEm ++WPFF   l++lEmvF K D  +A  yD  L  E+L+P
  gi|2378068   743 EDL--LKEMDQQWPFFHTRLEMLEMVFLKADLWLAEYYDLRLAPENLWPL 790

                     GksLRdkYvEtkdlLLkiAGHk.DlLEGDPYLKqrlRLRdsYittLnvfq
                     Gk+LR++ ++  + +L++   +++lL+  P++K  ++LR++Y   Lnv+q
  gi|2378068   791 GKRLRQELQDSINVVLQLLPKRgELLDDQPWIKESIKLRNPYTDPLNVLQ 840

                     AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                        L R R                 + +            ++v P ++
  gi|2378068   841 VELLHRSR-----------------ATP-------------DEVNPQVDQ 860

                     tLiLtmKGiAAGmqntG<-*
                      L++t+ GiAAGm ntG
  gi|2378068   861 ALMVTIAGIAAGMRNTG    877

gi|254508198|ref|ZP_05120323.1|: domain 1 of 1, from 1 to 880: score 794.3, E = 8.3e-236
                     *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                               +    K s    L     +L       ++D HGe+L E v
  gi|2545081     1    -------MTMNEKYS---ALRSNVSMLGHLLGNTIKDAHGEELLEKV 37

                     qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          ls        + + + L   +  L       vA+a+   LnL n+
  gi|2545081    38 ETIRKLSKSALAGNQADR-DSLIEEIKNLPNEQLTPVAHAFNQFLNLTNM 86
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                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AE  +   R                   E D   tl    ++ + s  +
gi|2545081    87 AEQYHTISRHCDAHVC-----------EPDALNTLFSKLSQNDISKLDT 124

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                 +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+ v ++
gi|2545081   125 AQAVRELNIELVLTAHPTEITRRTMINKLVKINECLSKLELGDLSVKERA 174

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                  +  L   i   +  D iR+ +PtP DE + G + +   +W+ vP FLR
gi|2545081   175 KTERRLEQLIAQSWHSDTIRKQRPTPLDEAKWGFAVVENSLWEAVPDFLR 224

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                 +D  LK   + E lP d+  ++FssWmGGDRDG nP vt  vtR+v LL
gi|2545081   225 EMDGRLKDY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTVTREVMLL 272

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                +R  Aa lY++ v +L+ Elsm  Cnd +R+ A E       d
gi|2545081   273 SRWKAADLYLNDVNELVSELSMTQCNDTIRALAGE-------D------- 308

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                         EPYR +L + R  L  t+E       +G   ++  A   ++
gi|2545081   309 -------EHEPYRAVLKELRNLLNETKE-ILDAKVHG-QKLAVKAPLQRI 349

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                E+  EPL  CY+sL eCG  +iADGsLLD LR +  FG+ Lv+LDiRqEs
gi|2545081   350 EQLWEPLYACYQSLHECGMGIIADGSLLDTLRRIKAFGVHLVRLDIRQES 399

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                 R+ Dvl  +t+ L+iG Y +WsE+ +  +L  EL  KRPLl+ D    E
gi|2545081   400 TRHSDVLSELTRYLGIGDYDQWSEQDKIAFLTNELASKRPLLPRDWEPSE 449

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                 vk+vld+ +++A  P ++FGaY+isma + sDvLAv LL  E g    +
gi|2545081   450 AVKEVLDTCKIVAAQPREAFGAYVISMARTASDVLAVHLLLQESGCPYRM 499

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                 v PLFE L DL+ A   +++L  iD Y+  i+  q vm+GYsDs KDAG
gi|2545081   500 DVCPLFETLDDLNNAESVIKQLMGIDLYRGFIQNHQMVMIGYSDSAKDAG 549

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 +sA W  Y A + ++KvA + Gv L+lFHGRGGt+GRGG P H A+Lsq
gi|2545081   550 VMSAGWAQYHAMDSLVKVAEEEGVELTLFHGRGGTIGRGGAPAHAALLSQ 599

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP  P
gi|2545081   600 PPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNLYASAILEANLLPPPEP 649

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                k EWR+Lm+ +  v  E YRsvv  EP Fv YFR AtPElE Gk+ +GsR
gi|2545081   650 KQEWRDLMDVLSEVSCEAYRSVVRGEPDFVPYFRQATPELELGKLPLGSR 699

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                PaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ +dK  + l
gi|2545081   700 PAKRNPKGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSVDKGHQAL 749

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  L+Em +eWPFF   l +lEmv+ K    i   yD+ Lv   L+P G++
gi|2545081   750 --LEEMCREWPFFSTRLGMLEMVYTKCNIEISRYYDERLVDPKLQPLGDR 797

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LRd+ +   + +L +     l+  DP+ +  +RLR+ Y+  Ln++qA  L
gi|2545081   798 LRDQLKKDIKAVLNVENNENLMQSDPWGQESIRLRNIYVEPLNMLQAELL 847

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                 R R            s E   E+                   LE+ L++
gi|2545081   848 YRTRQ-----------SEEASTEE-------------------LEEALMV 867

                tmKGiAAGmqntG<-*
                t+ GiAAGm ntG
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  gi|2545081   868 TIAGIAAGMRNTG    880

gi|262370772|ref|ZP_06064096.1|: domain 1 of 1, from 4 to 894: score 793.1, E = 1.8e-235
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      iDA LR               D  Ll   L++ L++  G+dL
  gi|2623707     4    QIDAPLRE--------------DVRLLGNLLgETLKEHAGQDLFNQ 35

                  vqECYEls.AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                  v     ls+   +G+ +++K   L     sL+  + + + +a+ H Ln A
  gi|2623707    36 VEQIRALSkGARDGQVEAEK--QLEQLFFSLEDDEILPLTRAFTHFLNFA 83

                  nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                  n+AE  ++   RR +            A     ++  + k       s +
  gi|2623707    84 NIAEQYHVVRSRRQSEFD-------ETAPSPNPLDHLFAKFKNND-ISTD 125

                  EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    F+ +    ++LvltAHPt   RR L+qK   i   L ++  + +t+ +
  gi|2623707   126 TLFQQICDLNIELVLTAHPTEVSRRTLIQKYDGINDALFKMDQQKLTPRE 175

                  KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                  ++ + E L   i  A+ tDEiR  +PtP DE + G   i  t+W+ vPKF
  gi|2623707   176 RQTVLEDLKQLICSAWQTDEIRQHRPTPVDEAKWGFTTIEQTLWNAVPKF 225

                  LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                  +R  D  +       RlP  v  ++F+sWmGGDRDG nP vt  +t +v
  gi|2623707   226 MRELDDMVIE-HCGQRLPLHVAPVRFASWMGGDRDG-NPNVTHNITQEVL 273

                  LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                   L+R  Aa lY+  +EDL +Els+  C dELR      +   + +
  gi|2623707   274 WLSRWKAADLYLRDIEDLRWELSIQSCSDELR------QALGQDH----- 312

                  YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi..seisEeAv
                             EPYR  L d R++L  t    RH LA  +++++  +  v
  gi|2623707   313 ----------PEPYREYLRDTRERLKAT----RHWLAEKLrgADADDSLV 348

                  ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                      +e L PL LCY+sL       iA G LLD++  v  FG+ L KLDi
  gi|2623707   349 IKAKDELLQPLLLCYRSLISSNLPEIANGKLLDFIHRVNCFGIELLKLDI 398

                  RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                  RqEs R+   + Ait+ L++G +  W E+ Rq +Ll EL+ KRPLl+  L
  gi|2623707   399 RQESGRHRQAISAITEYLGLGNFETWTEQARQNFLLQELQSKRPLLPKHL 448

                  PktE.......EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvEL
                      ++  +++Ev++v  ++r LA  P +s GaYiisma  PsDvLAv L
  gi|2623707   449 NEPAqslieqpEVQEVFATMRTLAAQPQESLGAYIISMAEYPSDVLAVLL 498

                  LqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevm
                  Lq+E g++++LrvvPLFE L DL+ A A+++ LF + WY+ +i+GK evm
  gi|2623707   499 LQKEAGIQHPLRVVPLFETLKDLDGAAATMNTLFNMHWYKQHIQGKHEVM 548

                  vGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRG
                  +GYsDs KDAG +sA W  Y+AqEE+  +AK +G++L+lFHGRGG + RG
  gi|2623707   549 IGYSDSAKDAGFMSANWAQYRAQEELTAIAKTHGIQLTLFHGRGGSISRG 598

                  GGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAt
                  G Pt  A+ sqPP  i G++Rvt qGE+i f FG E +  + L  +tAAt
  gi|2623707   599 GAPTQQALFSQPPGSISGAIRVTEQGEMIRFKFGLEGIALQNLEIYTAAT 648

                  LEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPE
                  LE  + PP  PkPEWR+Lm  m       YR  v   P Fv Y R  tPE
  gi|2623707   649 LEATLLPPPVPKPEWRELMHSMTDLSVQVYRQTVRENPHFVKYLRTVTPE 698

                  lEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAF
                  lE   + +GsRPaKRk  GGiesLRAiPW+FaWtq R  LP WLG GAA
  gi|2623707   699 LELQMLPLGSRPAKRKVTGGIESLRAIPWVFAWTQIRLMLPAWLGTGAAI 748

                  KhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL
                     id+  K    L Em   WP+F   +D+lEmv  K D  +A  y+  L
  gi|2623707   749 NQVIDQGHKA--TLDEMLVAWPYFQTLIDMLEMVLSKSDAHVALYYESHL 796
```

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                    v.aEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsY
                     + E+Lk  G+ LR++ +   + LL + G   lL     L q +R+R +Y
  gi|2623707   797 TdDEDLKVLGEHLRQRLKYAVQTLLALKGESKLLSSNEVLDQSMRVRKPY 846

                    ittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpte
                    +  L  +qA  +KR R               y +E              +
  gi|2623707   847 LLPLHLLQAELMKRRR--------------RYLEER-------------Q 869

                    rvaPGLEDtLiLtmKGiAAGmqntG<-*
                    +    ++  L++ + GiAAG+ ntG
  gi|2623707   870 ETNTPVDHALMVSIAGIAAGLRNTG    894

gi|242052357|ref|XP_002455324.1|: domain 1 of 1, from 16 to 1038: score 790.8, E = 9.1e-235
                    *->siDAqLRlLvPGKvsedekLieYDALLlD...kFLDiLqDLHGedLk
                       + +   RlL+    s     +  D LL + +++F+ iL        +
  gi|2420523    16    AFEDDCRLLA----S-----LLHDVLLRElgpRFIQILE-------R 46

                    EavqECYElsAeYEGKkDtkKLeE..LGakLtsLdPaDailvAkailHmL
                      +     +s    G +Dt  + E++L a L ++   Da+ vA+a++H L
  gi|2420523    47 NRILAQSAVSMRAAGMEDTAAVVErqLEADLAAMSLDDALCVARAFSHYL 96

                    nLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnK
                    nL  +AE     +R R  +        E       Di   + kL+  +
  gi|2420523    97 NLMGIAET---HHRVRKARNI------EQLSKSCDDI---FNKLIQSG-V 133

                    sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt
                     Pe  ++ +  q v++vltAHPtq  RR L  K+ R+   L      D+
  gi|2420523   134 PPEQLYDTVCKQEVEIVLTAHPTQINRRTLQYKHLRVAHLLEFNGRPDLS 183

                    veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGv
                     eDK+ L E L REi A + tDE+RR +PtP DE RaG+  +   +Wk +
  gi|2420523   184 HEDKEMLIEDLVREITAIWQTDELRRHKPTPVDEARAGLHIVEQSLWKAI 233

                    PKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                    P +LRRv  ALK       lP     ikF sWmGGDRDG nP vt  vtR
  gi|2420523   234 PHYLRRVSSALKK-HTGRPLPLTCTPIKFGSWMGGDRDG-NPNVTAKVTR 281

                    DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEly........
                    Dv LL+R mA  +Yi  ++ L FEls+ RC d +   A ++  +++ +++
  gi|2420523   282 DVSLLSRWMAIDFYIRELDNLSFELSIKRCSDKVASLANDIIlkesased 331

                    ..................................................
                     + ++ +++ ++++ + +++   + + +++ + ++ ++ ++++++ +  +
  gi|2420523   332 lkantwnktvpqnnaklhhnlalpaqlpsgadlpsctecsdgesqfrmin 381

                    .................................rtaardkvvKyYiE...
                     ++++++++  + +++ ++++ +++++++++ +rt+  +++ K + E++
  gi|2420523   382 lprnssrpgalnltekiedsplssptsrqpqlsRTSSGHQLRKLFKEshi 431

                    .....FWKqvPPt.......EPYRviLGdvRDKLYntRERaRHLLAtGis
                    +++++F K + P  +++++  PYRv+LG+v++KL  tR R   LL
  gi|2420523   432 grsssFQKLLEPSlsdrpgiTPYRVVLGNVKEKLVKTRRRLELLLEDLPC 481

                    eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                    +   e      ++ LEPL LC +sL  CG  v+ADG L Dl+R v tFG+
  gi|2420523   482 DYDTEEYCETSDQLLEPLLLCHQSLQSCGASVLADGRLADLIRRVATFGM 531

                    sLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKR
                     L+KLD+RqEs R+t+ lD +t  L++G Y eW EeK+ ++L  ELkGKR
  gi|2420523   532 VLMKLDVRQESGRHTEALDSVTSYLDLGVYSEWDEEKKLDFLTRELKGKR 581

                    PLlgsDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvEL
                    PL++  +    +vk+vld+f+v AEL +Ds GaY+isma   sDvLAvEL
  gi|2420523   582 PLVPQNIEVSADVKEVLDTFKVAAELGSDSLGAYVISMASNASDVLAVEL 631

                    LqRECgvkq...........tLrvvPLFEkLADLeAAPAavekLFsiDWY
                    Lq++  +  +++ +++ +++tLrvvPLFE + DL+AA  a+ kL siDWY
  gi|2420523   632 LQKDARLTVsgdlgrpcpggTLRVVPLFETVKDLQAAGSAIRKLLSIDWY 681

                    inri....dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGv
                    + +i ++++G qevmvGYsDsGKDAGR+ AAW LYkAqE+++    ++G+
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  gi|2420523   682 REHIiknhNGHQEVMVGYSDSGKDAGRFTAAWELYKAQEDVVAACNEFGI 731

                   KLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGE
                   K++lFHGRGG +GRGGGPt LAi sqPP  + G lR t qGE++   FG
  gi|2420523   732 KVTLFHGRGGSIGRGGGPTYLAIQSQPPGSVMGTLRSTEQGEMVQAKFGL 781

                   EnLCFrsLqRFtAAtLEHGmnPPvsPk.PEWRkLmeemAvvAtEEYRsvv
                    +   r L  +t A L   + PP  P++P WR +mee+       YR+ v
  gi|2420523   782 PQTAVRQLEIYTTAVLLATLRPPHPPRdPNWRTVMEEISRASCAHYRATV 831

                   vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaW
                   + +P F+ YF  AtP  E G++niGsRPaKRk + GGi sLRAiPW+FaW
  gi|2420523   832 YEDPEFITYFQEATPQAELGHLNIGSRPAKRKQAlGGISSLRAIPWVFAW 881

                   tqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEm
                   tqtR  LP WLGvG   + A+d+       L+ mY eWPFF  t+DL+Em
  gi|2420523   882 TQTRLVLPAWLGVGTGLQDALDRGHGA--ELRAMYGEWPFFQSTVDLIEM 929

                   vFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlL
                   v AK D  +Aa y+++Lva e +  G++LR +   t+  +L + GH  l
  gi|2420523   930 VTAKADAPVAAHYEEMLVAPERRAVGERLRKELARTERCVLAVSGHSKLT 979

                   EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                        L+  +  R +Y+  +n++q   L+R+R                d
  gi|2420523   980 AHNRSLRRLIESRLAYLNPINMLQVEVLRRLR----------------RD 1013

                   EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   ++          n        L D L++t+ GiAAGm ntG
  gi|2420523  1014 DD----------N------RRLRDALLITINGIAAGMRNTG    1038

gi|156972425|ref|YP_001443332.1|: domain 1 of 1, from 3 to 888: score 790.7, E = 9.7e-235
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +    R+    K +     ++    +l + L+  + D HGe++ E
  gi|1569724     3    VVFLRGRMTMNEKYA----ALKSNVRMLGHLLgNTIRDAHGEEIFEK 45

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls        + + e L   + sL       v +a+   LnL n
  gi|1569724    46 VETIRKLSKSAQAGNSADR-ESLIEEIKSLPDEQLTPVTRAFNQFLNLTN 94

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +   R   +         E +A     i   + kLv     s  +
  gi|1569724    95 IAEQYHTISRHCEEHIC------EPDA-----INSLFSKLVQND-VSKLD 132

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+   ++
  gi|1569724   133 TAQAVRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSFKER 182

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   k  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
  gi|1569724   183 KKTERRLEQLIVQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWEAVPDFL 232

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   R +   LK   + E lP d+  ++FssWmGGDRDG nP vt  vtR+v L
  gi|1569724   233 REMNDRLKSY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHSVTREVLL 280

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   L+R  Aa lY++ + +L+ Elsm  Cnd +R  A E +
  gi|1569724   281 LSRWKAADLYLNDINELISELSMTVCNDKVRELAGEDQH----------- 319

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                             EPYR iL + R  L  t++       +G   ++  A   k
  gi|1569724   320 ----------EPYRAILKQLRSLLNETKD-ILDAKVHG-QKLAVKAPLQK 357

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                   vE+  EPL  CY+sL eCG  viA GsLLD LR v  FG+ Lv+LDiRqE
  gi|1569724   358 VEQLWEPLYACYQSLNECGMGVIANGSLLDTLRRVKAFGIHLVRLDIRQE 407

                   seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                   s R+ Dvl  +t+ L+iG Y +WsE+ +  +L  EL  KRPLl+ D
  gi|1569724   408 STRHADVLSELTRYLGIGDYEQWSEQDKIAFLTNELASKRPLLPRDWEPS 457
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                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    E vk+vld+ +++A  P ++FGaY+isma + sDvLAv LL  E g
  gi|1569724   458 EPVKEVLDTCKIVAAQPREAFGAYVISMARTASDVLAVHLLLQEAGCPYR 507

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    + v PLFE L DL+ A A +++L  iD Y+  i+  q vm+GYsDs KDA
  gi|1569724   508 MDVCPLFETLDDLNNAEAVIKQLMGIDLYRGFIQNHQMVMIGYSDSAKDA 557

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G +sA W  Y A + ++KvA + Gv L+lFHGRGGt+GRGG P H A+Ls
  gi|1569724   558 GVMSAGWAQYHAMDSLVKVAEEEGVELTLFHGRGGTIGRGGAPAHAALLS 607

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|1569724   608 QPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNLYASAILEANLLPPPE 657

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EWR+Lm+ +  v  E YRsvv  EP Fv YFR AtPElE Gk+ +Gs
  gi|1569724   658 PKQEWRDLMDVLSEVSCESYRSVVRGEPDFVPYFRQATPELELGKLPLGS 707

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ +dK  +
  gi|1569724   708 RPAKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSVDKGHQA 757

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l  L+Em +eWPFF   l +lEmv+ K    i   yD+ Lv E L+P G+
  gi|1569724   758 L--LEEMCREWPFFSTRLGMLEMVYTKCNMDISRYYDQRLVDEPLQPLGD 805

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR++ +   + +L +     l+  DP+    +RLR+ Y+  Ln++qA
  gi|1569724   806 RLREQLQRDIKSVLNVENNENLMQSDPWGLESIRLRNIYVEPLNMLQAEL 855

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                                 te+ +  LE+ L+
  gi|1569724   856 LYRTRQ------------------------------TEEASANLEEALM 874

                    LtmKGiAAGmqntG<-*
                    +t+ GiAAGm ntG
  gi|1569724   875 VTIAGIAAGMRNTG    888

gi|5734703|gb|AAD49968.1|AC008075_1: domain 1 of 1, from 2 to 980: score 790.4, E = 1.2e-234
                    *->siDAqLRlLvPGKvsedekLieYDA.LLlDkFLDiLqDLHGedLkEa
                               +   +s   +  e D +LL   F D+Lq   G+   E
  gi|5734703     2    ---TDTTDDIAEEIS--FQSFEDDCkLLGSLFHDVLQREVGNPFMEK 43

                    vqECYEl..sA...eYEGKkDtkKLeE..LGakLtsLdPaDailvAkail
                    v     l +sA +    G +Dt  L E++L + +  +   +a+ +A+++
  gi|5734703    44 VERIRILaqSAlnlRMAGIEDTANLLEkqLTSEISKMPLEEALTLARTFT 93

                    HmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlk
                    H LnL  +A+                        t  s       +L
  gi|5734703    94 HSLNLMGIAD------------------------THHS-------QLLQS 112

                    lnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK
                    +  sP+E +  +  q v++vltAHPtq  RR L  K+ Ri   L
  gi|5734703   113 G-ISPDELYKTVCKQEVEIVLTAHPTQINRRTLQYKHIRIAHLLEYNTRS 161

                    DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvW
                    D+ veD++ L E L REi   + tDE+RR +PtP DE RaG+  +   +W
  gi|5734703   162 DLSVEDRETLIEDLVREITSLWQTDELRRQKPTPVDEARAGLNIVEQSLW 211

                    kGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPE
                    k vP++LRRv   LK       lP     +kF sWmGGDRDG nP vt
  gi|5734703   212 KAVPQYLRRVSNSLKKF-TGKPLPLTCTPMKFGSWMGGDRDG-NPNVTAK 259

                    vt.............RDvCLLaRmmAanlYisqvEDLmFElsmWRCndE
                    v      + +++++++  + LL+R mA  lYi  v+ L FEls  RC d
  gi|5734703   260 VSllifydlnskptghERISLLSRWMAIDLYIREVDSLRFELSTDRCSDR 309

                    LRvRAEEly.....................................r
                        A+ + +++  +++ +++++++ ++++ ++ +++++++ +++++ ++
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  gi|5734703   310 FSRLADKILekdymppnlqkqneqdfsesdwekidngsrsgltsrgsfsS 359

                    taardkvvKyYiE.......FWKqvPP.......tEPYRviLGdvRDKLY
                    t++     K + E++ ++++F K + P++ ++ +  PYR++LG+v++KL
  gi|5734703   360 TSQLLLQRKLFEEsqvgktsFQKLLEPpplkragSAPYRIVLGEVKEKLV 409

                    ntRERaRHLLAtGi.seisEeAvytkvEeFLEPLELCYksLCeCGDkviA
                     tR R   LL  G++ e      y   ++ LEPL LCY sL   G +v+A
  gi|5734703   410 KTR-RLLELLIEGLpCEYDPKNSYETSDQLLEPLLLCYESLQSSGARVLA 458

                    DGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWs
                    DG L Dl+R vstFG+ LvKLD+RqE+ R+ + lDAitt L++G Y eW
  gi|5734703   459 DGRLADLIRRVSTFGMVLVKLDLRQEAARHSEALDAITTYLDMGTYSEWD 508

                    EeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGaY
                    EeK+ E+L  ELkGKRPL++  +    +vk+vld+frv AEL ++s GaY
  gi|5734703   509 EEKKLEFLTRELKGKRPLVPQCIKVGPDVKEVLDTFRVAAELGSESLGAY 558

                    iismataPsDvLAvELLqRECgvkq..........tLrvvPLFEkLADL
                    +isma   sDvLAvELLq++  +  +++++++ +++tLrvvPLFE + DL
  gi|5734703   559 VISMASNASDVLAVELLQKDARLALtsehgkpcpggTLRVVPLFETVNDL 608

                    eAAPAavekLFsiDWYinri....dGKqevmvGYsDsGKDAGRlsAAWqL
                    +AA  ++ kL siDWY+ +i+++++G qevmvGYsDsGKDAGR+ AAW L
  gi|5734703   609 RAAGPSIRKLLSIDWYREHIqknhNGHQEVMVGYSDSGKDAGRFTAAWEL 658

                    YkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGs
                    YkAqE ++    ++G+K++lFHGRGG +GRGGGPt LAi sqPP  + Gs
  gi|5734703   659 YKAQENVVAACNEFGIKITLFHGRGGSIGRGGGPTYLAIQSQPPGSVMGS 708

                    lRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE.WRkL
                    lR t qGE++   FG  +   r L  +t A L   ++PP  P+ E+WR+L
  gi|5734703   709 LRSTEQGEMVQAKFGIPQTAVRQLEVYTTAVLLATLKPPQPPREEkWRNL 758

                    meemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs
                    mee+  +    YRs v+  P F  YF  AtP  E G +niGsRP++Rk s
  gi|5734703   759 MEEISGISCQHYRSTVYENPEFLSYFHEATPQAELGFLNIGSRPTRRKSS 808

                    GGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmY
                     Gi  LRAiPW+FaWtqtRF LP WLGvGA  K   +K       LkEmY
  gi|5734703   809 SGIGHLRAIPWVFAWTQTRFVLPAWLGVGAGLKGVSEKGHAD--DLKEMY 856

                    keWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvE
                    keWPFF  tl+L+Emv AK D  +   yD+ Lv+E  +  G +LR +
  gi|5734703   857 KEWPFFQSTLELIEMVLAKADIPMTKHYDEQLVSEKRRGLGTELRKELMT 906

                    tkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPs
                    t++++L i GH  lL     LK+ +  R +Y+  +n++q   LKR+R
  gi|5734703   907 TEKYVLVISGHEKLLQDNKSLKKLIDSRLPYLNAMNMLQVEILKRLR--- 953

                    ykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAA
                                 dE+          n        L D L++t+ GiAA
  gi|5734703   954 -------------RDED----------N------NKLRDALLITINGIAA 974

                    GmqntG<-*
                    Gm ntG
  gi|5734703   975 GMRNTG    980

gi|90407116|ref|ZP_01215305.1|: domain 1 of 1, from 6 to 877: score 789.9, E = 1.6e-234
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLH.GedLkEa
                          A LR    G v            Ll + L      H Ge+  +
  gi|9040711     6    ---ANLR----GNVN-----------LLGQLLGKSIGEHlGEEFLDK 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    + E   ls       ++   e L  +L  L   + + v +a+ H LnLAn
  gi|9040711    35 IEEIRQLSKSSRAGNESDG-ETLIRVLSNLSDDELVPVSRAFTHFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +      i++        E s      i E + kL      s eE
  gi|9040711    84 IAEQFHC-----ISRHT------ENSQDAPDPINEVINKLKNSN-VSKEE 121
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                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+ n s+ +vltAHPt   RR L+ K++ i  CL+ L   Dv   ++
  gi|9040711   122 MQKAINNLSMNMVLTAHPTEITRRTLIHKHTAINECLSLLEVSDVSNKER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L + L   i  A+ t +iR+ +PtP DE + G + i   +W+ vP ++
  gi|9040711   172 DQLLDRLEQLITQAWHTNDIRKKRPTPVDEAKWGFAVIENSLWEAVPLYV 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R  D  LK   +   lP d   i  +sWmGGDRDG nP vt  vt +v +
  gi|9040711   222 RELDEKLKT-ELDLCLPEDSSPINITSWMGGDRDG-NPFVTAKVTEEVLI 269

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                     +R +A nlY+  +  L  Elsm  C   LR            d
  gi|9040711   270 TSRWVAINLYLKDIKQLTEELSMDNCDATLR------NIVGDAD------ 307

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR iL   R  L  t       L    s+  +    t+
  gi|9040711   308 ----------EPYRAILRKLRIELKETLTALSAKLQGQTSDAKD--LITR 345

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     E+   P+ LCY sL  CG + iA G +LD+LR v  FG+ LvKLDiRq+
  gi|9040711   346 TEQLKTPIKLCYESLKKCGMHSIANGLILDILRRVACFGVNLVKLDIRQD 395

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                     eR+ D l  +tt L++G Y  W E ++qE+Ll ELk KRPL++s
  gi|9040711   396 GERHGDTLSELTTYLGLGDYNTWTEPQKQEFLLEELKSKRPLIPSKWKPS 445

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     E ++vld+ +v+A     + G Yiisma   sDvL v LL +E g
  gi|9040711   446 AEAQEVLDTCHVIAKTDPQALGIYIISMARQASDVLSVQLLLKETGCPFK 495

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    + v PLFE L DL+ A   +++LF++DWY+n i+G q+vm+GYsDs KDA
  gi|9040711   496 IAVAPLFETLDDLNNAKEVMQRLFAVDWYRNYINGEQHVMIGYSDSAKDA 545

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y+AqE ++K+  +  ++LvlFHGRGGt+GRGG P H A+Ls
  gi|9040711   546 GVIAANWAQYQAQEALVKICDDNNIQLVLFHGRGGTIGRGGAPAHQALLS 595

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f FG  ++  +sL  +tAA LE  + PP +
  gi|9040711   596 QPPGSLKGGLRVTEQGEMIRFKFGLPKIAIQSLNLYTAAILEANLLPPPA 645

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EWR++m++ A     EYR  v  EP Fv YFR+ tPElE Gk+ +Gs
  gi|9040711   646 PKQEWRDIMDQFAEQSCREYRHFVCDEPDFVPYFRSVTPELELGKLALGS 695

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKRk  GGiesLRAiPWiFaW q R  LP WLG G   K  +d   K
  gi|9040711   696 RPAKRKANGGIESLRAIPWIFAWSQNRLMLPAWLGTGGSLKTLLDEGKKE 745

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l  L+EmY +WPFF   l++lEm F K D G+   y++ Lv   L+P G+
  gi|9040711   746 L--LQEMYCNWPFFHTRLEMLEMLFLKTDAGLTKFYEERLVPKSLWPLGQ 793

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LRd+   t++ LL+    + l+   P++K  + LR++Y+  Ln++qA
  gi|9040711   794 RLRDNLSLTREVLLETIPEHKLMQEQPWIKESISLRNPYVDPLNMLQAEL 843

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                              n ++++ P ++  L+
  gi|9040711   844 LSRSRA----------------------------N-GDEICPVIDQALM 863

                    LtmKGiAAGmqntG<-*
                    +t+ GiAAG+ ntG
  gi|9040711   864 VTIAGIAAGLRNTG    877

gi|50086573|ref|YP_048083.1|: domain 1 of 1, from 4 to 894: score 789.6, E = 2.1e-234
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        iDA LR               D  Ll   L++ L+   G+dL
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gi|5008657     4    QIDAPLRE--------------DVRLLGNLLgETLKQHAGQDLFNQ 35

                    vqECYEls.AeYEGKkDt.kKLeELGakLtsLdPaDailvAkailHmLnL
                    +     l++   +G+ +t+kKLe L      L   + + + +a++  Ln
gi|5008657    36 IEQIRALAkGARDGQAETeKKLEQL---FLDLKDEEILPLTRAFSYFLNF 82

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                    An+AE  ++   RR +         E        i   + k       s
gi|5008657    83 ANIAEQYHVVRSRRRSEFD------EQGPPPNPLI-HLFEKFKQNQ-ISS 124

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    +  F+ + n s++LvltAHPt   RR L+qK   i   L++L  + +t+
gi|5008657   125 KQLFQQVSNLSIELVLTAHPTEVSRRTLIQKYDDINEGLSKLDQQKLTPR 174

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    +++ + + L   i  A+ tDEiR  +PtP DE + G   i  t+W+ vPK
gi|5008657   175 ERQQVLDDLKQLICSAWQTDEIRQNKPTPLDEAKWGFTTIEQTLWNAVPK 224

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    F+R  Dt L        lP d+  i+F+sWmGGDRDG nP vt  vt +v
gi|5008657   225 FVRELDT-LVHQHCDAHLPLDISPIRFASWMGGDRDG-NPNVTHNVTQEV 272

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      L+R  Aa lY+  +EDL +Els+  C +EL       +   +r+
gi|5008657   273 LWLSRWQAADLYLRDIEDLRWELSIQACSEELS------QTLGRRH---- 312

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                               EPYR  L   R++L  tR     L  +G+ +  +  +
gi|5008657   313 -----------PEPYREYLRSTRERLKATRQWLS-LRLQGL-DGDDSQII 349

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     +  e L+PL LC +sL eC    iA G LLD++  v  FG+ L KLDiR
gi|5008657   350 RHKQELLDPLLLCHRSLMECNLPEIANGKLLDFIYRVNCFGIELLKLDIR 399

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+   + Ait+ L++G + +W E+ Rq +L+ EL+ KRPLl+  L
gi|5008657   400 QESGRHRQAISAITEYLGLGNFESWTEQARQNFLIQELQSKRPLLPKYLN 449

                    ktE.......EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                      E++  ++++vk+v  ++r LAE P +s GaYiisma   sDvLAv LL
gi|5008657   450 EPEgsliehpDVKEVFATMRTLAEQPPESLGAYIISMAEYASDVLAVLLL 499

                    qRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmv
                    q+E g+ q+LrvvPLFE L DL+ A  ++e LF + WY+ +i+GK evm+
gi|5008657   500 QKEAGILQPLRVVPLFETLKDLDGAAKTMETLFNMHWYKQHIQGKHEVMI 549

                    GYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGG
                    GYsDs KDAG +sA W  Y+AqEE+  vAK +Gv+L+lFHGRGG + RGG
gi|5008657   550 GYSDSAKDAGFMSANWAQYRAQEELTAVAKSHGVQLTLFHGRGGSISRGG 599

                    GPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtL
                     Pt  A+ sqPP  i G++Rvt qGE+i f FG E +  + L  +tAAtL
gi|5008657   600 APTQQALFSQPPGSISGAIRVTEQGEMIRFKFGLEGVALQNLEIYTAATL 649

                    EHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPEl
                    E  + PP  Pk EWR+Lm +m  +    YR  v   P Fv Y R  tPEl
gi|5008657   650 EATLLPPPVPKQEWRDLMHQMTDISVRVYRETVRENPHFVQYLRTVTPEL 699

                    EYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFK
                    E   + +GsRPaKRk sGGiesLRAiPW+FaWtq R  LP WLG GAA
gi|5008657   700 ELQMLPLGSRPAKRKVSGGIESLRAIPWVFAWTQIRLMLPAWLGTGAAIN 749

                    hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLv
                      id   K +  L Em  eWP+F   +D+lEmv  K D  iA  y+  L
gi|5008657   750 QVIDENKKAV--LDEMLAEWPYFQTLIDMLEMVLSKSDANIALYYESHLT 797

                    .aEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYi
                    + E+Lk  G+ LR++  +  + LL + G   lL     L q + +R +Y+
gi|5008657   798 dNEDLKILGEMLRQRLNDAVQTLLSMKGESKLLSKNDVLDQAMQVRKPYL 847

                    ttLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpter
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                    L  +qA  +KR R               y +            n +er
  gi|5008657   848 LPLHLLQAELMKRRR--------------LYTAQS----------N-AER 872

                   vaPGLEDtLiLtmKGiAAGmqntG<-*
                    +  ++  L++ + GiAAG+ ntG
  gi|5008657   873 TP--VDHALMVSIAGIAAGLRNTG    894

gi|254229794|ref|ZP_04923201.1|: domain 1 of 1, from 3 to 888: score 788.8, E = 3.7e-234
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +    R     K +     ++    +l + L+  + D HGe++ E
  gi|2542297     3    VVFLRGRTTMNEKYA----ALKSNVRMLGHLLgNTIRDAHGEEIFEK 45

                   vqECYEl..sAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                   v     l++sA+   + D   L E    +  L       v +a+   LnL
  gi|2542297    46 VETIRKLskSAQAGNQADRDSLIE---EIKHLPDEQLTPVTRAFNQFLNL 92

                   AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                    n+AE  +   R   +         E +A     i   + kLv     s
  gi|2542297    93 TNIAEQYHTISRHCEEHIC------EPDA-----INSLFSKLVQND-VSK 130

                   eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    +  +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+
  gi|2542297   131 LDTAQAVRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSSK 180

                   DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                   ++k  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP
  gi|2542297   181 ERKKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWEAVPD 230

                   FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                   FLR +   LK   + E lP d+  ++FssWmGGDRDG nP vt  vtR+v
  gi|2542297   231 FLREMHDRLKSY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHSVTREV 278

                   CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                    LL+R  Aa lY++ + +L+ Elsm   nd +R  A E +
  gi|2542297   279 LLLSRWKAADLYLNDINELISELSMTVSNDQVRELAGEDQH--------- 319

                   yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                               EPYR iL + R  L  t++     + +G   ++  A
  gi|2542297   320 ------------EPYRAILKQLRTLLNETKDILDAKI-HG-QKLAVKAPL 355

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                    kvE+  EPL  CY+sL eCG  viA GsLLD LR v  FG+ Lv+LDiR
  gi|2542297   356 QKVEQLWEPLYACYQSLNECGMGVIANGSLLDTLRRVKAFGIHLVRLDIR 405

                   qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                   qEs R+ Dvl  +t+ L+iG Y +WsE+ +  +L  EL  KRPLl+ D
  gi|2542297   406 QESTRHSDVLSELTRYLGIGDYEQWSEQDKIAFLTNELASKRPLLPRDWE 455

                   ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                     E vk+vld+ +++A  P ++FGaY+isma + sDvLAv LL  E g
  gi|2542297   456 PSEPVKEVLDTCKIIAAQPREAFGAYVISMARTASDVLAVHLLLQEAGCP 505

                   qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                     + v PLFE L DL+ A   +++L  iD Y+  i+  q vm+GYsDs K
  gi|2542297   506 YRMDVCPLFETLDDLNNAESVIKQLMGIDLYRGFIQNHQMVMIGYSDSAK 555

                   DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                   DAG +sA W  Y A E ++KvA + Gv L+lFHGRGGtvGRGG P H A+
  gi|2542297   556 DAGVMSAGWAQYHAMESLVKVAEEEGVELTLFHGRGGTVGRGGAPAHAAL 605

                   LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                   LsqPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|2542297   606 LSQPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNLYASAILEANLLPP 655

                   vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                     Pk EWR+Lme +  v  E YR vv  EP Fv YFR AtPElE Gk+ +
  gi|2542297   656 PEPKQEWRDLMEVLSEVSCESYRNVVRGEPDFVPYFRQATPELELGKLPL 705

                   GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                   GsRPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ idK
  gi|2542297   706 GSRPAKRNPKGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSIDKGH 755
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                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    + l  L+Em +eWPFF   l +lEmv+ K    i   yD+ Lv E L+P
  gi|2542297   756 QAL--LEEMCREWPFFSTRLGMLEMVYSKCNIDISRYYDERLVDESLRPL 803

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G++LR++ +E  + +L +     l+  DP+    +RLR+ Y+  Ln++qA
  gi|2542297   804 GEKLRAQLQEDIKAVLNVENNENLMQHDPWGLESIRLRNIYVEPLNMLQA 853

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R                                 te+ +  LE+
  gi|2542297   854 ELLYRTRQ------------------------------TEEASANLEEA 872

                    LiLtmKGiAAGmqntG<-*
                    L++t+ GiAAGm ntG
  gi|2542297   873 LMVTIAGIAAGMRNTG    888

gi|145297649|ref|YP_001140490.1|: domain 1 of 1, from 6 to 877: score 787.7, E = 7.7e-234
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          A LR+ v G              Ll k    ++D  G+   + +
  gi|1452976     6    ---AALRANV-GMLG----------QLLGK---SIKDHQGQAFLDKI 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         l A    K      e L   L  L   + + vA+a++  LnLAn+
  gi|1452976    36 ETIRQL-AKSSRKGNEADRERLLETLRTLSDDELLPVARAFSQFLNLANV 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +   RR  ++             t   +E  + kL      s e +
  gi|1452976    85 AEQFHTISRRCEEQVC-----------TPDPLEQMFAKLKASN-LSQEAI 122

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     +A++   +DLvltAHPt   RR L+ K+  +  CL  L   D+ + ++
  gi|1452976   123 IQAVRELDIDLVLTAHPTEVTRRTLIHKHVQLNDCLEALELSDLLPRERD 172

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +   +   +  A+ t EiR  +PtP DE + G + +   +W  +P F+R
  gi|1452976   173 KILNRIEQLVNQAWHTNEIREQRPTPVDEAKWGFAVVENSLWPAIPEFMR 222

                    RvDtALKn.iGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                      D  L+ ++G+  RlP d+  +kF+sWmGGDRDG nP vt  vt +v
  gi|1452976   223 NLDERLQQhLGV--RLPLDAAPVKFTSWMGGDRDG-NPFVTAKVTAEVLE 269

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L R mA  l++  + +L  Elsm  C d +R R          d
  gi|1452976   270 LGRWMAVSLFYKDIKELTSELSMSDCTDAVRERV--------GD------ 305

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vyt
                              EPYR ++ + R+ L  t E    L A+   ++sE  +  t
  gi|1452976   306 --------HPEPYRALVRELREALRETQE---YLTAKVQGQVSESRdLIT 344

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                       +  EPLELCY+s+  CG   iADG LLD+LR+   FG+ LvKLDiRq
  gi|1452976   345 TTAQLREPLELCYHSMHACGMGNIADGMLLDVLRKLACFGIHLVKLDIRQ 394

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    + eR+  v   +t+ L++G Y eWsE+ +q +Ll EL  +RPL++ D
  gi|1452976   395 DGERHGQVFSELTRYLGMGDYAEWSEDDKQAFLLNELNSRRPLIPTDWEP 444

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     +E ++ +d+ rv+A    D+FG Yiisma aPsDvLAv LL +E g k
  gi|1452976   445 SDETRETIDTCRVIAQHDPDAFGIYIISMAGAPSDVLAVQLLLKEAGCKF 494

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                     ++v PLFE   DL A  A +e+L s+DWY+  i+G+q vm+GYsDs KD
  gi|1452976   495 RMPVAPLFETQEDLMAGTAVMERLLSVDWYRGYIQGRQYVMIGYSDSAKD 544

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y A E ++  A     +L+lFHGRGGtvGRGG P H AiL
  gi|1452976   545 AGMMAAGWAQYAAMESLVALAEASNLRLTLFHGRGGTVGRGGAPAHQAIL 594

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
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                    sqPP  + G lRvt qGE+i f FG  ++  +sL  +t A LE  + PP
  gi|1452976   595 SQPPGSLRGGLRVTEQGEMIRFKFGLPKVAIHSLNLYTSAVLEGNLLPPP 644

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR +me++A v  + YRs+v   P Fv YFR AtPE+E Gk+ +G
  gi|1452976   645 KPKESWRAVMEQLATVSCDHYRSIVRGHPDFVPYFRAATPEMELGKLPLG 694

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKRkP GG+esLRAiPWiFaWtq R  LP WLG      hAi    K
  gi|1452976   695 SRPAKRKPNGGVESLRAIPWIFAWTQNRLMLPAWLGAHKGLEHAITDGQK 744

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     +  L+Em ++WPFFR  l++lEmvF K D  +A  yD  Lv  eL+  G
  gi|1452976   745 SV--LEEMSRQWPFFRTRLEMLEMVFLKADLWLAEYYDTRLVPQELWNLG 792

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    k+LR++  +  +++L++    DlL+  P++K  + LR++Y   Lnv+q
  gi|1452976   793 KQLRQELADAIQIVLQLRPQGDLLDDQPWIKESINLRNPYTDPLNVLQVE 842

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                                 te   P L+  L
  gi|1452976   843 LLGRSRS------------------------------HTETLHPELDQAL 862

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|1452976   863 MVTIAGIAAGMRNTG    877

gi|149189173|ref|ZP_01867460.1|: domain 1 of 1, from 3 to 888: score 787.6, E = 8.5e-234
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q R     K +     ++    +l + L+  +++ HG+++ E
  gi|1491891     3    VVKLQGRTTMNEKYA----PLKSNVRMLGHLLgNTIKEAHGDEILEK 45

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls            e L   +t L       vA+a+   LnL n
  gi|1491891    46 VEKIRKLSKSVVRAGNEADRELLIEEITNLPNEQLTPVARAFNQFLNLTN 95

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +A+  +   R           + Ea+      i   + kL ++ n s  +
  gi|1491891    96 IADQYHTISR-----------SCEADVCEPDPISSLFSKL-SQENISKLD 133

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      +A++   ++LvltAHPt   RR ++ K  +i  CL++L   ++ v ++
  gi|1491891   134 SAQAVRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELNELSVKER 183

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    k  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
  gi|1491891   184 KRTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWEAVPEFL 233

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R  D  LK   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
  gi|1491891   234 REFDEKLKGF-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHKITREVML 281

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa lY+    +L+ Elsm +Cnd +R  A E      ++
  gi|1491891   282 LSRWKAAELYLKDFQELITELSMVKCNDQVRELAGE------QH------ 319

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR iL  vR  L nt E     +     e++   +  +
  gi|1491891   320 ----------EPYRAILKPVRTLLMNTLEVIEAQINR--QEVPNKPILED 357

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     ++   PL  CYksL e G  ++ADGsLLD LR v  FG+ Lv+LDiRqE
  gi|1491891   358 ADQLWQPLMACYKSLRESGMAIVADGSLLDTLRRVKAFGVHLVRLDIRQE 407

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+ Dv+  +t+ L++G Y +WsE+ +  +L+ EL+ KRPll+ D
  gi|1491891   408 STRHSDVISELTRYLGLGDYDQWSEQDKVSFLINELSSKRPLLPRDWEPS 457

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    E+v++vld+ rv+A    ++FGaY+isma + sDvLAv L+  ECg k
  gi|1491891   458 EDVQEVLDTCRVIASQSREAFGAYVISMARTASDVLAVHLILQECGCKFR 507
```

```
                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    + v PLFE L DL+   A +++LF iDWY+  i+  q vm+GYsDs KDA
  gi|1491891   508 MDVCPLFETLDDLNNSEAVMKQLFDIDWYRGYIQNHQMVMIGYSDSAKDA 557

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G +sA W  Y A E ++ v  + G+ ++lFHGRGGt+GRGG P H A+Ls
  gi|1491891   558 GVMSAGWAQYSAMESLVEVGEQAGIDITLFHGRGGTIGRGGAPAHAALLS 607

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|1491891   608 QPPKSLKGGLRVTEQGEMIRFKLGLPEIAVNSFNLYASAILEANLLPPPE 657

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk  WR+Lme +  v  E YR vv  EP Fv YFR AtPElE Gk+ +Gs
  gi|1491891   658 PKQAWRDLMEVLSEVSCEAYRKVVRGEPDFVPYFRQATPELELGKLPLGS 707

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ idK  +
  gi|1491891   708 RPAKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSIDKGHQA 757

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l  L+Em +eWPFF   l +lEmv+ K    i   yD+ L a eL P G+
  gi|1491891   758 L--LEEMCREWPFFSTRLGMLEMVYTKCNMEISRYYDQRLAAPELLPLGD 805

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR++ +   + +L +  H  l+  DP+ +  +RLR+ Y+  Ln++qA
  gi|1491891   806 KLRAQLQQDIKAVLNVENHNHLMQSDPWGQESIRLRNTYVEPLNMLQAEL 855

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                                +e     LE+ L+
  gi|1491891   856 LYRTRQ------------------------------SEDTEAELEEALM 874

                    LtmKGiAAGmqntG<-*
                    +t+ GiAAGm ntG
  gi|1491891   875 VTIAGIAAGMRNTG    888

gi|262280608|ref|ZP_06058392.1|: domain 1 of 1, from 4 to 894: score 787.3, E = 1e-233
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        iDA LR                D  Ll   L++ L+   G++L
  gi|2622806     4    QIDAPLRE--------------DVRLLGNLLgETLKQHAGQELFNQ 35

                    vqECYEls.AeYEGKkDtkK.LeELGakLtsLdPaDail.vAkailHmLn
                    +     l++   +G+ +++K+Le L   L    P D +l++ +a++H Ln
  gi|2622806    36 IEQIRALAkGARDGQAEAQKqLEQLFLNL----PDDELLpLTRAFSHFLN 81

                    LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                     An+AE  ++   RR         +D  s      + E +K
  gi|2622806    82 FANIAEQYHVVRSRRQAEFD----SDANSPNPLVHLFEKFKDKSIST--- 124

                    PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                     e  F+ +    ++LvltAHPt   RR L+qK   i  CL+qL  + +t+
  gi|2622806   125 -EKLFQQVCDLDIELVLTAHPTEVSRRTLIQKYDDINACLSQLDQQKLTP 173

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                     +++     L   i  A+ tDEiR  +PtP DE + G + i  t+W+ vP
  gi|2622806   174 RERQSALANLKQQISSAWQTDEIRQHRPTPVDEAKWGFATIEQTLWNAVP 223

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                    KF+R     ++       lP ++  ++F+sWmGGDRDG nP vt  +t +
  gi|2622806   224 KFIRELNELVQE-NCQQNLPLNIAPVRFASWMGGDRDG-NPNVTHQITQE 271

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                    v  L+R  Aa lY+  +E L +Els+  C +E+      ++    ++
  gi|2622806   272 VLWLSRWQAADLYLRDIENLRWELSIQTCSEEM------IQAIGNQH--- 312

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe..
                                EPYR  L + R++L  t    RH LA+ +  +  +++
  gi|2622806   313 ------------AEPYREYLRATRERLKAT----RHWLAQRLQGLEADdt 346

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
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                    v    +e L PL LCY+sL +     iA G LLD++  v  FG+ L KL
  gi|2622806   347 NVIKSKDELLQPLLLCYRSLIDSNLPEIANGQLLDFIYRVNCFGIELLKL 396

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    DiRqEs R+   + Ait+ L++G + +W E+ Rq +L+ EL+ KRPLl+
  gi|2622806   397 DIRQESGRHRQAISAITEYLGLGNFESWTEQARQNFLIQELQSKRPLLPK 446

                    DLPktE.......EvkDvldafrvLAELPiDsFGaYiismataPsDvLAv
                     +   E++  ++++v++v  ++r LA+ P +s GaYiisma  PsDvLAv
  gi|2622806   447 YINEPEgslighpDVQEVFATMRTLADQPPESLGAYIISMAEYPSDVLAV 496

                    ELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqe
                     LLq+E g++++LrvvPLFE L DL+ A  +++ LF + WY+ +i+GK e
  gi|2622806   497 LLLQKEAGIQHPLRVVPLFETLKDLDGAATTMNTLFNMHWYKQHIQGKHE 546

                    vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                    vm+GYsDs KDAG +sA W  Y+AqEE+  +A+ +Gv+L+lFHGRGG +
  gi|2622806   547 VMIGYSDSAKDAGFMSANWAQYRAQEELTAIAQTHGVQLTLFHGRGGSIS 596

                    RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                    RGG Pt  A+ sqPP  i G++Rvt qGE+i f FG E +  + L  +tA
  gi|2622806   597 RGGAPTQQALFSQPPGSISGAIRVTEQGEMIRFKFGLEGIAMQNLEIYTA 646

                    AtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAt
                    AtLE  + PP  Pk EWR+Lm++m       YR  v   P Fv Y R  t
  gi|2622806   647 ATLEATLLPPPEPKAEWRELMNRMTDHSVKVYRQTVRENPHFVKYLRTVT 696

                    PElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGA
                    PElE   + +GsRPaKRk sGGiesLRAiPW+FaWtq R  LP WLG GA
  gi|2622806   697 PELELQMLPLGSRPAKRKVSGGIESLRAIPWVFAWTQIRLMLPAWLGTGA 746

                    AFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDk
                    A    i    K    L Em ++WP+F   +D+lEmv  K D  iA  y+
  gi|2622806   747 AINEVIADQQKA--TLDEMLQQWPYFQTLIDMLEMVLSKADANIALYYES 794

                    LLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRd
                     L  +E+Lk  G++LR++ ++  + LL +     lL     L q + +R
  gi|2622806   795 HLTEdEDLKVLGNQLRQRLKDAVETLLALKDESKLLSNNEVLDQSMQVRK 844

                    sYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnp
                    +Y+  L  +qA  +KR RD              y +E
  gi|2622806   845 PYLLPLHLLQAELMKRRRD--------------YLAER------------ 868

                    tervaPGLEDtLiLtmKGiAAGmqntG<-*
                      +  P ++  L++ + GiAAG+ ntG
  gi|2622806   869 QAENTP-VDHALMVSIAGIAAGLRNTG    894

gi|45505267|gb|AAS67005.1|: domain 1 of 1, from 2 to 1032: score 787.1, E = 1.2e-233
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                            +   +   +s   +  + D  Ll   L+DiLq   G +L +
  gi|4550526     2    ---TDITGDIAEEIS--FQSFDDDCRLLGNLLnDILQREVGTNLLDK 43

                    vqECYEls.....AeYEGKkDtkKLeE..LGakLtsLdPaDailvAkail
                    +     l++++ +    G      + E++L + L  +   +a  +A+a++
  gi|4550526    44 IERTRVLAqsgcnMRQAGIVNMAEMLEkqLASELSKMTLEEAFTLARAFS 93

                    HmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlk
                    H L L  +AE     +R R              A      ++ + +Lv
  gi|4550526    94 HYLTLMGIAET---HHRVRKGGNM---------AQIAKSCDDIFNQLVQG 131

                    lnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK
                    +   PeE ++ +    v++vltAHPtq  RR L  K+ Ri   L
  gi|4550526   132 G-VPPEELYDTVCKREVEIVLTAHPTQINRRTLQFKHIRIAHLLDYNDRP 180

                    DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvW
                    D+  eD++ + E L REi   + tDE+RR +PtP DE RaG   +   +W
  gi|4550526   181 DLSTEDREMVIEDLVREITSIWQTDELRRQKPTPVDEARAGFNIVEQSLW 230

                    kGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPE
                    k vP +LRRv  ALK       lP     ikF sWmGGDRDG nP vt
  gi|4550526   231 KAVPHYLRRVSNALKK-HTGKPLPLTCTPIKFGSWMGGDRDG-NPNVTAK 278
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                    vtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrt...
                    vt+Dv LL+R mA  lYi  v+ L FElsm  C d L   A E+   +++
  gi|4550526   279 VTKDVSLLSRWMAIDLYIREVDSLRFELSMNQCSDRLSRLAHEILEAkhe 328

                    .....................aardkv.......................
                    +++++ +++ +++ + +++ +ar ++++  +++++++++ + + ++  ++
  gi|4550526   329 nrrenwnqsanrsltlptqlPARAHLpsiaengesrhprldipapdymqs 378

                    ....................................vKyYiE....
                    ++++++ + ++++++  +++++ +++++ +++ ++   ++ K Y E++++
  gi|4550526   379 nhkdggvsvssttsklanpntrlpgtssanssassaalgqKKLYAEsqtg 428

                    ...FWK.......qvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                    +++F K  ++  +q+P   PYR++LG+v+DKL   R R   LL     +
  gi|4550526   429 kstFQKllepmlpQLPGIAPYRIVLGNVKDKLEKSRRRLEILLEDVACDY 478

                    sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                         y   ++ LEPL LCY sL  CG  v+ADG L Dl+R v tFG+ L
  gi|4550526   479 DPLDYYETSDQLLEPLLLCYESLQSCGSGVLADGRLADLIRRVATFGMVL 528

                    vKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPL
                    +KLD+RqEs R+ + lDAit+ L++G Y eW EeK+ ++L  ELkGKRPL
  gi|4550526   529 MKLDLRQESGRHAEALDAITQYLDMGTYSEWDEEKKLDFLTRELKGKRPL 578

                    lgsDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLq
                    ++  +    +vk+vld+fr+ AEL +Ds GaY+isma   sDvLAvELLq
  gi|4550526   579 VPVSIEVHPDVKEVLDTFRIAAELGSDSLGAYVISMASNASDVLAVELLQ 628

                    RECgvkq...........tLrvvPLFEkLADLeAAPAavekLFsiDWYin
                    ++  +   ++ ++  +++tLrvvPLFE + DL+ A   + kL siDWY
  gi|4550526   629 KDARLAAigelgkacpggTLRVVPLFETVKDLRGAGSVIRKLLSIDWYHE 678

                    ri....dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                    +i ++++G qevmvGYsDsGKDAGR+ AAW LYkAqE+++    +yG+K+
  gi|4550526   679 HIvknhNGHQEVMVGYSDSGKDAGRFTAAWELYKAQEDVVAACNDYGIKV 728

                    vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                    +lFHGRGG +GRGGGPt LAi sqPP  + G lR t qGE++E  FG  +
  gi|4550526   729 TLFHGRGGSIGRGGGPTYLAIQSQPPGSVMGTLRSTEQGEMVEAKFGLPQ 778

                    LCFrsLqRFtAAtLEHGmnPPvsPkPE.WRkLmeemAvvAtEEYRsvvvK
                    +  r L  +t A L   + PP+ P+ E+WR++mee+  +     R vv+
  gi|4550526   779 IAVRQLEIYTTAVLLATLRPPIPPREEkWRNVMEEISNISCQCDRNVVYE 828

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                     P F  YF  AtPE E G +niGsRP++Rk s Gi  LRAiPW+FaWtqt
  gi|4550526   829 NPEFLAYFHEATPEAELGFLNIGSRPTRRKSSVGIGHLRAIPWLFAWTQT 878

                    RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                    RF LP WLGvGA  K A +K       Lk mYkeWPFF  t+DL+Emv
  gi|4550526   879 RFVLPAWLGVGAGLKGACEKGYTE--ELKAMYKEWPFFQSTIDLIEMVLG 926

                    KGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                    K D  iA  yD++Lv+ e +  G++LR +    +++++ i GH  l
  gi|4550526   927 KADIPIAKHYDEVLVTKERQELGHELRSELMTAEKFVMVISGHEKLQQNN 976

                    PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                      L+  +  R +++  Ln++q   LKR+R                d++
  gi|4550526   977 RSLRRLIENRLPFLNPLNMLQVEILKRLR----------------RDDD- 1009

                    kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                             n        + D L++t+ GiAAGm+ntG
  gi|4550526  1010 ---------N------RKIRDALLITINGIAAGMKNTG    1032

gi|255318037|ref|ZP_05359282.1|: domain 1 of 1, from 4 to 894: score 787.0, E = 1.3e-233
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLH.GedLkEa
                        iDA LR               D  Ll   L     LH G+dL
  gi|2553180     4    QIDAPLRE--------------DVRLLGNLLGETLKLHaGQDLFNQ 35

                    vqECYEls..AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
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                +     l+++A    K+  k+LeEL      L   + + + +a++H Ln
gi|2553180    36 IEQIRALAkgARDGQKEAEKQLEEL---FSTLKDEEILPLTRAFSHFLNF 82

                AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                An+AE  +l   RR +           +A     ++  ++k   k   s
gi|2553180    83 ANIAEQYHLVRSRRQHEFD-------ENAPSPNPLDHLFQKFKQKD-ISA 124

                eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                +  ++ +    ++LvltAHPt   RR L+qK   i  CL+ L  + +t+
gi|2553180   125 DALYQQVCELKIELVLTAHPTEVSRRTLIQKYDGINQCLSRLDQQKLTPH 174

                DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                +++ + + +   i  A+ tDEiR  +PtP DE + G   i  t+W+ vPK
gi|2553180   175 ERQSVLDEMKQLICSAWQTDEIRQHRPTPIDEAKWGFTTIEQTLWNAVPK 224

                FLRRvD.tALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                F+   D+  L   G    lP +v  i+F+sWmGGDRDG nP vt  vt +
gi|2553180   225 FIHELDqLVLEHCG--RPLPLEVAPIRFASWMGGDRDG-NPNVTHQVTQE 271

                vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                v  L+R  Aa lY+  +E L +Els+  C +E+    E l  t
gi|2553180   272 VLWLSRWQAADLYVRDIEALRWELSIQNCSEEM---SEALGYTH------ 312

                KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.
                             EPYR  L + R++L  t    RH LA+ +     +A+
gi|2553180   313 ------------PEPYREYLRQTRERLRAT----RHWLAQKLQGQDADAs 346

                .vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                 v    +e L PL LCY+sL  C    iA G LLD++R v  FG+ L KL
gi|2553180   347 lVIHSKDELLQPLLLCYRSLMACNLPEIANGRLLDFIRRVNCFGIELLKL 396

                DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                D+RqEs R+   + Ait+ L++G +  W E+ Rq +Ll EL+ KRPLl+
gi|2553180   397 DVRQESGRHRQAISAITEYLGLGNFDTWTEQARQNFLLQELQSKRPLLPK 446

                D.......LPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAv
                  +++ ++L    +v++v  +++ LAE P++s GaYiisma  PsDvLAv
gi|2553180   447 HfnepaqsLILHPDVQEVFATMQTLAEQPSESLGAYIISMAEYPSDVLAV 496

                ELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqe
                 LLq+E g++++LrvvPLFE L DL+ A A+++ LF + WY+ +i+GK e
gi|2553180   497 LLLQKEAGIQRPLRVVPLFETLKDLDGAAATMATLFNMHWYRQHIQGKHE 546

                vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                vm+GYsDs KDAG +sA W  Y+AqEE+  vA+++ v+L+lFHGRGG +
gi|2553180   547 VMIGYSDSAKDAGFMSANWAQYRAQEELTAVARQHAVQLTLFHGRGGSIS 596

                RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                RGG Pt  A+ sqPP  i G++Rvt qGE+i f FG E +  + L  +tA
gi|2553180   597 RGGAPTQQALFSQPPGSISGAIRVTEQGEMIRFKFGVEGIALQNLEIYTA 646

                AtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAt
                AtLE  + PP  Pk EWR+Lm  m       YR  v   P Fv Y R  t
gi|2553180   647 ATLEATLLPPPEPKAEWRELMHCMTDLSVQVYRQTVRENPHFVQYLRTVT 696

                PElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGA
                PElE   + +GsRPaKRk sGGiesLRAiPW+FaWtq R  LP WLG GA
gi|2553180   697 PELELQMLPLGSRPAKRKVSGGIESLRAIPWVFAWTQIRLMLPAWLGTGA 746

                AFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDk
                A    +d+  K l  L Em ++WP+F   +D+lEmv  K D  +A  y+
gi|2553180   747 ALNQVLDQGQKEL--LDEMLQQWPYFQTLIDMLEMVLSKADAHVALYYEA 794

                LLvaE.eLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRd
                 L  ++eLk  G++LR++ ++  + LL + G   lL     L q +R+R
gi|2553180   795 HLTDDpELKALGQELRQRLQDAVQTLLALKGESKLLSHNEVLDQSMRVRK 844

                sYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnp
                +Y+  L  +qA  +KR R               y +E+        +L
gi|2553180   845 PYLLPLHLLQAKLMKRRR--------------IYLAEQ--------QLE- 871
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                    tervaPGLEDtLiLtmKGiAAGmqntG<-*
                         P ++  L++ + GiAAG+ ntG
  gi|2553180   872 ---HTP-VDHALMVSIAGIAAGLRNTG    894

gi|90580872|ref|ZP_01236674.1|: domain 1 of 1, from 1 to 876: score 786.9, E = 1.3e-233
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                K s    L     +L       ++  HG++L + v
  gi|9058087     1    ---------MNEKYS---TLKSNVSMLGHLLGNTIKTAHGDELLDKV 35

                    qECYEl..sAeYEGKkDtkKLeELGakLtsLdPaDail.vAkailHmLnL
                         l++sA     +D  KL +    L  L P D +l+vA+a++  LnL
  gi|9058087    36 ETIRKLskSAHSGSEEDRAKLID---ELQNL-PDDQLLpVARAFSQFLNL 81

                    AnLAEEvelAyRRRikkkkhGDFaDEa.sAttEsDiEEtlKkLvlklnKs
                     n+AE  +   R     +   D  DE  +  t+ D        v +l
  gi|9058087    82 TNIAEQYHTISRQCETTLCSPDALDELfNKLTDND--------VNQL--- 120

                    PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                      +  eA++   +DLvltAHPt  +RR ++ K   i  CL+qL   ++
  gi|9058087   121 --DSIEAVRELNIDLVLTAHPTEIARRTMIHKLVQINKCLSQLELSELST 168

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                     ++  ++  L   i  A+  D iR  +PtP DE + G + i   +W+ vP
  gi|9058087   169 SERARIEQRLEQLIAQAWHSDVIRQQRPTPIDEAKWGYAVIENSLWQAVP 218

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                     FLR  D  L+   + E lP d+  + FssWmGGDRDG nP vt  vtR+
  gi|9058087   219 EFLRLFDEKLQQ-HLGEALPLDASPVTFSSWMGGDRDG-NPFVTSNVTRE 266

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                    v  L+R  Aa lY++ + +L+ Elsm  Cn+ +R  A E       +
  gi|9058087   267 VLSLSRWKAADLYLNDIQELINELSMTQCNETVRELAGE-------E--- 306

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                                  EPYR iL + R KL  tR+     + +G    s + v
  gi|9058087   307 ------------HEPYRAILKQLRNKLVHTRDNLDAKI-HGQKPTS-DIV 342

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                      ++ e  +PL  CY+sL eCG  +iADG LLD LR v  FG+ Lv+LDi
  gi|9058087   343 IEDIAELWDPLYACYQSLHECGMAIIADGLLLDTLRRVKCFGVHLVRLDI 392

                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    RqEs R+ Dv+  +t+ L++G Y +WsE+ +  +L+ EL+ KRPLl+ D
  gi|9058087   393 RQESTRHSDVISELTRYLGLGDYDQWSEQDKIAFLVRELSSKRPLLPRDW 442

                    PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                        Evk+v+++ + +AE   ++ G+Y+isma + sDvLAv LL  E g
  gi|9058087   443 EPSAEVKEVIETCKTIAEQSREALGSYVISMARTASDVLAVHLLLQEAGC 492

                    kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsG
                       + v PLFE L DL+     +e+L  iDWY+  i+  q vm+GYsDs
  gi|9058087   493 PFRMDVCPLFETLDDLNNGADVIEQLLNIDWYRGFIQNHQMVMIGYSDSA 542

                    KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                    KDAG +sA W  Y A E ++ v  + Gv ++lFHGRGG +GRGG P H A
  gi|9058087   543 KDAGVMSAGWAQYSAMEKLVDVCEQAGVEITLFHGRGGSIGRGGAPAHAA 592

                    iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP
                    +LsqPP  ++G lRvt qGE+i f  G  ++   sL  ++ AtLE  + P
  gi|9058087   593 LLSQPPRSLKGGLRVTEQGEMIRFKLGLPEVAINSLSLYASATLEANLLP 642

                    PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmn
                    P +Pk EWR+Lm+ +  v  E YR vv  +P Fv YFR AtPElE Gk+
  gi|9058087   643 PPAPKQEWRELMDVLSEVSCEAYRNVVRVDPEFVPYFRAATPELELGKLP 692

                    iGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                    +GsRPaKR P GG+esLRAiPWiFaW q R  LP WLG G A ++ i+K
  gi|9058087   693 LGSRPAKRNPQGGVESLRAIPWIFAWSQNRLLLPAWLGAGEAIQYSINKG 742

                    iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP
                       l  L++m +eWPFF   l +lEmv+ K   GiA  yD+ L  E L+P
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  gi|9058087   743 HAKL--LEDMCREWPFFSTRLGMLEMVYTKTNTGIAKYYDERLTDESLWP 790

                   FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfq
                    G++LRd+     + +L +     l+E DP+    +RLR+ Y+  Ln++q
  gi|9058087   791 LGQKLRDQLGKDIKAVLTVENNDHLMEQDPWGAESIRLRNIYVEPLNMLQ 840

                   AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                   A  L R R                                 e+ +P LE+
  gi|9058087   841 AELLYRTRQ------------------------------QEELPPALEE 859

                   tLiLtmKGiAAGmqntG<-*
                    L++t+ GiA Gm ntG
  gi|9058087   860 ALMVTIAGIATGMRNTG    876

gi|262380617|ref|ZP_06073771.1|: domain 1 of 1, from 4 to 894: score 786.7, E = 1.5e-233
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLH.GedLkEa
                       iDA LR               D  Ll   L     LH G+dL
  gi|2623806     4    QIDAPLRE--------------DVRLLGNLLGETLKLHaGQDLFNQ 35

                   vqECYEls..AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                   +     l+++A    K+  k+LeEL      L   + + + +a++H Ln
  gi|2623806    36 IEQIRALAkgARDGQKEAEKQLEEL---FSTLKDEEILPLTRAFSHFLNF 82

                   AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                   An+AE  +l   RR +           +A     ++  ++k   k   s
  gi|2623806    83 ANIAEQYHLVRSRRQHEFD-------ENAPSPNPLDHLFQKFKQKD-ISA 124

                   eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                   +  ++ +    ++LvltAHPt   RR L+qK   i  CL+ L  + +t+
  gi|2623806   125 DALYQQVCELKIELVLTAHPTEVSRRTLIQKYDGINQCLSRLDQQKLTPH 174

                   DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                   +++ + + +   i  A+ tDEiR  +PtP DE + G   i  t+W+ vPK
  gi|2623806   175 ERQSVLDEMKQLICSAWQTDEIRQHRPTPIDEAKWGFTTIEQTLWNAVPK 224

                   FLRRvD.tALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                   F+   D+  L   G    lP +v  i+F+sWmGGDRDG nP vt  vt +
  gi|2623806   225 FIHELDqLVLEHCG--RPLPLEVAPIRFASWMGGDRDG-NPNVTHQVTQE 271

                   vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                   v  L+R  Aa lY+  +E L +Els+  C +E+    E l  t
  gi|2623806   272 VLWLSRWQAADLYVRDIEALRWELSIQNCSEEM---SEALGYTH------ 312

                   KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.
                               EPYR  L + R++L  t    RH LA+ +     +A+
  gi|2623806   313 ------------PEPYREYLRQTRERLRAT----RHWLAQKLQGQDADAs 346

                   .vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                    v    +e L PL LCY+sL  C    iA G LLD++R v  FG+ L KL
  gi|2623806   347 lVIHSKDELLQPLLLCYRSLMACNLPEIANGRLLDFIRRVNCFGIELLKL 396

                   DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                   D+RqEs R+   + Ait+ L++G +  W E+ Rq +Ll EL+ KRPLl+
  gi|2623806   397 DVRQESGRHRQAISAITEYLGLGNFDTWTEQARQNFLLQELQSKRPLLPK 446

                   D.......LPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAv
                     +++ ++L    +v++v  +++ LAE P +s GaYiisma  PsDvLAv
  gi|2623806   447 HfnepaqsLILHPDVQEVFATMQTLAEQPTESLGAYIISMAEYPSDVLAV 496

                   ELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqe
                    LLq+E g++++LrvvPLFE L DL+ A A+++ LF + WY+ +i+GK e
  gi|2623806   497 LLLQKEAGIQRPLRVVPLFETLKDLDGAAATMATLFNMHWYRQHIQGKHE 546

                   vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                   vm+GYsDs KDAG +sA W  Y+AqEE+  vA+++ v+L+lFHGRGG +
  gi|2623806   547 VMIGYSDSAKDAGFMSANWAQYRAQEELTAVARQHAVQLTLFHGRGGSIS 596

                   RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                   RGG Pt  A+ sqPP  i G++Rvt qGE+i f FG E +  + L  +tA
  gi|2623806   597 RGGAPTQQALFSQPPGSISGAIRVTEQGEMIRFKFGVEGIALQNLEIYTA 646
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                    AtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAt
                    AtLE  + PP  Pk EWR+Lm +m       YR  v   P Fv Y R  t
  gi|2623806   647 ATLEATLLPPPEPKAEWRELMHRMTDLSVQVYRQTVRENPHFVQYLRTVT 696

                    PElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGA
                    PElE   + +GsRPaKRk sGGiesLRAiPW+FaWtq R  LP WLG GA
  gi|2623806   697 PELELQMLPLGSRPAKRKVSGGIESLRAIPWVFAWTQIRLMLPAWLGTGA 746

                    AFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDk
                    A    +d+  K l  L Em ++WP+F   +D+lEmv  K D  +A  y+
  gi|2623806   747 ALNQVLDQGQKEL--LDEMLQQWPYFQTLIDMLEMVLSKADAHVALYYEA 794

                    LLvaE.eLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRd
                     L  ++eLk  G++LR++ ++  + LL + G   lL     L q +R+R
  gi|2623806   795 HLTDDpELKALGQELRQRLQDAVQTLLALKGESKLLSHNEVLDQSMRVRK 844

                    sYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnp
                    +Y+  L  +qA  +KR R               y +E+        +L
  gi|2623806   845 PYLLPLHLLQAKLMKRRR--------------IYLAEQ--------QLE- 871

                    tervaPGLEDtLiLtmKGiAAGmqntG<-*
                         P ++  L++ + GiAAG+ ntG
  gi|2623806   872 ---HTP-VDHALMVSIAGIAAGLRNTG    894

gi|271498759|ref|YP_003331784.1|: domain 1 of 1, from 1 to 879: score 786.0, E = 2.5e-233
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  ++    vs           +l k L+D ++D  G ++ E
  gi|2714987     1    -MNEQYSAMR-SNVS-----------MLGKLLgDTIKDALGANILER 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       +t++ +EL + L  L   + + vA+a++  LnL n
  gi|2714987    35 VETIRKLSKASRAGSETHR-QELLTTLQNLSNEELLPVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +       +   hG+ a   +A     +   ++ L ++ n s ++
  gi|2714987    84 TAEQYH-------SISPHGEAASNPEA-----LATVFRNLKSRDNLSDKD 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + +A+   s++LvltAHPt   RR L+ K   +  CL qL   D+   ++
  gi|2714987   122 IRNAVESLSIELVLTAHPTEITRRTLIHKLVEVNTCLKQLDHNDLADYER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + +   L   i   + tDEiR+ +PtP DE + G + +   +W+GvP FL
  gi|2714987   172 HQIMRRLRQLIAQYWHTDEIRKIRPTPVDEAKWGFAVVENSLWEGVPAFL 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R  D  ++K +G   RlP d   ++F+sWmGGDRDG nP vt E+tR v
  gi|2714987   222 RELDEQMdKELGY--RLPVDSVPVRFTSWMGGDRDG-NPNVTSEITRRVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  Aa l++  v  L+ Elsm  C   L       ++ a  d v
  gi|2714987   269 LLSRWKAADLFLRDVQVLVSELSMTTCTPKL-------QQLAGGDEV--- 308

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                              +EPYR ++ + R +L  t +     L +G   ++ +
  gi|2714987   309 ----------QEPYRELMKNLRAQLTATLDYLDARL-KGEQRVPPNDLLV 347

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                      ++  EPL  CY+sL  CG  +iADG LLD LR v  FG+ Lv++D+Rq
  gi|2714987   348 TNDQLWEPLYACYQSLHACGMGIIADGQLLDTLRRVRCFGVPLVRIDVRQ 397

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+tD l  it+ L++G Y +WsE  +q +L+ EL  KRPLl+
  gi|2714987   398 ESTRHTDALAEITRYLGLGDYESWSESDKQAFLIRELNSKRPLLPRQWEP 447

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      + ++vl++ rv+AE P Ds  aY+isma +PsDvLAv LL +E g
  gi|2714987   448 SADTQEVLETCRVIAETPRDSIAAYVISMARTPSDVLAVHLLLKEAGCPY 497

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    +L+v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
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  gi|2714987   498 SLPVAPLFETLDDLNNADSVMIQLLNIDWYRGFIQGKQMVMIGYSDSAKD 547

                   AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                   AG ++A W  Y+Aq+ +iK   kyG+ L+lFHGRGG +GRGG P H A+L
  gi|2714987   548 AGVMAASWAQYRAQDALIKTCEKYGIALTLFHGRGGSIGRGGAPAHAALL 597

                   sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                   sqPP  ++G lRvt qGE+i f FG  ++   sL  +t A LE  + PP
  gi|2714987   598 SQPPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLSLYTSAILEANLLPPP 647

                   sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                    PkPEW ++m+e+  +  + YR  v   P Fv YFR AtPElE Gk+ +G
  gi|2714987   648 EPKPEWHHIMDELSRISCDMYRGYVRENPDFVPYFRAATPELELGKLPLG 697

                   sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                   sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA +  idK  +
  gi|2714987   698 SRPAKRRPNGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQDVIDKGHQ 747

                   nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                      +L+ m ++WPFF   + +lEmvFAK D  +A  yD+ Lv E L+  G
  gi|2714987   748 S--QLETMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVDEKLWSLG 795

                   ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                   k+LR++ +   + +L i     l+   P++   + LR+ Y   Lnv+qA
  gi|2714987   796 KQLREQLEKDIQAVLTISNDDHLMADLPWIAESIALRNVYTDPLNVLQAE 845

                   tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    L R R                                +   P +E  L
  gi|2714987   846 LLHRSRQ------------------------------QDMTDPQVEQAL 864

                   iLtmKGiAAGmqntG<-*
                   ++t+ G+AAGm ntG
  gi|2714987   865 MVTIAGVAAGMRNTG    879

gi|292826793|gb|EFF85158.1|: domain 1 of 1, from 4 to 894: score 785.9, E = 2.6e-233
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       iDA LR               D  Ll   L++ L+   G++L
  gi|2928267     4    QIDAPLRE--------------DVRLLGNLLgETLKQHAGQELFNQ 35

                   vqECYEls.AeYEGKkDtkK.LeELGakLtsLdPaDail.vAkailHmLn
                   +     l++   +G+ +++K+Le L   L    P + +l++ +a++H Ln
  gi|2928267    36 IEQIRALAkGARDGQAEAEKqLEQLFLEL----PDEELLpLTRAFSHFLN 81

                   LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                    An+AE  ++   RR            ++A     +   ++k   k   s
  gi|2928267    82 FANIAEQYHVVRSRRQAEFD-------SDANSPNPLVHLFQKFKDKS-IS 123

                   PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                    e  F+ +    ++LvltAHPt   RR L+qK   i  CL+qL  + +t+
  gi|2928267   124 TEKLFQQICDLKIELVLTAHPTEVSRRTLIQKYDDINACLSQLDQQKLTP 173

                   eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                    +++     L   i  A+ tDEiR  +PtP DE + G + i  t+W+ vP
  gi|2928267   174 RERQNALANLKQQISSAWQTDEIRQHRPTPVDEAKWGFATIEQTLWNAVP 223

                   KFLRRvDtALK.niGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                   KF+R     +++n  +n  lP ++  ++F+sWmGGDRDG nP vt  +t
  gi|2928267   224 KFIRELNELVQeNCQLN--LPLNIAPVRFASWMGGDRDG-NPNVTHQITQ 270

                   DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                   +v  L+R  Aa lY+  +E L +Els+  C +E+      ++    ++
  gi|2928267   271 EVLWLSRWQAADLYLRDIENLRWELSIQTCSEEM------IQAIGSQH-- 312

                   vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe.
                                EPYR  L + R++L  t    RH LA+ +  +  ++
  gi|2928267   313 -------------AEPYREYLRATRERLKAT----RHWLAQRLQGLEADd 345

                   .AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                   + v    +e L PL LCY+sL +     iA G LLD++  v  FG+ L K
  gi|2928267   346 sNVIKSKDELLQPLLLCYRSLIDSNLPEIANGQLLDFIYRVNCFGIELLK 395
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                    LDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlg
                    LDiRqEs R+   + Ait+ L++G + +W E+ Rq +L+ EL+ KRPLl+
  gi|2928267   396 LDIRQESGRHRQAISAITEYLGLGNFESWTEQARQNFLIQELQSKRPLLP 445

                    sDLPktE.......EvkDvldafrvLAELPiDsFGaYiismataPsDvLA
                      +   E++  ++++v++v  ++r LA+ P +s GaYiisma  PsDvLA
  gi|2928267   446 KYINEPEgslighpDVQEVFATMRTLADQPPESLGAYIISMAEYPSDVLA 495

                    vELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKq
                    v LLq+E g++++LrvvPLFE L DL+ A  +++ LF + WY+ +i+GK
  gi|2928267   496 VLLLQKEAGIQHPLRVVPLFETLKDLDGAATTMNTLFNMHWYKQHIQGKH 545

                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                    evm+GYsDs KDAG +sA W  Y+AqEE+  +A+ +Gv+L+lFHGRGG +
  gi|2928267   546 EVMIGYSDSAKDAGFMSANWAQYRAQEELTAIAQTHGVQLTLFHGRGGSI 595

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                     RGG Pt  A+ sqPP  i G++Rvt qGE+i f FG E +  + L  +t
  gi|2928267   596 SRGGAPTQQALFSQPPGSISGAIRVTEQGEMIRFKFGLEGIAMQNLEIYT 645

                    AAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlA
                    AAtLE  + PP  Pk EWR++m++m       YR  v   P Fv Y R
  gi|2928267   646 AATLEATLLPPPEPKAEWREIMNRMTDHSVKVYRQTVRENPHFVKYLRTV 695

                    tPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvG
                    tPElE   + +GsRPaKRk sGGiesLRAiPW+FaWtq R  LP WLG G
  gi|2928267   696 TPELELQMLPLGSRPAKRKVSGGIESLRAIPWVFAWTQIRLMLPAWLGTG 745

                    AAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyD
                    AA    i    K    L Em ++WP+F   +D+lEmv  K D  iA  y+
  gi|2928267   746 AAINEVIADQQKA--TLDEMLQQWPYFQTLIDMLEMVLSKADANIALYYE 793

                    kLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLR
                      L  +E+Lk  G++LR++ ++  + LL +     lL     L q + +R
  gi|2928267   794 SHLTEdEDLKVLGNQLRQRLKDAVQTLLTLKDESKLLSNNDVLDQSMQVR 843

                    dsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLn
                     +Y+  L  +qA  +KR RD              y +E
  gi|2928267   844 KPYLLPLHLLQAELMKRRRD--------------YLAER----------- 868

                    ptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       +  P ++  L++ + GiAAG+ ntG
  gi|2928267   869 -QAEHTP-VDHALMVSIAGIAAGLRNTG    894

gi|149374698|ref|ZP_01892472.1|: domain 1 of 1, from 1 to 868: score 785.8, E = 2.9e-233
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedL.kEa
                                                      +L +L G+++++
  gi|1493746     1    ---------------------------------MLGELLGQSIqRHP 14

                    vqECYElsAeYEGKkDtkKLeELGa......kLtsLdPaDailvAkailH
                     q+CYEl  e      + + +E G++++  + L  L   + + v +a+
  gi|1493746    15 GQDCYELIEEVRAAAKADRRQESGSgqrlvnLLGKLRDDELLPVTRAFNQ 64

                    mLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkl
                     LnLAnLAE  +   R+R ++              Es + + + +L   +
  gi|1493746    65 FLNLANLAEQYHGIRRKRGHQSD---------LMVES-LGDVFSRLKKGG 104

                    nKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKD
                      s +E    +    ++ vltAHPt  +RR L+ K   +  CLa L   D
  gi|1493746   105 -VSADELHRRVADLRIEYVLTAHPTEVARRTLIMKYDEMSDCLARLDHED 153

                    vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWk
                    + + +++E+   L   +  A+ tDEiR  +Pt  DE + G + i   +W+
  gi|1493746   154 LLPAEREEIVGRLSQLVTEAWHTDEIRHDRPTAVDEAKWGFAVIENSLWQ 203

                    GvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEv
                      P+FLR  D  L     n  lP d+  i+ +sWmGGDRDG nP vt Ev
  gi|1493746   204 ALPRFLRSLDLSLSDATGNG-LPLDASPIRIASWMGGDRDG-NPNVTHEV 251

                    tRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaard
                    tR v LL R mAa lY+  +  L  ElsmW   dELR  A +
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  gi|1493746   252 TRKVFLLGRWMAADLYLRDIQSLRAELSMWQASDELRDIAGDTR------ 295

                    kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                                EPYR +L   R+KL  tR+ a   +A   ++ +
  gi|1493746   296 ----------------EPYRQVLAGLREKLIKTRDWAEARVAGEPAD-AT 328

                    eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                       + + E+F  PLELCY+sL +CG   iA G LLD +R   tFGL L++
  gi|1493746   329 GILFAN-EDFTGPLELCYRSLVDCGLESIANGPLLDTIRRAHTFGLPLIR 377

                    LDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlg
                    LDiRqEs R+ + +  +   L++G Y +WsE+ Rq++L+ ELkG+RPL++
  gi|1493746   378 LDIRQESTRHAEAVAEMVDYLGLGDYLSWSEQERQDFLVRELKGRRPLIP 427

                    sDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRE
                          EEv++vl + +v+AE   ++ G+Y+isma  PsDvL v LL RE
  gi|1493746   428 RHWQPSEEVAEVLATCEVVAEQTPEALGSYVISMASKPSDVLNVILLLRE 477

                    CgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYs
                     g+k+++rvvPLFE L DL+ AP +++ L+s+DWY+   +G+qevm+GYs
  gi|1493746   478 AGMKNPMRVVPLFETLDDLRGAPDSMAALYSVDWYRDYCEGRQEVMIGYS 527

                    DsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPt
                    Ds KDAG + AAW  Y+AqE +  vA ++Gv L+lFHGRGGtvGRGGGP
  gi|1493746   528 DSSKDAGQMMAAWAQYQAQEKLTEVANQHGVHLTLFHGRGGTVGRGGGPA 577

                    HLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHG
                      AiLsqPP  +nGs R+t qGE+i f FG   L  +sL  +t A +E
  gi|1493746   578 NRAILSQPPGSVNGSFRITEQGEMIRFKFGLPRLAEQSLTLYTTAVIEAT 627

                    mnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYG
                    + PP  P PEWR+ m+ +       YR vv   P Fv YFR  tPE   G
  gi|1493746   628 LAPPRGPEPEWREAMDWLTERSLKAYRDVVRENPDFVPYFRQVTPEQALG 677

                    kmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAi
                    k+ +GsRPa+RkP+GG+esLRAiPWiFaWtq R  LP WLG   A   A
  gi|1493746   678 KLALGSRPARRKPGGGVESLRAIPWIFAWTQMRMMLPSWLGSDVALEEAF 727

                    dKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaE.
                    + D   +  L+Em ++WPFF+  +D+lEmv AK D  iA+ y+k Lv ++
  gi|1493746   728 HND--RVPVLREMMQQWPFFKTYVDMLEMVLAKSDLRIASYYEKTLVDDp 775

                    eLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittL
                     L   Gk+LR++ +     LL++     lLE +P     +R+R++Y   L
  gi|1493746   776 KLLELGKNLRERLQGCIRHLLELKQQDTLLEQEPVFAHSMRVRNPYTDPL 825

                    nvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaP
                      +qA  LKR R+                E               +v+
  gi|1493746   826 HYLQAELLKRDRE----------------GEG------------KGEVPE 847

                    GLEDtLiLtmKGiAAGmqntG<-*
                     +E  L +tm GiAAGm ntG
  gi|1493746   848 MVERALKVTMAGIAAGMRNTG    868

gi|239502757|ref|ZP_04662067.1|: domain 1 of 1, from 4 to 894: score 785.7, E = 3e-233
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        iDA LR               D  Ll   L++ L+   G++L
  gi|2395027     4    QIDAPLRE--------------DVRLLGNLLgETLKQHAGQELFNQ 35

                    vqECYEls.AeYEGKkDtkK.LeELGakLtsLdPaDail.vAkailHmLn
                    +     l++   +G+ +++K+Le L   L    P + +l++ +a++H Ln
  gi|2395027    36 IEQIRALAkGARDGQAEAEKqLEQLFLEL----PDEELLpLTRAFSHFLN 81

                    LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                     An+AE  ++   RR             +A     +   +Kk   k   s
  gi|2395027    82 FANIAEQYHVVRSRRQAEFD-------PDANSPNPLVHLFKKFKDKN-IS 123

                    PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                     e  F+ +    ++LvltAHPt   RR L+qK   i  CL+qL  + +t+
  gi|2395027   124 TEKLFQQICDLKIELVLTAHPTEVSRRTLIQKYDDINACLSQLDQQKLTP 173
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                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                     +++     L   i  A+ tDEiR  +PtP DE + G + i  t+W+ vP
  gi|2395027   174 RERQNALANLKQQISSAWQTDEIRQHRPTPVDEAKWGFATIEQTLWNAVP 223

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                    KF+R     ++       lP  +  ++F+sWmGGDRDG nP vt  +t +
  gi|2395027   224 KFIRELNELVQD-NCQQNLPLHIAPVRFASWMGGDRDG-NPNVTHQITQE 271

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                    v  L+R  Aa lY+  +E L +Els+  C +E+      ++     +
  gi|2395027   272 VLWLSRWQAADLYLRDIENLRWELSIQSCSEEM------VQAIGSPH--- 312

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe..
                                EPYR  L + R++L  t    RH LA+ +  +  +++
  gi|2395027   313 ------------PEPYREYLRATRERLKAT----RHWLAQRLQGLEADds 346

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                     v    +e L PL LCY+sL +     iA G LLD++  v  FG+ L KL
  gi|2395027   347 NVIKSKDELLQPLLLCYRSLIDSNLPEIANGQLLDFIYRVNCFGIELLKL 396

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    DiRqEs R+   + Ait+ L++G + +W E+ Rq +L+ EL+ KRPLl+
  gi|2395027   397 DIRQESGRHCQAISAITEYLGLGNFESWTEQARQNFLIQELQSKRPLLPK 446

                    DLPktE.......EvkDvldafrvLAELPiDsFGaYiismataPsDvLAv
                     +   E++  ++++v++v  ++r LA+ P +s GaYiisma  PsDvLAv
  gi|2395027   447 YINEPEgslighpDVQEVFATMRTLADQPPESLGAYIISMAEYPSDVLAV 496

                    ELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqe
                     LLq+E g++++LrvvPLFE L DL+ A  +++ LF + WY+ +i+GK e
  gi|2395027   497 LLLQKEAGIQHPLRVVPLFETLKDLDGAATTMNTLFNMHWYKQHIQGKHE 546

                    vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                    vm+GYsDs KDAG +sA W  Y+AqEE+  +A+k+Gv+L+lFHGRGG +
  gi|2395027   547 VMIGYSDSAKDAGFMSANWAQYRAQEELTAIARKHGVQLTLFHGRGGSIS 596

                    RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                    RGG Pt  A+ sqPP  i G++Rvt qGE+i f FG E +  + L  +tA
  gi|2395027   597 RGGAPTQQALFSQPPGSISGAIRVTEQGEMIRFKFGLEGIAMQNLEIYTA 646

                    AtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAt
                    AtLE  + PP  Pk EWR+Lm++m       YR  v   P Fv Y R  t
  gi|2395027   647 ATLEATLLPPPEPKAEWRELMNRMTDHSVKVYRQTVRENPHFVKYLRTVT 696

                    PElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGA
                    PElE   + +GsRPaKRk sGGiesLRAiPW+FaWtq R  LP WLG GA
  gi|2395027   697 PELELQMLPLGSRPAKRKVSGGIESLRAIPWVFAWTQIRLMLPAWLGTGA 746

                    AFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDk
                    A    i    K    L Em ++WP+F   +D+lEmv  K D  iA  y+
  gi|2395027   747 AINEVIADQQKA--TLDEMLQQWPYFQTLIDMLEMVLSKADANIALYYES 794

                    LLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRd
                     L  +E+Lk  G++LR++ ++  + LL +     lL     L q + +R
  gi|2395027   795 HLTEdEDLKVLGNQLRQRLKDAVETLLTLKDESKLLSDNEVLDQSMQVRK 844

                    sYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnp
                    +Y+  L  +qA  +KR RD              y +E
  gi|2395027   845 PYLLPLHLLQAELMKRRRD--------------YLAER------------ 868

                    tervaPGLEDtLiLtmKGiAAGmqntG<-*
                      +  P ++  L++ + GiAAG+ ntG
  gi|2395027   869 QAEHTP-VDHALMVSIAGIAAGLRNTG    894

gi|152972745|ref|YP_001337891.1|: domain 1 of 1, from 1 to 891: score 785.3, E = 4e-233
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                            +R  v G + e+   ++    +l k L+D ++D  Ge++ +
  gi|1529727     1    -----MRWGVWGNMNEQYSALRSNVSMLGKVLgDTIKDALGENILDR 42

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++ + +EL + L  L   + + vA+a++  LnLAn
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gi|1529727    43 VETIRKLSKSSRAGNEANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 91

                 LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  AE  +      i+         Ea    E  i  tl+kL  + n   e
gi|1529727    92 TAEQYH-----SISANG------EAASNPEV-IARTLRKLKDQPNLNEET 129

                 vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                 + +A+   s +LvltAHPt   RR L+ K   + nCL qL  KD+   +
gi|1529727   130 IKQAVESLSLELVLTAHPTEITRRTLIHKMVEVNNCLKQLDNKDIADYEH 179

                 kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                 + L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
gi|1529727   180 HQLMRRLRQLIAQSWHTDEIRKHRPSPVDEAKWGFAVVENSLWEGVPNYL 229

                 RRvDtALK.niGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                 R     L  n+G    lP d   ++F+sWmGGDRDG nP vt ++tR v
gi|1529727   230 RELNEQLEaNLGY--QLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVL 276

                 LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                 LL+R  A+ l++  v  L+ Elsm  C dELR+ A      a
gi|1529727   277 LLSRWKATDLFLKDVQVLISELSMVECTDELRALA-----GAEGA----- 316

                 YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                           +EPYR ++   R +L  t       L +G          t
gi|1529727   317 ----------QEPYRYLMKKLRSQLMETQAWLEARL-KGQKLPKPAGLIT 355

                 kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                 + E+  EPL  CYksL  CG  +iA G LLD LR v  FG+ Lv++DiRq
gi|1529727   356 QNEQLWEPLYACYKSLQACGMGIIANGELLDTLRRVKSFGVPLVRIDIRQ 405

                 EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                 Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
gi|1529727   406 ESTRHTEALGEMTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRQWEP 455

                 tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                  EE ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
gi|1529727   456 SEETREVLDTCKVIAEAPRGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 505

                 tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                 +L+v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
gi|1529727   506 ALPVAPLFETLDDLNNANDVMTQLLNIDWYRGFIQGKQMVMIGYSDSAKD 555

                 AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                 AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
gi|1529727   556 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 605

                 sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                 sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
gi|1529727   606 SQPPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLSLYTSAILEANLLPPP 655

                 sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                  Pk EWR++m e+  v    YR  v     Fv YFR+AtPE E Gk+ +G
gi|1529727   656 EPKAEWRDIMAELSDVSCKMYRGYVRENKDFVPYFRSATPEQELGKLPLG 705

                 sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                 sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA +  ++   +
gi|1529727   706 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQKVVEGGKQ 755

                 nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     L+ m ++WPFF   l +lEmv+ K D  +A  yD+ Lv  eL+  G
gi|1529727   756 S--ELEAMCRDWPFFSTRLGMLEMVYSKADLWLAEYYDQRLVKPELWALG 803

                 ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                  +LR       + +L iA    l+   P++   + LR+ Y   Lnv+qA
gi|1529727   804 SELRKLLAADINVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 853

                 tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                  L R R                A+E+ k +d            P +E  L
gi|1529727   854 LLHRSRQ--------------AEEEGKDPD-----------PRVEQAL 876

                 iLtmKGiAAGmqntG<-*
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                  ++t+ G+AAGm ntG
  gi|1529727   877 MVTIAGVAAGMRNTG    891

gi|121999069|ref|YP_001003856.1|: domain 1 of 1, from 1 to 883: score 784.9, E = 5.6e-233
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                             +   + s  +  ++ D   l   L+  L +  G +L E
  gi|1219990     1    --------MEEHQDS--DSALREDIRDLGELLgATLREQGGTELFET 37

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v E   + A      D +  +EL   L  L P     vA+a++  LnLAn
  gi|1219990    38 V-ERVRVLAKTARAGDDQAAQELERTLSELPPEQVTPVARAFSQFLNLAN 86

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  +AE  +   R R   +       Ea+    s + Et+ +L       Pe
  gi|1219990    87 IAEQHHRVRRSREWART-----PEAQPLFGS-LAETVPRLAADM--EPEQ 128

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    eA+    + Lv+tAHPt   RR +LqK  Ri   L        t+ +
  gi|1219990   129 LHEAICSMDINLVFTAHPTEVQRRTMLQKYNRIAGLLDNRDRFGQTPTEV 178

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   E   AL REi AA+  DEiRR +PtPqDE R G++ +  t+W+ vP++L
  gi|1219990   179 AETRLALKREITAAWHSDEIRRRRPTPQDEARWGLAVVEQTLWDAVPRYL 228

                  RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                  R  D  L+       lP d   i F sWmGGDRDG nP vt  vtRDv +
  gi|1219990   229 RSLDHTLRE-HTGRPLPLDCAPITFGSWMGGDRDG-NPNVTHRVTRDVAI 276

                  LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                  L+R mAa lY   +  L+  ls+  C dELR   +E+
  gi|1219990   277 LSRWMAAYLYERDIQRLVSTLSLQVCDDELR---DEVGG---------- 312

                  iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                   E W      EPYRv+L   R +L  t   a   L  G    +E  + t+
  gi|1219990   313 -EAW------EPYRVVLKRLRARLRQTMRWAEAKLQGGRP--PESDILTE 353

                  vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                  vE+   PL  CY sL   G  v+A+G LLD +R vs FGL L+ +DiRq
  gi|1219990   354 VEDLRQPLLRCYYSLQRVGAGVVAEGELLDTIRRVSCFGLTLMPMDIRQH 403

                  seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                  ++R+t  lDAit+ +++GsY eW Ee Rq WL  EL+ +RPL++ D
  gi|1219990   404 ADRHTAALDAITQAVGLGSYSEWDEETRQQWLFQELSHRRPLIPLDFKPE 453

                  EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                   Ev++vld++++L E+  D+ GaYi+s a  PsD+LAvELLq+ECg+ ++
  gi|1219990   454 REVQEVLDTIHMLEEIGPDAVGAYIVSHASKPSDILAVELLQKECGLTHP 503

                  LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                   rvvPLFE    L  A  ++e LF  DWY+ ri G+qe+m+GYsDs KDA
  gi|1219990   504 TRVVPLFETRDTLARAADTMEVLFKSDWYRQRIGGRQEIMIGYSDSTKDA 553

                  GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                  G l A W LY+AqE ++   ++  v L+lFHGRGG +GRGGGPtH AiL+
  gi|1219990   554 GHLTATWTLYQAQEQLVALSRRQRVDLTLFHGRGGSIGRGGGPTHAAILA 603

                  qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                  qPP  ++G lRvt qGEv+   FG   +  r L  +t   LE  + PP
  gi|1219990   604 QPPGSVDGTLRVTEQGEVMQAKFGLPGIALRNLELYTTSVLEATVRPPEP 653

                  PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                  P   WR+++e++   A   YR  v   P F++YF  AtP  E  ++ iGs
  gi|1219990   654 PPKRWREILERLSDRAMTAYRQTVKERPEFMDYFQAATPIDEISRLTIGS 703

                  RPaKRkP.sGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                  RPaKR P+   ++sLRAiPW+FaWtqtR  LP WLGvG A   Ai+
  gi|1219990   704 RPAKRAPdQMTVDSLRAIPWVFAWTQTRLMLPAWLGVGEALEEAIEEGLT 753

                  nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                      L+Em+  WPFF   lD++Emv AK +PG+  Ly++ Lv +eL+  G
  gi|1219990   754 E--ELQEMFARWPFFEAFLDMVEMVVAKAEPGVNRLYEHALVPDELHSVG 801
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                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    ++LRd++  t+d +L + GH + L   P +K  + +R++Y+  Ln +q
  gi|1219990   802 DELRDRFARTRDAVLTVTGHEEPLSDFPVVKRAVEVRNPYVDPLNLLQVE 851

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L+R R                +++s +    v +n
  gi|1219990   852 LLRRSR---------------MCEDDSLRRGLQVVIN------------- 873

                    iLtmKGiAAGmqntG<-*
                         GiAAGm ntG
  gi|1219990   874 -----GIAAGMRNTG    883

gi|126643456|ref|YP_001086440.1|: domain 1 of 1, from 4 to 894: score 784.8, E = 5.8e-233
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        iDA LR                D  Ll   L++ L+   G++L
  gi|1266434     4    QIDAPLRE---------------DVRLLGNLLgETLKQHAGQELFNQ 35

                    vqECYEls.AeYEGKkDtkK.LeELGakLtsLdPaDail.vAkailHmLn
                    +     l++   +G+ +++K+Le L   L    P + +l++ +a++H Ln
  gi|1266434    36 IEQIRALAkGARDGQAEAEKqLEQLFLEL----PDEELLpLTRAFSHFLN 81

                    LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                     An+AE  ++   RR             +A     +   +Kk   k   s
  gi|1266434    82 FANIAEQYHVVRSRRQAEFD-------PDANSPNPLVHLFKKFKDKN-IS 123

                    PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                     e  F+ +    ++LvltAHPt   RR L+qK   i  CL+qL  + +t+
  gi|1266434   124 TEKLFQQICDLKIELVLTAHPTEVSRRTLIQKYDDINACLSQLDQQKLTP 173

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                     +++     L   i  A+ tDEiR  +PtP DE + G + i  t+W+ vP
  gi|1266434   174 RERQNALANLKQQISSAWQTDEIRQHRPTPVDEAKWGFATIEQTLWNAVP 223

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                    KF+R     ++       lP  +  ++F+sWmGGDRDG nP vt  +t +
  gi|1266434   224 KFIRELNELVQD-NCQQNLPLHIAPVRFASWMGGDRDG-NPNVTHQITQE 271

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                    v  L+R  Aa lY+  +E L +Els+  C +E+      ++     +
  gi|1266434   272 VLWLSRWQAADLYLRDIENLRWELSIQSCSEEM------VQAIGSPH--- 312

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe..
                                 EPYR  L + R++L  t    RH LA+ +  +  +++
  gi|1266434   313 ------------PEPYREYLRATRERLKAT----RHWLAQRLQGLEADds 346

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                     v    +e L PL LCY+sL +     iA G LLD++  v  FG+ L KL
  gi|1266434   347 NVIKSKDELLQPLLLCYRSLIDSNLPEIANGQLLDFIYRVNCFGIELLKL 396

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    DiRqEs R+   + Ait+ L++G + +W E+ Rq +L+ EL+ KRPLl+
  gi|1266434   397 DIRQESGRHRQAISAITEYLGLGNFESWTEQARQNFLIQELQSKRPLLPK 446

                    DLPktE.......EvkDvldafrvLAELPiDsFGaYiismataPsDvLAv
                     +   E++  ++++v++v  ++r LA+ P +s GaYiisma  PsDvLAv
  gi|1266434   447 YINEPEgslighpDVQEVFATMRTLADQPPESLGAYIISMAEYPSDVLAV 496

                    ELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqe
                     LLq+E g++++LrvvPLFE L DL+ A  +++ LF + WY+ +i+GK e
  gi|1266434   497 LLLQKEAGIQHPLRVVPLFETLKDLDGAATTMNTLFNMHWYKQHIQGKHE 546

                    vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                    vm+GYsDs KDAG +sA W  Y+AqEE+  +A+k+Gv+L+lFHGRGG +
  gi|1266434   547 VMIGYSDSAKDAGFMSANWAQYRAQEELTAIARKHGVQLTLFHGRGGSIS 596

                    RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                    RGG Pt  A+ sqPP  i G++Rvt qGE+i f FG E +  + L  +tA
  gi|1266434   597 RGGAPTQQALFSQPPGSISGAIRVTEQGEMIRFKFGLEGIAMQNLEIYTA 646

                    AtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAt
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                    AtLE  + PP  Pk EWR+Lm++m       YR  v   P Fv Y R  t
  gi|1266434   647 ATLEATLLPPPEPKAEWRELMNRMTDHSVKVYRQTVRENPHFVKYLRTVT 696

                    PElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGA
                    PElE   + +GsRPaKRk sGGiesLRAiPW+FaWtq R  LP WLG GA
  gi|1266434   697 PELELQMLPLGSRPAKRKVSGGIESLRAIPWVFAWTQIRLMLPAWLGTGA 746

                    AFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDk
                    A    i    K    L Em ++WP+F   +D+lEmv  K D  iA  y+
  gi|1266434   747 AINEVIADQQKA--TLDEMLQQWPYFQTLIDMLEMVLSKADANIALYYES 794

                    LLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRd
                     L  +E+Lk  G++LR++ ++  + LL +     lL     L q + +R
  gi|1266434   795 HLTEdEDLKVLGNQLRQRLKDAVETLLTLKDESKLLSDNEVLDQSMQVRK 844

                    sYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnp
                    +Y+  L  +qA  +KR RD              y +E
  gi|1266434   845 PYLLPLHLLQAELMKRRRD--------------YLAER------------ 868

                    tervaPGLEDtLiLtmKGiAAGmqntG<-*
                      +  P ++  L++ + GiAAG+ ntG
  gi|1266434   869 QAEHTP-VDHALMVSIAGIAAGLRNTG    894

gi|169634906|ref|YP_001708642.1|: domain 1 of 1, from 4 to 894: score 784.8, E = 6e-233
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        iDA LR               D  Ll   L++ L+   G++L
  gi|1696349     4    QIDAPLRE---------------DVRLLGNLLgETLKQHAGQELFNQ 35

                    vqECYEls.AeYEGKkDtkK.LeELGakLtsLdPaDail.vAkailHmLn
                    +     l++   +G+ +++K+Le L   L    P + +l++ +a++H Ln
  gi|1696349    36 IEQIRALAkGARDGQAEAEKqLEQLFLEL----PDEELLpLTRAFSHFLN 81

                    LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                     An+AE  ++   RR             +A     +   +Kk   k   s
  gi|1696349    82 FANIAEQYHVVRSRRQAEFD-------PDANSPNPLVHLFKKFKDKN-IS 123

                    PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                     e  F+ +    ++LvltAHPt   RR L+qK   i  CL+qL  + +t+
  gi|1696349   124 TEKLFQQICDLKIELVLTAHPTEVSRRTLIQKYDDINACLSQLDQQKLTP 173

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                     +++     L + i  A+ tDEiR  +PtP DE + G + i  t+W+ vP
  gi|1696349   174 RERQNALANLKKQISSAWQTDEIRQHRPTPVDEAKWGFATIEQTLWNAVP 223

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                    KF+R     ++       lP  +  ++F+sWmGGDRDG nP vt  +t +
  gi|1696349   224 KFIRELNELVQD-NCQQNLPLHIAPVRFASWMGGDRDG-NPNVTHQITQE 271

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                    v  L+R  Aa lY+  +E L +Els+  C +E+      ++     +
  gi|1696349   272 VLWLSRWQAADLYLRDIENLRWELSIQSCSEEM------VQAIGSPH--- 312

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe..
                                  EPYR  L + R++L  t    RH LA+ +  +  +++
  gi|1696349   313 ------------PEPYREYLRATRERLKAT----RHWLAQRLQGLEADds 346

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                     v    +e L PL LCY+sL +     iA G LLD++  v  FG+ L KL
  gi|1696349   347 NVIKSKDELLQPLLLCYRSLIDSNLPEIANGQLLDFIYRVNCFGIELLKL 396

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    DiRqEs R+   + Ait+ L++G + +W E+ Rq +L+ EL+ KRPLl+
  gi|1696349   397 DIRQESGRHRQAISAITEYLGLGNFDSWTEQARQNFLIQELQSKRPLLPK 446

                    DLPktE.......EvkDvldafrvLAELPiDsFGaYiismataPsDvLAv
                     +   E++  ++++v++v  ++r LA+ P +s GaYiisma  PsDvLAv
  gi|1696349   447 YINEPEgslighpDVQEVFATMRTLADQPPESLGAYIISMAEYPSDVLAV 496

                    ELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqe
                     LLq+E g++++LrvvPLFE L DL+ A  +++ LF + WY+ +i+GK e
  gi|1696349   497 LLLQKEAGIQHPLRVVPLFETLKDLDGAATTMNTLFNMHWYKQHIQGKHE 546
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                    vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                    vm+GYsDs KDAG +sA W  Y+AqEE+  +A+k+Gv+L+lFHGRGG +
  gi|1696349   547 VMIGYSDSAKDAGFMSANWAQYRAQEELTAIARKHGVQLTLFHGRGGSIS 596

                    RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                    RGG Pt  A+ sqPP  i G++Rvt qGE+i f FG E +  + L  +tA
  gi|1696349   597 RGGAPTQQALFSQPPGSISGAIRVTEQGEMIRFKFGLEGIAMQNLEIYTA 646

                    AtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAt
                    AtLE  + PP  Pk EWR+Lm++m       YR  v   P Fv Y R  t
  gi|1696349   647 ATLEATLLPPPEPKAEWRELMNRMTDHSVKVYRQTVRENPHFVKYLRTVT 696

                    PElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGA
                    PElE   + +GsRPaKRk sGGiesLRAiPW+FaWtq R  LP WLG GA
  gi|1696349   697 PELELQMLPLGSRPAKRKVSGGIESLRAIPWVFAWTQIRLMLPAWLGTGA 746

                    AFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDk
                    A    i    K    L Em ++WP+F   +D+lEmv  K D  iA  y+
  gi|1696349   747 AINEVIADQQKA--TLDEMLQQWPYFQTLIDMLEMVLSKADANIALYYES 794

                    LLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRd
                     L  +E+Lk  G++LR++ ++  + LL +     lL     L q + +R
  gi|1696349   795 HLTEdEDLKVLGNQLRQRLKDAVETLLALKDESKLLSDNEVLDQSMQVRK 844

                    sYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnp
                    +Y+  L  +qA  +KR RD              y +E
  gi|1696349   845 PYLLPLHLLQAELMKRRRD--------------YLAER------------ 868

                    tervaPGLEDtLiLtmKGiAAGmqntG<-*
                      +  P ++  L++ + GiAAG+ ntG
  gi|1696349   869 QAEHTP-VDHALMVSIAGIAAGLRNTG    894

gi|50119147|ref|YP_048314.1|: domain 1 of 1, from 1 to 879: score 784.5, E = 7e-233
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +  q  ++    vs          +L     D +++  Ge++ + v
  gi|5011914     1    -MNEQYSAMR-SNVS----------MLGTLLGDTIKEALGENILDKV 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       + ++ +EL + L  L   + + vA+a++  LnL n
  gi|5011914    36 ETIRKLSKSSRAGNEKHR-QELLTTLQNLSNDELLPVARAFSQFLNLTNT 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +           hG+      A   + +   +K+L    + s  ++
  gi|5011914    85 AEQYH-------TISPHGE-----AASNPAQLSSAFKRLKESKDLSERDI 122

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     +A+   s++LvltAHPt   RR L+ K   +  CL qL   D+   ++
  gi|5011914   123 RDAVESLSIELVLTAHPTEITRRTLIHKLVEVNTCLKQLDHNDLADYERN 172

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +   L   i   + tDEiR+ +PtP DE + G + +   +W+GvP FLR
  gi|5011914   173 QVMRRLRQLIAQSWHTDEIRKIRPTPVDEAKWGFAVVENSLWEGVPAFLR 222

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                      D  L       RlP d+  ++F+sWmGGDRDG nP vt EvtR v LL
  gi|5011914   223 ELDEQLEQ-AFGYRLPVDAVPVRFTSWMGGDRDG-NPNVTAEVTRHVLLL 270

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    +R  Aa l++  +  L+ Elsm  C  EL     El   +  +
  gi|5011914   271 SRWKAADLFLRDIQVLVSELSMSECTPELL----ELAGGSEVQ------- 309

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             EPYR i+   R +L  t       L tG   ++
  gi|5011914   310 ---------EPYRAIMKSLRSQLSCTLSYLEARL-TGEERLPPKDLLITN 349

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+  EPL  CY+sL  CG  +iADGsLLD LR v  FG+ Lv++D+RqEs
  gi|5011914   350 EQLWEPLHACYQSLKTCGMGIIADGSLLDTLRRVRCFGVPLVRIDVRQES 399

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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                     R+tD l  it+ L++G Y +WsE  +q +L+ EL+ KRPLl+
  gi|5011914   400 TRHTDALAEITRYLGLGDYESWSESDKQAFLIRELSSKRPLLPRYWEPSA 449

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   + k+vld+ rv+A  P  s  aY+isma +PsDvLAv LL +E g   +L
  gi|5011914   450 DTKEVLDTCRVIAKAPQGSIAAYVISMARTPSDVLAVQLLLKEAGCPFAL 499

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +v PLFE L DL+ A   + +L siDWY+  i+GKq vm+GYsDs KDAG
  gi|5011914   500 PVAPLFETLDDLNNADDVMTQLLSIDWYRGFIQGKQMVMIGYSDSAKDAG 549

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Lsq
  gi|5011914   550 VMAASWAQYRAQDALIKTCEKAGIALTLFHGRGGSIGRGGAPAHAALLSQ 599

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP  P
  gi|5011914   600 PPGSLKGGLRVTEQGEMIRFKYGLPDVTISSLALYTGAILEANLLPPPEP 649

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   k EW ++m+e+  v  + YR  v   P Fv YFR AtPElE Gk+ +GsR
  gi|5011914   650 KQEWHEVMDELSRVSCDMYRGYVRENPDFVPYFRAATPELELGKLPLGSR 699

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKR+P GG+esLRAiPWiFaWtq R  LP WLG GA  +  +d D K
  gi|5011914   700 PAKRRPNGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQKVVD-DGKQE 748

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q L+Em ++WPFF   + +lEmvFAK D  +A  yD+ Lv E L+P Gk+
  gi|5011914   749 Q-LEEMCRNWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVEEKLWPLGKQ 797

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LRd+     +++L i     l+   P++   + LR+ Y   Lnv+qA  L
  gi|5011914   798 LRDQLAADINIVLAISNDDHLMADLPWIAESIALRNVYTDPLNVLQAELL 847

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    R R                     k++d  ++L             L++
  gi|5011914   848 HRSRQ------------------QKQPDADLELA------------LMV 866

                   tmKGiAAGmqntG<-*
                   t+ G+AAGm ntG
  gi|5011914   867 TIAGVAAGMRNTG    879

gi|226945972|ref|YP_002801045.1|: domain 1 of 1, from 3 to 878: score 784.1, E = 9.5e-233
                   *->siDAqLRlLvPGKvsedekLieY.DALLlDkFLDiLqDLHGedLkEa
                       iDA LR  v  +    e L eY  A   + F D +  +
  gi|2269459     3    EIDARLREDV--RLL-GELLGEYiHAQCGEVFFDKIERIR------L 40

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                         l  e    + t+ L+EL  +   L+P     vA+a+   LnLAn
  gi|2269459    41 GAKTGRLGSEEGAEQLTRTLGEL--REDELQP-----VARAFNQFLNLAN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +   RRR        Fa  a       + E l +L   +  + +
  gi|2269459    84 IAEQYH-EIRRRAPEEP-PPFAVRA-------LPELLDRLLAGG-HAADA 123

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                       L    +DLvltAHPt   RR L+ K   i   La L   D+ + ++
  gi|2269459   124 LARQLGRLEIDLVLTAHPTEVTRRTLIRKYEAIAAELAVLDHGDLLPAER 173

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   + + E L R i  A+ tDEiRR++PtP DE + G s i   +W+ vP FL
  gi|2269459   174 EAVHERLRRLIAEAWHTDEIRRSRPTPVDEAKWGFSVIEHSLWQAVPAFL 223

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   R vD AL        lP ++  i+FssWmGGDRDG nP vt  vtR+v L
  gi|2269459   224 RGVDRALHE-ATGLHLPLEAAPIRFSSWMGGDRDG-NPNVTAAVTREVLL 271

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   LaR  Aa l +  vE L  Elsm    +ELR+R  E+      d
  gi|2269459   272 LARWAAADLHLRDVEQLAAELSMQEASSELRARTGEV------D------ 309
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                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYRv+L + R++L+ tR+ a   L +G   +   Av  +
  gi|2269459   310 ----------EPYRVLLKQLRERLFATRDWAAAAL-HG-EAVRSPAVLQN 347

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      e L PLELCY+sL  CG   iADG LLD LR   tFGL Lv+LDiRq+
  gi|2269459   348 NRELLQPLELCYRSLHACGMGLIADGPLLDSLRRAATFGLFLVRLDIRQD 397

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    + R+   l  it+ L++G Y +W Ee R  +L+ EL  +RPLl+   P
  gi|2269459   398 AARHAAALSEITEYLGLGRYADWNEETRTAFLMRELDSRRPLLPVHFPAS 447

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     E ++vl + r +A  P  s G+Y+isma aPsDvLAv LL +ECg++++
  gi|2269459   448 AETAEVLATCREVAQAPAASLGSYVISMAAAPSDVLAVQLLLKECGLQRP 497

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    +rvvPLFE L DL+ A  +ve+L  +  Y+ r+ G qevm+GYsDs KD
  gi|2269459   498 MRVVPLFETLTDLDNAAPTVERLLLLPGYRARLHGPQEVMIGYSDSAKDG 547

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G  +AAW  Y+AqE ++ v ++ Gv L lFHGRGGtvGRGGGP H AiLs
  gi|2269459   548 GTTAAAWAQYRAQEGLVEVCRRQGVELLLFHGRGGTVGRGGGPAHAAILS 597

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  + G  R t qGE+i f FG  +   +sL  +  A LE  + PP +
  gi|2269459   598 QPPGSVPGRFRTTEQGEMIRFKFGLPDTAVQSLNLYLSAVLEATLLPPPA 647

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    P P WR+Lm+++A      YRsvv   P FvEYFR AtPE E G++ +Gs
  gi|2269459   648 PEPAWRELMDRLAAEGLAAYRSVVREHPQFVEYFRQATPEQELGRLPLGS 697

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+ +GGiesLRAiPWiFaWtqtR  LP WLG   A   A+ +
  gi|2269459   698 RPAKRR-AGGIESLRAIPWIFAWTQTRLMLPAWLGWETALGNALARGEGE 746

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l  L+ m + WPFF   +D+lEmv AK D  iA LyD+ Lv   L P G+
  gi|2269459   747 L--LRRMSRHWPFFGTRIDMLEMVLAKSDAAIAQLYDERLVEPGLLPLGQ 794

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR         +L++     lL   P ++    +R+ Y+  L  +q
  gi|2269459   795 QLRGLLSQACAAVLELTEQDRLLGHNPEVRAAFSVRNTYLDPLHLLQVEL 844

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R           l +E A  +                   LE  L+
  gi|2269459   845 LARYR-----------LHQEQACSP-------------------LEQALL 864

                    LtmKGiAAGmqntG<-*
                    + + GiAAG+ ntG
  gi|2269459   865 VSVAGIAAGLRNTG    878

gi|260553863|ref|ZP_05826131.1|: domain 1 of 1, from 4 to 894: score 784.0, E = 1e-232
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        i A LR               D  Ll   L++ L+   G++L
  gi|2605538     4    QINAPLRE--------------DVRLLGNLLgETLKQHAGQELFNQ 35

                    vqECYEls.AeYEGKkDtkK.LeELGakLtsLdPaDail.vAkailHmLn
                    +     l++   +G+ +++K+Le L   L    P + +l++ +a++H Ln
  gi|2605538    36 IEQIRALAkGARDGQAEAEKqLEQLFLEL----PDEELLpLTRAFSHFLN 81

                    LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                     An+AE  ++   RR            ++A     +   ++k   k   s
  gi|2605538    82 FANIAEQYHVVRSRRQAEFD-------SEANSPNPLVHLFQKFKDKS-IS 123

                    PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                     e  F+ +    ++LvltAHPt   RR L+qK   i  CL+qL  + +t+
  gi|2605538   124 TEKLFQQICDLKIELVLTAHPTEVSRRTLIQKYDDINACLSQLDQQKLTP 173

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
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                    +++     L   i  A+ tDEiR  +PtP DE + G + i  t+W+ vP
  gi|2605538   174 RERQNALANLKQQISSAWQTDEIRQHRPTPVDEAKWGFATIEQTLWNAVP 223

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                    KF+R     ++       lP ++  ++F+sWmGGDRDG nP vt  +t +
  gi|2605538   224 KFIRELNELVQD-NCQQNLPLNIAPVRFASWMGGDRDG-NPNVTHQITQE 271

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                    v  L+R  Aa lY+  +E L +Els+  C +E+      ++     +
  gi|2605538   272 VLWLSRWQAADLYLRDIENLRWELSIQACSEEM------IQAIGSPH--- 312

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe..
                                EPYR  L + R++L  t    RH LA+ +  +  +++
  gi|2605538   313 ------------PEPYREYLRATRERLKAT----RHWLAQRLQGLEADds 346

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                     v    +e L PL LCY+sL +     iA G LLD++  v  FG+ L KL
  gi|2605538   347 NVIKSKDELLQPLLLCYRSLIDSNLPEIANGQLLDFIYRVNCFGIELLKL 396

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    DiRqEs R+   + Ait+ L++G + +W E+ Rq +L+ EL+ KRPLl+
  gi|2605538   397 DIRQESGRHRQAISAITEYLGLGNFESWTEQARQNFLIQELQSKRPLLPK 446

                    DLPktE.......EvkDvldafrvLAELPiDsFGaYiismataPsDvLAv
                     +   E++  ++++v++v  ++r LA+ P +s GaYiisma  PsDvLAv
  gi|2605538   447 YINEPEgslighpDVQEVFATMRTLADQPPESLGAYIISMAEYPSDVLAV 496

                    ELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqe
                     LLq+E g++++LrvvPLFE L DL+ A  +++ LF + WY+ +i+GK e
  gi|2605538   497 LLLQKEAGIQHPLRVVPLFETLKDLDGAATTMNTLFNMHWYKQHIQGKHE 546

                    vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                    vm+GYsDs KDAG +sA W  Y+AqEE+  +A+k+Gv+L+lFHGRGG +
  gi|2605538   547 VMIGYSDSAKDAGFMSANWAQYRAQEELTAIARKHGVQLTLFHGRGGSIS 596

                    RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                    RGG Pt  A+ sqPP  i G++Rvt qGE+i f FG E +  + L  +tA
  gi|2605538   597 RGGAPTQQALFSQPPGSISGAIRVTEQGEMIRFKFGLEGIAMQNLEIYTA 646

                    AtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAt
                    AtLE  + PP  Pk EWR+Lm++m       YR  v   P Fv Y R  t
  gi|2605538   647 ATLEATLLPPPEPKVEWRELMNRMTDHSVKVYRQTVRENPHFVKYLRTVT 696

                    PElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGA
                    PElE   + +GsRPaKRk sGGiesLRAiPW+FaWtq R  LP WLG GA
  gi|2605538   697 PELELQMLPLGSRPAKRKVSGGIESLRAIPWVFAWTQIRLMLPAWLGTGA 746

                    AFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDk
                    A    i    K    L Em ++WP+F   +D+lEmv  K D  iA  y+
  gi|2605538   747 AINEVIADQQKA--TLDEMLQQWPYFQTLIDMLEMVLSKADANIALYYES 794

                    LLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRd
                     L  +E+Lk  G++LR++ ++  + LLk+     lL     L q + +R
  gi|2605538   795 HLTEdEDLKVLGNQLRQRLKDAVETLLKLKDESKLLSNNEVLDQSMQVRK 844

                    sYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnp
                    +Y+  L  +qA  +KR RD              y +E
  gi|2605538   845 PYLLPLHLLQAELMKRRRD--------------YLAER------------ 868

                    tervaPGLEDtLiLtmKGiAAGmqntG<-*
                      +  P ++  L++ + GiAAG+ ntG
  gi|2605538   869 QAEHTP-VDHALMVSIAGIAAGLRNTG    894

gi|229588773|ref|YP_002870892.1|: domain 1 of 1, from 3 to 875: score 783.6, E = 1.3e-232
                    *->siDAqLR..lLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                        iDA LR+++   G    +    +Y     D FLD +     e+++
  gi|2295887     3    DIDARLRedVHLLGELLGNTIREQYG----DAFLDKI-----EQIRK 40

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                      +      A+  G  D     EL a L  L+  + + vA+a+   LnLA
  gi|2295887    41 GAK------ADRRGAGD-----ELSASLNQLQENELLPVARAFNQFLNLA 79
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                nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiE.EtlKkLvlklnKsP
                n+AE  +l +RR  ++              Es + +E l +L + +  s
gi|2295887    80 NIAEQYQLIHRRDESQPA----------PFESRVLpELLARLQSEG-HSN 118

                eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                e     L    ++LvltAHPt  +RR L+qK   i   La    +D+t
gi|2295887   119 ESLARQLGRLEIELVLTAHPTEVARRTLIQKYDAIAAQLALQDHRDLTTA 168

                DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                +++ +   L R i  A+ t+EiRR++PtP DE + G + i   +W+ +P
gi|2295887   169 EREQIRQRLQRLIAEAWHTEEIRRTRPTPVDEAKWGFAVIEHSLWHAIPN 218

                FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                +LR+ D AL       RlP ++  i+F+sWmGGDRDG nP vt  vtR+v
gi|2295887   219 YLRKADQALHA-ATGLRLPLEAAPIRFASWMGGDRDG-NPNVTAPVTREV 266

                CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                 LLaR mAa lY+  ++ L  Elsm      L ++  +      +
gi|2295887   267 LLLARWMAADLYLRDIDHLASELSMQQASPALQAKVGD------SV---- 306

                yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                            EPYR +L + R++L  tR  a   L       +E  v
gi|2295887   307 ------------EPYRALLKQLRERLRATRQWAHTALSSSTPAPAE--VL 342

                tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                 +  + LEPLELCY+sL eCG  viADG LLD LR   tFGL Lv+LD+R
gi|2295887   343 QNNRDLLEPLELCYQSLHECGMGVIADGPLLDCLRRAVTFGLFLVRLDVR 392

                qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                q+s R+   +  it  L++G Y +W Ee R  +L+ EL  +RPLl+
gi|2295887   393 QDSSRHSAAMTEITDYLGLGRYEDWDEEARISFLMKELANRRPLLPGYFK 442

                ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                   + ++vl++ + +A  P  s G+Y+isma a sDvLAv LL +E gv+
gi|2295887   443 PSADTAEVLNTCKEVAAAPAASLGSYVISMAGAASDVLAVQLLLKESGVQ 492

                qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                +++rvvPLFE LADL+ A   +e+L  +  Y+ r++G qevm+GYsDs K
gi|2295887   493 RPMRVVPLFETLADLDNAGPVIEQLLLLPGYRTRLQGPQEVMIGYSDSAK 542

                DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                DAG  +AAW  Y+AqE ++ + ++  v L lFHGRGGtvGRGGGP H Ai
gi|2295887   543 DAGTTAAAWAQYRAQERLVDICREQQVELLLFHGRGGTVGRGGGPAHAAI 592

                LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                LsqPP  + G  R t qGE+i f FG  ++  + L  + AA LE  + PP
gi|2295887   593 LSQPPGSVAGRFRTTEQGEMIRFKFGLPDIAEQNLNLYLAAVLEATLLPP 642

                vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                  P P WR+Lm+e+A      YR+vv   P FvEYFR  tPE E G++ +
gi|2295887   643 PPPEPAWRHLMDELAADGVSAYRAVVRENPQFVEYFRQSTPEQELGRLPL 692

                GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                GsRPaKR+ +GGiesLRAiPWiF WtqtR  LP WLG  AA   A+++
gi|2295887   693 GSRPAKRR-AGGIESLRAIPWIFGWTQTRLMLPAWLGWEAALSKALERGE 741

                KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                  l  L  m ++WPFFR  +D+lEmv AK D  iA LyD+ Lv  +L P
gi|2295887   742 GEL--LGQMREQWPFFRTRIDMLEMVLAKADADIARLYDERLVQPDLLPL 789

                GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                G  LRd        +L + G   lL   P     +RLR+ Y+  L  +qA
gi|2295887   790 GTHLRDLLSQACSVVLGLTGQSQLLAHSPDTLEFIRLRNTYLDPLHLLQA 839

                YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                  L R R             +E A++                     LE
gi|2295887   840 ELLARSRQ------------QEAAQDS------------------PLEQA 859

                LiLtmKGiAAGmqntG<-*
                L++ + GiAAG+ ntG
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  gi|2295887   860 LLVSVAGIAAGLRNTG    875

gi|169794232|ref|YP_001712025.1|: domain 1 of 1, from 4 to 894: score 782.9, E = 2.2e-232
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      iDA LR               D  Ll   L++ L+   G++L
  gi|1697942     4    QIDAPLRE--------------DVRLLGNLLgETLKQHAGQELFNQ 35

                  vqECYEls.AeYEGKkDtkK.LeELGakLtsLdPaDail.vAkailHmLn
                  +     l++   +G+ +++K+Le L   L    P + +l++ +a++H Ln
  gi|1697942    36 IEQIRALAkGARDGQAEAEKqLEQLFLEL----PDEELLpLTRAFSHFLN 81

                  LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                   An+AE  ++   RR             +A     +   +Kk   k   s
  gi|1697942    82 FANIAEQYHVVRSRRQAEFD-------PDANSPNPLVHLFKKFKDKN-IS 123

                  PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                   e  F+ +    ++LvltAHPt   RR L+qK   i  CL+qL  + +t+
  gi|1697942   124 TEKLFQQICDLKIELVLTAHPTEVSRRTLIQKYDDINACLSQLDQQKLTP 173

                  eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                   +++     L   i  A+ tDEiR  +PtP DE + G + i  t+W+ vP
  gi|1697942   174 RERQNALANLKQQISSAWQTDEIRQHRPTPVDEAKWGFATIEQTLWNAVP 223

                  KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                  KF+R     ++       lP  +  ++F+sWmGGDRDG nP vt  +t +
  gi|1697942   224 KFIRELNELVQD-NCQQNLPLHIAPVRFASWMGGDRDG-NPNVTHQITQE 271

                  vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                  v  L+R  Aa lY+  +E L +Els+  C +E+    E + +
  gi|1697942   272 VLWLSRWQAADLYLRDIENLRWELSIQSCSEEM---VEAIGS-------- 310

                  KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe..
                            P  EPYR  L + R++L  t    RH LA+ +  +  +++
  gi|1697942   311 ----------PHPEPYREYLRATRERLKAT----RHWLAQRLQGLEADds 346

                  AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                   v    +e L PL LCY+sL +     iA G LLD++  v  FG+ L KL
  gi|1697942   347 NVIKSKDELLQPLLLCYRSLIDSNLPEIANGQLLDFIYRVNCFGIELLKL 396

                  DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                  DiRqEs R+   + Ait+ L++G + +W E+ Rq +L+ EL+ KRPLl+
  gi|1697942   397 DIRQESGRHRQAISAITEYLGLGNFESWTEQARQNFLIQELQSKRPLLPK 446

                  DLPktE.......EvkDvldafrvLAELPiDsFGaYiismataPsDvLAv
                   +   E++  ++++v++v  ++r LA+ P +s GaYiisma  PsDvLAv
  gi|1697942   447 YINEPEgslighpDVQEVFATMRTLADQPPESLGAYIISMAEYPSDVLAV 496

                  ELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqe
                   LLq+E g++++LrvvPLFE L DL+ A  +++ LF + WY+ +i+GK e
  gi|1697942   497 LLLQKEAGIQHPLRVVPLFETLKDLDGAATTMNTLFNMHWYKQHIQGKHE 546

                  vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                  vm+GYsDs KDAG +sA W  Y+AqEE+  +A+k+Gv+L+lFHGRGG +
  gi|1697942   547 VMIGYSDSAKDAGFMSANWAQYRAQEELTAIARKHGVQLTLFHGRGGSIS 596

                  RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                  RGG Pt  A+ sqPP  i G++Rvt qGE+i f FG E +  + L  +tA
  gi|1697942   597 RGGAPTQQALFSQPPGSISGAIRVTEQGEMIRFKFGLEGIAMQNLEIYTA 646

                  AtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAt
                  AtLE  + PP  Pk EWR+Lm++m       YR  v   P Fv Y R  t
  gi|1697942   647 ATLEATLLPPPEPKAEWRELMNRMTDHSVKVYRQTVRENPHFVKYLRTVT 696

                  PElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGA
                  PElE   + +GsRPaKRk sGGiesLRAiPW+FaWtq R  LP WLG GA
  gi|1697942   697 PELELQMLPLGSRPAKRKVSGGIESLRAIPWVFAWTQIRLMLPAWLGTGA 746

                  AFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDk
                  A    i    K    L Em ++WP+F   +D+lEmv  K D  iA  y+
  gi|1697942   747 AINEVIADQQKA--TLDEMLQQWPYFQTLIDMLEMVLSKADANIALYYES 794
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                    LLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRd
                     L  +E+Lk  G++LR++ ++  + LL +     lL     L q + +R
  gi|1697942   795 HLTEdEDLKVLGNQLRQRLKDAVETLLTLKDESKLLSDNEVLDQSMQVRK 844

                    sYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnp
                    +Y+  L  +qA  +KR RD              y +E
  gi|1697942   845 PYLLPLHLLQAELMKRRRD--------------YLAER------------ 868

                    tervaPGLEDtLiLtmKGiAAGmqntG<-*
                      +  P ++  L++ + GiAAG+ ntG
  gi|1697942   869 QAEHTP-VDHALMVSIAGIAAGLRNTG    894

gi|213158772|ref|YP_002321193.1|: domain 1 of 1, from 4 to 894: score 782.8, E = 2.3e-232
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        iDA LR                D  Ll   L++ L+   G++L
  gi|2131587     4    QIDAPLRE---------------DVRLLGNLLgETLKQHAGQELFNQ 35

                    vqECYEls.AeYEGKkDtkK.LeELGakLtsLdPaDail.vAkailHmLn
                    +     l++   +G+ +++K+Le L   L    P + +l++ +a++H Ln
  gi|2131587    36 IEQIRALAkGARDGQAEAEKqLEQLFLEL----PDEELLpLTRAFSHFLN 81

                    LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                     An+AE  ++   RR             +A     +   +Kk   k   s
  gi|2131587    82 FANIAEQYHVVRSRRQAEFD-------PDANSPNPLVHLFKKFKDKN-IS 123

                    PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                     e  F+ +    ++LvltAHPt   RR L+qK   i  CL+qL  + +t+
  gi|2131587   124 TEKLFQQICDLKIELVLTAHPTEVSRRTLIQKYDDINACLSQLDQQKLTP 173

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                     +++     L   i  A+ tDEiR  +PtP DE + G + i  t+W+ vP
  gi|2131587   174 RERQNALANLKQQISSAWQTDEIRQHRPTPVDEAKWGFATIEQTLWNAVP 223

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                    KF+R     ++       lP  +  ++F+sWmGGDRDG nP vt  +t +
  gi|2131587   224 KFIRELNELVQD-NCQQNLPLHIAPVRFASWMGGDRDG-NPNVTHQITQE 271

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                    v  L+R  Aa lY+  +E L +Els+  C +E+      ++     +
  gi|2131587   272 VLWLSRWQAADLYLRDIENLRWELSIQSCSEEM------VQAIGSPH--- 312

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe..
                                EPYR  L + R++L  t    RH LA+ +  +  +++
  gi|2131587   313 ------------PEPYREYLRATRERLKAT----RHWLAQRLQGLEADds 346

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                     v    +e L PL LCY+sL +     iA G LLD++  v  FG+ L KL
  gi|2131587   347 NVIKSKDELLQPLLLCYRSLIDSNLPEIANGQLLDFIYRVNCFGIELLKL 396

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    DiRqEs R+   + Ait+ L++G + +W E+ Rq +L+ EL+ KRPLl+
  gi|2131587   397 DIRQESGRHRQAISAITEYLGLGNFESWTEQARQNFLIQELQSKRPLLPK 446

                    DLPktE.......EvkDvldafrvLAELPiDsFGaYiismataPsDvLAv
                     +   E++  ++++v++v  ++r LA+ P +s GaYiisma  PsDvLAv
  gi|2131587   447 YINEPEgslighpDVQEVFATMRTLADQPPESLGAYIISMAEYPSDVLAV 496

                    ELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqe
                     LLq+E g++++LrvvPLFE L DL+ A  +++ LF + WY+ +i+GK e
  gi|2131587   497 LLLQKEAGIQHPLRVVPLFETLKDLDGAATTMNTLFNMHWYKQHIQGKHE 546

                    vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                    vm+GYsDs KDAG +sA W  Y+AqEE+  +A+k+G++L+lFHGRGG +
  gi|2131587   547 VMIGYSDSAKDAGFMSANWAQYRAQEELTAIARKHGIQLTLFHGRGGSIS 596

                    RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                    RGG Pt  A+ sqPP  i G++Rvt qGE+i f FG E +  + L  +tA
  gi|2131587   597 RGGAPTQQALFSQPPGSISGAIRVTEQGEMIRFKFGLEGIAMQNLEIYTA 646

                    AtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAt
                    AtLE  + PP  Pk EWR+Lm++m       YR  v   P Fv Y R  t
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  gi|2131587   647 ATLEATLLPPPEPKAEWRELMNRMTDHSVKVYRQTVRENPHFVKYLRTVT 696

                   PElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGA
                   PElE   + +GsRPaKRk sGGiesLRAiPW+FaWtq R  LP WLG GA
  gi|2131587   697 PELELQMLPLGSRPAKRKVSGGIESLRAIPWVFAWTQIRLMLPAWLGTGA 746

                   AFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDk
                   A    i    K    L Em ++WP+F   +D+lEmv  K D  iA  y+
  gi|2131587   747 AINEVIADQQKA--TLDEMLQQWPYFQTLIDMLEMVLSKADANIALYYES 794

                   LLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRd
                    L  +E+Lk  G++LR++ ++  + LL +     lL     L q + +R
  gi|2131587   795 HLTEdEDLKVLGNQLRQRLKDAVETLLALKDESKLLSDNEVLDQSMQVRK 844

                   sYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnp
                   +Y+  L  +qA  +KR RD              y +E
  gi|2131587   845 PYLLPLHLLQAELMKRRRD--------------YLAER------------ 868

                   tervaPGLEDtLiLtmKGiAAGmqntG<-*
                     +  P ++  L++ + GiAAG+ ntG
  gi|2131587   869 QAEHTP-VDHALMVSIAGIAAGLRNTG    894

gi|251791486|ref|YP_003006207.1|: domain 1 of 1, from 1 to 879: score 782.7, E = 2.5e-232
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  q  ++    vs           +l k L+D +++  G ++ E
  gi|2517914     1    -MNEQYSAMR-SNVS-----------MLGKLLgDTIKEALGANILER 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls       +t++ +EL + L  L   + + vA+a++  LnL n
  gi|2517914    35 VETIRKLSKASRAGSETHR-QELLTTLQNLSNEELLPVARAFSQFLNLTN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    AE  +       +   hG+ a   +A     +   ++ L  + n s ++
  gi|2517914    84 TAEQYH-------SISPHGEAASNPEA-----LATVFRNLKNRDNLSDKD 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   + +A+   s++LvltAHPt   RR L+ K   +  CL qL   D+   ++
  gi|2517914   122 IRDAVESLSIELVLTAHPTEITRRTLIHKLVEVNTCLKQLDHDDLADYER 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   + +   L   i   + tDEiR+ +PtP DE + G + +   +W+GvP FL
  gi|2517914   172 HQIMRRLRQLIAQYWHTDEIRKIRPTPVDEAKWGFAVVENSLWEGVPAFL 221

                   RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   R  D  ++K +G   RlP d   ++F+sWmGGDRDG nP vt E+tR v
  gi|2517914   222 RELDEQMdKELGY--RLPVDSVPVRFTSWMGGDRDG-NPNVTAEITRRVL 268

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                   LL+R  Aa l++  v  L+ Elsm  C  EL       ++ a  d
  gi|2517914   269 LLSRWKAADLFLRDVQVLVSELSMTTCTPEL-------QQLAGGD----- 306

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                             +EPYR ++ + R +L  t +     L +G   ++
  gi|2517914   307 --------EIQEPYRELMKALRAQLTSTLDYLDARL-KGEQRVPPKDLLV 347

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                     E+   PL  CY+sL  CG  +iADG LLD LR v  FG+ Lv++D+Rq
  gi|2517914   348 TNEQLWQPLYACYQSLHACGMGIIADGQLLDTLRRVRCFGVPLVRIDVRQ 397

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   Es R+tD l  it+ L++G Y +WsE  +q +L+ EL  KRPLl+
  gi|2517914   398 ESTRHTDALAEITRYLGLGDYESWSESDKQAFLIRELNSKRPLLPRQWEP 447

                   tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     + ++vl++ rv+AE P Ds  aY+isma +PsDvLAv LL +E g
  gi|2517914   448 SADTQEVLETCRVIAETPRDSIAAYVISMARTPSDVLAVHLLLKEAGCPY 497

                   tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                   +L+v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|2517914   498 ALPVAPLFETLDDLNNADSVMIQLLNIDWYRGFIQGKQMVMIGYSDSAKD 547
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                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+Aq+ +iK   kyG+ L+lFHGRGG +GRGG P H A+L
  gi|2517914   548 AGVMAASWAQYRAQDALIKTCEKYGIALTLFHGRGGSIGRGGAPAHAALL 597

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f FG  ++   sL  +t A LE  + PP
  gi|2517914   598 SQPPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLSLYTSAILEANLLPPP 647

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     PkPEW ++m+e+  +  + YR  v   P Fv YFR AtPElE Gk+ +G
  gi|2517914   648 EPKPEWHHIMDELSRISCDMYRGYVRENPDFVPYFRAATPELELGKLPLG 697

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA +  id   +
  gi|2517914   698 SRPAKRRPNGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQKVIDDGNQ 747

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                    n  +L+ m ++WPFF   + +lEmvFAK D  +A  yD+ Lv E L+  G
  gi|2517914   748 N--QLEAMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVEEKLWSLG 795

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    k+LR++     + +L i     l+   P++   + LR+ Y   Lnv+qA
  gi|2517914   796 KQLREQLAKDIKAVLTISNDDHLMADLPWIAESIALRNVYTDPLNVLQAE 845

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                 ++          L       P +E  L
  gi|2517914   846 LLHRSRQ----------------QDT---------LD------PQVEQAL 864

                    iLtmKGiAAGmqntG<-*
                    ++t+ G+AAGm ntG
  gi|2517914   865 MVTIAGVAAGMRNTG    879

gi|262393083|ref|YP_003284937.1|: domain 1 of 1, from 1 to 877: score 782.3, E = 3.3e-232
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                               + e    ++    +l + L+  + D HGe++ E
  gi|2623930     1    -------------MNEKYAALKSNVRMLGHLLgNTIRDAHGEEIFEK 34

                    vqECYEl..sAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    v     l++sA+   + D   L E    +  L       v +a+   LnL
  gi|2623930    35 VETIRKLskSAQAGNQADRDSLIE---EIKHLPDEQLTPVTRAFNQFLNL 81

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                     n+AE  +   R   +         E +A     i   + kLv     s
  gi|2623930    82 TNIAEQYHTISRHCEEHIC------EPDA-----INSLFSKLVQND-VSK 119

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                     +  +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+
  gi|2623930   120 LDTAQAVRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSSK 169

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++k  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP
  gi|2623930   170 ERKKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWEAVPD 219

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    FLR +   LK   + E lP d+  ++FssWmGGDRDG nP vt  vtR+v
  gi|2623930   220 FLREMHDRLKSY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHSVTREV 267

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                     LL+R  Aa lY++ + +L+ Elsm   nd +R  A E +
  gi|2623930   268 LLLSRWKAADLYLNDINELISELSMTVSNDQVRELAGEDQH--------- 308

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                                EPYR iL + R  L  t++     + +G   ++  A
  gi|2623930   309 ------------EPYRAILKQLRTLLNETKDILDAKI-HG-QKLAVKAPL 344

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     kvE+  EPL  CY+sL eCG  viA GsLLD LR v  FG+ Lv+LDiR
  gi|2623930   345 QKVEQLWEPLYACYQSLNECGMGVIANGSLLDTLRRVKAFGIHLVRLDIR 394

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+ Dvl  +t+ L+iG Y +WsE+ +  +L  EL  KRPLl+ D
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  gi|2623930   395 QESTRHSDVLSELTRYLGIGDYEQWSEQDKIAFLTNELASKRPLLPRDWE 444

                   ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                     E vk+vld+ +++A  P ++FGaY+isma + sDvLAv LL  E g
  gi|2623930   445 PSEPVKEVLDTCKIIAAQPREAFGAYVISMARTASDVLAVHLLLQEAGCP 494

                   qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                     + v PLFE L DL+ A   +++L  iD Y+  i+  q vm+GYsDs K
  gi|2623930   495 YRMDVCPLFETLDDLNNAESVIKQLMGIDLYRGFIQNHQMVMIGYSDSAK 544

                   DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                   DAG +sA W  Y A E ++KvA + Gv L+lFHGRGGtvGRGG P H A+
  gi|2623930   545 DAGVMSAGWAQYHAMESLVKVAEEEGVELTLFHGRGGTVGRGGAPAHAAL 594

                   LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                   LsqPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|2623930   595 LSQPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNLYASAILEANLLPP 644

                   vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                     Pk EWR+Lme +  v  E YR vv  EP Fv YFR AtPElE Gk+ +
  gi|2623930   645 PEPKQEWRDLMEVLSEVSCESYRNVVRGEPDFVPYFRQATPELELGKLPL 694

                   GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                   GsRPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ idK
  gi|2623930   695 GSRPAKRNPKGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSIDKGH 744

                   KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                   + l  L+Em +eWPFF   l +lEmv+ K    i   yD+ Lv E L+P
  gi|2623930   745 QAL--LEEMCREWPFFSTRLGMLEMVYSKCNIDISRYYDERLVDESLRPL 792

                   GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                   G++LR++ +E  + +L +     l+  DP+    +RLR+ Y+  Ln++qA
  gi|2623930   793 GEKLRAQLQEDIKAVLNVENNENLMQHDPWGLESIRLRNIYVEPLNMLQA 842

                   YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                     L R R                                 te+ +  LE+
  gi|2623930   843 ELLYRTRQ------------------------------TEEASANLEEA 861

                   LiLtmKGiAAGmqntG<-*
                   L++t+ GiAAGm ntG
  gi|2623930   862 LMVTIAGIAAGMRNTG    877

gi|261823543|ref|YP_003261649.1|: domain 1 of 1, from 1 to 879: score 782.0, E = 4e-232
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  q  ++    vs           +l k L+D +++  Ge++ +
  gi|2618235     1    -MNEQYSAMR-SNVS-----------MLGKLLgDTIKEALGENILDK 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls       + ++ +EL + L  L   + + vA+a++  LnL n
  gi|2618235    35 VETIRKLSKSSRAGNEKHR-QELLTTLQNLSNDELLPVARAFSQFLNLTN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    AE  +           hG+      A   + +   + +L    + +  +
  gi|2618235    84 TAEQYH-------TISPHGE-----AASNPAQLSNAFERLKENKDLTERD 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvteDK
                   + +A+   s++LvltAHPt   RR L+ K   +  CL qL   D+   ++
  gi|2618235   122 IRDAVESLSIELVLTAHPTEITRRTLIHKLVEVNTCLKQLDHNDLADYER 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     +   L   i   + tDEiR+ +PtP DE + G + +   +W+GvP FL
  gi|2618235   172 NQIMRRLRQLIAQSWHTDEIRKIRPTPVDEAKWGFAVVENSLWEGVPAFL 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   R  D  L       RlP d+  ++F+sWmGGDRDG nP vt EvtR v L
  gi|2618235   222 RELDEQLEQ-AFGYRLPVDAVPVRFTSWMGGDRDG-NPNVTAEVTRHVLL 269

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   L+R  Aa l++  +  L+ Elsm  C  EL     El      +
  gi|2618235   270 LSRWKAADLFLRDIQVLVSELSMSECTPELL----ELAGGNEVQ------ 309
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                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR i+   R +L  t       L tG   ++
  gi|2618235   310 ----------EPYRAIMKSLRSQLSSTLSYLEARL-TGEERLPPKDLLIT 348

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     E+  EPL  CY+sL  CG  +iADG LLD LR v  FG+ Lv++D+RqE
  gi|2618235   349 NEQLWEPLHACYQSLKTCGMGIIADGRLLDTLRRVRCFGVPLVRIDVRQE 398

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+tD l  it+ L++G Y +WsE  +q +L+ EL+ KRPLl+
  gi|2618235   399 STRHTDALAEITRYLGLGDYESWSESDKQAFLIRELSSKRPLLPRYWEPS 448

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     + k+vld+ rv+A  P  s  aY+isma +PsDvLAv LL +E g   +
  gi|2618235   449 ADTKEVLDTCRVIAKAPQGSIAAYVISMARTPSDVLAVQLLLKEAGCPFA 498

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    L+v PLFE L DL+ A   + +L siDWY+  i+GKq vm+GYsDs KDA
  gi|2618235   499 LPVAPLFETLDDLNNADDVMTQLLSIDWYRGFIQGKQMVMIGYSDSAKDA 548

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Ls
  gi|2618235   549 GVMAASWAQYRAQDALIKTCEKAGIALTLFHGRGGSIGRGGAPAHAALLS 598

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2618235   599 QPPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLALYTGAILEANLLPPPE 648

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EW ++m+e+  v  + YR  v   P Fv YFR AtPElE Gk+ +Gs
  gi|2618235   649 PKQEWHQVMDELSRVSCDMYRGYVRENPDFVPYFRAATPELELGKLPLGS 698

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA +  +d D K
  gi|2618235   699 RPAKRRPNGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQKVVD-DGKQ 747

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                     q L+Em ++WPFF   + +lEmvFAK D  +A  yD+ Lv E L+P Gk
  gi|2618235   748 GQ-LEEMCRNWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVEEKLWPLGK 796

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LRd+      ++L i     l+   P++   + LR+ Y   Lnv+qA
  gi|2618235   797 QLRDQLAADISIVLAISNDDHLMADLPWIAESIALRNVYTDPLNVLQAEL 846

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                 +E+   +d  ++L             L+
  gi|2618235   847 LHRSRQ----------------QEQ---PDADLELA------------LM 865

                    LtmKGiAAGmqntG<-*
                    +t+ G+AAGm ntG
  gi|2618235   866 VTIAGVAAGMRNTG    879

gi|117621332|ref|YP_855124.1|: domain 1 of 1, from 6 to 877: score 781.7, E = 4.9e-232
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          A LR+ v G              Ll k    ++D  G+   + +
  gi|1176213     6    ---AALRANV-GMLG----------QLLGK---SIKDHQGQAFLDKI 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         l A    K      e L   L  L   + + vA+a++  LnLAn+
  gi|1176213    36 ETIRQL-AKSSRKGNETDRERLLDTLRNLSDDELLPVARAFSQFLNLANV 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +   RR  ++            t   +E  + kL      s e +
  gi|1176213    85 AEQFHTISRRCEEQVC----------TPDPLEQMFDKLKASN-LSQEAI 122

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     +A++   +DLvltAHPt   RR L+ K+  +  CL  L   D+ + ++
  gi|1176213   123 IQAVRELDIDLVLTAHPTEVTRRTLIHKHVQLNDCLEALELSDLLPRERD 172

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +   +   +  A+ t EiR  +PtP DE + G + +   +W  +P F+R
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  gi|1176213   173 KILNRIEQLVNQAWHTNEIREQRPTPVDEAKWGFAVVENSLWPAIPEFMR 222

                    RvDtALK.niGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                      D  L++ +G+  RlP d+  +kF+sWmGGDRDG nP vt  vt +v
  gi|1176213   223 NLDERLQhHLGV--RLPLDAAPVKFTSWMGGDRDG-NPFVTAKVTAEVLE 269

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L R mA  l++  + +L  Elsm  C d +R R          d
  gi|1176213   270 LGRWMAVSLFYKDIKELTSELSMSDCTDAVRERV--------GD------ 305

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR ++ + R++L  t E    L A+   + sE     k
  gi|1176213   306 --------HPEPYRALVRELREQLRETQE---FLTAKVQGQASESRDLVK 344

                    vEeFL.EPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                        L+EPLELCY+sL  CG   iADG LLD+LR+   FG+ LvKLDiRq
  gi|1176213   345 TTAQLrEPLELCYHSLHACGMGNIADGMLLDVLRKLACFGIHLVKLDIRQ 394

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    + eR+  v   +t+ L++G Y eWsE+ +q +Ll EL  +RPL++ D
  gi|1176213   395 DGERHGQVFSELTRYLGMGDYAEWSEDDKQAFLLNELNSRRPLIPTDWEP 444

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     +E ++ ld+ +v+A    D+FG Yiisma aPsDvLAv LL +E g k
  gi|1176213   445 SDETRETLDTCKVIAQHDPDAFGIYIISMAGAPSDVLAVQLLLKEAGCKF 494

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                     ++v PLFE   DL A  A +e+L s+DWY+  i+G+q vm+GYsDs KD
  gi|1176213   495 RMPVAPLFETQEDLMAGTAVMERLLSVDWYRGYIQGRQYVMIGYSDSAKD 544

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y A E ++  A     +L+lFHGRGGtvGRGG P H AiL
  gi|1176213   545 AGMMAAGWAQYAAMESLVALAEANNLRLTLFHGRGGTVGRGGAPAHQAIL 594

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  + G lRvt qGE+i f FG  ++  +sL  +t A LE  + PP
  gi|1176213   595 SQPPGSLRGGLRVTEQGEMIRFKFGLPKVAIQSLNLYTSAVLEGNLLPPP 644

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR +me++A v  + YRs+v   P Fv YFR AtPE+E Gk+ +G
  gi|1176213   645 KPKECWRAVMEQLASVSCDHYRSIVRGHPDFVPYFRAATPEMELGKLPLG 694

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRP+KRkP GG+esLRAiPWiFaWtq R  LP WLG     + Ai    K
  gi|1176213   695 SRPSKRKPNGGVESLRAIPWIFAWTQNRLMLPAWLGAHKGLQQAIADGQK 744

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     +  L+Em ++WPFFR  l++lEmvF K D  +A  yD  Lv  eL+  G
  gi|1176213   745 GV--LEEMSRQWPFFRTRLEMLEMVFLKADVWLAEYYDTRLVPKELWGLG 792

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    k+LR++  +  + +L++    DlL+  P++K  ++LR++Y   Lnv+q
  gi|1176213   793 KQLRQELADSIQVVLELRPQGDLLDDQPWIKESIKLRNPYTDPLNVLQVE 842

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                              n +e   P L+  L
  gi|1176213   843 LLGRSR------------------------------NHAETLHPELDQAL 862

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|1176213   863 MVTIAGIAAGMRNTG    877

gi|262273438|ref|ZP_06051252.1|: domain 1 of 1, from 1 to 876: score 781.7, E = 5.1e-232
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  +  +L    vs           +l + L+  ++D HGe L
  gi|2622734     1    -MNEKYDALK-SNVS-----------MLGHLLgNTIKDAHGEALLAK 34

                    vqECYEl..sAeYEGKkDtkKLeELGakLtsLdPaDail.vAkailHmLn
                    v E   l++sA    K+D  KL ++   L    P D +l+vA+a++  Ln
  gi|2622734    35 VEEIRQLskSASAGNKEDHAKLIDVLQNL----PNDQLLpVARAFSQFLN 80
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                LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                L n+AE  +   R   ++          +  t  D+   + +L      s
gi|2622734    81 LTNIAEQYHSVSRHCAEQVC--------NPDTLDDL---FIRLKHAD-VS 118

                PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                 +E  +A+    ++LvltAHPt  +RR  + K   i  CL++L   D+
gi|2622734   119 DNERDNAVDDLKIELVLTAHPTEIARRTTIHKLVQINKCLSKLELGDLSS 168

                eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                 ++   +  L   i  A+  D iR+ +PtP DE + G + i   +W+ vP
gi|2622734   169 GERAKTELRLEQLIAQAWHSDVIRKQRPTPLDEAKWGYAVIENSLWQAVP 218

                KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                 FLR  D  +Kn  +   l  d+  i+ ssWmGGDRDG nP vt +vt +
gi|2622734   219 EFLRQFDQKMKN-HLGRGLGVDASPIQISSWMGGDRDG-NPFVTADVTHE 266

                vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                v LL+R  Aa lY+  + +L+ Elsm RCnd +R+ A +      ++
gi|2622734   267 VLLLSRWKAADLYLGDIQELISELSMTRCNDVVRAMAGD------QH--- 307

                KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                             EPYR iL   R  L nt       +    s+  E  +
gi|2622734   308 -------------EPYRAILKSLRQTLTNTLKYLDEKIHGRRSD--EKDI 342

                ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                 t++++   PL  CY+sL eCG  +iADG LLD LR + tFG+ L+KLDi
gi|2622734   343 LTHIDQLWTPLHACYQSLHECGMGIIADGLLLDTLRRIRTFGVNLIKLDI 392

                RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                RqEs R+ Dvl  +t+ L++G Y +WsE+ +q +L+ EL+ KRPLl+ D
gi|2622734   393 RQESTRHADVLSEVTRTLGMGDYSQWSEQDKQAFLIRELSSKRPLLPRDW 442

                PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                   +Ev++vld+ r++A  P ++ GaY+isma + sDvLAv LL +E g
gi|2622734   443 EPSDEVQEVLDTCRIVAQQPREALGAYVISMARTASDVLAVHLLLKEAGC 492

                kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsG
                   + v PLFE L DL+ A   +++L siDWY+  i+  q vm+GYsDs
gi|2622734   493 PFRMDVCPLFETLDDLNNAKSVIKQLLSIDWYRGFIQNFQMVMIGYSDSA 542

                KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                KDAG ++A W  YkA E ++      Gv LvlFHGRGG +GRGG P H A
gi|2622734   543 KDAGVMAAGWAQYKAMEQLVELCESAGVDLVLFHGRGGSIGRGGAPAHAA 592

                iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP
                +LsqPP  ++G lRvt qGE+i f  G  ++  +sL  ++ A LE  + P
gi|2622734   593 LLSQPPRSLKGGLRVTEQGEMIRFKLGLPDVAIQSLNLYASAILEANLLP 642

                PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmn
                P  Pk EWR+Lme +  v  E YR vv     Fv YFR AtPElE Gk+
gi|2622734   643 PPEPKQEWRDLMETLSEVSCEAYRDVVRGHKDFVPYFRAATPELELGKLP 692

                iGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                +GsRP+KR P GG+esLRAiPWiFaW q R  LP WLG G A ++ idK
gi|2622734   693 LGSRPSKRNPNGGVESLRAIPWIFAWSQNRLLLPAWLGAGQAIQFSIDKG 742

                iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP
                   l+ L+Em +eWPFF   l +lEmvF K  P i   yD+ Lv   L+
gi|2622734   743 H--LKSLEEMCREWPFFSTRLGMLEMVFTKTSPSISRYYDEKLVDPSLWT 790

                FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfq
                 Gk+LR +  E  + +L +     l+E  P+    +RLR+ Y+  Ln++q
gi|2622734   791 LGKELRKRLAEDIKAVLMVENNAHLMEQNPWGAESIRLRNIYVEPLNMLQ 840

                AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                A  L R R  +               E           n te     L++
gi|2622734   841 AELLCRTRATN---------------EG----------N-TE-----LDE 859

                tLiLtmKGiAAGmqntG<-*
                 L++t+ GiAAGm ntG
gi|2622734   860 ALMVTIAGIAAGMRNTG    876
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gi|77457296|ref|YP_346801.1|: domain 1 of 1, from 3 to 876: score 781.6, E = 5.3e-232
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      iDA LR      v           LL +     + D  Ge   + +
  gi|7745729     3    DIDARLRE----DVH----------LLGELLGNTIRDQYGEAFLDKI 35

                  qECYE.lsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                       +  A+  G  D+    EL a L  L   + + vA+a+   LnLAn
  gi|7745729    36 EQIRKgAKADRRGSMDA----ELSASLNQLSEDELLPVARAFNQFLNLAN 81

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiE.EtlKkLvlklnKsPe
                  +AE  +l +RR   +              Es + +E l +L   +  s e
  gi|7745729    82 IAEQYQLIHRREETQAA----------PFESRVLpELLARLRNEG-HSAE 120

                  EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                       L    ++LvltAHPt  +RR L+qK   i   La    +D+t  +
  gi|7745729   121 SLARQLARLEIELVLTAHPTEVARRTLIQKYDAIAAQLAAQDHRDLTTAE 170

                  KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                  ++ +   L R i  A+ t+EiRR++PtP DE + G + i   +W+ +P
  gi|7745729   171 REQIHNTLQRLIAEAWHTEEIRRTRPTPVDEAKWGFAVIEHSLWQAIPHH 220

                  LRRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                  +R+ D AL    G+  RlP ++  i+F+sWmGGDRDG nP vt  vtR+v
  gi|7745729   221 MRKADQALfAATGL--RLPLEAAPIRFASWMGGDRDG-NPNVTAAVTREV 267

                  CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                   LLaR mAa lY+  v+ L  Elsm    d L++RA +      +
  gi|7745729   268 LLLARWMAADLYLRDVDHLAAELSMQQASDALKARAGD------SA---- 307

                  yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                               EPYR +L + R++L  tR  a H   t     + + v
  gi|7745729   308 ------------EPYRAVLKQLRERLRATRNWA-HASLTATTPAPAD-VL 343

                  tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                   +  + L+PLELC+ sL eCG  viADG LLD LR   tFGL Lv+LD+R
  gi|7745729   344 HNNRDLLDPLELCFNSLHECGMGVIADGPLLDCLRRAVTFGLFLVRLDVR 393

                  qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                  q+s R+   +  it  L++G Y eW Ee+R  +L  EL+ +RPLl++
  gi|7745729   394 QDSSRHSAAMTEITDYLGLGKYEEWDEEQRISFLTRELQNRRPLLPAHFK 443

                  ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                     + ++vl + + +A  P  s G+Y+isma a sDvLAv LL +E gv
  gi|7745729   444 PSADTAEVLATCKEIAAAPGASLGSYVISMAGAASDVLAVQLLLKESGVL 493

                  qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                  +++rvvPLFE LADL+ A   +e+L  +  Y+ r++G qevm+GYsDs K
  gi|7745729   494 RPMRVVPLFETLADLDNAGPVIERLLLLPGYRARLQGPQEVMIGYSDSAK 543

                  DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                  DAG  +AAW  Y+AqE ++ + ++  v L lFHGRGGtvGRGGGP H Ai
  gi|7745729   544 DAGTTAAAWAQYRAQERLVEICREQQVELLLFHGRGGTVGRGGGPAHAAI 593

                  LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                  LsqPP  + G  R t qGE+i f FG  ++  + L  + AA LE  + PP
  gi|7745729   594 LSQPPGSVAGRFRTTEQGEMIRFKFGLPDIAEQNLNLYLAAVLEATLLPP 643

                  vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                    P PEWR+Lm+e+A      YR+vv   P FvEYFR  tPE E G++ +
  gi|7745729   644 PPPTPEWRHLMDELAADGVAAYRAVVRENPQFVEYFRQSTPEQELGRLPL 693

                  GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                  GsRPaKR+ +GGiesLRAiPWiF WtqtR  LP WLG   A   A+++
  gi|7745729   694 GSRPAKRR-AGGIESLRAIPWIFGWTQTRLMLPAWLGWETALSKALERGE 742

                  KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    l  L  m ++WPFFR  +D+lEmv AK D  iA  yD+ Lv  +L P
  gi|7745729   743 GEL--LGQMREQWPFFRTRIDMLEMVLAKADADIALSYDERLVEPDLLPL 790

                  GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
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                  G  LRd        +L + G   lL   P     +RLR+ Y+  L  +qA
  gi|7745729   791 GAHLRDLLSQACSVVLGLTGQSQLLAHSPDTLEFIRLRNTYLDPLHLLQA 840

                  YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                    L R R                            + n  e+ +P +E
  gi|7745729   841 ELLARSR----------------------------RQN-VEQGSP-VEQA 860

                  LiLtmKGiAAGmqntG<-*
                  L++ + GiAAG+ ntG
  gi|7745729   861 LLVSVAGIAAGLRNTG    876

gi|91227300|ref|ZP_01261725.1|: domain 1 of 1, from 1 to 877: score 781.4, E = 6.3e-232
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                  + e    ++    +l + L+  + D HGe++ E
  gi|9122730     1    -------------MNEKYAALKSNVRMLGHLLgNTIRDAHGEEIFEK 34

                  vqECYEl..sAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                  v     l++sA+   + D   L E    +  L       v +a+   LnL
  gi|9122730    35 VETIRKLskSAQAGNQADRDSLIE---EIKHLPDEQLTPVTRAFNQFLNL 81

                  AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                   n+AE  +   R   +         E +A     i   + kLv     s
  gi|9122730    82 TNIAEQYHTISRHCEEHIC------EPDA-----INSLFSKLVQND-VSK 119

                  eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                   +  +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+
  gi|9122730   120 LDTAQAVRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSSK 169

                  DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                  +++  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP
  gi|9122730   170 ERRKTERRLEQLIAQGWHSDVIRQQRPTPLDEAKWGFAVVENSLWEAVPD 219

                  FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                  FLR +   LK   + E lP d+  ++FssWmGGDRDG nP vt  vtR+v
  gi|9122730   220 FLREMNDRLKSY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHNVTREV 267

                  CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                   LL+R  Aa lY++ + +L+ Elsm   nd +R  A E +
  gi|9122730   268 LLLSRWKAADLYLNDINELISELSMTVSNDQVRELAGEDQH--------- 308

                  yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                             EPYR iL + R  L  t++     + +G   ++  A
  gi|9122730   309 ------------EPYRAILKQLRTLLNETKDILDAKI-HG-QKLAVKAPL 344

                  tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                   kvE+  EPL  CY+sL eCG  viA GsLLD LR v  FG+ Lv+LDiR
  gi|9122730   345 QKVEQLWEPLYACYQSLNECGMGVIANGSLLDTLRRVKAFGIHLVRLDIR 394

                  qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                  qEs R+ Dvl  +t+ L+iG Y +WsE+ +  +L  EL  KRPLl+ D
  gi|9122730   395 QESTRHSDVLSELTRYLGIGDYEQWSEQDKIAFLTNELASKRPLLPRDWE 444

                  ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                    E vk+vld+ +++A  P ++FGaY+isma + sDvLAv LL  E g
  gi|9122730   445 PSEPVKEVLDTCKIVAAQPREAFGAYVISMARTASDVLAVHLLLQEAGCP 494

                  qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                    + v PLFE L DL+ A   +++L  iD Y+  i+  q vm+GYsDs K
  gi|9122730   495 YRMDVCPLFETLDDLNNAESVIKQLMGIDLYRGFIQNHQMVMIGYSDSAK 544

                  DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                  DAG +sA W  Y A E ++KvA + Gv L+lFHGRGGtvGRGG P H A+
  gi|9122730   545 DAGVMSAGWAQYHAMESLVKVAEEEGVELTLFHGRGGTVGRGGAPAHAAL 594

                  LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                  LsqPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|9122730   595 LSQPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNLYASAILEANLLPP 644

                  vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                    Pk EWR+Lme +  v  E YR vv  EP Fv YFR AtPElE Gk+ +
  gi|9122730   645 PEPKQEWRDLMEVLSEVSCESYRNVVRGEPDFVPYFRQATPELELGKLPL 694
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                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ idK
  gi|9122730   695 GSRPAKRNPKGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSIDKGH 744

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    + l  L+Em +eWPFF   l +lEmv+ K    i   yD+ Lv E L+P
  gi|9122730   745 QAL--LEEMCREWPFFSTRLGMLEMVYSKCNIDISRYYDERLVDESLRPL 792

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G++LR++ +E  + +L +     l+  DP+    +RLR+ Y+  Ln++qA
  gi|9122730   793 GEKLRAQLQEDIKAVLNVENNENLMQHDPWGLESIRLRNIYVEPLNMLQA 842

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R                                 te+ +  LE+
  gi|9122730   843 ELLYRTRQ------------------------------TEEASANLEEA 861

                    LiLtmKGiAAGmqntG<-*
                    L++t+ GiAAGm ntG
  gi|9122730   862 LMVTIAGIAAGMRNTG    877

gi|71735722|ref|YP_276003.1|: domain 1 of 1, from 3 to 878: score 781.2, E = 7.2e-232
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        iDA LR      v           LL +     + +  G +  + +
  gi|7173572     3    DIDARLRE----DVH----------LLGELLGNTIREQRGAEFLDKI 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E     A    +  ++  e L a + +L   + + vA+a+   LnLAn+
  gi|7173572    36 -ERIRKGAKAGRRGSAEGAEQLSASVDGLGDDELLPVARAFNQFLNLANI 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiE.EtlKkLvlklnKsPeE
                    AE  +l +RR   +             Es + +E l +L   +  +P+
  gi|7173572    85 AEQYQLMHRRDDTQPL----------PFESRVLpELLDRLKTEG-HTPDA 123

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                        L    ++LvltAHPt  +RR L+qK   i   La L  +D+   ++
  gi|7173572   124 LARQLSKLEIELVLTAHPTEVARRTLIQKYDAIAAQLAALDHRDLNSTER 173

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L R i  A+ t+EiRR +PtP DE + G + i   +W+ +P +L
  gi|7173572   174 AQITSRLQRLIAEAWHTEEIRRIRPTPVDEAKWGFAVIEHSLWHAIPNYL 223

                    RRvDtALKni.GinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R+ D AL   +G+n  lP ++  i+F+sWmGGDRDG nP vt  vtR+v
  gi|7173572   224 RKADHALHAAtGLN--LPLEAAPIRFASWMGGDRDG-NPNVTAIVTREVL 270

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LLaR mAa lY+  v+ L  Elsm    d LR+R  +      +
  gi|7173572   271 LLARWMAADLYLRDVDNLAAELSMQQASDALRARVGD------SA----- 309

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR  L   R++L  tR  a   L   +   + eAv
  gi|7173572   310 -----------EPYRAELKRLRERLRATRNWANASLSETLP--APEAVLR 346

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  e L+PL LC++sL eCG  viADG LLD LR   tFGL Lv+LD+Rq
  gi|7173572   347 DNRELLDPLLLCFQSLHECGMGVIADGPLLDCLRRAVTFGLFLVRLDVRQ 396

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    +s R+   +  it  L++G Y eW E+ R ++Ll EL  +RPLl+
  gi|7173572   397 DSSRHCAAMTEITDYLGLGRYEEWDEQTRIDFLLRELNNRRPLLPGYFKP 446

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      + ++vl + rv+A  P  s G+Y+isma + sDvLAv LL +E g+++
  gi|7173572   447 AADTAEVLATCRVVAAAPTASLGSYVISMAGSASDVLAVQLLLKEAGLQR 496

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    ++rvvPLFE LADL+ A   +ekL  +  Y+ r+ G qevm+GYsDs KD
  gi|7173572   497 PMRVVPLFETLADLDNAGPVIEKLLGLPGYRSRLHGPQEVMIGYSDSAKD 546

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
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                    AG  +AAW  Y+AqE ++ + ++  v L lFHGRGGtvGRGGGP H AiL
  gi|7173572   547 AGTTAAAWAQYRAQEKLVEICREQQVELLLFHGRGGTVGRGGGPAHAAIL 596

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  + G  R t qGE+i f FG  ++  + L  + AA LE  + PP
  gi|7173572   597 SQPPGSVAGRFRTTEQGEMIRFKFGLPDIAEQNLNLYLAAVLEATLLPPP 646

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     P+P WR +m++mA      YR+vv   P FvEYFR AtPE E G++ +G
  gi|7173572   647 PPQPSWRTMMDQMAADGVGAYRAVVRENPEFVEYFRQATPEQELGRLPLG 696

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+  GG+esLRAiPWiFaWtqtR  LP WLG  AA   A+++
  gi|7173572   697 SRPAKRR-EGGVESLRAIPWIFAWTQTRLMLPAWLGWEAALSKALERGEG 745

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     +  L  m ++WPFFR  +D+lEmv AK D  iA LyD+ Lv+ eL+  G
  gi|7173572   746 TV--LAQMREQWPFFRTRIDMLEMVLAKADSDIARLYDERLVSAELQHLG 793

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                      LRd      + +L + G k lL   P     + LR+ Y+  L  +qA
  gi|7173572   794 AHLRDLLSQACNVVLGLTGQKQLLAHSPETLEFISLRNTYLDPLHLLQAE 843

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R            s+E   +                    LE  L
  gi|7173572   844 LLSRSR------------SREASLDS-----------------PLELAL 863

                    iLtmKGiAAGmqntG<-*
                    ++ + GiAAG+ ntG
  gi|7173572   864 LVSVAGIAAGLRNTG    878

gi|89075195|ref|ZP_01161626.1|: domain 1 of 1, from 1 to 876: score 780.8, E = 9.1e-232
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                  K s    L     +L       ++  HG++L + v
  gi|8907519     1    ---------MNEKYS---TLKSNVSMLGHLLGNTIKTAHGDELLDKV 35

                    qECYEl..sAeYEGKkDtkKLeELGakLtsLdPaDail.vAkailHmLnL
                         l++sA     +D  KL +    L  L P D +l+vA+a++  LnL
  gi|8907519    36 ETIRKLskSAHSGSEEDRAKLID---ELQNL-PDDQLLpVARAFSQFLNL 81

                    AnLAEEvelAyRRRikkkkhGDFaDEa.sAttEsDiEEtlKkLvlklnKs
                     n+AE  +   R     +   D  DE  +  t+ D        v +l
  gi|8907519    82 TNIAEQYHTISRQCETTLCSPDALDELfNKLTDND--------VNQL--- 120

                    PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                      +  eA++   +DLvltAHPt  +RR ++ K   i  CL+qL   ++
  gi|8907519   121 --DSIEAVRELNIDLVLTAHPTEIARRTMIHKLVQINKCLSQLELSELST 168

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                     ++  ++  L   i  A+  D iR  +PtP DE + G + i   +W+ vP
  gi|8907519   169 SERARIEQRLEQLIAQAWHSDVIRQQRPTPIDEAKWGYAVIENSLWQAVP 218

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                     FLR  D  L+   + E lP d+  + FssWmGGDRDG nP vt  vtR+
  gi|8907519   219 EFLRLFDEKLQQ-HLGEALPLDASPVTFSSWMGGDRDG-NPFVTSNVTRE 266

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                    v  L+R  Aa lY++ + +L+ Elsm  Cn+ +R  A E       +
  gi|8907519   267 VLALSRWKAADLYLNDIQELINELSMTQCNETVRELAGE-------E--- 306

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                                EPYR iL + R KL  tR+     + +G    s + v
  gi|8907519   307 ------------HEPYRAILKQLRTKLVHTRDNLDAKI-HGQKPAS-DIV 342

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                      ++ e   PL  CY+sL eCG  +iADG LLD LR v  FG+ Lv+LDi
  gi|8907519   343 IEDIAELWGPLHACYQSLHECGMAIIADGLLLDTLRRVKCFGVHLVRLDI 392

                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    RqEs R+ Dv+  +t+ L++G Y +WsE+ +  +L+ EL+ KRPLl+ D
  gi|8907519   393 RQESTRHSDVISELTRYLGLGDYDQWSEQDKIAFLVRELSSKRPLLPRDW 442
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                    PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                        Evk+v+++ + +AE   ++ G+Y+isma + sDvLAv LL  E g
  gi|8907519   443 EPSAEVKEVIETCKTIAEQSREALGSYVISMARTASDVLAVHLLLQEAGC 492

                    kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsG
                       + v PLFE L DL+     +e+L  iDWY+  i+  q vm+GYsDs
  gi|8907519   493 PFRMDVCPLFETLDDLNNGADVIEQLLNIDWYRGFIQNHQMVMIGYSDSA 542

                    KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                    KDAG +sA W  Y A E ++ v  + Gv ++lFHGRGG +GRGG P H A
  gi|8907519   543 KDAGVMSAGWAQYSAMEKLVDVCEQAGVEITLFHGRGGSIGRGGAPAHAA 592

                    iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP
                    +LsqPP  ++G lRvt qGE+i f  G  ++   sL  ++ AtLE  + P
  gi|8907519   593 LLSQPPRSLKGGLRVTEQGEMIRFKLGLPEVAINSLSLYASATLEANLLP 642

                    PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmn
                    P +Pk EWR+Lm+ +  v  E YR vv  +P Fv YFR AtPElE Gk+
  gi|8907519   643 PPAPKQEWRELMDVLSEVSCEAYRNVVRVDPEFVPYFRAATPELELGKLP 692

                    iGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                    +GsRPaKR P GG+esLRAiPWiFaW q R  LP WLG G A ++ i+K
  gi|8907519   693 LGSRPAKRNPQGGVESLRAIPWIFAWSQNRLLLPAWLGAGEAIQYSINKG 742

                    iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP
                       l  L++m +eWPFF   l +lEmv+ K   GiA  yD+ L  E L+P
  gi|8907519   743 HAKL--LEDMCREWPFFSTRLGMLEMVYTKTNTGIAKYYDERLTDESLWP 790

                    FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfq
                     G++LRd+     + +L +     l+E DP+    +RLR+ Y+  Ln++q
  gi|8907519   791 LGQKLRDQLGKDIKAVLTVENNDHLMEQDPWGAESIRLRNIYVEPLNMLQ 840

                    AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                    A  L R R                                 e+ +  LE+
  gi|8907519   841 AELLYRTRQ------------------------------QEELPSALEE 859

                    tLiLtmKGiAAGmqntG<-*
                     L++t+ GiA Gm ntG
  gi|8907519   860 ALMVTIAGIATGMRNTG    876

gi|253690426|ref|YP_003019616.1|: domain 1 of 1, from 1 to 879: score 780.7, E = 1e-231
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  ++    vs           +l k L+D +++  Ge++ +
  gi|2536904     1    -MNEQYSAMR-SNVS-----------MLGKLLgDTIKEALGENILDK 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       + ++ +EL + L  L   + + vA+a++  LnL n
  gi|2536904    35 VETIRKLSKSSRAGNEKHR-QELLTTLQNLSNDELLPVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +           hG+      A   + +   + +L    + +  +
  gi|2536904    84 TAEQYH-------TISPHGE-----AASNPAQLSSAFERLKESKDLTERD 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + +A+   s++LvltAHPt   RR L+ K   +  CL qL   D+   ++
  gi|2536904   122 IRDAVESLSIELVLTAHPTEITRRTLIHKLVEVNTCLKQLDHNDLADYER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L   i   + tDEiR+ +PtP DE + G + +   +W+GvP FL
  gi|2536904   172 NQIMRRLRQLIAQSWHTDEIRKIRPTPVDEAKWGFAVVENSLWEGVPAFL 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R  D  L       RlP d+  ++F+sWmGGDRDG nP vt EvtR v L
  gi|2536904   222 RELDEQLEQ-AFGYRLPVDAVPVRFTSWMGGDRDG-NPNVTAEVTRHVLL 269

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa l++  +  L+ Elsm  C  EL     El   +  +
  gi|2536904   270 LSRWKAADLFLRDIQVLVSELSMSECTPELL----ELAGGSEVQ------ 309

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
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                          EPYR i+   R +L  t       L tG   ++
  gi|2536904   310 ----------EPYRAIMKSLRSQLSSTLSYLEARL-TGEERLPPKDLLIT 348

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    E+  EPL  CY+sL  CG  +iADG LLD LR v  FG+ Lv++D+RqE
  gi|2536904   349 NEQLWEPLHACYQSLKSCGMGIIADGRLLDTLRRVRCFGVPLVRIDVRQE 398

                   seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                   s R+t+ l  it+ L++G Y +WsE  +q +L+ EL+ KRPLl+
  gi|2536904   399 STRHTEALAEITRYLGLGDYESWSESDKQAFLIRELSSKRPLLPRYWEPS 448

                   EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    + k+vld+ rv+A  P  s  aY+isma +PsDvLAv LL +E g   +
  gi|2536904   449 ADTKEVLDTCRVIAKAPQGSIAAYVISMARTPSDVLAVHLLLKEAGCSFA 498

                   LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                   L+v PLFE L DL+ A   + +L siDWY+  i+GKq vm+GYsDs KDA
  gi|2536904   499 LPVAPLFETLDDLNNADDVMTQLLSIDWYRGFIQGKQMVMIGYSDSAKDA 548

                   GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                   G ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Ls
  gi|2536904   549 GVMAASWAQYRAQDALIKTCEKAGIALTLFHGRGGSIGRGGAPAHAALLS 598

                   qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                   qPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2536904   599 QPPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLALYTGAILEANLLPPPE 648

                   PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                   Pk EW ++m+e+  v  + YR  v   P Fv YFR AtPElE Gk+ +Gs
  gi|2536904   649 PKQEWHEVMDELSRVSCDMYRGYVRENPDFVPYFRAATPELELGKLPLGS 698

                   RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                   RPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA +  +d D K
  gi|2536904   699 RPAKRRPNGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQKVVD-DGKQ 747

                   lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    q L+Em ++WPFF   + +lEmvFAK D  +A  yD+ Lv E L+P Gk
  gi|2536904   748 EQ-LEEMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVDEKLWPLGK 796

                   sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                   +LRd+     +++L i     l+   P++   + LR+ Y   Lnv+qA
  gi|2536904   797 QLRDQLAADINIVLAISNDDHLMADLPWIAESIALRNVYTDPLNVLQAEL 846

                   LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                   L R R                 +E    +d  ++L             L+
  gi|2536904   847 LHRSRQ----------------QEK---PDADLELA------------LM 865

                   LtmKGiAAGmqntG<-*
                   +t+ G+AAGm ntG
  gi|2536904   866 VTIAGVAAGMRNTG    879

gi|28807771|dbj|BAC61024.1|: domain 1 of 1, from 3 to 888: score 780.4, E = 1.2e-231
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +    R     K +     ++    +l + L+  + D HGe++ E
  gi|2880777     3    VVFLRGRTTMNEKYA----ALKSNVRMLGHLLgNTIRDAHGEEIFEK 45

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls        + + e L   +  L       v +a+   LnL n
  gi|2880777    46 VETIRKLSKSAQAGNQADR-ESLIEEIKHLPDEQLTPVTRAFNQFLNLTN 94

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +   R   +         E +A     i   + kLv     s  +
  gi|2880777    95 IAEQYHTISRHCEEHIC------EPDA-----INSLFSKLVQND-VSKLD 132

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+   ++
  gi|2880777   133 TAQAVRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSSKER 182

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   k  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
  gi|2880777   183 KKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWEAVPDFL 232
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                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R +   LK   + E lP d+  ++FssWmGGDRDG nP vt  vtR+v L
  gi|2880777   233 REMNDRLKSY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHSVTREVLL 280

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa lY++ + +L+ Elsm   nd +R  A E +
  gi|2880777   281 LSRWKAADLYLNDINELISELSMTVSNDQVRELAGEDQH----------- 319

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR iL + R  L  t++     + +G   ++  A   k
  gi|2880777   320 ----------EPYRAILKQLRALLNETKDILDAKI-HG-QKLAVKAPLQK 357

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    vE+  +PL  CY+sL eCG  viADGsLLD LR v  FG+ Lv+LDiRqE
  gi|2880777   358 VEQLWDPLYACYQSLHECGMGVIADGSLLDTLRRVKAFGVHLVRLDIRQE 407

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+ Dvl  +t+ L+iG Y +WsE+ +  +L  EL  KRPLl+ D
  gi|2880777   408 STRHADVLSELTRYLGIGDYEQWSEQDKIAFLTNELASKRPLLPRDWEPS 457

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    E vk+vld+ +++A  P ++FGaY+isma + sDvLAv LL  E g
  gi|2880777   458 EPVKEVLDTCKIIALQPREAFGAYVISMARTASDVLAVHLLLQEAGCPYR 507

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    + v PLFE L DL+ A   +++L siD Y+  i+  q vm+GYsDs KDA
  gi|2880777   508 MDVCPLFETLDDLNNAESVIKQLMSIDLYRGFIQNHQMVMIGYSDSAKDA 557

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G +sA W  Y A E ++KvA + Gv L+lFHGRGGtvGRGG P H A+Ls
  gi|2880777   558 GVMSAGWAQYHAMESLVKVAEDEGVELTLFHGRGGTVGRGGAPAHAALLS 607

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|2880777   608 QPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNLYASAILEANLLPPPE 657

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EWR+Lme +  v  E YR vv  EP Fv YFR AtPElE Gk+ +Gs
  gi|2880777   658 PKQEWRDLMEVLSEVSCEAYRGVVRGEPDFVPYFRQATPELELGKLPLGS 707

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ +dK  +
  gi|2880777   708 RPAKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSVDKGHQA 757

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l  L+Em +eWPFF   l +lEmv+ K    i   yD+ Lv  +L+P G+
  gi|2880777   758 L--LEEMCREWPFFSTRLGMLEMVYTKCNMEISRYYDQRLVEPQLQPLGD 805

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR++ +   + +L +     l+  DP+ +  +RLR+ Y+  Ln++qA
  gi|2880777   806 RLREQLQRDIKSVLNVENNENLMQSDPWGQESIRLRNIYVEPLNMLQAEL 855

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                                 te+ +  LE+ L+
  gi|2880777   856 LYRTRQ------------------------------TEEASANLEEALM 874

                    LtmKGiAAGmqntG<-*
                    +t+ GiAAGm ntG
  gi|2880777   875 VTIAGIAAGMRNTG    888

gi|70728529|ref|YP_258278.1|: domain 1 of 1, from 3 to 876: score 779.7, E = 2e-231
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        iDA LR      v           LL +     + D  Ge   + +
  gi|7072852     3    DIDARLRE----DVH----------LLGELLGNTIRDQYGEAFLDKI 35

                    qECYE.lsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                         +  A+  G    +   EL a L  L   + + vA+a+   LnLAn
  gi|7072852    36 EQIRKgAKADRRG----SPGAELSASLDQLSEDELLPVARAFNQFLNLAN 81

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
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                +AE  +l +RR  ++        Ea       + E l +L   +  s +
gi|7072852    82 IAEQYQLIHRRDESQPA----PFEARV-----LPELLARLRAEG-HSADA 121

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    L    ++LvltAHPt  +RR L+qK   i   La    +D+t  ++
gi|7072852   122 LARQLGRLEIELVLTAHPTEVARRTLIQKYDAIAGQLAAQDHRDLTSAER 171

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  + E L R i  A+ t+EiRR++PtP DE + G + i   +W+ +P +L
gi|7072852   172 GQIQERLQRLIAEAWHTEEIRRTRPTPVDEAKWGFAVIEHSLWQAIPNYL 221

                RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                R+ D AL    G+   lP +   i+F+sWmGGDRDG nP vt  vtR+v
gi|7072852   222 RKADKALfEATGL--HLPLESAPIRFASWMGGDRDG-NPNVTAAVTREVL 268

                LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                LLaR mAa lY+  ++ L  Elsm      L +RA +      +
gi|7072852   269 LLARWMAADLYLRDIDHLAAELSMQQASPALLARAGD------SA----- 307

                YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                           EPYR +L + R++L  tR  a   L   +   +E  v
gi|7072852   308 -----------EPYRALLKQLRERLRATRNWAHAALSAAVPAGAE--VLH 344

                kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                +  + LEPL LCY+sL eCG  viADG LLD LR   tFGL Lv+LD+Rq
gi|7072852   345 NNRDLLEPLQLCYQSLHECGMGVIADGPLLDCLRRAVTFGLFLVRLDVRQ 394

                EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                +s R+t  +  it  L++G Y +WsEe R  +L+ EL+ +RPLl+
gi|7072852   395 DSSRHTSAMTEITDYLGLGRYEDWSEEDRITFLMRELSSRRPLLPGYFKP 444

                tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                  + ++vl + r +A  P  s G+Y+isma a sDvLAv LL +E gv +
gi|7072852   445 SADTAEVLATCREIAGAPAASLGSYVISMAGAASDVLAVQLLLKESGVLR 494

                tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                ++rvvPLFE LADL+ A   +ekL  +  Y+ r++G qevm+GYsDs KD
gi|7072852   495 PMRVVPLFETLADLDNAGPVMEKLLHMPGYRSRLQGPQEVMIGYSDSAKD 544

                AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                AG  +AAW  Y+AqE ++ + ++  v L lFHGRGGtvGRGGGP H AiL
gi|7072852   545 AGTTAAAWAQYRAQERLVDICREQQVELLLFHGRGGTVGRGGGPAHAAIL 594

                sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                sqPP  + G  R t qGE+i f FG  ++  + L  + AA LE  + PP
gi|7072852   595 SQPPGSVAGRFRTTEQGEMIRFKFGLPDIAEQNLNLYLAAVLEATLLPPP 644

                sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                 P+P WR+Lm+e+A      YR vv   P FvEYFR  tPE E G++ +G
gi|7072852   645 PPQPAWRHLMDELASDGVRAYREVVRDNPQFVEYFRQSTPEQELGRLPLG 694

                sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                sRPaKR+ +GGiesLRAiPWiF WtqtR  LP WLG  AA   A+ +
gi|7072852   695 SRPAKRR-AGGIESLRAIPWIFGWTQTRLMLPAWLGWEAALSKALARGEG 743

                nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                 l  L  m ++WPFFR  +D+lEmv AK D  iA  yD+ Lv  eL P G
gi|7072852   744 DL--LGQMREQWPFFRTRIDMLEMVLAKADADIARSYDERLVEAELLPLG 791

                ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                + LRd        +L + G   lL   P     +RLR+ Y+  L  +qA
gi|7072852   792 EHLRDLLSQACAVVLGLTGQSQLLAHSPDTLEFIRLRNTYLDPLHLLQAE 841

                tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                 L R R             K  A                   +P +E  L
gi|7072852   842 LLARSR-------------KQQAPQG----------------SP-VEQAL 861

                iLtmKGiAAGmqntG<-*
                ++ + GiAAG+ ntG
gi|7072852   862 LVSVAGIAAGLRNTG    876
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gi|242237649|ref|YP_002985830.1|: domain 1 of 1, from 1 to 880: score 778.7, E = 4e-231
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                 K s     ++    +l k L+D ++D  Ge++ +
  gi|2422376     1    ---------MNEKYS----AMRSNVSMLGKLLgDTIKDALGENILDR 34

                  vqECYEls.AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                  v     ls+A   G +  k  +EL + L  L   + + vA+a++  LnL
  gi|2422376    35 VETIRKLSkASRAGSE--KHRQELLTTLQNLSNDELLPVARAFSQFLNLT 82

                  nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                  n AE  +       +   hG+      A     + + ++ L ++ n s
  gi|2422376    83 NTAEQYH-------SISPHGE-----AAGNPGMLADAFRSLKSRDNLSDS 120

                  EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                   + eA+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   +
  gi|2422376   121 AIREAVESLSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHNDLADYE 170

                  KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                  ++ +   L   i   + tDEiRR +PtP DE R G + +   +W+GvP F
  gi|2422376   171 RHQIMRRLRQLIAQYWHTDEIRRDRPTPVDEARWGFAVVENSLWDGVPAF 220

                  LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                  LR  D  L n     RlP +   ++F+sWmGGDRDG nP vt E+tR v
  gi|2422376   221 LRELDEQLEN-AFGFRLPVESVPVRFTSWMGGDRDG-NPNVTSEITRHVL 268

                  LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                  LL+R  Aa l++  +  L+ Elsm  C    R            +
  gi|2422376   269 LLSRWKAADLFLRDIQVLVSELSMTQCTPAFR----QWLGCGEEE----- 309

                  YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAt..GiseisEeAv
                            +EPYRv++   R +L   RE    L A+ +G +  +
  gi|2422376   310 ----------QEPYRVVMKHLRAQL---RETLTYLTAQvkGEAAAPPKDL 346

                  ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                   t+  +  EPL  CY+sL  CG  +iADG LLD LR v  FG+ Lv++D+
  gi|2422376   347 ITHNQQLWEPLYACYQSLHACGMGIIADGQLLDTLRRVRCFGVPLVRIDV 396

                  RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                  RqEs R+t+ +  it+ L++G Y +WsE  +q +L+ EL  KRPLl+
  gi|2422376   397 RQESTRHTEAIAEITRYLGLGDYENWSESDKQAFLIRELNSKRPLLPRQW 446

                  PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                      E ++vl++ +v+AE P D+  +Y+isma +PsDvLAv LL +E g
  gi|2422376   447 EPSAETREVLETCQVIAETPRDAIASYVISMARTPSDVLAVHLLLKEAGC 496

                  kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsG
                    +L+v PLFE L DL+ A   + +L  iDWY+  i+G+q vm+GYsDs
  gi|2422376   497 PYALPVAPLFETLDDLNNADSVMTQLLNIDWYRGFIQGRQMVMIGYSDSA 546

                  KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                  KDAG ++A W  Y+Aq+ +iK   k+G+ L+lFHGRGG +GRGG P H A
  gi|2422376   547 KDAGVMAASWAQYRAQDALIKTCDKFGIALTLFHGRGGSIGRGGAPAHAA 596

                  iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP
                  +LsqPP  ++G lRvt qGE+i f FG  ++   sL  +t A LE  + P
  gi|2422376   597 LLSQPPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLSLYTSAILEANLLP 646

                  PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmn
                  P  Pk EW ++m+e+  +  + YR  v   P Fv YFR AtPElE Gk+
  gi|2422376   647 PPEPKQEWHHIMDELSRISCDMYRGYVRENPGFVPYFRAATPELELGKLP 696

                  iGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                  +GsRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA +  id
  gi|2422376   697 LGSRPAKRRPNGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQKVIDDG 746

                  iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP
                   +   +L+ m ++WPFF   + +lEmvFAK D  +A  yD+ Lv E L+P
  gi|2422376   747 HQD--QLETMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVDETLWP 794

                  FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfq
                   G++LR++ +   + +L i     l+   P++   + LR+ Y   Lnv+q
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  gi|2422376   795 LGQQLREQLEKDIKAVLTISNDDHLMADLPWIAESIALRNVYTDPLNVLQ 844

                   AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                   A  L R R                ++          L       P +E
  gi|2422376   845 AELLHRSRQ----------------QDT---------LD------PQVEQ 863

                   tLiLtmKGiAAGmqntG<-*
                    L++t+ G+AAGm ntG
  gi|2422376   864 ALMVTIAGVAAGMRNTG    880

gi|227327296|ref|ZP_03831320.1|: domain 1 of 1, from 1 to 879: score 778.5, E = 4.6e-231
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  q  ++    vs           +l k L+D +++  Ge++ +
  gi|2273272     1    -MNEQYSAMR-SNVS-----------MLGKLLgDTIKEALGENILDK 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls       + ++ +EL + L  L   + + vA+a++  LnL n
  gi|2273272    35 VETIRKLSKSSRAGNEKHR-QELLTTLQNLSNDELLPVARAFSQFLNLTN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    AE  +           hG+      A   + +   + +L    + +  +
  gi|2273272    84 TAEQYH-------TISPHGE-----AASNPAQLSHAFERLKESKDLTERD 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   + +A+   s++LvltAHPt   RR L+ K   +  CL qL   D+   ++
  gi|2273272   122 IRDAVESLSIELVLTAHPTEITRRTLIHKLVEVNTCLKQLDHNDLADYER 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     +   L   i   + tDEiR+ +PtP DE + G + +   +W+GvP FL
  gi|2273272   172 NQIMRRLRQLIAQSWHTDEIRKIRPTPVDEAKWGFAVVENSLWEGVPAFL 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   R  D  L       RlP d+  ++F+sWmGGDRDG nP vt EvtR v L
  gi|2273272   222 RELDEQLEQ-AFGYRLPVDAVPVRFTSWMGGDRDG-NPNVTAEVTRHVLL 269

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   L+R  Aa l++  +  L+ Elsm  C  EL     El   +  +
  gi|2273272   270 LSRWKAADLFLRDIQVLVSELSMSECTPELL----ELAGGSEVQ------ 309

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                            EPYR i+   R +L  t       L tG   ++
  gi|2273272   310 ----------EPYRAIMKSLRSQLSSTLSYLEARL-TGEERLPPKDLLIT 348

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    E+  EPL  CY+sL  CG  +iADG LLD LR v  FG+ Lv++D+RqE
  gi|2273272   349 NEQLWEPLHACYQSLKTCGMGIIADGRLLDTLRRVRCFGVPLVRIDVRQE 398

                   seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                   s R+t+ l  it+ L++G Y +WsE  +q +L+ EL+ KRPLl+
  gi|2273272   399 STRHTEALAEITRYLGLGDYESWSESDKQAFLIRELSSKRPLLPRYWEPS 448

                   EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    + k+vld+ rv+A  Pi s  aY+isma +PsDvLAv LL +E g   +
  gi|2273272   449 ADTKEVLDTCRVVAKAPIGSVAAYVISMARTPSDVLAVHLLLKEAGCPFA 498

                   LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                   L+v PLFE L DL+ A   + +L siDWY+  i+GKq vm+GYsDs KDA
  gi|2273272   499 LPVAPLFETLDDLNNADDVMTQLLSIDWYRGFIQGKQMVMIGYSDSAKDA 548

                   GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                   G ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Ls
  gi|2273272   549 GVMAASWAQYRAQDALIKTCEKAGIALTLFHGRGGSIGRGGAPAHAALLS 598

                   qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                   qPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2273272   599 QPPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLALYTGAILEANLLPPPE 648

                   PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                   Pk EW ++m+++  v  E YR  v   P Fv YFR AtPElE Gk+ +Gs
  gi|2273272   649 PKQEWHEVMDDLSRVSCEMYRGYVRENPDFVPYFRAATPELELGKLPLGS 698
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                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA +  +d D K
  gi|2273272   699 RPAKRRPNGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQKVVD-DGKQ 747

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                     q L+ m ++WPFF   + +lEmvFAK D  +A  yD+ Lv E L+P Gk
  gi|2273272   748 EQ-LEAMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVEEKLWPLGK 796

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LRd+     + +L i     l+   P++   + LR+ Y   Lnv+qA
  gi|2273272   797 QLRDQLAADINVVLAISNDDHLMADLPWIAESIALRNVYTDPLNVLQAEL 846

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                +E+   +d  ++L             L+
  gi|2273272   847 LHRSRQ----------------QEQ---PDADLELA------------LM 865

                    LtmKGiAAGmqntG<-*
                    +t+ G+AAGm ntG
  gi|2273272   866 VTIAGVAAGMRNTG    879

gi|163802795|ref|ZP_02196685.1|: domain 1 of 1, from 1 to 877: score 778.4, E = 5e-231
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                + e    ++    +l + L+  + D HGe++ E
  gi|1638027     1    -------------MNEKYAALKSNVRMLGHLLgNTIRDAHGEEIFEK 34

                    vqECYEl..sAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    v     l++sA+   + D + L E    + sL       v +a+   LnL
  gi|1638027    35 VETIRKLskSAQAGNRADRESLIE---EIKSLPGEQLTPVTRAFNQFLNL 81

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                     n+AE  +   R   +         E +A     i   + kL      s
  gi|1638027    82 TNIAEQYHTISRHCEEHIC------EPDA-----INSLFAKLEQND-VSK 119

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                     E  +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+
  gi|1638027   120 LETAQAIRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSFK 169

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++k  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP
  gi|1638027   170 ERKKTERRLEQLIVQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWEAVPD 219

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    FLR +   LK   + E lP d+  ++FssWmGGDRDG nP vt  vtR+v
  gi|1638027   220 FLREMNDRLKSY-LGEDLPIDARPVHFSSWMGGDRDG-NPFVTHSVTREV 267

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                     LL+R  Aa lY++ + +L+ Elsm  Cnd +R  A E +
  gi|1638027   268 LLLSRWKAADLYLNDINELISELSMTVCNDKVRELAGEDQH--------- 308

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                                EPYR iL + R  L  t++       +G   ++  A
  gi|1638027   309 ------------EPYRAILKQLRSLLSETKD-ILDAKVHG-QKLAVKAPL 344

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     kvE+  EPL  CY+sL eCG  viA GsLLD LR v  FG+ Lv+LDiR
  gi|1638027   345 QKVEQLWEPLYACYQSLNECGMGVIANGSLLDTLRRVKAFGIHLVRLDIR 394

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+ Dvl  +t+ L+iG Y +WsE+ +  +L  EL  KRPll+ D
  gi|1638027   395 QESTRHADVLSELTRYLGIGDYEQWSEQDKIAFLTNELASKRPLLPRDWE 444

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                      E vk+vld+ +++A  P ++FGaY+isma + sDvLAv LL  E g
  gi|1638027   445 PSEPVKEVLDTCKIVAAQPREAFGAYVISMARTASDVLAVHLLLQEAGCP 494

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                      + v PLFE L DL+ A A +++L  iD Y+  i+  q vm+GYsDs K
  gi|1638027   495 YRMDVCPLFETLDDLNNAEAVIKQLMGIDLYRGFIQNHQMVMIGYSDSAK 544

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG +sA W  Y A + ++ vA + Gv L+lFHGRGGt+GRGG P H A+
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  gi|1638027   545 DAGVMSAGWAQYHAMDSLVNVAEEEGVELTLFHGRGGTIGRGGAPAHAAL 594

                   LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                   LsqPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|1638027   595 LSQPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNLYASAILEANLLPP 644

                   vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                     Pk EWR+Lm+ +  v  E YRs+v  EP Fv YFR AtPElE Gk+ +
  gi|1638027   645 PEPKQEWRDLMDVLSEVSCEAYRSIVRGEPDFVPYFRQATPELELGKLPL 694

                   GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                   GsRPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ +dK
  gi|1638027   695 GSRPAKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSVDKGH 744

                   KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                   + l  L+Em +eWPFF   l +lEmv+ K    i   yD+ Lv ++L+P
  gi|1638027   745 QAL--LEEMCREWPFFSTRLGMLEMVYTKCNMEISHYYDQRLVDDQLQPL 792

                   GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                   G++LR + +   + +L +     l+  DP+    +RLR+ Y+  Ln++qA
  gi|1638027   793 GDRLRKQLQQDIKSVLNVENNENLMQSDPWGLESIRLRNTYVEPLNMLQA 842

                   YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                     L R R                                 te+ +  LE+
  gi|1638027   843 ELLYRTRQ-------------------------------TEEASANLEEA 861

                   LiLtmKGiAAGmqntG<-*
                   L++t+ GiAAGm ntG
  gi|1638027   862 LMVTIAGIAAGMRNTG    877

gi|260779573|ref|ZP_05888463.1|: domain 1 of 1, from 1 to 877: score 777.9, E = 6.9e-231
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  +  +L    vs           +l + L+  ++D HG+ L E
  gi|2607795     1    -MNEKYSALR-SNVS-----------MLGHLLgNTIKDAHGDALLEK 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls        + + e L   + sL       vA+a+   LnL n
  gi|2607795    35 VETIRKLSKSALSGNQSDR-ESLIEEIKSLPDEQLTPVAHAFNQFLNLTN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +   R             E +A     i   + kL      s  +
  gi|2607795    84 MAEQYHTISRHCDAHVC------EPDA-----INNLFSKLSQND-ISKLD 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+   ++
  gi|2607795   122 TAQAVRALNIELVLTAHPTEITRRTMINKLVKINKCLSKLELNDLSAKER 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   +  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
  gi|2607795   172 QKTERRLEQLIAQGWHSDTIRQQRPTPLDEAKWGFAVVENSLWEAVPDFL 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   R  D  L+   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
  gi|2607795   222 RELDGRLRGY-LEEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITREVML 269

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   L+R  Aa lY++ + +L+ Elsm RCnd +R  A E       d
  gi|2607795   270 LSRWKAADLYLNDINELVSELSMTRCNDAVRSLAGE-------D------ 306

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi..seisEeAvy
                             EPYR +L + R  L  t+E    +L   +++  ++  A
  gi|2607795   307 --------EHEPYRAVLKQLRALLTETKE----ILDAKVngQKLAVKAPL 344

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     vE+  EPL  CY+sL eCG  +iADGsLLD LR +  FG+ Lv+LDiR
  gi|2607795   345 QCVEQLWEPLYACYQSLHECGMGIIADGSLLDTLRRIKAFGVHLVRLDIR 394

                   qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                   qEs R+ D l  +t+ L+iG Y +WsE+ +  +L  EL  KRPLl+ D
  gi|2607795   395 QESTRHSDALSELTRYLGIGDYNQWSEQDKIAFLTNELASKRPLLPRDWQ 444
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                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                      E v++vld+ +++A  P ++FGaY+isma + sDvLAv LL  E g
  gi|2607795   445 PSEQVQEVLDTCKIVAAQPREAFGAYVISMARTASDVLAVHLLLQEAGCP 494

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                      + v PLFE L DL+ A   +++L  iD Y+  i+  q vm+GYsDs K
  gi|2607795   495 YRMDVCPLFETLDDLNNAESVIKQLMGIDLYRGFIQNHQMVMIGYSDSAK 544

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG +sA W  Y A E ++KvA + Gv L+lFHGRGGt+GRGG P H A+
  gi|2607795   545 DAGVMSAGWAQYHAMEALVKVAEEEGVELTLFHGRGGTIGRGGAPAHAAL 594

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|2607795   595 LSQPPKSLKGGLRVTEQGEMIRFKLGLPEVAVNSFNLYASAILEANLLPP 644

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      Pk EWR+Lm+ +  v  E YRsvv  EP Fv YFR AtPElE Gk+ +
  gi|2607795   645 PEPKQEWRDLMNVLSEVSCEAYRSVVRGEPDFVPYFRQATPELELGKLPL 694

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ idK
  gi|2607795   695 GSRPAKRNPKGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSIDKGH 744

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    + l  L+Em +eWPFF   l +lEmv+ K    i   yD+ L    L P
  gi|2607795   745 QAL--LEEMCREWPFFSTRLGMLEMVYTKCNLEISRYYDERLADPKLLPL 792

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G++LR++ +   + +L +     l+  DP+ +  +RLR+ Y+  Ln++qA
  gi|2607795   793 GDKLRAQLQQDIKAVLNVENNENLMQSDPWGQESIRLRNIYVEPLNMLQA 842

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R                                 ++  +P LE+
  gi|2607795   843 ELLYRTRQ------------------------------SDAASPELEEA 861

                    LiLtmKGiAAGmqntG<-*
                    L++t+ GiAAGm ntG
  gi|2607795   862 LMVTIAGIAAGMRNTG    877

gi|227114312|ref|ZP_03827968.1|: domain 1 of 1, from 1 to 879: score 777.8, E = 7.7e-231
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  ++    vs           +l k L+D +++  Ge++ +
  gi|2271143     1    -MNEQYSAMR-SNVS-----------MLGKLLgDTIKEALGENILDK 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       + ++ +EL + L  L   + + vA+a++  LnL n
  gi|2271143    35 VETIRKLSKSSRAGNEKHR-QELLTTLQNLSNDELLPVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +           hG+      A   + +   + +L    + +  +
  gi|2271143    84 TAEQYH-------TISPHGE-----AASNPAQLSHAFERLKESKDLTERD 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + +A+   s++LvltAHPt   RR L+ K   +  CL qL   D+   ++
  gi|2271143   122 IRDAVESLSIELVLTAHPTEITRRTLIHKLVEVNTCLKQLDHNDLADYER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L   i   + tDEiR+ +PtP DE + G + +   +W+GvP FL
  gi|2271143   172 NQIMRRLRQLIAQSWHTDEIRKIRPTPVDEAKWGFAVVENSLWEGVPAFL 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R  D  L       RlP d+  ++F+sWmGGDRDG nP vt EvtR v L
  gi|2271143   222 RELDEQLEQ-AFGYRLPVDAVPVRFTSWMGGDRDG-NPNVTAEVTRHVLL 269

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa l++  +  L+ Elsm  C  EL     El   +  +
  gi|2271143   270 LSRWKAADLFLRDIQVLVSELSMSECTPELL----ELAGGSEVQ------ 309

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR i+   R +L  t       L tG   ++
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  gi|2271143   310 ----------EPYRAIMKSLRSQLSSTLSYLEARL-TGEERLPPKDLLIT 348

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     E+  EPL  CY+sL  CG  +iADG LLD LR v  FG+ Lv++D+RqE
  gi|2271143   349 NEQLWEPLHACYQSLKTCGMGIIADGRLLDTLRRVRCFGVPLVRIDVRQE 398

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+t+ l  it+ L++G Y +WsE  +q +L+ EL+ KRPLl+
  gi|2271143   399 STRHTEALAEITRYLGLGDYESWSESDKQAFLIRELSSKRPLLPRYWEPS 448

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     + k+vld+ rv+A  Pi s  aY+isma +PsDvLAv LL +E g   +
  gi|2271143   449 ADTKEVLDTCRVIAKAPIGSVAAYVISMARTPSDVLAVHLLLKEAGCPFA 498

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    L+v PLFE L DL+ A   +++L siDWY+  i+GKq vm+GYsDs KDA
  gi|2271143   499 LPVAPLFETLDDLNNADDVMKQLLSIDWYRGFIQGKQMVMIGYSDSAKDA 548

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Ls
  gi|2271143   549 GVMAASWAQYRAQDALIKTCEKAGIALTLFHGRGGSIGRGGAPAHAALLS 598

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2271143   599 QPPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLALYTGAILEANLLPPPE 648

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EW ++m+e+  v  + YR  v   P Fv YFR AtPElE Gk+ +Gs
  gi|2271143   649 PKQEWHEVMDELSRVSCDMYRGYVRENPDFVPYFRAATPELELGKLPLGS 698

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA +  +d D K
  gi|2271143   699 RPAKRRPNGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQKVVD-DGKQ 747

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                     q L+ m ++WPFF   + +lEmvFAK D  +A  yD+ Lv E L+P Gk
  gi|2271143   748 EQ-LEAMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVEEKLWPLGK 796

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LRd+     + +L i     l+   P++   + LR+ Y   Lnv+qA
  gi|2271143   797 QLRDQLAADINVVLAISNDDHLMADLPWIAESIALRNVYTDPLNVLQAEL 846

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                 +E    +d  ++L             L+
  gi|2271143   847 LHRSRQ----------------QEK---PDADLELA------------LM 865

                    LtmKGiAAGmqntG<-*
                    +t+ G+AAGm ntG
  gi|2271143   866 VTIAGVAAGMRNTG    879

gi|238892353|ref|YP_002917087.1|: domain 1 of 1, from 1 to 883: score 777.6, E = 8.3e-231
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L+D ++D  Ge++ +
  gi|2388923     1    -MNEQYSALR-SNVS-----------MLGKVLgDTIKDALGENILDR 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++ + +EL + L  L   + + vA+a++  LnLAn
  gi|2388923    35 VETIRKLSKSSRAGNEANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+         Ea    E  i  tl+kL  + n   e
  gi|2388923    84 TAEQYH-----SISANG------EAASNPEV-IARTLRKLKDQPNLNEET 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + +A+   s +LvltAHPt   RR L+ K   + nCL qL  KD+   +
  gi|2388923   122 IKQAVESLSLELVLTAHPTEITRRTLIHKMVEVNNCLKQLDNKDIADYEH 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|2388923   172 HQLMRRLRQLIAQSWHTDEIRKHRPSPVDEAKWGFAVVENSLWEGVPNYL 221
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                    RRvDtALK.niGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L  n+G    lP d   ++F+sWmGGDRDG nP vt ++tR v
  gi|2388923   222 RELNEQLEaNLGY--QLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  A+ l++  v  L+ Elsm  C dELR+ A      a
  gi|2388923   269 LLSRWKATDLFLKDVQVLISELSMVECTDELRALA-----GAEGA----- 308

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                              +EPYR ++   R +L  t       L +G          t
  gi|2388923   309 ----------QEPYRYLMKKLRSQLMETQAWLEARL-KGQKLPKPAGLIT 347

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    + E+  EPL  CYksL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|2388923   348 QNEQLWEPLYACYKSLQACGMGIIANGELLDTLRRVKSFGVPLVRIDIRQ 397

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|2388923   398 ESTRHTEALGEMTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRQWEP 447

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     EE ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|2388923   448 SEETREVLDTCKVIAEAPRGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    +L+v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|2388923   498 ALPVAPLFETLDDLNNANDVMTQLLNIDWYRGFIQGKQMVMIGYSDSAKD 547

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|2388923   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2388923   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLSLYTSAILEANLLPPP 647

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk EWR++m e+  v    YR  v     Fv YFR+AtPE E Gk+ +G
  gi|2388923   648 EPKAEWRDIMAELSDVSCKMYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA +  ++   +
  gi|2388923   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQKVVEGGKQ 747

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        L+ m ++WPFF   l +lEmv+ K D  +A  yD+ Lv  eL+  G
  gi|2388923   748 S--ELEAMCRDWPFFSTRLGMLEMVYSKADLWLAEYYDQRLVKPELWALG 795

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                     +LR       + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|2388923   796 SELRKLLAADINVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 845

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R               A+E+ k +d            P +E  L
  gi|2388923   846 LLHRSRQ--------------AEEEGKDPD------------PRVEQAL 868

                    iLtmKGiAAGmqntG<-*
                    ++t+ G+AAGm ntG
  gi|2388923   869 MVTIAGVAAGMRNTG    883

gi|146308379|ref|YP_001188844.1|: domain 1 of 1, from 3 to 878: score 777.4, E = 9.7e-231
                    *->siDAqLR..lLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                        iDA LR+++   G      + i+    L D FLD +     e ++
  gi|1463083     3    EIDARLReeVHLLGELL--GQTIR--TQLGDDFLDKI-----ERIRK 40

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                      +     sA           e L + L  L   + + vA+a+   LnLA
  gi|1463083    41 GAKAGRRGSA--------AGAEQLTSTLGDLGDDELLPVARAFNQFLNLA 82

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE        R+++++     DE +      ++E l +L   + + P+
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  gi|1463083    83 NIAEQ-----QHRVRRRR----PDEPEPFELRVLDELLERLLAAG-QKPD 122

                   EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                   E    L    ++LvltAHPt  +RR L+qK   i   L+ L   D+ + +
  gi|1463083   123 ELARQLGRLDIELVLTAHPTEVARRTLIQKYDAIAAQLTALDHSDLLPAE 172

                   KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                   ++ +   L R i  A+ t+EiRR++P P DE + G + i   +W+ vP+F
  gi|1463083   173 RERIAQRLQRLIAEAWHTEEIRRSRPSPVDEAKWGFAVIEHSLWQAVPQF 222

                   LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   LRR D  L+      RlP ++  i+F+sWmGGDRDG nP vt  vtR+v
  gi|1463083   223 LRRADRSLQA-ATGLRLPLEAAPIRFASWMGGDRDG-NPNVTARVTREVL 270

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                   LLaR mAa lY+  v+ L  Elsm     ELR+      +   +
  gi|1463083   271 LLARWMAADLYLRDVDQLAAELSMQQASAELRA------QVGDSA----- 309

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                              EPYR +L + R++L  tR  a   L   i+  +  Av
  gi|1463083   310 -----------EPYRALLKQLRERLRETRSWAQQALTADIA--PGAAVLQ 346

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   +  + L PL LCY+sL  CG  viADG LLD LR   tFGL Lv+LD+Rq
  gi|1463083   347 DNHDLLAPLQLCYQSLHACGMGVIADGPLLDCLRRAATFGLFLVRLDVRQ 396

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   +s R+   l  it  L++G Y eW Ee+R  +L  EL  +RPLl+sD
  gi|1463083   397 DSTRHAAALSEITDYLGLGRYAEWDEEQRLAFLQRELDSRRPLLPSDYRP 446

                   tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     + ++vl + r +A  P  + G+Y+isma a sDvLAv LL +E g+++
  gi|1463083   447 SADTAEVLATCREVAAAPAAALGSYVISMAGAASDVLAVQLLLKEAGLRR 496

                   tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                   ++rvvPLFE LADL+ A   +++L  +  Y+ r+ G qevm+GYsDs KD
  gi|1463083   497 PMRVVPLFETLADLDNAGPVIDRLLGLPGYRVRLHGPQEVMIGYSDSAKD 546

                   AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                   AG  +AAW  Y+AqEE+++   ++ v L lFHGRGGtvGRGGGP H AiL
  gi|1463083   547 AGTTAAAWAQYRAQEELVRLCGEHQVELLLFHGRGGTVGRGGGPAHAAIL 596

                   sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                   sqPP  + G  R t qGE+i f FG  ++  + L  + AA LE  + PP
  gi|1463083   597 SQPPGSVAGRFRTTEQGEMIRFKFGLPDIAEQNLNLYLAAVLEATLLPPP 646

                   sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                   +P P WR +m+++A v    YR vv   P Fv YFR AtPE E G++ +G
  gi|1463083   647 APEPSWRAMMDRLADVGVKAYRGVVREHPQFVAYFRQATPEQELGRLPLG 696

                   sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                   sRPaKR+  GG+esLRAiPWiFaWtqtR  LP WLG   A   A+
  gi|1463083   697 SRPAKRR-EGGVESLRAIPWIFAWTQTRLMLPAWLGWEQALGQALAGGEG 745

                   nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                    l  Lk m ++WPFFR  +D+lEmv AK D  iAaLyD+ Lv   L+P G
  gi|1463083   746 EL--LKNMREQWPFFRTRIDMLEMVLAKADASIAALYDQRLVEPALQPLG 793

                   ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    +LRd        +L++ G   lL   P     + +R+ Y+  L  +qA
  gi|1463083   794 AQLRDLLSQACAAVLELTGQSRLLAHSPETLESISVRNTYLDPLHLLQAE 843

                   tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    L R R             +  A E                    LE  L
  gi|1463083   844 LLARCR------------LRQQAPES-----------------PLEQAL 863

                   iLtmKGiAAGmqntG<-*
                   ++ + GiAAG+ ntG
  gi|1463083   864 LVSVAGIAAGLRNTG    878
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gi|120555149|ref|YP_959500.1|: domain 1 of 1, from 1 to 881: score 777.2, E = 1.1e-230

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                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEa.
                         +  L P                    + +L DL G+++  ++
gi|1205551     1    -----MTELHPDLRE---------------NVRLLGDLLGQSILRFp 27

                  vqECYElsAeYEGKkDtkKLeELGa.....kLtsLdPaDail.vAkailH
                   q+CY+   e      + + +E G++++  kL +    D +l+v +a+
gi|1205551    28 GQDCYDRIEEIRAAAKADRRQESGSgqrlvKLLGQLSDDELLpVTRAFNQ 77

                  mLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkl
                   LnLAnLAE  +      i++k+ G  +D      Es + E + +L + +
gi|1205551    78 FLNLANLAEQYH-----GIRRKQ-GHPSD---LMVES-LGEVFDRLKSGG 117

                  nKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKD
                     P+E    +    ++ vltAHPt  +RR L+ K   +  CL+ L   D
gi|1205551   118 -IDPQELHRKVADLRIEFVLTAHPTEVARRTLILKYDEMSDCLSRLDHDD 166

                  vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWk
                  + + +++E+ + L   i  A+ tDEiR  +Pt  DE + G + i   +W+
gi|1205551   167 LMPGEREEIVDRLSLLIAEAWHTDEIRHERPTAVDEAKWGFAVIENSLWQ 216

                  GvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEv
                    PKFLR  Dt L        lP +v  i+ +sWmGGDRDG nP vt Ev
gi|1205551   217 ALPKFLRSLDTSLSE-ATGQGLPLQVSPIRIASWMGGDRDG-NPNVTHEV 264

                  tRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaard
                  tR+v LL R mAa lY+  +  L  ElsmW   dELR+          +
gi|1205551   265 TREVFLLGRWMAADLYLRDIQALRAELSMWQASDELRA------EVGDSR 308

                  kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                                 EPYR +L + R++L  tRE a    A    e ++
gi|1205551   309 ----------------EPYRQVLAQLRERLIKTREWAE---ASVKGEPAD 339

                  eA.vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                  + ++  + E+   PLELCY+sL eCG   iA G LLD +R   tFGL L+
gi|1205551   340 DSgILFENEDLTGPLELCYRSLMECGLETIANGPLLDTIRRAHTFGLPLI 389

                  KLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLl
                  +LDiRqE+ R+ + +  +   L++G Y +WsE+ Rq +L+ ELkG+RPL+
gi|1205551   390 RLDIRQEASRHAEAVAEMVNYLGLGDYLSWSEQERQAFLVKELKGRRPLV 439

                  gsDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqR
                  +      E v++vl + +v+A    ++ G+Y+isma  PsDvL v LL R
gi|1205551   440 PRNWQPSEPVREVLATCEVVAGQTPEALGSYVISMASKPSDVLNVILLLR 489

                  ECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGY
                  E g+  ++rvvPLFE L DL+ AP +++ L+ +DWY+    G+qevm+GY
gi|1205551   490 EAGMAFPMRVVPLFETLDDLKGAPDSMAALYEVDWYREYCSGRQEVMIGY 539

                  sDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGP
                  sDs KDAG l AAW  Y+AqE +  vA +yGv L+lFHGRGGtvGRGGGP
gi|1205551   540 SDSSKDAGQLMAAWAQYQAQEKLTEVANRYGVHLTLFHGRGGTVGRGGGP 589

                  tHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEH
                     AiLsqPP  +nGs R+t qGE+i f FG   L  +sL  +t A +E
gi|1205551   590 ANRAILSQPPGSVNGSFRITEQGEMIRFKFGLPRLAVQSLTLYTTAVIEA 639

                  GmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEY
                   + PP  Pk EWR++m+ +       YR vv   P Fv YFR  tPE+
gi|1205551   640 TLAPPPVPKDEWREVMDWLTERSLRSYREVVRENPDFVPYFRQVTPETAL 689

                  GkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhA
                  Gk+ +GsRPa+Rk  GG+esLRAiPWiFaWtq R  LP WLG   A   A
gi|1205551   690 GKLALGSRPARRKATGGVESLRAIPWIFAWTQMRLMLPSWLGSDVALEQA 739

                  idKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva.
                   + D   l  L+Em + WPFFR  +D+lEmv AK D  iA+ y++ Lv +
gi|1205551   740 AQAD--RLPELREMMQGWPFFRTYVDMLEMVLAKADLRIASYYEQTLVEd 787

                  EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYitt
                  E L   G+sLR++ +   + LL++   + lLE +P     +++R++Y
gi|1205551   788 EHLLALGQSLRQRLQGCIERLLELKQQQTLLEQEPVFAHSMKVRNPYTDP 837
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                    LnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpterva
                    L  +qA  L+R R+                E + k  eLv+
  gi|1205551   838 LHYLQAELLRRDRE----------------SEGAGKVPELVERA------ 865

                    PGLEDtLiLtmKGiAAGmqntG<-*
                          L +tm Gi AGm ntG
  gi|1205551   866 ------LKVTMAGISAGMRNTG    881

gi|37199939|dbj|BAC95768.1|: domain 1 of 1, from 3 to 888: score 777.1, E = 1.2e-230
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        i    R+    K +    L     +L       +q+ HG+++ E v
  gi|3719993     3    VIFLRGRMTMNEKYA---ALKSNVSMLGHLLGNTIQEAHGDEILEKV 46

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls        + + + L   + sL       vA+a+   LnL n+
  gi|3719993    47 ETIRKLSKSARAGNQADR-NNLIEEIKSLPDEQLTPVARAFNQFLNLTNI 95

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +   R             E +A     i   + kL   +     +
  gi|3719993    96 AEQYHTISRHCDAHVC------EPDA-----INTLFAKLGQNG-INKLDT 133

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+   +++
  gi|3719993   134 AQAIRELNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSYKERH 183

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                      +  L   i   +  D iR+ +PtP DE + G + +   +W+ vP FLR
  gi|3719993   184 KTEKRLEQLIAQSWHSDVIRKQRPTPLDEAKWGFAVVENSLWEAVPDFLR 233

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                      D  LK   +   lP d+  ++FssWmGGDRDG nP vt  vtR+v LL
  gi|3719993   234 ELDEKLKDY-LDQGLPIDARPVHFSSWMGGDRDG-NPFVTHTVTREVLLL 281

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    +R  Aa lY+  + +L+ Elsm +Cnd +R  A E       d
  gi|3719993   282 SRWKAADLYLKDINELISELSMTKCNDTVRQLAGE-------D------- 317

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi..seisEeAvyt
                             EPYR iL + R  L  t+E    +L   i++  ++  A
  gi|3719993   318 -------EHEPYRAILKQLRTLLSDTKE----ILDAKIngQKLAVKAPLQ 356

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                     vE+  +PL  CY+sL eCG   iA+GsLLD LR v  FG+ Lv+LDiRq
  gi|3719993   357 SVEQLWDPLFACYQSLRECGMSMIAEGSLLDTLRRVKAFGVHLVRLDIRQ 406

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+ Dvl  +t+ L+iG Y  WsE+ +  +L  EL  KRPLl+ D
  gi|3719993   407 ESTRHADVLSELTRYLGIGDYNHWSEQDKIAFLTNELASKRPLLPRDWQP 456

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     E vk+vld+ +++A    ++FGaY+isma + sDvLAv LL  E g
  gi|3719993   457 SEPVKEVLDTCKIIAAQSREAFGAYVISMAKTASDVLAVHLLLQESGCPY 506

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                     + v PLFE L DL+ A A +++L siD Y+  i+  q vm+GYsDs KD
  gi|3719993   507 RMDVCPLFETLDDLNNAEAVIKQLMSIDLYRGFIQNHQMVMIGYSDSAKD 556

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y A E ++ vA + G+ L+lFHGRGGt+GRGG P H A+L
  gi|3719993   557 AGVMAAGWAQYHAMEALVNVAEQEGIELTLFHGRGGTIGRGGAPAHAALL 606

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|3719993   607 SQPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNMYASAILEANLLPPP 656

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk EWR+Lme +  v  E YRsvv  EP Fv YFR AtPElE Gk+ +G
  gi|3719993   657 EPKQEWRDLMEVLSQVSCEAYRSVVRGEPDFVPYFRQATPELELGKLPLG 706

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
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                    sRPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ idK  +
  gi|3719993   707 SRPAKRNPNGGVESLRAIPWIFSWSQNRLLLPAWLGAGEAIQYSIDKGHQ 756

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     l  L+Em +eWPFF   l +lEmv+ K    i   yD+ L    L P G
  gi|3719993   757 AL--LEEMCREWPFFSTRLGMLEMVYLKCNSEISRYYDERLADKSLLPLG 804

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    ++LRd+ +   + +L +     l+  DP+ +  +RLR+ Yi  Ln++qA
  gi|3719993   805 DRLRDQLQSDIKAVLNVENNENLMQSDPWGQESIRLRNIYIEPLNMLQAE 854

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                        +++v           LE+ L
  gi|3719993   855 LLYRTRQ----------------------AGVVSEE--------LEEAL 873

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|3719993   874 MVTIAGIAAGMRNTG    888

gi|46911906|emb|CAG18704.1|: domain 1 of 1, from 9 to 892: score 777.0, E = 1.3e-230
                    *->siDAqLR..lLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                           +LR++     K s    L     +L       ++D HGe L +
  gi|4691190     9    ---TKLRdgCDMNEKYS---ALRSNVSMLGHMLGNTIKDAHGEPLFD 49

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDail.vAkailHmLnL
                     v     ls       D+ +   L   L  L P D +l+vA+a++  LnL
  gi|4691190    50 KVETIRKLSKSARAGNDSDR-AKLIDELQNL-PDDQLLpVARAFSQFLNL 97

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                     n+AE  +   R   ++                 i+  + kL      s
  gi|4691190    98 TNIAEQYHTISRHCEEQIC-----------SPDSIDSLFGKLNANS-ISQ 135

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                     +  +A++   ++LvltAHPt  +RR ++ K   i  CL+ L   ++
  gi|4691190   136 LDSIQAVRDLNIELVLTAHPTEIARRTMIHKLVQINKCLSNLELSELSHS 185

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    +++ ++  L   i  A+  D iR+ +PtP DE + G + +   +W+ vP
  gi|4691190   186 ERQRVEQRLEQLIAQAWHSDVIRKQRPTPLDEAKWGFAVVENSLWHAVPE 235

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    FLR  D  L    + E+lP d+  +kF+sWmGGDRDG nP vt EvtR+v
  gi|4691190   236 FLRQFDEKLMR-HLGEKLPLDASPVKFTSWMGGDRDG-NPFVTSEVTREV 283

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                     LL+R  Aa l++  + +L+ Elsm +Cnd +R  A E       +
  gi|4691190   284 MLLSRWKAADLFLGDIQELVSELSMVKCNDQVRELAGE-------E---- 322

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi..seisEeA
                                EPYR iL d R KL ntR+    +LA  i++ + +  A
  gi|4691190   323 ----------HEPYRAILKDLRTKLTNTRD----VLAAKInkQDAPNLA 357

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                       +v++   PL  CY+sL eCG  +iADG LLD+LR +  FG+ Lv+LD
  gi|4691190   358 TIDDVDQLWTPLHACYQSLRECGMGIIADGLLLDVLRRIKCFGIHLVRLD 407

                    iRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
                    iRqEs R+ Dv+  +t+ L++G Y +W E+ +  +L+ EL  KRPLl+
  gi|4691190   408 IRQESTRHSDVISELTRYLGLGDYEQWNEQDKVAFLVRELASKRPLLPLA 457

                    LPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECg
                         Ev++vld+ + +AE   ++ GaY+isma + sDvLAv LL +E g
  gi|4691190   458 WQPSAEVQEVLDTCKAVAEQSREALGAYVISMARTASDVLAVHLLLKEAG 507

                    vkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDs
                        L v PLFE L DL+     ++ L siDWY+  i+  q vm+GYsDs
  gi|4691190   508 CPFRLDVCPLFETLDDLNNGASVIKELMSIDWYRGFIQNHQMVMIGYSDS 557

                    GKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHL
                     KDAG ++A W  Y+A EE++ v  +  v L+lFHGRGG +GRGG P H
  gi|4691190   558 AKDAGVMAAGWAQYRAMEELVEVCEDASVELTLFHGRGGSIGRGGAPAHA 607
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                    AiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmn
                    A+LsqPP  ++G lRvt qGE+i f  G  ++   sL  ++ AtLE  +
  gi|4691190   608 ALLSQPPRSLKGGLRVTEQGEMIRFKLGLPDVAVNSLSLYASATLEANLL 657

                    PPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkm
                    PP +Pk EW +Lm+ +  v  E YR vv     Fv YFR AtPElE Gk+
  gi|4691190   658 PPPAPKKEWCDLMDVLSEVSCESYRNVVRGSEEFVPYFRAATPELELGKL 707

                    niGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidK
                     +GsRPaKR P GG+esLRAiPWiFaW q R  LP WLG G A ++ idK
  gi|4691190   708 PLGSRPAKRNPNGGVESLRAIPWIFAWSQNRLLLPAWLGAGEAIQYSIDK 757

                    DiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk
                         q L++m +eWPFF   l +lEmv+ K   GiA  yD+ L    L+
  gi|4691190   758 GHA--QLLEDMCREWPFFSTRLGMLEMVYTKTNVGIAEYYDQRLTDKSLW 805

                    PFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvf
                    P G++LRd+ +   + +L +     l+E  P+    +RLR+ Y+  Ln++
  gi|4691190   806 PLGQKLRDQLQQDIKAVLNVENNAHLMEQNPWGAEAIRLRNIYVEPLNML 855

                    qAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLE
                    qA  L R R                dE+               +P LE
  gi|4691190   856 QAELLYRTRQ---------------QDEP----------------SPILE 874

                    DtLiLtmKGiAAGmqntG<-*
                    + L++ + GiA Gm ntG
  gi|4691190   875 EALMVSIAGIATGMRNTG    892

gi|205359957|ref|ZP_02833529.2|: domain 1 of 1, from 17 to 912: score 776.4, E = 2e-230
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +   q R  v G + e+   ++    +l k L++ ++D  Ge + +
  gi|2053599    17    AGQLQQRWGVWGHMNEQYSALRSNVSMLGKVLgETIKDALGEHILDR 63

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++ + +EL + L  L   + + vA+a++  LnLAn
  gi|2053599    64 VETIRKLSKSSRAGNEANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 112

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+ k       Ea    E  i  tl+kL  + +   +
  gi|2053599   113 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPDLNDAT 150

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K + i nCL qL   D+   ++
  gi|2053599   151 IKKAVESLSLELVLTAHPTEITRRTLIHKMGEINNCLKQLDNTDIADYER 200

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + +   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|2053599   201 HQVMRRLRQLIAQSWHTDEIRKQRPSPVDEAKWGFAVVENSLWQGVPNYL 250

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G   +lP d   ++F+sWmGGDRDG nP vt ++tR v
  gi|2053599   251 RELNEQLeENLGY--KLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVL 297

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  A+ l++  +  L+ Elsm     EL +   E     a++
  gi|2053599   298 LLSRWKATDLFLKDIHVLVSELSMVDATPELLALVGE---EGASE----- 339

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vy
                                  PYR ++   R +L  t       L      ++  A+
  gi|2053599   340 ------------PYRYLMKKLRARLMATQSWLEARLKG--EKLPKPAgLL 375

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                    t+ E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiR
  gi|2053599   376 TQNEQLWEPLYACYQSLQACGMGIIANGELLDTLRRVKCFGVPLVRIDIR 425

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+t+ l  it+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|2053599   426 QESTRHTEALGEITRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWE 475

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
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                      + ++vl++ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|2053599   476 PSNDTREVLETCKVIAEAPKGSIAAYVISMAKTPSDVLAVHLLLKEAGIG 525

                   qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                    +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs K
  gi|2053599   526 FAMPVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAK 575

                   DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                   DAG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+
  gi|2053599   576 DAGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAAL 625

                   LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                   LsqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2053599   626 LSQPPGSLKGGLRVTEQGEMIRFKYGLPEVTVSSLSLYTSAILEANLLPP 675

                   vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                     Pk  WR++m+e+ v+  E YR  v     Fv YFR+AtPE E Gk+ +
  gi|2053599   676 PEPKDSWRHIMDELSVISCETYRGYVRENKDFVPYFRSATPEQELGKLPL 725

                   GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                   GsRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D
  gi|2053599   726 GSRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DG 774

                   KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                   K    L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lva  L+P
  gi|2053599   775 KQ-SELEAMCRDWPFFSTRLGMLEMVFSKADLWLADYYDQRLVAKTLWPL 823

                   GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                   Gk+LRd  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|2053599   824 GKELRDLLEEDIKVVLAIANDSHLMADLPWIAESIQLRNVYTDPLNVLQA 873

                   YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                     L R R                +E+ k +d            P +E
  gi|2053599   874 ELLYRSR---------------LTEEQGKSPD------------PRVEQA 896

                   LiLtmKGiAAGmqntG<-*
                   L++t+ G+AAGm ntG
  gi|2053599   897 LMVTIAGVAAGMRNTG    912

gi|261254127|ref|ZP_05946700.1|: domain 1 of 1, from 1 to 877: score 775.8, E = 2.9e-230
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  +  +L    vs           +l + L+  ++D HG+ L E
  gi|2612541     1    -MNEKYSALR-SNVS-----------MLGHLLgNTIKDAHGDVLLEK 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls          + + L   + sL       vA+a+   LnL n
  gi|2612541    35 VETIRKLSKSALAGNQKNR-DSLIEEIKSLPNEQLTPVAHAFNQFLNLTN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +   R             E +A     i   + kL      s  +
  gi|2612541    84 MAEQYHTISRHCDAHVC------EPDA-----INSLFSKLAQND-ISKLD 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     +A++   ++LvltAHPt   RR ++ K  +i  CL++L   ++ v ++
  gi|2612541   122 TAQAVRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELGELSVKER 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
  gi|2612541   172 AKTERRLEQLIAQSWHSDTIRQQRPTPLDEAKWGFAVVENSLWEAVPDFL 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   R  D  L    + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
  gi|2612541   222 RELDQRLEGY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITREVLL 269

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   L+R  Aa lY+  + +L+ Elsm  Cnd +R+ A E       d
  gi|2612541   270 LSRWKAADLYLGDINELVSELSMTQCNDAVRALAGE-------D------ 306

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                             EPYR +L + R  L  t+E     + +G   ++  A   +
  gi|2612541   307 --------EHEPYRAVLKELRALLNETKEILDAKI-HG-QKLAVKAPLQR 346
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                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    +E+  EPL  CY+sL eCG  +iADGsLLD LR +  FG+ Lv+LDiRqE
  gi|2612541   347 IEQLWEPLYACYQSLHECGMGIIADGSLLDTLRRIKAFGVHLVRLDIRQE 396

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+ Dvl  +t+ L+iG Y +WsE+ +  +L  EL  KRPLl+ D
  gi|2612541   397 STRHSDVLSELTRYLGIGDYDQWSEQDKVAFLTNELASKRPLLPRDWEPS 446

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    E vk+vld+ +++A  P ++FGaY+isma + sDvLAv LL  E g
  gi|2612541   447 ESVKEVLDTCKIVALQPREAFGAYVISMARTASDVLAVHLLLQESGCPYR 496

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    + v PLFE L DL+ A A +++L  iD Y+  i+  q vm+GYsDs KDA
  gi|2612541   497 MDVCPLFETLDDLNNAEAVIKQLMGIDLYRGFIQNHQMVMIGYSDSAKDA 546

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G +sA W  Y A + ++KvA + Gv L+lFHGRGGt+GRGG P H A+Ls
  gi|2612541   547 GVMSAGWAQYHAMDSLVKVAEEEGVELTLFHGRGGTIGRGGAPAHAALLS 596

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|2612541   597 QPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNLYASAILEANLLPPPE 646

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EWR+Lm+ +  v  E YR vv  EP Fv YFR AtPElE Gk+ +Gs
  gi|2612541   647 PKQEWRELMDVLSEVSCEAYRKVVRGEPDFVPYFRQATPELELGKLPLGS 696

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ +dK  +
  gi|2612541   697 RPAKRNPKGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSVDKGHQA 746

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l  L+Em +eWPFF   l +lEmv+ K    i   yD+ Lv  eL P G+
  gi|2612541   747 L--LEEMCREWPFFSTRLGMLEMVYTKCNLEISRYYDERLVDSELLPLGD 794

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LRd+ +   + +L +     l+  DP+    +RLR+ Y+  Ln++qA
  gi|2612541   795 RLRDQLQQDIKAVLNVENNENLMQSDPWGLESIRLRNIYVEPLNMLQAEL 844

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                                 +e+ aP LE+ L+
  gi|2612541   845 LYRTRQ------------------------------SEESAPELEEALM 863

                    LtmKGiAAGmqntG<-*
                    +t+ GiAAGm ntG
  gi|2612541   864 VTIAGIAAGMRNTG    877

gi|262376807|ref|ZP_06070034.1|: domain 1 of 1, from 4 to 894: score 775.6, E = 3.4e-230
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLH.GedLkEa
                        iDA LR               D  Ll   L     LH G+dL
  gi|2623768     4    QIDAPLRE--------------DVRLLGNLLGETLKLHaGQDLFNQ 35

                    vqECYEls.AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    +     ls+   +G+ +++K   L     sL+ a+ + + +a+ H Ln A
  gi|2623768    36 IEQIRALSkGARDGQVEAEK--QLEQLFLSLEDAEILPLTRAFTHFLNFA 83

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE  ++  RRR +     D a+  +      + E +K+         +
  gi|2623768    84 NIAEQYHVVRRRRQSEFD--DTAESPNPLVP--LFEKFKQQEISA----D 125

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                      ++ +    ++LvltAHPt   RR L+qK   i n L++   + +t+ +
  gi|2623768   126 TLYQQICELKIELVLTAHPTEVSRRTLIQKYDGINNALSKFDQQKLTPRE 175

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    ++ +   L   i  A+ tDEiR  +PtP DE + G   i  t+W+ vPKF
  gi|2623768   176 RQAVLADLKQLISSAWQTDEIRQHRPTPIDEAKWGFTTIEQTLWNAVPKF 225

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
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                    +R     +        lP dv  ++F+sWmGGDRDG nP vt  vt +v
  gi|2623768   226 IRELNSMVTE-QCAQNLPLDVAPVRFASWMGGDRDG-NPNVTHTVTQEVL 273

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     L+R  Aa lY+  +E L +Els+  C         E+     +d
  gi|2623768   274 WLSRWKAADLYLRDIENLRWELSIQQC-------SPEISEALGQD----- 311

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi..seisEeAv
                              EPYR  L d R +L  t    RH LA  +++ +  +  v
  gi|2623768   312 ---------HPEPYREYLRDTRSRLKAT----RHWLAEKLkgNDADDSLV 348

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                        +e L PL  CY+sL +C    iA GsLLD++  v  FG+ L KLDi
  gi|2623768   349 IKSKDELLQPLLTCYRSLMDCNLAEIANGSLLDFIYRVNSFGIELLKLDI 398

                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    RqEs R+   + Ait+ L++G +  W E+ Rq +Ll EL+ KRPLl+  L
  gi|2623768   399 RQESGRHRQAISAITEYLGLGNFETWTEQARQNFLLQELQSKRPLLPKHL 448

                    PktE.......EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvEL
                        ++  ++++v++v  ++r LAE P++s GaYiisma  PsDvLAv L
  gi|2623768   449 NEPAgsliehpDVQEVFATMRTLAEQPSESLGAYIISMAEYPSDVLAVLL 498

                    LqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevm
                    Lq+E g+k++LrvvPLFE L DL+ A  ++  LF + WY+ +i+GK evm
  gi|2623768   499 LQKEAGIKHALRVVPLFETLKDLDGAAETMSTLFNMHWYKQHIQGKHEVM 548

                    vGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRG
                    +GYsDs KDAG +sA W  Y+AqEE+  +A+++Gv+L+lFHGRGG + RG
  gi|2623768   549 IGYSDSAKDAGFMSANWAQYRAQEELTTIAQQHGVQLTLFHGRGGSISRG 598

                    GGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAt
                    G Pt  A+ sqPP  i G +Rvt qGE+i f FG E++  + L  +tAAt
  gi|2623768   599 GAPTQQALFSQPPGSISGTIRVTEQGEMIRFKFGLEEIALQNLEIYTAAT 648

                    LEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPE
                    LE  + PP  Pk EWR+Lm +m       YR  v   P Fv Y R  tPE
  gi|2623768   649 LEATLLPPPEPKQEWRDLMHQMTELSVQVYRQTVRENPHFVKYLRTVTPE 698

                    lEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAF
                    lE   + +GsRPaKRk sGGiesLRAiPW+FaWtq R  LP WLG GAA
  gi|2623768   699 LELQMLPLGSRPAKRKVSGGIESLRAIPWVFAWTQIRLMLPAWLGTGAAL 748

                    KhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL
                       +d+  + +  L Em  eWP+F   +D+lEmv  K D  +A  y+  L
  gi|2623768   749 NKVLDQGQRAV--LDEMLAEWPYFQTLIDMLEMVLSKADAHVALYYESHL 796

                    va.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsY
                      +E+Lk  G +LR++ ++  + LL +     lL     L q +++R +Y
  gi|2623768   797 TQdEDLKVLGTELRQRLQDAVQTLLTLKDESKLLSSNGVLDQSMKVRKPY 846

                    ittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpte
                    +  L  +qA  +KR          r  l +  A+
  gi|2623768   847 LLPLHLLQAELMKR---------RRLYLQQQQAENT-------------- 873

                    rvaPGLEDtLiLtmKGiAAGmqntG<-*
                         ++  L++ + GiAAG+ ntG
  gi|2623768   874 ----PVDHALMVSIAGIAAGLRNTG    894

gi|289626060|ref|ZP_06459014.1|: domain 1 of 1, from 3 to 878: score 775.3, E = 4.1e-230
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        iDA LR      v           LL +     + +  G +  + +
  gi|2896260     3    DIDARLRE----DVH----------LLGELLGNTIREQRGAEFLDKI 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E     A    +  ++  e L a + +L   + + vA+a+   LnLAn+
  gi|2896260    36 -ERIRKGAKAGRRGSAEGAEQLSASVDGLGDDELLPVARAFNQFLNLANI 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiE.EtlKkLvlklnKsPeE
                    AE  +l +RR   +              Es + +E l +L   +  +P+
  gi|2896260    85 AEQYQLMHRRDDTQPL----------PFESRVLpELLDRLKTEG-HTPDA 123
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                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                        L    ++LvltAHPt  +RR L+qK   i   La L  +D+   ++
  gi|2896260   124 LARQLSKLEIELVLTAHPTEVARRTLIQKYDAIAAQLAALDHRDLNSTER 173

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L R i  A+ t+EiRR +PtP DE + G + i   +W+ +P +L
  gi|2896260   174 AQITSRLQRLIAEAWHTEEIRRIRPTPVDEAKWGFAVIEHSLWHAIPNYL 223

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R+ D AL        lP ++  i+F+sWmGGDRDG nP vt  vtR+v L
  gi|2896260   224 RKADHALHA-ATGLHLPLEAAPIRFASWMGGDRDG-NPNVTAKVTREVLL 271

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    LaR mAa lY+  v+ L  Elsm    d LR+      +   +
  gi|2896260   272 LARWMAADLYLRDVDNLAAELSMQQASDALRA------SVGDSA------ 309

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR  L   R++L  tR  a   L   +   + eAv  +
  gi|2896260   310 ----------EPYRAELKRLRERLRATRNWANASLSETLP--APEAVLRD 347

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      e L+PL LC++sL eCG  viADG LLD LR   tFGL Lv+LD+Rq+
  gi|2896260   348 NRELLDPLLLCFQSLHECGMGVIADGPLLDCLRRAVTFGLFLVRLDVRQD 397

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+   +  it  L++G Y eW E+ R ++Ll EL  +RPLl+s
  gi|2896260   398 SSRHCAAMTEITDYLGLGRYEEWDEQTRIDFLLRELNNRRPLLPSYFKPA 447

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     + ++vl + rv+A  P  s G+Y+isma + sDvLAv LL +E g++++
  gi|2896260   448 ADTAEVLATCRVVAAAPAASLGSYVISMAGSASDVLAVQLLLKESGLQRP 497

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    +rvvPLFE LADL+ A   +e L  +  Y+ r+ G qevm+GYsDs KDA
  gi|2896260   498 MRVVPLFETLADLDNAGPVIETLLGLPGYRSRLHGPQEVMIGYSDSAKDA 547

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G  +AAW  Y+AqE ++ +  +  v L lFHGRGGtvGRGGGP H AiLs
  gi|2896260   548 GTTAAAWAQYRAQEKLVEICGEQQVELLLFHGRGGTVGRGGGPAHAAILS 597

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  + G  R t qGE+i f FG  ++  + L  + AA LE  + PP
  gi|2896260   598 QPPGSVAGRFRTTEQGEMIRFKFGLPDIAEQNLNLYLAAVLEATLLPPPP 647

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    P+P WR +m++mA      YR+vv   P FvEYFR AtPE E G++ +Gs
  gi|2896260   648 PQPSWRTMMDQMAADGVGAYRAVVRENPEFVEYFRQATPEQELGRLPLGS 697

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+  GG+esLRAiPWiFaWtqtR  LP WLG  AA   A+++
  gi|2896260   698 RPAKRR-EGGVESLRAIPWIFAWTQTRLMLPAWLGWEAALSKALERGEGS 746

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    +  L  m ++WPFFR  +D+lEmv AK D  iA LyD+ Lv+ eL+  G
  gi|2896260   747 V--LAQMREQWPFFRTRIDMLEMVLAKADSDIARLYDERLVSAELQHLGA 794

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                     LRd      + +L + G k lL   P     + LR+ Y+  L  +qA
  gi|2896260   795 HLRDLLSQACNVVLGLTGQKQLLAHSPETLEFISLRNTYLDPLHLLQAEL 844

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R            s+E   +                   LE  L+
  gi|2896260   845 LSRSR------------SREASLDS-----------------PLELALL 864

                    LtmKGiAAGmqntG<-*
                    + + GiAAG+ ntG
  gi|2896260   865 VSVAGIAAGLRNTG    878

gi|104780469|ref|YP_606967.1|: domain 1 of 1, from 3 to 875: score 775.3, E = 4.3e-230
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
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                  iD  LR      v           LL +   + +   HGe    +
gi|1047804     3    DIDQRLRE----DVH----------LLGELLGETIRQQHGEA---FL 32

                 qECYElsAeYEGKkDtkKLeE.LGakLtsLdPaDailvAkailHmLnLAn
                 q   ++      K D +  +E+L + L  L+  D + vA+a+   LnLAn
gi|1047804    33 QKIEDI--RHSAKADRRGEGEqLSSTLGDLAEEDLLPVARAFNQFLNLAN 80

                 LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                 +AE  +l +RR   +        Ea       + E l +L   +    +
gi|1047804    81 IAEQYQLIHRRDTDQPE----PFEARV-----LPELLARLKAAG-HGNDA 120

                 vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     L    + LvltAHPt  +RR L+qK   i   La    +D+ + ++
gi|1047804   121 LARQLARLDIQLVLTAHPTEVARRTLIQKYDAIAAQLAAQDHRDLIPAER 170

                 kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                 + + E L R i  A+ t+EiRR++PtP DE + G + i   +W+ vP  L
gi|1047804   171 QQVRERLRRLIAEAWHTEEIRRTRPTPVDEAKWGFAVIEHSLWQAVPNHL 220

                 RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                 R+vD AL    G+  RlP +   ++F+sWmGGDRDG nP vt  vtR+v
gi|1047804   221 RKVDKALfEATGL--RLPLESAPVRFASWMGGDRDG-NPNVTAAVTREVL 267

                 LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                 LLaR mAa l++  ++ L  Elsm      LR   E +   a
gi|1047804   268 LLARWMAADLFLRDIDYLAAELSMQQASGALR---EQVGDSA-------- 306

                 YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                              EPYR +L + RD+L  tR  a   LA    + +  Av
gi|1047804   307 -----------EPYRALLKQLRDRLRATRAWAHASLAG--PQPASAAVLV 343

                 kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                 +  + + PLELCY+sL  CG  viADG LLD LR   tFGL Lv+LD+Rq
gi|1047804   344 DNRDLIAPLELCYQSLHACGMGVIADGPLLDSLRRAVTFGLFLVRLDVRQ 393

                 EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                 ++ R+ D l  it  L++G Y +W Ee+R E+L  ELk +RPLl++
gi|1047804   394 DAARHRDALSEITDYLGLGRYADWDEERRIEFLQHELKNRRPLLPAHFKP 443

                 tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                   E ++vl + r +A  P  s G+Y+isma a sDvLAv LL +E g+ +
gi|1047804   444 AAETAEVLATCREIAAAPAASLGSYVISMAGAASDVLAVQLLLKEAGLTR 493

                 tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                 ++rvvPLFE LADL+ A   +e+L  +  Y+  + G qevm+GYsDs KD
gi|1047804   494 PMRVVPLFETLADLDNAGPVMERLLGLPGYRAGLHGPQEVMIGYSDSAKD 543

                 AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                 AG  +AAW  Y+AqE ++++ +++ v L lFHGRGGtvGRGGGP H AiL
gi|1047804   544 AGTTAAAWAQYRAQENLVRICREHQVELLLFHGRGGTVGRGGGPAHAAIL 593

                 sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                 sqPP  + G  R t qGE+i f FG   +  + L  + AA LE  + PP
gi|1047804   594 SQPPGSVGGRFRTTEQGEMIRFKFGLPGIAEQNLNLYLAAVLEATLLPPP 643

                 sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                  P P WR Lm+++A      YR vv   P FvEYFR  tPE E G++ +G
gi|1047804   644 PPEPAWRALMDQLAADGVKAYRGVVRDNPEFVEYFRQSTPEQELGRLPLG 693

                 sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                 sRPaKR+ +GGiesLRAiPWiF WtqtR  LP WLG   A   A+ +
gi|1047804   694 SRPAKRR-AGGIESLRAIPWIFGWTQTRLMLPAWLGWETALSNALARGQA 742

                 nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                  l  L  m ++WPFFR  +D+lEmv AK D  iA  yD+ Lv   L P G
gi|1047804   743 DL--LAQMREQWPFFRTRIDMLEMVLAKADAQIAEAYDQRLVQPRLLPLG 790

                 ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                   LRd      + +L + G + lL   P     +RLR+ Y+  L  +qA
gi|1047804   791 AHLRDLLSQSCQVVLGLTGQQVLLAHSPETLEFIRLRNTYLDPLHRLQAE 840
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                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R            s+E A +                    LE  L
  gi|1047804   841 LLARSR------------SREAALDS------------------PLEQAL 860

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAG+ ntG
  gi|1047804   861 LVTVAGIAAGLRNTG    875

gi|66806573|ref|XP_637009.1|: domain 1 of 1, from 10 to 931: score 775.2, E = 4.6e-230
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                               + P        + ++  +L     D+  D  Ge++   v
  gi|6680657    10    ----DFGEIKPDDLD--KSITKFQNILSNCIKDLETD--GEEIIKLV 48

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    +    +  +  G + t+ +eE   k+  L  ++a+ v + ++H+LnL n+
  gi|6680657    49 KTL--ILTQSPGERTTEFIEEYLKKISNLSNTEALNVSRVLSHLLNLINV 96

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +l    R + +         +       E t+++L  ++    e v
  gi|6680657    97 AEQHHLVRSVRESFLN-------NEDDLKYSCENTIQQLLNQG-LDKESV 138

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    ++AL  q ++LvltAHPtq  RR ++ Kn+ +   L+ L  + +t  +++
  gi|6680657   139 YNALIQQKIELVLTAHPTQIMRRTIISKNSAMGEALSSLDNQQLTMFERE 188

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    + +  L RE+   + tDE+RR++ t   E   G s i  t+W+  PKF++
  gi|6680657   189 DYEKRLIREVGGSWLTDEVRRSKVTVEMEAQGGFSVIEQTLWHALPKFIK 238

                    RvD.tALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                       +  +K +G    lP     i+ +sW+GGDRDG n  vt EvtR v
  gi|6680657   239 ILNrCCVKYLG--KELPPTFANIHVASWVGGDRDG-NHNVTAEVTRQVSY 285

                    LaRmmAanlYisqvEDLmFElsmWRCndEL....RvRAEElyrtaardkv
                     +R +Aa lY+  ++ L+FElsm R n  L++  R   E    t +   +
  gi|6680657   286 FSRWIAATLYYKEIDALLFELSMVRHNKTLeelaRHSIEKRSGTVKLRYL 335

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAt..GiseisE
                    +  Y EF   +P  E YR+++ + RDK+  t+ +   L+A ++    ++
  gi|6680657   336 TTLYKEFKEGIPSKECYRIVMAELRDKMLLTKRKYEDLIAAksDTQYLPG 385

                    eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                    e  + + +e L  L +CY sL e G k +ADG LLD +R    FGL L K
  gi|6680657   386 ET-FENADEILQVLQVCYDSLVEVGAKEVADGRLLDNIRRLKSFGLTLSK 434

                    LDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlg
                    +DiRqEs R+ Dv+  +t+ L++G Y +W E K+q +L+ EL+ KRPL++
  gi|6680657   435 MDIRQESTRHSDVINCVTEYLGLGTYNDWDEPKKQAFLIGELESKRPLIP 484

                    sDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRE
                     DLP   Ev++vld+f+v A LP  s GaY+ism+  PsD+LAv LLq+
  gi|6680657   485 HDLPCSSEVREVLDTFKVAASLPNGSLGAYVISMCRNPSDILAVHLLQKA 534

                    CgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYs
                     g k++ rvvPLFE  ADL+  P ++e LF   WY   i+G qe+m+GYs
  gi|6680657   535 VGNKNPQRVVPLFETAADLDSSPKTMEELFLQQWYLKSINGEQEIMLGYS 584

                    DsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPt
                    Ds KD GR+   W L+kAqE ++    k+ vKL+lFHGRGGt  RGGG
  gi|6680657   585 DSAKDSGRFMSCWELFKAQERLASLTEKFNVKLTLFHGRGGTAARGGGNS 634

                    HLAiLsqPPDtin.GslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEH
                    H  i+sqP   +++ s Rvt+qGE+i+  +G      r    Ft A L
  gi|6680657   635 HEGIMSQPGGSLKsASTRVTIQGEMIDSHYGQIGASIRNFELFTTALLKQ 684

                    GmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEY
                     + PP  Pk  WR++me++ +     YRsvv   P F+ YFR  t   E
  gi|6680657   685 SLTPPPPPKQRWREIMEQLSITSCKKYRSVVRENPSFIQYFRTSTVQPEM 734

                    GkmniGsRPaKRkP..sGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFK
                      +niGsRPaKR   +s G+e LRAiPW+F++ q R  LPvWLG+  A
```

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  gi|6680657   735 VYLNIGSRPAKRIAakSFGLEHLRAIPWVFSFSQNRLNLPVWLGIEDAIL 784

                   hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLv
                    A  K       + EmYkeWPFF  t+DL+Emv  K DP i   y ++Lv
  gi|6680657   785 EAKTKGWGS--DINEMYKEWPFFSSTIDLVEMVLLKTDPQISLRYNQMLV 832

                   aEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYit
                     +++P G ++ d+   t + +L++  Hk l      L+  + +R  ++
  gi|6680657   833 PAQVQPLGIEMIDELTKTTNAILELTKHKTLQQDNKILQHFVSIRRTFMD 882

                   tLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpterv
                    +n +q  tLKR+R      t +P       d            n  +
  gi|6680657   883 PINYIQVETLKRLRS-----TQKP-------DGT----------N--DDA 908

                   aPGLEDtLiLtmKGiAAGmqntG<-*
                    P L DtLi+t  Gi AGm+ntG
  gi|6680657   909 DPILIDTLIITFNGISAGMKNTG    931

gi|197336287|ref|YP_002157103.1|: domain 1 of 1, from 1 to 876: score 774.6, E = 6.7e-230
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  +  +L    vs           +l + L+  + D HGe+L
  gi|1973362     1    -MNEKYAALK-SNVS-----------MLGHLLgNTIRDAHGEELLAK 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDail.vAkailHmLnLA
                   v     ls       D  + + L   + sL P D + +vA+a++  LnL
  gi|1973362    35 VETIRKLSKTARAGSDEDR-NALIEEIKSL-PDDQLTpVARAFSQFLNLT 82

                   nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                   n+AE  +   R                    E D   tl    ++ n s
  gi|1973362    83 NMAEQYHTISRHCEAHVC-----------EPDAISTLFSKLSQSNVSKL 120

                   EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                   +  +A++   ++LvltAHPt  +RR ++ K  +i  CL++L   D+   +
  gi|1973362   121 DTAQAVRELNIELVLTAHPTEIARRTMINKLVKINECLSKLELGDISFSE 170

                   KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                   +   +  L   i  A+  D iR  +PtP DE + G + +   +W+G+P F
  gi|1973362   171 RDKTERRLEQLIAQAWHSDVIRQERPTPLDEAKWGFAVVENSLWQGIPEF 220

                   LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   LR  D  L    + E lP d+  ++ ssWmGGDRDG nP vt  +tR+v
  gi|1973362   221 LREFDQRLEG-HLGEGLPIDARPVHMSSWMGGDRDG-NPFVTHKITREVM 268

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                   LL+R  Aa lY+  + +L+ Elsm +C dE+R  A +      ++
  gi|1973362   269 LLSRWKAADLYLKDINELISELSMVKCTDEVRELAGD------QH----- 307

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                              EPYR iL + R  L  t E     +   +  ++  A+ t
  gi|1973362   308 -----------EPYRAILKQLRTLLGDTLESLDAQMKGEL--VPNKAILT 344

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   + ++   PL  CY+sL  CG  +iADGsLLD LR v  FG  Lv+LDiRq
  gi|1973362   345 DADQLWNPLYACYQSLHACGMGIIADGSLLDTLRRVKAFGAHLVRLDIRQ 394

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   Es R+ Dvl  +t+ L+iG Y +WsE+ +  +L+ EL+ KRPLl+
  gi|1973362   395 ESTRHSDVLSELTRYLGIGDYDQWSEQDKISFLVNELSSKRPLLPRKWEP 444

                   tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     Ev++v+d+ rv+AE   ++ G+Y+isma + sDvLAv LL  E g
  gi|1973362   445 SPEVQEVIDTCRVVAEQSKEALGSYVISMARTASDVLAVHLLLQEAGCPF 494

                   tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    + v PLFE L DL+     +e+LFsiDWY+  i+  q vm+GYsDs KD
  gi|1973362   495 RMDVCPLFETLDDLNRSKEVMEQLFSIDWYRGFIQNHQMVMIGYSDSAKD 544

                   AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                   AG +sA W  Y A E ++ v  k  + L+lFHGRGGt+GRGG P H A+L
  gi|1973362   545 AGVMSAGWAQYSAMEALVEVCEKESIELTLFHGRGGTIGRGGAPAHAALL 594
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                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|1973362   595 SQPPKSLKGGLRVTEQGEMIRFKLGLPEVAVNSFNLYASAILEANLLPPP 644

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk EWR+Lme +  v  E YR vv  E  Fv YFR AtPElE Gk+ +G
  gi|1973362   645 EPKQEWRDLMEVLSEVSCEAYRNVVRGEKDFVPYFRAATPELELGKLPLG 694

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ idK  +
  gi|1973362   695 SRPAKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSIDKGHQ 744

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     l  L+Em +eWPFF   l +lEmv+ K  P +   yD+ L    L+P G
  gi|1973362   745 EL--LEEMCREWPFFSTRLGMLEMVYTKCNPQMSEYYDQRLTDKSLWPLG 792

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    ++LR++ +   + +L +     l+E DP+    +RLR+ Y+  Ln++qA
  gi|1973362   793 ERLRNQLQTDIKAVLNVENNDHLMERDPWGSESIRLRNIYVDPLNMLQAE 842

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                                 e+ +P LE+ L
  gi|1973362   843 LLFRTRQ------------------------------QEETSPELEEAL 861

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|1973362   862 MVTIAGIAAGMRNTG    876

gi|197300985|ref|ZP_02662800.2|: domain 1 of 1, from 17 to 912: score 774.5, E = 7.4e-230
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +   q R  v   + e+   ++    +l k L++ ++D  Ge + +
  gi|1973009    17    AGQLQQRWGVWDHMNEQYSALRSNVSMLGKVLgETIKDALGEHILDR 63

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++ + +EL + L  L   + + vA+a++  LnLAn
  gi|1973009    64 VETIRKLSKSSRAGNEANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 112

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+ k       Ea    E  i  tl+kL  + +   +
  gi|1973009   113 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPDLNDAT 150

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K + i nCL qL   D+   ++
  gi|1973009   151 IKKAVESLSLELVLTAHPTEITRRTLIHKMGEINNCLKQLDNTDIADYER 200

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + +   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|1973009   201 HQVMRRLRQLIAQSWHTDEIRKQRPSPVDEAKWGFAVVENSLWQGVPNYL 250

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G   +lP d   ++F+sWmGGDRDG nP vt ++tR v
  gi|1973009   251 RELNEQLeENLGY--KLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVL 297

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  A+ l++  +  L+ Elsm     EL +   E     a++
  gi|1973009   298 LLSRWKATDLFLKDIHVLVSELSMVDATPELLALVGE---EGASE----- 339

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                                PYR ++   R +L  t       L +G      +   t
  gi|1973009   340 ------------PYRYLMKKLRARLMATQSWLEARL-KGEKLPKPDGLLT 376

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    + E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|1973009   377 QNEQLWEPLYACYQSLQACGMGIIANGELLDTLRRVKCFGVPLVRIDIRQ 426

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+t+ l  it+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|1973009   427 ESTRHTEALGEITRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWEP 476

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      + ++vl++ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
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  gi|1973009   477 SNDTREVLETCKVIAEAPKGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 526

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|1973009   527 AMPVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 576

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|1973009   577 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 626

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|1973009   627 SQPPGSLKGGLRVTEQGEMIRFKYGLPEVTVSSLSLYTSAILEANLLPPP 676

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR++m+e+ v+  E YR  v     Fv YFR+AtPE E Gk+ +G
  gi|1973009   677 EPKDSWRHIMDELSVISCETYRGYVRENKDFVPYFRSATPEQELGKLPLG 726

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
  gi|1973009   727 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 775

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lva  L+P G
  gi|1973009   776 Q-SELEAMCRDWPFFSTRLGMLEMVFSKADLWLADYYDQRLVAKTLWPLG 824

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    k+LRd  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|1973009   825 KELRDLLEEDIKVVLAIANDSHLMADLPWIAESIQLRNVYTDPLNVLQAE 874

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                +E+ k +d           P +E  L
  gi|1973009   875 LLYRSR---------------LTEEQGKSPD------------PRVEQAL 897

                    iLtmKGiAAGmqntG<-*
                    ++t+ G+AAGm ntG
  gi|1973009   898 MVTIAGVAAGMRNTG    912

gi|161936338|ref|YP_128506.2|: domain 1 of 1, from 1 to 876: score 774.3, E = 8.4e-230
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                K s    L     +L       ++D HGe L + v
  gi|1619363     1    ---------MNEKYS---ALRSNVSMLGHMLGNTIKDAHGEPLFDKV 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDail.vAkailHmLnLAn
                         ls       D+ +   L   L  L P D +l+vA+a++  LnL n
  gi|1619363    36 ETIRKLSKSARAGNDSDR-AKLIDELQNL-PDDQLLpVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R   ++                 i+  + kL      s  +
  gi|1619363    84 IAEQYHTISRHCEEQIC-----------SPDSIDSLFGKLNANS-ISQLD 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      +A++   ++LvltAHPt  +RR ++ K   i  CL+ L   ++   ++
  gi|1619363   122 SIQAVRDLNIELVLTAHPTEIARRTMIHKLVQINKCLSNLELSELSHSER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + ++  L   i  A+  D iR+ +PtP DE + G + +   +W+ vP FL
  gi|1619363   172 QRVEQRLEQLIAQAWHSDVIRKQRPTPLDEAKWGFAVVENSLWHAVPEFL 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R  D  L    + E+lP d+  +kF+sWmGGDRDG nP vt EvtR+v L
  gi|1619363   222 RQFDEKLMR-HLGEKLPLDASPVKFTSWMGGDRDG-NPFVTSEVTREVML 269

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa l++  + +L+ Elsm +Cnd +R  A E       +
  gi|1619363   270 LSRWKAADLFLGDIQELVSELSMVKCNDQVRELAGE-------E------ 306

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi..seisEeAvy
                              EPYR iL d R KL ntR+    +LA  i++ + +  A
  gi|1619363   307 ---------HEPYRAILKDLRTKLTNTRD----VLAAKInkQDAPNLATI 343
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                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     +v++   PL  CY+sL eCG  +iADG LLD+LR +  FG+ Lv+LDiR
  gi|1619363   344 DDVDQLWTPLHACYQSLRECGMGIIADGLLLDVLRRIKCFGIHLVRLDIR 393

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+ Dv+  +t+ L++G Y +W E+ +  +L+ EL  KRPLl+
  gi|1619363   394 QESTRHSDVISELTRYLGLGDYEQWNEQDKVAFLVRELASKRPLLPLAWQ 443

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                       Ev++vld+ + +AE   ++ GaY+isma + sDvLAv LL +E g
  gi|1619363   444 PSAEVQEVLDTCKAVAEQSREALGAYVISMARTASDVLAVHLLLKEAGCP 493

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                      L v PLFE L DL+     ++ L siDWY+  i+  q vm+GYsDs K
  gi|1619363   494 FRLDVCPLFETLDDLNNGASVIKELMSIDWYRGFIQNHQMVMIGYSDSAK 543

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG ++A W  Y+A EE++ v  +  v L+lFHGRGG +GRGG P H A+
  gi|1619363   544 DAGVMAAGWAQYRAMEELVEVCEDASVELTLFHGRGGSIGRGGAPAHAAL 593

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPP  ++G lRvt qGE+i f  G  ++   sL  ++ AtLE  + PP
  gi|1619363   594 LSQPPRSLKGGLRVTEQGEMIRFKLGLPDVAVNSLSLYASATLEANLLPP 643

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                     +Pk EW +Lm+ +  v  E YR vv     Fv YFR AtPElE Gk+ +
  gi|1619363   644 PAPKKEWCDLMDVLSEVSCESYRNVVRGSEEFVPYFRAATPELELGKLPL 693

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKR P GG+esLRAiPWiFaW q R  LP WLG G A ++ idK
  gi|1619363   694 GSRPAKRNPNGGVESLRAIPWIFAWSQNRLLLPAWLGAGEAIQYSIDKGH 743

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                       q L++m +eWPFF   l +lEmv+ K   GiA  yD+ L    L+P
  gi|1619363   744 A--QLLEDMCREWPFFSTRLGMLEMVYTKTNVGIAEYYDQRLTDKSLWPL 791

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G++LRd+ +   + +L +     l+E  P+    +RLR+ Y+  Ln++qA
  gi|1619363   792 GQKLRDQLQQDIKAVLNVENNAHLMEQNPWGAEAIRLRNIYVEPLNMLQA 841

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R                 dE+                +P LE+
  gi|1619363   842 ELLYRTRQ---------------QDEP----------------SPILEEA 860

                    LiLtmKGiAAGmqntG<-*
                    L++ + GiA Gm ntG
  gi|1619363   861 LMVSIAGIATGMRNTG    876

gi|170723273|ref|YP_001750961.1|: domain 1 of 1, from 3 to 875: score 774.1, E = 9.4e-230
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        iD  LR      v           +L +   + +   HG+    +
  gi|1707232     3    DIDVRLRE----DVH----------VLGELLGETIRQQHGDA---FL 32

                    qECYElsAeYEGKkDtkKLeE.LGakLtsLdPaDailvAkailHmLnLAn
                    q   ++      K D +  +E+L + L  L+  D + vA+a+   LnLAn
  gi|1707232    33 QKIEDI--RHSAKADRRSAGEqLSSTLANLAEEDLLPVARAFNQFLNLAN 80

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +l  RR  ++        Ea       + E l +L   +    +
  gi|1707232    81 MAEQYQLIRRRDAEQPE----PFEARV-----LPELLARLKRAG-HKDDA 120

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                       L    + LvltAHPt  +RR L+qK   i   La    +D+t+ ++
  gi|1707232   121 LARQLAKLDIQLVLTAHPTEVARRTLIQKYDAIAGQLAAQDHRDLTPGER 170

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + + E L R i  A+ t+EiRR++PtP DE + G + i   +W+ +P  L
  gi|1707232   171 QQVRERLRRLIAEAWHTEEIRRTRPTPVDEAKWGFAVIEHSLWHAIPSHL 220

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R+vD AL       RlP ++  ++F+sWmGGDRDG nP vt  vtR+v L
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  gi|1707232   221 RKVDKALFD-ATGLRLPLEAAPVRFASWMGGDRDG-NPNVTAAVTREVLL 268

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   LaR mAa l++  v+ L  Elsm    + +R   E +  t+
  gi|1707232   269 LARWMAADLFLRDVDALAAELSMQQASSAVR---ERVGDTP--------- 306

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                            EPYR +L + RD+L  tR  a   L     + +   v  +
  gi|1707232   307 ----------EPYRAVLKQLRDRLRATRAWAHASLTA--TQPASADVLVD 344

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     + + PLELCY+sL eCG  viADG LLD LR   tFGL L +LD+Rq+
  gi|1707232   345 NRDLIAPLELCYQSLHECGMGVIADGPLLDSLRRAVTFGLFLGRLDVRQD 394

                   seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                   + R+ D l  it  L++GsY +W E+KR  +L aELk +RPLl++
  gi|1707232   395 AARHRDALSEITDYLGMGSYADWDEDKRIAFLQAELKNRRPLLPAHFTPQ 444

                   EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    + ++vl + r +A  P  s G+Y+isma a sDvLAv LL +E g+ ++
  gi|1707232   445 ADTAEVLATCREIAAAPGASLGSYVISMAGAASDVLAVQLLLKEAGLTRP 494

                   LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                   +rvvPLFE LADL+ A   +e+L  +  Y+  + G qevm+GYsDs KDA
  gi|1707232   495 MRVVPLFETLADLDNAGPVMERLLGLPGYRAGLRGPQEVMIGYSDSAKDA 544

                   GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                   G  +AAW  Y+AqE ++++ +++ v L lFHGRGGtvGRGGGP H AiLs
  gi|1707232   545 GTTAAAWAQYRAQENLVRICRDHQVELLLFHGRGGTVGRGGGPAHAAILS 594

                   qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                   qPP  + G  R t qGE+i f FG   +  + L  + AA LE  + PP
  gi|1707232   595 QPPGSVAGRFRTTEQGEMIRFKFGLPSIAEQNLNLYLAAVLEATLLPPPP 644

                   PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                   P P WR Lm+++A      YRsvv   P FvEYFR  tPE E G++ +Gs
  gi|1707232   645 PEPAWRALMDQLAADGVKAYRSVVRENPDFVEYFRQSTPEQELGRLPLGS 694

                   RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                   RPaKR+ +GGiesLRAiPWiF WtqtR  LP WLG   A   A+ +
  gi|1707232   695 RPAKRR-AGGIESLRAIPWIFGWTQTRLMLPAWLGWETALSNALARGQGE 743

                   lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                   l  L  m ++WPFFR  +D+lEmv AK D  iA  yD+ Lv  eL P G
  gi|1707232   744 L--LAQMREQWPFFRTRIDMLEMVLAKADAQIAEAYDERLVQPELLPLGA 791

                   sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    LRd      + +L + G + lL   P     + LR+ Y+  L  +qA
  gi|1707232   792 HLRDLLSQSCQVVLGLTGQQVLLAHSPETLEFISLRNTYLDPLHRLQAEL 841

                   LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                   L R R            s+E A +                    LE  L+
  gi|1707232   842 LARSR------------SREAALDS------------------PLEQALL 861

                   LtmKGiAAGmqntG<-*
                   +t+ GiAAG+ ntG
  gi|1707232   862 VTVAGIAAGLRNTG    875

gi|153839017|ref|ZP_01991684.1|: domain 1 of 1, from 1 to 877: score 774.1, E = 9.9e-230
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                  + e    ++    +l + L+  + D HGe++ E
  gi|1538390     1    -------------MNEKYAALKSNVRMLGHLLgNTIRDAHGEEIFEK 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls        + + e L   +  L       v +a+   LnL n
  gi|1538390    35 VETIRKLSKSAQAGNQADR-ESLIEEIKHLPDEQLTPVTRAFNQFLNLTN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +   R   +         E +A     i   + kLv     s  +
  gi|1538390    84 IAEQYHTISRHCEEHIC------EPDA-----INSLFSKLVQND-VSKLD 121
```

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                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+   ++
  gi|1538390   122 TAQAVRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSSKER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    k  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
  gi|1538390   172 KKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWEAVPDFL 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R +   LK   + E lP d+  ++FssWmGGDRDG nP vt  vtR+v L
  gi|1538390   222 REMNDRLKSY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHSVTREVLL 269

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa lY++ + +L+ Elsm   nd +R  A E +
  gi|1538390   270 LSRWKAADLYLNDINELISELSMTVSNDQVRELAGEDQH----------- 308

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR iL + R  L  t++     + +G   ++  A   k
  gi|1538390   309 ----------EPYRAILKQLRALLNETKDILDAKI-HG-QKLAVKAPLQK 346

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    vE+  +PL  CY+sL eCG  viADGsLLD LR v  FG+ Lv+LDiRqE
  gi|1538390   347 VEQLWDPLYACYQSLHECGMGVIADGSLLDTLRRVKAFGVHLVRLDIRQE 396

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+ Dvl  +t+ L+iG Y +WsE+ +  +L  EL  KRPLl+ D
  gi|1538390   397 STRHADVLSELTRYLGIGDYEQWSEQDKIAFLTNELASKRPLLPRDWEPS 446

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    E vk+vld+ +++A  P ++FGaY+isma + sDvLAv LL  E g
  gi|1538390   447 EPVKEVLDTCKIIALQPREAFGAYVISMARTASDVLAVHLLLQEAGCPYR 496

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    + v PLFE L DL+ A   +++L siD Y+  i+  q vm+GYsDs KDA
  gi|1538390   497 MDVCPLFETLDDLNNAESVIKQLMSIDLYRGFIQNHQMVMIGYSDSAKDA 546

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G +sA W  Y A E ++KvA + Gv L+lFHGRGGtvGRGG P H A+Ls
  gi|1538390   547 GVMSAGWAQYHAMESLVKVAEDEGVELTLFHGRGGTVGRGGAPAHAALLS 596

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|1538390   597 QPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNLYASAILEANLLPPPE 646

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EWR+Lme +  v  E YR vv  EP Fv YFR AtPElE Gk+ +Gs
  gi|1538390   647 PKQEWRDLMEVLSEVSCEAYRGVVRGEPDFVPYFRQATPELELGKLPLGS 696

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ +dK  +
  gi|1538390   697 RPAKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSVDKGHQA 746

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l  L+Em +eWPFF   l +lEmv+ K    i   yD+ Lv  +L+P G+
  gi|1538390   747 L--LEEMCREWPFFSTRLGMLEMVYTKCNMEISRYYDQRLVEPQLQPLGD 794

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR++ +   + +L +     l+  DP+ +  +RLR+ Y+  Ln++qA
  gi|1538390   795 RLREQLQRDIKSVLNVENNENLMQSDPWGQESIRLRNIYVEPLNMLQAEL 844

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                                 te+ +  LE+ L+
  gi|1538390   845 LYRTRQ------------------------------TEEASANLEEALM 863

                    LtmKGiAAGmqntG<-*
                    +t+ GiAAGm ntG
  gi|1538390   864 VTIAGIAAGMRNTG    877

gi|268593405|ref|ZP_06127626.1|: domain 1 of 1, from 1 to 879: score 773.6, E = 1.4e-229
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  ++    vs           +l k L+D +++  Ged+ +
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gi|2685934     1    -MNQQYSAMR-SNVS-----------MLGKLLgDTIKEALGEDILDK 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       + ++ + L   L  L   + + vA+a+   LnL n
gi|2685934    35 VESIRKLSKSSRAGNEVQR-QKLLMTLQNLSNDELLPVARAFNQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +       +   hG+ a    A     +   + +L  k   +  +
gi|2685934    84 VAEQYH-------SISPHGEAASNPVA-----LKNLFSRLKGKN-FTDGD 120

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s++LvltAHPt  +RR L+ K   + nCL+qL   D+   ++
gi|2685934   121 IQKAVEQLSIELVLTAHPTEIARRTLIHKLVEVNNCLSQLDHDDIADYER 170

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L   +   + tDEiR+ +PtP DE + G + +   +W+GvP FL
gi|2685934   171 NNIMRRLRQLVAQSWHTDEIRKIRPTPIDEAKWGFAVVENSLWEGVPAFL 220

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R     L    i   lP ++  i+F+sWmGGDRDG nP vt +vtR v L
gi|2685934   221 REFNEQLED-SIGAVLPVEANPIRFTSWMGGDRDG-NPNVTADVTRQVLL 268

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa l++  +  L+ Elsm     ELR+ A         d
gi|2685934   269 LSRWKAADLFLKDIQVLVSELSMTEATPELRALA------GGDD------ 306

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                             EPYR i  + R +L+ t E     + +G   ++      +
gi|2685934   307 --------VDEPYRQIAKNLRSQLFSTLEYLERRV-KGEQVLPPADLLVD 347

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      +  +PL  CY+sL  C  k+iA G LLD LR +  FGL Lv++D+RqE
gi|2685934   348 NAQLWDPLYACYQSLIACNMKIIANGQLLDTLRRIRSFGLQLVRIDVRQE 397

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+t+ +  +t+ L++G Y +WsEe +q +LlaEL+  RPL++ D
gi|2685934   398 STRHTEAIAELTQYLGLGDYSQWSEEEKQQFLLAELQSLRPLIPQDWQPS 447

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     E ++v ++ rv+A    Ds  aY+isma  PsDvLAv LL +E g
gi|2685934   448 AETQEVFETCRVIAKAKNDSVAAYVISMAKVPSDVLAVKLLLKENGASVR 497

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    L+v PLFE L DL+ A   + kL si+WY+n id +q vm+GYsDs KDA
gi|2685934   498 LPVAPLFETLEDLNNAESVMTKLLSIEWYRNLIDDRQMVMIGYSDSAKDA 547

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y+Aq+ +iK   k Gv L+lFHGRGGt+GRGG P H A+Ls
gi|2685934   548 GVMAASWAQYRAQDALIKLCEKEGVTLTLFHGRGGTIGRGGAPAHSALLS 597

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP
gi|2685934   598 QPPGSLKGGLRVTEQGEMIRFKFGLPQVTISSLALYASAILEANLLPPPE 647

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EW+ +m+ +  v    YR  v   P Fv YFR AtPElE Gk+ +Gs
gi|2685934   648 PKDEWKSVMDSLSDVSCAMYRDYVREQPDFVPYFRAATPELELGKLPLGS 697

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+P GG+e+LRAiPWiFaWtq R  LP WLG GAA Kh i+K+ K
gi|2685934   698 RPAKRRPTGGVETLRAIPWIFAWTQNRLMLPAWLGAGAALKHVIEKEGKQ 747

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                       L Em+++WPFF   + +lEmv+AK D  +A  yD+ Lv E L+P G+
gi|2685934   748 -AILDEMWQQWPFFNTRIAMLEMVYAKADLWLAEYYDHRLVEERLWPLGQ 796

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LRd+  E  + +L +     l+   P++   + LR+ Y   Lnv+qA
gi|2685934   797 KLRDQLSEDIKSVLAVSKDEALMADLPWIAESIALRNVYTDPLNVLQAEL 846

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
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                    L R R                 +E+   +d            P +E  L+
  gi|2685934   847 LHRSRQ----------------QEQ---PD------------PRVEQALM 865

                    LtmKGiAAGmqntG<-*
                    +t+ G+AAGm ntG
  gi|2685934   866 VTIAGVAAGMRNTG    879

gi|209696160|ref|YP_002264090.1|: domain 1 of 1, from 1 to 876: score 772.7, E = 2.5e-229
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  +  +L    vs           +l + L+  + D HGe+L
  gi|2096961     1    -MNEKYAALK-SNVS-----------MLGHLLgNTIRDAHGEELLAK 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDail.vAkailHmLnLA
                    v     ls       D  + + L   + sL P D + +vA+a++  LnL
  gi|2096961    35 VETIRKLSKTARAGSDNDR-NALIEEIKSL-PNDQLTpVARAFSQFLNLT 82

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE  +   R   +         E +A     i   + kL ++ n s
  gi|2096961    83 NMAEQYHTISRHCEEHVC------EPDA-----ISSLFSKL-SQNNISKL 120

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    +  +A++   ++LvltAHPt  +RR ++ K  +i  CL++L   D+   +
  gi|2096961   121 DTVQAVRELNIELVLTAHPTEIARRTMINKLVKINECLSKLELSDISFSE 170

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    ++  +  L   i  A+  D iR  +PtP DE + G + +   +W+G+P F
  gi|2096961   171 REKTERRLEQLIAQAWHSDVIRQERPTPLDEAKWGFAVVENSLWQGIPDF 220

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    LR  D  L n  + E lP d+  ++ ssWmGGDRDG nP vt  +tR+v
  gi|2096961   221 LREFDQRLEN-HLGEGLPIDARPVHMSSWMGGDRDG-NPFVTHTITREVM 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  Aa lY+  v +L+ Elsm +C dE+R       + a  +
  gi|2096961   269 LLSRWKAADLYLKDVNELISELSMVKCTDEVR-------KLAGDQ----- 306

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vy
                                EPYR iL + R  L  t E    L A+   e+  + ++
  gi|2096961   307 ----------HEPYRAILKQLRTLLNDTLE---NLDAQMKGELTNNKpIL 343

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     + E+   PL  CY+sL  CG  +iA+GsLLD LR v  FG  Lv+LDiR
  gi|2096961   344 RNAEQLWLPLHACYQSLHACGMGIIAEGSLLDTLRRVKAFGAHLVRLDIR 393

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+  vl  +t+ L+iG Y +WsE+ +  +L+ EL+ KRPLl+ D
  gi|2096961   394 QESTRHSNVLSELTRYLGIGDYDQWSEQDKISFLVNELSSKRPLLPRDWT 443

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                     t Ev++v+d+ +++AE   ++ G+Y+isma + sDvLAv LL  E g
  gi|2096961   444 PTAEVQEVIDTCKIVAEQSKEALGSYVISMARTASDVLAVHLLLQEAGCP 493

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                      + v PLFE L DL+     +e+LFsiDWY+  i+  q vm+GYsDs K
  gi|2096961   494 FRMDVCPLFETLDDLNRSKEVMEQLFSIDWYRGFIQNHQMVMIGYSDSAK 543

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG +sA W  Y A E ++ v  k  + L+lFHGRGGt+GRGG P H A+
  gi|2096961   544 DAGVMSAGWAQYSAMEALVDVCEKESIELTLFHGRGGTIGRGGAPAHAAL 593

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|2096961   594 LSQPPKSLKGGLRVTEQGEMIRFKLGLPEVAVNSFNLYASAILEANLLPP 643

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      Pk EWR+Lme +  v  E YR +v  E  Fv YFR AtPElE Gk+ +
  gi|2096961   644 PEPKQEWRDLMEVLSEVSCEAYRNIVRGEKDFVPYFRAATPELELGKLPL 693

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ idK
  gi|2096961   694 GSRPAKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSIDKGH 743
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                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    + l  L+Em +eWPFF   l +lEmv+ K  P +   yD+ L    L+P
  gi|2096961   744 QEL--LEEMCREWPFFSTRLGMLEMVYTKCNPQMSEYYDQRLTDKSLWPL 791

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G +LR++ +   + +L +     l+E DP+    +RLR+ Y+  Ln++qA
  gi|2096961   792 GVRLRNQLQADIKAVLNVENSDHLMESDPWGSESIRLRNIYVDPLNMLQA 841

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R                                  e+ +P LE+
  gi|2096961   842 ELLYRTRQ------------------------------QEETSPELEEA 860

                    LiLtmKGiAAGmqntG<-*
                    L++t+ GiAAGm ntG
  gi|2096961   861 LMVTIAGIAAGMRNTG    876

gi|218551053|ref|YP_002384844.1|: domain 1 of 1, from 1 to 883: score 772.0, E = 4.2e-229
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L++ ++D  Ge + +
  gi|2185510     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILDR 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       D+ + +EL + L  L   + + vA+a++  LnLAn
  gi|2185510    35 VETIRKLSKSSRAGNDADR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+ k       Ea    E  i  tl+kL  + + s +
  gi|2185510    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPDLSEAT 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K   +  CL qL  KD+   ++
  gi|2185510   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNTCLKQLDNKDLADYER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|2185510   172 NQLMRRLRQLIAQSWHTDEIRKQRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G   +lP d   ++F+sWmGGDRDG nP vt ++tR v
  gi|2185510   222 RELNEQLeENLGF--KLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  A+ l++  +  L+ Elsm     EL +   E       +
  gi|2185510   269 LLSRWKATDLFLKDIQVLVSELSMVEATPELLALVGE-------E----- 306

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR ++ + R +L  t       L +G      e   t
  gi|2185510   307 --------GAAEPYRYLMKNLRSRLMTTQAWLEARL-KGQKLPKPEGLLT 347

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    + Ee  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|2185510   348 QNEELWEPLYACYQSLQACGMGIIANGDLLDTLRRVKCFGVPLVRIDIRQ 397

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|2185510   398 ESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWQP 447

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|2185510   448 SAETREVLDTCQVIAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|2185510   498 AMPVAPLFETLDDLNNANDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 547

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|2185510   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
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                    sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2185510   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPP 647

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR++m+e+ v+  + YR  v     Fv YFR+AtPE E Gk+ +G
  gi|2185510   648 EPKESWRRIMDELSVISCDVYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
  gi|2185510   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lva eL+P G
  gi|2185510   747 Q-SELETMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVAKELWPLG 795

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    k+LR+  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|2185510   796 KELRNLLEEDIKVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 845

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                         L + n +++  P +E  L
  gi|2185510   846 LLHRSR-------------------------LTEQN-GKEPDPRVEQAL 868

                    iLtmKGiAAGmqntG<-*
                    ++t+ G+AAGm ntG
  gi|2185510   869 MVTIAGVAAGMRNTG    883

gi|27364763|ref|NP_760291.1|: domain 1 of 1, from 1 to 877: score 771.7, E = 5.3e-229
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  +  +L    vs           +l + L+  +q+ HG+++ E
  gi|2736476     1    -MNEKYAALK-SNVS-----------MLGHLLgNTIQEAHGDEILEK 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls        + + + L   + sL       vA+a+   LnL n
  gi|2736476    35 VETIRKLSKSARAGNQADR-NNLIEEIKSLPDEQLTPVARAFNQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R             E +A     i   + kL   +     +
  gi|2736476    84 IAEQYHTISRHCDAHVC------EPDA-----INTLFAKLGQNG-INKLD 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+   ++
  gi|2736476   122 TAQAIRELNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSYKER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +  +  L   i   +  D iR+ +PtP DE + G + +   +W+ vP FL
  gi|2736476   172 HKTEKRLEQLIAQSWHSDVIRKQRPTPLDEAKWGFAVVENSLWEAVPDFL 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R  D  LK   +   lP d+  ++FssWmGGDRDG nP vt  vtR+v L
  gi|2736476   222 RELDEKLKDY-LDQGLPIDARPVHFSSWMGGDRDG-NPFVTHTVTREVLL 269

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa lY+  + +L+ Elsm +Cnd +R  A E       d
  gi|2736476   270 LSRWKAADLYLKDINELISELSMTKCNDTVRQLAGE-------D------ 306

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi..seisEeAvy
                              EPYR iL + R  L  t+E    +L   i++  ++  A
  gi|2736476   307 --------EHEPYRAILKQLRTLLSDTKE----ILDAKIngQKLAVKAPL 344

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                      vE+  +PL  CY+sL eCG   iA+GsLLD LR v  FG+ Lv+LDiR
  gi|2736476   345 QSVEQLWDPLFACYQSLRECGMSMIAEGSLLDTLRRVKAFGVHLVRLDIR 394

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+ Dvl  +t+ L+iG Y  WsE+ +  +L  EL  KRPLl+ D
  gi|2736476   395 QESTRHADVLSELTRYLGIGDYNHWSEQDKIAFLTNELASKRPLLPRDWQ 444

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                      E vk+vld+ +++A    ++FGaY+isma + sDvLAv LL  E g
  gi|2736476   445 PSEQVKEVLDTCKIIAAQSREAFGAYVISMAKTASDVLAVHLLLQESGCP 494
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                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                      + v PLFE L DL+ A A +++L siD Y+  i+  q vm+GYsDs K
  gi|2736476   495 YRMDVCPLFETLDDLNNAEAVIKQLMSIDLYRGFIQNHQMVMIGYSDSAK 544

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG ++A W  Y A E ++ vA + G+ L+lFHGRGGt+GRGG P H A+
  gi|2736476   545 DAGVMAAGWAQYHAMEALVNVAEQEGIELTLFHGRGGTIGRGGAPAHAAL 594

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|2736476   595 LSQPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNMYASAILEANLLPP 644

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      Pk EWR+Lme +  v  E YRsvv  EP Fv YFR AtPElE Gk+ +
  gi|2736476   645 PEPKQEWRDLMEVLSQVSCEAYRSVVRGEPDFVPYFRQATPELELGKLPL 694

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ idK
  gi|2736476   695 GSRPAKRNPNGGVESLRAIPWIFSWSQNRLLLPAWLGAGEAIQYSIDKGH 744

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    + l  L+Em +eWPFF   l +lEmv+ K    i   yD+ L    L P
  gi|2736476   745 QAL--LEEMCREWPFFSTRLGMLEMVYLKCNSEISRYYDERLADKSLLPL 792

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G++LRd+ +   + +L +     l+  DP+ +  +RLR+ Yi  Ln++qA
  gi|2736476   793 GDRLRDQLQSDIKAVLNVENNENLMQSDPWGQESIRLRNIYIEPLNMLQA 842

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R                        +++v           LE+
  gi|2736476   843 ELLYRTRQ----------------------AGVVSEA--------LEEA 861

                    LiLtmKGiAAGmqntG<-*
                    L++t+ GiAAGm ntG
  gi|2736476   862 LMVTIAGIAAGMRNTG    877

gi|194471160|ref|ZP_03077144.1|: domain 1 of 1, from 17 to 912: score 771.6, E = 5.6e-229
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +   q R  v   + e+   ++    +l k L++ ++D  Ge + +
  gi|1944711    17    AGQLQQRWGVWDHMNEQYSALRSNVSMLGKVLgETIKDALGEHILDR 63

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++ + +EL + L  L   + + vA+a++  LnLAn
  gi|1944711    64 VETIRKLSKSSRAGNEANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 112

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+ k       Ea    E  i  tl+kL  + +   +
  gi|1944711   113 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPDLNDAT 150

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K + i nCL qL   D+   ++
  gi|1944711   151 IKKAVESLSLELVLTAHPTEITRRTLIHKMGEINNCLKQLDNTDIADYER 200

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + +   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|1944711   201 HQVMRRLRQLIAQSWHTDEIRKQRPSPVDEAKWGFAVVENSLWQGVPNYL 250

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G   +lP d   ++F+sWmGGDRDG nP vt ++tR v
  gi|1944711   251 RELNEQLeENLGY--KLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVL 297

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  A+ l++  +  L+ Elsm     EL +   E     a++
  gi|1944711   298 LLSRWKATDLFLKDIHVLVSELSMVDATPELLALVGE---EGASE----- 339

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vy
                                PYR ++   R +L  t       L      ++  A+
  gi|1944711   340 ------------PYRYLMKKLRARLMATQSWLEARLKG--EKLPKPAgLL 375

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
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                    t+ E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiR
  gi|1944711   376 TQNEQLWEPLYACYQSLQACGMGIIANGELLDTLRRVKCFGVPLVRIDIR 425

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+t+ l  it+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|1944711   426 QESTRHTEALGEITRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWE 475

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                       + ++vl++ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|1944711   476 PSNDTREVLETCKVIAEAPKGSIAAYVISMAKTPSDVLAVHLLLKEAGIG 525

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                     +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs K
  gi|1944711   526 FAMPVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAK 575

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+
  gi|1944711   576 DAGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAAL 625

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|1944711   626 LSQPPGSLKGGLRVTEQGEMIRFKYGLPEVTVSSLSLYTSAILEANLLPP 675

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      Pk  WR++m+e+ v+  E YR  v     Fv YFR+AtPE E Gk+ +
  gi|1944711   676 PEPKDSWRHIMDELSVISCETYRGYVRENKDFVPYFRSATPEQELGKLPL 725

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D
  gi|1944711   726 GSRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DG 774

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    K    L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lva  L+P
  gi|1944711   775 KQ-SELEAMCRDWPFFSTRLGMLEMVFSKADLWLADYYDQRLVAKTLWPL 823

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    Gk+LRd  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|1944711   824 GKELRDLLEEDIKVVLAIANDSHLMADLPWIAESIQLRNVYTDPLNVLQA 873

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R                +E+ k +d            P +E
  gi|1944711   874 ELLYRSR---------------LTEEQGKSPD------------PRVEQA 896

                    LiLtmKGiAAGmqntG<-*
                    L++t+ G+AAGm ntG
  gi|1944711   897 LMVTIAGVAAGMRNTG    912

gi|26988237|ref|NP_743662.1|: domain 1 of 1, from 3 to 875: score 771.4, E = 6.2e-229
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        iD  LR      v           +L +   + +   HG+    +
  gi|2698823     3    DIDVRLRE----DVH----------VLGELLGETIRQQHGDA---FL 32

                    qECYElsAeYEGKkDtkKLeE.LGakLtsLdPaDailvAkailHmLnLAn
                    q   ++      K D +  +E+L + L  L+  D + vA+a+   LnLAn
  gi|2698823    33 QKIEDI--RHSAKADRRGPGEqLSSTLADLAEEDLLPVARAFNQFLNLAN 80

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +l  RR   +        Ea+      + E l +L   +  s +
  gi|2698823    81 MAEQYQLIRRRDADQPE----PFEAQV-----LPELLGRLKQAG-HSNDA 120

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                        L    + LvltAHPt  +RR L+qK   i   La    +D+t+ ++
  gi|2698823   121 LARQLAKLDIQLVLTAHPTEVARRTLIQKYDAIAGQLAAQDHRDLTPAER 170

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + + E L R i  A+ t+EiRR++PtP DE + G + i   +W+ +P  L
  gi|2698823   171 QQVRERLRRLIAEAWHTEEIRRTRPTPVDEAKWGFAVIEHSLWHAIPSHL 220

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R+vD AL       RlP ++  i+F+sWmGGDRDG nP vt  vtR+v L
  gi|2698823   221 RKVDKALLE-ATGLRLPLEAAPIRFASWMGGDRDG-NPNVTAAVTREVLL 268
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                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    LaR mAa l++  ++ L  Elsm   nd LR
  gi|2698823   269 LARWMAADLFLRDIDALAAELSMQQANDTLR------------------ 299

                    iEFWKqv.PPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vy
                        Kqv+   EPYR +L + RD+L  tR  a   L    s+ +  A+v
  gi|2698823   300 ----KQVgDSAEPYRAVLKQLRDRLRATRAWAHSALT---SNQPAGAdVL 342

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     +  e + PLELCY+sL eCG  viA+G LLD LR   tFGL L +LD+R
  gi|2698823   343 VDNRELIAPLELCYQSLHECGMGVIAEGPLLDCLRRAVTFGLFLGRLDVR 392

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    q++ R+ D l  it  L++G Y +W Ee+R  +L aELk +RPLl++
  gi|2698823   393 QDAARHRDALTEITDYLGLGRYADWDEEQRIAFLQAELKNRRPLLPAHFK 442

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                       + ++vl + r +A  P  s G+Y+isma a sDvLAv LL +E g+
  gi|2698823   443 PQADTAEVLATCREVAAAPAASLGSYVISMAGAASDVLAVQLLLKEAGLT 492

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                    +++rvvPLFE LADL+ A   +++L  +  Y+  + G qevm+GYsDs K
  gi|2698823   493 RPMRVVPLFETLADLDNAGPVMQRLLGLPGYRAGLRGPQEVMIGYSDSAK 542

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG  +AAW  Y+AqE ++++  ++ v L lFHGRGGtvGRGGGP H Ai
  gi|2698823   543 DAGTTAAAWAQYRAQENLVRICAEHQVELLLFHGRGGTVGRGGGPAHAAI 592

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPP  + G  R t qGE+i f FG   +  + L  + AA LE  + PP
  gi|2698823   593 LSQPPGSVAGRFRTTEQGEMIRFKFGLPGIAEQNLNLYLAAVLEATLLPP 642

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      P+P WR++m+++A      YRsvv   P FvEYFR  tPE E G++ +
  gi|2698823   643 PPPQPAWREVMDQLAADGVQAYRSVVRENPDFVEYFRQSTPEQELGRLPL 692

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKR+ +GGiesLRAiPWiF WtqtR  LP WLG   A   A+ +
  gi|2698823   693 GSRPAKRR-AGGIESLRAIPWIFGWTQTRLMLPAWLGWETALTNALARGQ 741

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                      l  L  m ++WPFFR  +D+lEmv AK D  iA  yD+ Lv   L+P
  gi|2698823   742 GEL--LAQMREQWPFFRTRIDMLEMVLAKADAQIAEAYDERLVQPHLRPL 789

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G  LRd      + +L + G   lL   P     + LR+ Y+  L  +qA
  gi|2698823   790 GAHLRDLLSQSCQVVLGLTGQPVLLAHSPETLEFISLRNTYLDPLHRLQA 839

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R            s+E A +                     LE
  gi|2698823   840 ELLARSR------------SREAALDS------------------PLEQA 859

                    LiLtmKGiAAGmqntG<-*
                    L++t+ GiAAG+ ntG
  gi|2698823   860 LLVTVAGIAAGLRNTG    875

gi|261211215|ref|ZP_05925504.1|: domain 1 of 1, from 1 to 876: score 771.3, E = 6.7e-229
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  +  +L    vs           +l + L+  +q   G+ + E
  gi|2612112     1    -MNEKYAALK-SNVS-----------MLGRLLgQTIQAADGDVILEK 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls        + + e L   +  L       vA+a+   LnL n
  gi|2612112    35 VETIRKLSKSARTGNQADR-ELLIEEIKNLPNHQLTPVARAFNQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R   +         E +A     +   + kL      s  +
  gi|2612112    84 IAEQYHTISRHCESHVN------ELDA-----VGSLFAKLAQNS-VSKFD 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
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                    +A++   ++LvltAHPt   RR ++ K  +i  CL++L   ++   ++
  gi|2612112   122 TAQAIRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSELSSKER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
  gi|2612112   172 HKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWNAVPEFL 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R  D  +K   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
  gi|2612112   222 RELDEQVKS-HLGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITREVLL 269

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa lY+  + +L+ Elsm +Cn+ +Rv A E       +
  gi|2612112   270 LSRWKAADLYLTDINELVSELSMTKCNEAVRVLAGE-------E------ 306

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR iL + R  L  t +     L      ++  A   +
  gi|2612112   307 ---------HEPYRAILKQLRGLLQETIDILEAKLNG--QKLAVKAPLQN 345

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    v++  EPL  CY+sL eCG  viADGsLLD LR +  FG+ Lv+LDiRqE
  gi|2612112   346 VDQLWEPLYACYQSLHECGMGVIADGSLLDTLRRIKAFGVHLVRLDIRQE 395

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+ +v+  +t+HL+iG Y +WsE+ +  +L +EL  KRPll+ D
  gi|2612112   396 SSRHAEVISELTRHLGIGDYNQWSEQDKIAFLTTELNSKRPLLPRDWQPS 445

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    E vk+vld+ +++A    D+FGaY+isma + sDvLAv LL  E g
  gi|2612112   446 EPVKEVLDTCKIIAAQSKDAFGAYVISMARTASDVLAVHLLLQEAGCPYR 495

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    + v PLFE L DL+ A   + +L siD Y+  i+  q vm+GYsDs KDA
  gi|2612112   496 MDVCPLFETLDDLNNAESVIRQLMSIDLYRGFIQNHQMVMIGYSDSAKDA 545

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y+A + ++Kv  + G+ L+lFHGRGGt+GRGG P H A+Ls
  gi|2612112   546 GVMAAGWAQYRAMDALVKVSEEAGIELTLFHGRGGTIGRGGAPAHAALLS 595

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|2612112   596 QPPKSLKGGLRVTEQGEMIRFKLGLPEVAVNSFNMYASAILEANLLPPPE 645

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EWR+Lm+ +  v  E YR vv  EP Fv YFR AtPElE Gk+ +Gs
  gi|2612112   646 PKQEWRDLMDVLSEVSCEAYRHVVRGEPDFVPYFRQATPELELGKLPLGS 695

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RP+KR P GG+esLRAiPWiF+W q R  LP WLG G A ++ idK  +
  gi|2612112   696 RPSKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQFSIDKGHQA 745

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv   L+P G+
  gi|2612112   746 L--LEEMCREWPFFSTRLGMLEMVYTKCSAEIARYYDERLVEPALRPLGE 793

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR++ +   + +L +     l+  DP+ +  +RLR+ Y+  Ln++qA
  gi|2612112   794 KLRAQLQKDIKTVLNVENNENLMQSDPWGQESIRLRNIYVEPLNMLQAEL 843

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                                 +e+ aP LE+ L+
  gi|2612112   844 LYRTRQ------------------------------SEHLAPELEEALM 862

                    LtmKGiAAGmqntG<-*
                    +t+ GiAAGm ntG
  gi|2612112   863 VTIAGIAAGMRNTG    876

gi|167032123|ref|YP_001667354.1|: domain 1 of 1, from 3 to 875: score 771.1, E = 8e-229
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        iD  LR      v           +L +   + +   HG+    +
  gi|1670321     3    DIDVRLRE----DVH----------VLGELLGETIRQQHGDA---FL 32
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                qECYElsAeYEGKkDtkKLeE.LGakLtsLdPaDailvAkailHmLnLAn
                q   ++      K D +  +E+L + L  L+  D + vA+a+   LnLAn
gi|1670321    33 QKIEDI--RHSAKADRRGPGEqLSSTLADLAEDDLLPVARAFNQFLNLAN 80

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                +AE  +l  RR   +        Ea       + E l +L   +  s +
gi|1670321    81 MAEQYQLIRRRDADQPE----PFEARV-----LPELLARLKQAG-HSNDA 120

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    L    + LvltAHPt  +RR L+qK   i   La    +D+ + ++
gi|1670321   121 LARQLAKLDIQLVLTAHPTEVARRTLIQKYDAIAGQLAAQDHRDLSPAER 170

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                + + E L R i  A+ t+EiRR++PtP DE + G + i   +W+ +P  L
gi|1670321   171 QQVRERLRRLIAEAWHTEEIRRTRPTPVDEAKWGFAVIEHSLWHAIPSHL 220

                RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                R+vD AL       RlP ++  i+F+sWmGGDRDG nP vt  vtR+v L
gi|1670321   221 RKVDKALLE-ATGLRLPLEAAPIRFASWMGGDRDG-NPNVTAAVTREVLL 268

                LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                LaR mAa l++  ++ L  Elsm   nd LR R  +      +
gi|1670321   269 LARWMAADLFLRDIDALAAELSMQQANDALRERVGD------SA------ 306

                iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vyt
                          EPYR +L + RD+L  tR  a   LA   s+ +  A+v
gi|1670321   307 ----------EPYRAVLKQLRDRLRATRAWAHSALA---SNQPAGAeVLV 343

                kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                +  + + PLELCY+sL +CG  viA+G LLD LR   tFGL L +LD+Rq
gi|1670321   344 DNRDLIAPLELCYQSLHDCGMGVIAEGPLLDCLRRAVTFGLFLGRLDVRQ 393

                EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                ++ R+ D l  it  L++G Y +W Ee+R  +L aELk +RPLl++
gi|1670321   394 DAARHRDALTEITDYLGLGRYADWDEEQRIGFLQAELKNRRPLLPAHFKP 443

                tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                  + ++vl + r +A  P  s G+Y+isma a sDvLAv LL +E g+ +
gi|1670321   444 QADTAEVLATCREVAAAPAASLGSYVISMAGAASDVLAVQLLLKEAGLTR 493

                tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                ++rvvPLFE LADL+ A   +++L  +  Y+  + G qevm+GYsDs KD
gi|1670321   494 PMRVVPLFETLADLDNAGPVMQRLLGLPGYRAGLRGPQEVMIGYSDSAKD 543

                AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                AG  +AAW  Y+AqE ++++  ++ v L lFHGRGGtvGRGGGP H AiL
gi|1670321   544 AGTTAAAWAQYRAQENLVRICAEHQVELLLFHGRGGTVGRGGGPAHAAIL 593

                sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                sqPP  + G  R t qGE+i f FG   +  + L  + AA LE  + PP
gi|1670321   594 SQPPGSVAGRFRTTEQGEMIRFKFGLPGIAEQNLNLYLAAVLEATLLPPP 643

                sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                 P+P WR+Lm+++A      YRsvv   P FvEYFR  tPE E G++ +G
gi|1670321   644 PPQPAWRELMDQLAADGVKAYRSVVRENPDFVEYFRQSTPEQELGRLPLG 693

                sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                sRPaKR+ +GGiesLRAiPWiF WtqtR  LP WLG   A   A+ +
gi|1670321   694 SRPAKRR-AGGIESLRAIPWIFGWTQTRLMLPAWLGWETALSNALARGQG 742

                nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                 l  L  m ++WPFFR  +D+lEmv AK D  iA  yD+ Lv   L P G
gi|1670321   743 EL--LAQMREQWPFFRTRIDMLEMVLAKADAQIAEAYDERLVQPHLLPLG 790

                ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                  LRd      + +L + G   lL   P     + LR+ Y+  L  +qA
gi|1670321   791 AHLRDLLSQSCQVVLGLTGQPVLLAHSPETLEFISLRNTYLDPLHRLQAE 840

                tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                 L R R            s+E A +                   LE  L
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  gi|1670321   841 LLARSR------------SREAALDS------------------PLEQAL 860

                   iLtmKGiAAGmqntG<-*
                   ++t+ GiAAG+ ntG
  gi|1670321   861 LVTVAGIAAGLRNTG    875

gi|170769681|ref|ZP_02904134.1|: domain 1 of 1, from 1 to 883: score 771.0, E = 8.2e-229
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  q  +L    vs           +l k L++ ++D  Ge + E
  gi|1707696     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILER 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls       D+ + +EL + L  L   + + vA+a++  LnLAn
  gi|1707696    35 VETIRKLSKSSRAGNDANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    AE  +      i+ k       Ea    E  i  tl+kL  + +   +
  gi|1707696    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPDLDAAT 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   +  A+   s +LvltAHPt   RR L+ K   +  CL qL  KD+   ++
  gi|1707696   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNTCLKQLDNKDIADYER 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|1707696   172 NQLMRRLRQLIAQSWHTDEIRKQRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                   RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   R     L+ n+G   +lP +   ++F+sWmGGDRDG nP vt ++tR v
  gi|1707696   222 RELNEQLeENLGY--KLPVEFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                   LL+R  A+ l++  +  L+ Elsm     EL +   E       +
  gi|1707696   269 LLSRWKATDLFLKDIQVLVSELSMVDATPELLALVGE-------E----- 306

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                             EPYR ++ + R +L  t       L +G      e   t
  gi|1707696   307 --------GAAEPYRYLMKNLRSRLMATQAWLEARL-KGEELPKPEGLLT 347

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   + Ee  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|1707696   348 QNEELWEPLYACYQSLQACGMGIIANGDLLDTLRRVKCFGVPLVRIDIRQ 397

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|1707696   398 ESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWQP 447

                   tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     E ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|1707696   448 SAETREVLDTCQVIAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                   tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                   +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|1707696   498 AMPVAPLFETLDDLNNANDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 547

                   AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                   AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|1707696   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                   sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                   sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|1707696   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPP 647

                   sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                    Pk  WR++m+e+ v+  + YR  v     Fv YFR+AtPE E Gk+ +G
  gi|1707696   648 EPKESWRRIMDELSVISCDVYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                   sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                   sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++   +
  gi|1707696   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVEDGKQ 747
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                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                    n   L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lva eL+  G
  gi|1707696   748 N--ELETMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVAKELWSLG 795

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    k+LR+  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|1707696   796 KELRNLQEEDIKVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 845

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                +E            + +  P +E  L
  gi|1707696   846 LLHRSRQ----------------AEK-----------EGHEPDPRVEQAL 868

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|1707696   869 MVTIAGIAAGMRNTG    883

gi|161486595|ref|NP_935797.2|: domain 1 of 1, from 1 to 877: score 770.7, E = 1e-228
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  +  +L    vs           +l + L+  +q+ HG+++ E
  gi|1614865     1    -MNEKYAALK-SNVS-----------MLGHLLgNTIQEAHGDEILEK 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls        + + + L   + sL       vA+a+   LnL n
  gi|1614865    35 VETIRKLSKSARAGNQADR-NNLIEEIKSLPDEQLTPVARAFNQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R             E +A     i   + kL   +     +
  gi|1614865    84 IAEQYHTISRHCDAHVC------EPDA-----INTLFAKLGQNG-INKLD 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+   ++
  gi|1614865   122 TAQAIRELNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSYKER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +  +  L   i   +  D iR+ +PtP DE + G + +   +W+ vP FL
  gi|1614865   172 HKTEKRLEQLIAQSWHSDVIRKQRPTPLDEAKWGFAVVENSLWEAVPDFL 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R  D  LK   +   lP d+  ++FssWmGGDRDG nP vt  vtR+v L
  gi|1614865   222 RELDEKLKDY-LDQGLPIDARPVHFSSWMGGDRDG-NPFVTHTVTREVLL 269

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa lY+  + +L+ Elsm +Cnd +R  A E       d
  gi|1614865   270 LSRWKAADLYLKDINELISELSMTKCNDTVRQLAGE-------D------ 306

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi..seisEeAvy
                              EPYR iL + R  L  t+E    +L   i++  ++  A
  gi|1614865   307 --------EHEPYRAILKQLRTLLSDTKE----ILDAKIngQKLAVKAPL 344

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                      vE+  +PL  CY+sL eCG   iA+GsLLD LR v  FG+ Lv+LDiR
  gi|1614865   345 QSVEQLWDPLFACYQSLRECGMSMIAEGSLLDTLRRVKAFGVHLVRLDIR 394

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+ Dvl  +t+ L+iG Y  WsE+ +  +L  EL  KRPLl+ D
  gi|1614865   395 QESTRHADVLSELTRYLGIGDYNHWSEQDKIAFLTNELASKRPLLPRDWQ 444

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                      E vk+vld+ +++A    ++FGaY+isma + sDvLAv LL  E g
  gi|1614865   445 PSEPVKEVLDTCKIIAAQSREAFGAYVISMAKTASDVLAVHLLLQESGCP 494

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                      + v PLFE L DL+ A A +++L siD Y+  i+  q vm+GYsDs K
  gi|1614865   495 YRMDVCPLFETLDDLNNAEAVIKQLMSIDLYRGFIQNHQMVMIGYSDSAK 544

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG ++A W  Y A E ++ vA + G+ L+lFHGRGGt+GRGG P H A+
  gi|1614865   545 DAGVMAAGWAQYHAMEALVNVAEQEGIELTLFHGRGGTIGRGGAPAHAAL 594

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
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  gi|1614865   595 LSQPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNMYASAILEANLLPP 644

                   vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                     Pk EWR+Lme +  v  E YRsvv  EP Fv YFR AtPElE Gk+ +
  gi|1614865   645 PEPKQEWRDLMEVLSQVSCEAYRSVVRGEPDFVPYFRQATPELELGKLPL 694

                   GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                   GsRPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ idK
  gi|1614865   695 GSRPAKRNPNGGVESLRAIPWIFSWSQNRLLLPAWLGAGEAIQYSIDKGH 744

                   KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                   + l  L+Em +eWPFF   l +lEmv+ K    i   yD+ L    L P
  gi|1614865   745 QAL--LEEMCREWPFFSTRLGMLEMVYLKCNSEISRYYDERLADKSLLPL 792

                   GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                   G++LRd+ +   + +L +     l+  DP+ +  +RLR+ Yi  Ln++qA
  gi|1614865   793 GDRLRDQLQSDIKAVLNVENNENLMQSDPWGQESIRLRNIYIEPLNMLQA 842

                   YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                     L R R                        +++v           LE+
  gi|1614865   843 ELLYRTRQ----------------------AGVVSEE--------LEEA 861

                   LiLtmKGiAAGmqntG<-*
                   L++t+ GiAAGm ntG
  gi|1614865   862 LMVTIAGIAAGMRNTG    877

gi|91213504|ref|YP_543490.1|: domain 1 of 1, from 1 to 883: score 770.6, E = 1.1e-228
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  q  +L    vs           +l k L++ ++D  Ge + E
  gi|9121350     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILER 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls       D+ + +EL + L  L   + + vA+a++  LnLAn
  gi|9121350    35 VETIRKLSKSSRAGNDANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    AE  +      i+ k       Ea    E  i  tl+kL  + + s +
  gi|9121350    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPELSEDT 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   +  A+   s +LvltAHPt   RR L+ K   +  CL qL  KD+   +
  gi|9121350   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNACLKQLDNKDIADYEH 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|9121350   172 NQLMRRLRQLIAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                   RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   R     L+ n+G   +lP +   ++F+sWmGGDRDG nP vt ++tR v
  gi|9121350   222 RELNEQLeENLGY--KLPVEFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                   LL+R  A+ l++  +  L+ Elsm     EL +   E       +
  gi|9121350   269 LLSRWKATDLFLKDIQVLVSELSMVEATPELLALVGE-------E----- 306

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                                EPYR ++ + R +L  t       L +G      e   t
  gi|9121350   307 --------GAAEPYRYLMKNLRSRLMATQAWLEARL-KGEELPKPEGLLT 347

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   + Ee  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|9121350   348 QNEELWEPLYACYQSLQACGMGIIANGDLLDTLRRVKCFGVPLVRIDIRQ 397

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|9121350   398 ESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWQP 447

                   tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     E ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|9121350   448 SAETREVLDTCQVIAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497
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                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|9121350   498 AMPVAPLFETLDDLNNANDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 547

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|9121350   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|9121350   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPP 647

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR++m+e+ v+  + YR  v     Fv YFR+AtPE E Gk+ +G
  gi|9121350   648 EPKESWRRIMDELSVISCDVYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++   +
  gi|9121350   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVEDGKQ 747

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                    n   L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lv   L+P G
  gi|9121350   748 N--ELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVDKALWPLG 795

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    k+LR+  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|9121350   796 KELRNLQEEDIKVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 845

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                 +E             +++  P +E  L
  gi|9121350   846 LLHRSRQ----------------AEK-----------EGQEPDPRVEQAL 868

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|9121350   869 MVTIAGIAAGMRNTG    883

gi|148977256|ref|ZP_01813883.1|: domain 1 of 1, from 1 to 876: score 770.5, E = 1.2e-228
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  +  +L    vs           +l + L+  +qD HG+ + E
  gi|1489772     1    -MNEKYAALK-SNVS-----------MLGRLLgNTIQDAHGDVILEK 34

                    vqECYEl..sAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    v     l++sA    K D   L E    +  L       vA+a+   LnL
  gi|1489772    35 VETIRKLskSARAGNKADRDSLVE---EIKNLPNEQLTPVARAFNQFLNL 81

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                     n+AE  +   R   +               E D+   l     + + s
  gi|1489772    82 TNMAEQYHTISRHCEEHVC------------EPDVLQSLFSKLNQNDISK 119

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                     +  +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+
  gi|1489772   120 LDAAQAVRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSHK 169

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++   +  L   i   +  D iR  +PtP DE + G + +   +W+ vP
  gi|1489772   170 ERAKTERRLEQLIAQGWHSDVIRQQRPTPLDEAKWGFAVVENSLWEAVPD 219

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    FLR +D  LK   + E lP d+  ++FssWmGGDRDG nP vt  +t++v
  gi|1489772   220 FLREMDGRLKGY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITKEV 267

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      L+R  Aa lY+  v +L+ Elsm +Cnd +R         a  +
  gi|1489772   268 LRLSRWKAADLYLGDVNELITELSMTKCNDAVR-------ELAGDE---- 306

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                                E YR iL + R  L nt E     L     e++
  gi|1489772   307 -----------HEAYRAILKNLRTLLNNTLEVLDAKLHD--TEVPKKETL 343

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     ++++   PL  CY+sL eCG  viADGsLLD LR    FG+ Lv+LD+R
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  gi|1489772   344 QNIDQLWTPLYACYQSLHECGMGVIADGSLLDTLRRLKAFGVHLVRLDVR 393

                   qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                   qEs R+ Dvl  +t+ L+iG Y +WsE+ +  +L  EL+ KRPLl+ D
  gi|1489772   394 QESTRHSDVLSELTRYLGIGDYDQWSEQDKIAFLTNELSSKRPLLPRDWE 443

                   ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                     E vk+vld+ +v+A  P ++FGaY+isma + sDvLAv LL  ECg
  gi|1489772   444 PSEQVKEVLDTCKVIAAQPREAFGAYVISMARTASDVLAVHLLLQECGCP 493

                   qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                     + v PLFE L DL+   A +++L siD Y+  i+  q vm+GYsDs K
  gi|1489772   494 YRMDVCPLFETLDDLNNSEAVMKQLMSIDLYRGFIQNHQMVMIGYSDSAK 543

                   DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                   DAG +sA W  Y A + ++Kv  + G+ L+lFHGRGGtvGRGG P H A+
  gi|1489772   544 DAGVMSAGWAQYDAMDKLVKVCDEEGIELTLFHGRGGTVGRGGAPAHAAL 593

                   LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                   LsqPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|1489772   594 LSQPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNLYASAILEANLLPP 643

                   vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                     Pk EWR+Lme +  v  E YR vv  E +Fv YFR AtPElE Gk+ +
  gi|1489772   644 PEPKQEWRDLMEVLSQVSCEAYRNVVRGEEKFVPYFRQATPELELGKLPL 693

                   GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                   GsRPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ +d+
  gi|1489772   694 GSRPAKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSVDQGH 743

                   KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                   + l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv EeL P
  gi|1489772   744 QAL--LEEMCREWPFFSTRLGMLEMVYSKCNMEIAKYYDQRLVDEELLPL 791

                   GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                   G+ LR++ +   + +L +     l+  DP+    +RLR+ Y+  Ln++qA
  gi|1489772   792 GELLREQLQKDIKAVLNVENNENLMQSDPWGLESIRLRNIYVEPLNMLQA 841

                   YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                     L R R                   E   +++e             LE+
  gi|1489772   842 ELLYRTRKC----------------ET--PPAE-------------LEEA 860

                   LiLtmKGiAAGmqntG<-*
                   L++t+ GiAAGm ntG
  gi|1489772   861 LMVTIAGIAAGMRNTG    876

gi|90413609|ref|ZP_01221599.1|: domain 1 of 1, from 1 to 876: score 770.2, E = 1.5e-228
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                  K s    L     +L       ++D HGe L + v
  gi|9041360     1    ---------MNEKYS---ALRSNVSMLGHMLGNTIKDAHGEALFDKV 35

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDail.vAkailHmLnLAn
                        ls       D+ +   L   L  L P D +l+vA+a++  LnL n
  gi|9041360    36 ETIRKLSKSARAGDDSDR-AKLIDELQNL-PDDQLLpVARAFSQFLNLTN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +   R   ++                 i+  + kL      s  +
  gi|9041360    84 IAEQYHTISRHCEEQVC----------SPDSIDSLFGKLNANS-ISQFD 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     +A++   ++LvltAHPt  +RR ++ K   i  CL+ L   ++   ++
  gi|9041360   122 SIQAVRDLNIELVLTAHPTEIARRTMIHKLVQINKCLSNLELSELSHSER 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   + ++  L   i  A+  D iR+ +PtP DE + G + +   +W+ vP FL
  gi|9041360   172 QRVEQRLEQLIAQAWHSDVIRKQRPTPLDEAKWGFAVVENSLWHAVPEFL 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   R  D  L    + E lP d+  +kF+sWmGGDRDG nP vt +vtR+v L
  gi|9041360   222 RQFDEKLVQ-HLGENLPLDASPVKFTSWMGGDRDG-NPFVTSDVTREVML 269
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                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa l++  + +L+ Elsm +Cnd +R  A E       +
  gi|9041360   270 LSRWKAADLFLGDIQELVSELSMVKCNDQVRELAGE-------E------ 306

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR iL d R KL ntR+     + +   +++  A+  +
  gi|9041360   307 ---------HEPYRAILKDLRTKLTNTRDVLDAKIKK--QDVPNLAIIDD 345

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    v++   PL  CY+sL eCG  +iADG LLD+LR +  FG+ Lv+LDiRqE
  gi|9041360   346 VDQLWTPLHACYQSLRECGMGIIADGLLLDVLRRIKCFGIHLVRLDIRQE 395

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+ Dv+  +t+ L++G Y +W E+ +  +L+ EL  KRPLl+
  gi|9041360   396 STRHSDVISELTRYLGLGDYEQWNEQDKVAFLVRELASKRPLLPLAWQPS 445

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     Ev++vld+ + +AE   ++ GaY+isma + sDvLAv LL +E g
  gi|9041360   446 AEVQEVLDTCKAVAEQSREALGAYVISMARTASDVLAVHLLLKEAGCPFR 495

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    L v PLFE L DL+     ++ L siDWY+  i+  q vm+GYsDs KDA
  gi|9041360   496 LDVCPLFETLEDLNNGASVIKELMSIDWYRGFIQNHQMVMIGYSDSAKDA 545

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y+A EE++ v  +  v L+lFHGRGG +GRGG P H A+Ls
  gi|9041360   546 GVMAAGWAQYRAMEELVEVCEDASVELTLFHGRGGSIGRGGAPAHAALLS 595

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f  G  ++   sL  ++ AtLE  + PP +
  gi|9041360   596 QPPRSLKGGLRVTEQGEMIRFKLGLPDVAVNSLSLYASATLEANLLPPPA 645

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EW +Lm+ +  v  E YR vv     Fv YFR AtPElE Gk+ +Gs
  gi|9041360   646 PKKEWCDLMDVLSEVSCESYRNVVRGSEEFVPYFRAATPELELGKLPLGS 695

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR P GG+esLRAiPWiFaW q R  LP WLG G A ++ idK
  gi|9041360   696 RPAKRNPNGGVESLRAIPWIFAWSQNRLLLPAWLGAGEAIQYSIDKGHA- 744

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                     q L++m +eWPFF   l +lEmv+ K   GiA  yD+ L    L+P G+
  gi|9041360   745 -QLLEDMCREWPFFSTRLGMLEMVYTKTNVGIAEYYDQRLTDKSLWPLGQ 793

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LRd+ +   + +L +     l+E  P+    +RLR+ Y+  Ln++qA
  gi|9041360   794 KLRDQLQQDIKAVLNVENNAHLMEQNPWGAEAIRLRNIYVEPLNMLQAEL 843

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                 dE+                +P LE+ L+
  gi|9041360   844 LYRTRQ---------------QDEP----------------SPILEEALM 862

                    LtmKGiAAGmqntG<-*
                    + + GiA Gm ntG
  gi|9041360   863 VSIAGIATGMRNTG    876

gi|261346852|ref|ZP_05974496.1|: domain 1 of 1, from 1 to 879: score 769.9, E = 1.8e-228
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  ++    vs           +l k L+D +++  Ged+ +
  gi|2613468     1    -MNQQYSAMR-SNVS-----------MLGKLLgDTIKEALGEDILDK 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       + ++   L + L  L   + + vA+a+   LnL n
  gi|2613468    35 VESIRKLSKSSRAGNEVQRQKLLVS-LQNLTNDELLPVARAFNQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +       +   hG+ a    A     +   + +L      s  +
  gi|2613468    84 VAEQYH-------SISPHGEAASNPVA-----LQKLFGRLKEHD-FSHGD 120

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s++LvltAHPt  +RR L+ K   +  CL+qL   D+   ++
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  gi|2613468   121 IQKAVEELSIELVLTAHPTEIARRTLIHKLVEVNTCLSQLDHDDLADYER 170

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L    +   + tDEiR+ +PtP DE + G + +   +W+GvP FL
  gi|2613468   171 NNIMRRLRQLVAQSWHTDEIRKIRPTPIDEAKWGFAVVENSLWEGVPAFL 220

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R     L    i   lP ++  i+F+sWmGGDRDG nP vt EvtR v L
  gi|2613468   221 REFNEQLEE-SIGAELPVEANPIRFTSWMGGDRDG-NPNVTAEVTRHVLL 268

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa l++  +  L+ Elsm     ELR+ A         d
  gi|2613468   269 LSRWKAADLFLKDIQVLVSELSMTEATPELRALA------GGDD------ 306

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR i  + R +L+ t E     + +G   ++     t+
  gi|2613468   307 --------VDEPYRQIAKNLRSQLFSTLEYLEGRV-KGEQVLPPADLLTD 347

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      +  +PL  CY+sL  C  k+iA GsLLD LR +  FGL Lv++D+RqE
  gi|2613468   348 NAQLWDPLYACYQSLIACNMKIIANGSLLDTLRRIRSFGLQLVRIDVRQE 397

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+t+ l  +t+ L++G Y eWsEe +q +Ll+EL+ +RPL++ D
  gi|2613468   398 STRHTEALSELTEYLGLGNYGEWSEEEKQRFLLTELQSRRPLIPQDWQPS 447

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     E ++v ++ rv+A    Ds  aY+isma  PsDvLAv LL +  g
  gi|2613468   448 AETQEVFETCRVIAKAKKDSIAAYVISMAKVPSDVLAVKLLLKASGACIK 497

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    L+v PLFE L DL+ A   + kL si+WY+n i   q vm+GYsDs KDA
  gi|2613468   498 LPVAPLFETLEDLNNAESVMTKLLSIEWYRNLIGDHQMVMIGYSDSAKDA 547

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y Aq+ +iK  Kk GvKL+lFHGRGGt+GRGG P H A+Ls
  gi|2613468   548 GVMAASWAQYHAQDSLIKLCKKEGVKLTLFHGRGGTIGRGGAPAHSALLS 597

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP
  gi|2613468   598 QPPGSLKGGLRVTEQGEMIRFKFGLPQVTISSLAMYASAILEANLLPPAE 647

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EW+ +m+ +  v  E YR  v   P Fv YFR AtPElE Gk+ +Gs
  gi|2613468   648 PKEEWKAVMNTLSEVSCEMYRDYVREQPDFVPYFRAATPELELGKLPLGS 697

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+P GG+e+LRAiPWiFaWtq R  LP WLG GAA Kh i+K+ K
  gi|2613468   698 RPAKRRPTGGVETLRAIPWIFAWTQNRLMLPAWLGAGAALKHVIEKEGKQ 747

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                       L Em++eW FF+  + +lEmv+AK D  +A  yD+ Lv   L+P G+
  gi|2613468   748 -AVLDEMWQEWTFFKTRIAMLEMVYAKADLWLAEYYDHRLVEKRLWPLGQ 796

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LRd+  E  + +L +     l+   P++   + LR+ Y   Lnv+qA
  gi|2613468   797 KLRDQLSEDIKSVLAVSKDEALMADLPWVAESIALRNVYTDPLNVLQAEL 846

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                  +E    +d            P +E  L+
  gi|2613468   847 LHRSRQ---------------QEH---PD------------PRVEQALM 865

                    LtmKGiAAGmqntG<-*
                    +t+ G+AAGm ntG
  gi|2613468   866 VTIAGVAAGMRNTG    879

gi|212712498|ref|ZP_03320626.1|: domain 1 of 1, from 1 to 879: score 769.8, E = 2e-228
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  ++    vs           +l k L+D ++D  Ged+ +
  gi|2127124     1    -MNQQYSAMR-SNVS-----------MLGKLLgDTIKDALGEDILDK 34
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                vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                v     ls       + ++ + L   L  L   + + vA+a+   LnL n
gi|2127124    35 VESIRKLSKSSRAGNEVQR-QKLLMTLQTLTNDELLPVARAFNQFLNLTN 83

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                +AE  +       +   hG+ a    A     +   + +L      s e+
gi|2127124    84 VAEQYH-------SISPHGEAASNPVA-----LQKLFGRLKEHD-FSHED 120

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                +  A+   s++LvltAHPt  +RR L+ K   +  CL+qL   D+   ++
gi|2127124   121 IQKAVEELSIELVLTAHPTEIARRTLIHKLVEVNTCLSQLDHDDLADYER 170

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  +   L   +   + tDEiR+ +PtP DE + G + +   +W+GvP FL
gi|2127124   171 NNIMRRLRQLVAQSWHTDEIRKIRPTPIDEAKWGFAVVENSLWEGVPAFL 220

                RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                R     L    i   lP ++  i+F+sWmGGDRDG nP vt EvtR v L
gi|2127124   221 REFNEQLEE-SIGAQLPVEANPIRFTSWMGGDRDG-NPNVTAEVTRHVLL 268

                LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                L+R  Aa l++  +  L+ Elsm     ELR+    l      d
gi|2127124   269 LSRWKAADLFLKDIQVLVSELSMTEATPELRA----LAGGDEVD------ 308

                iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                          EPYR i  + R +L+ t E     + +G   ++     t+
gi|2127124   309 ----------EPYRQIAKNLRSQLFSTLEYLERRV-KGEQVLPPADLLTD 347

                vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                  +  +PL  CY+sL  C   +iA GsLLD LR +  FGL Lv++D+RqE
gi|2127124   348 NAQLWDPLYACYQSLVACNMSIIANGSLLDTLRRIRSFGLQLVRIDVRQE 397

                seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                s R+tD l  +t+ L++G Y +WsE+ +q++Ll+EL+ +RPL++     t
gi|2127124   398 STRHTDALSELTEYLGLGNYGDWSEQEKQDFLLTELQSRRPLIPQNWQPT 447

                EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                 E ++v ++ rv+A    Ds  aY+isma  PsDvLAv LL +E g
gi|2127124   448 PETQEVFETCRVIAKAKNDSIAAYVISMAKVPSDVLAVKLLLKEAGASIK 497

                LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                L+v PLFE L DL+ A   + kL si+WY+  id +q vm+GYsDs KDA
gi|2127124   498 LPVAPLFETLEDLNNAESVMTKLLSIEWYRDLIDDRQMVMIGYSDSAKDA 547

                GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                G ++A W  Y+Aq+ +iK   k GvKL+lFHGRGGt+GRGG P H A+Ls
gi|2127124   548 GVMAASWAQYRAQDALIKLCDKEGVKLTLFHGRGGTIGRGGAPAHSALLS 597

                qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                qPP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP
gi|2127124   598 QPPGSLKGGLRVTEQGEMIRFKFGLPQVTISSLAMYASAILEANLLPPPE 647

                PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                Pk  W+ +m+ +  v    YR  v   P Fv YFR AtPElE Gk+ +Gs
gi|2127124   648 PKEAWKSVMNSLSDVSCAMYRDYVREQPDFVPYFRAATPELELGKLPLGS 697

                RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                RPaKR+P GG+e+LRAiPWiFaWtq R  LP WLG GAA Kh i+K+ K
gi|2127124   698 RPAKRRPTGGVETLRAIPWIFAWTQNRLMLPAWLGAGAALKHVIEKEGKQ 747

                lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                   L Em++eW FF+  + +lEmv+AK D  +A  yD+ Lv   L+P G+
gi|2127124   748 -AVLDEMWQEWTFFKTRIAMLEMVYAKADLWLAEYYDHCLVEKRLWPLGQ 796

                sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                +LRd+  E  + +L +     l+   P++   + LR+ Y   Lnv+qA
gi|2127124   797 KLRDQLSEDIKSVLAVSKDEALMADLPWIAESIALRNVYTDPLNVLQAEL 846

                LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                L+R R                +E    +d            P +E  L+
gi|2127124   847 LQRSRQ----------------QEH---PD------------PRVEQALM 865
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                  LtmKGiAAGmqntG<-*
                  +t+ G+AAGm ntG
  gi|2127124   866 VTIAGVAAGMRNTG    879

gi|260770868|ref|ZP_05879797.1|: domain 1 of 1, from 1 to 877: score 769.6, E = 2.2e-228
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      +  +  +L    vs           +l + L+  +qD  G+ + E
  gi|2607708     1    -MNEKYAALK-SNVS-----------MLGRLLgQTIQDADGDVILEK 34

                  vqECYEl..sAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                  v     l++sA    + D   L E    + sL+  +   vA+a+   LnL
  gi|2607708    35 VETIRKLskSARAGNQADHANLIE---EIKSLNNDELTPVARAFNQFLNL 81

                  AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                   n+A+  +   R             E +A     +   + +L   +  s
  gi|2607708    82 TNIADQYHTISRHCEAHVC------EPDA-----VHSLFSQLSQNG-ISK 119

                  eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                   +  +A++   ++LvltAHPt   RR ++    +i  CL++L   ++
  gi|2607708   120 LDTAQAVRDLNIELVLTAHPTEITRRTMINNLVKINECLSKLELSELSSK 169

                  DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                  ++   +  L   i   +  D iR+ +PtP DE + G + +   +W+ vP
  gi|2607708   170 ERLKTERRLEQLIAQGWHSDVIRKQRPTPLDEAKWGFAVVENSLWQAVPE 219

                  FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                  FLR     +K   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v
  gi|2607708   220 FLRELNESVKGY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHSITREV 267

                  CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                   LL+R  Aa lY+  + +L+ Elsm +Cnd LR  A E       +
  gi|2607708   268 MLLSRWKAADLYLGDISELVAELSMTKCNDTLRELAGE------EE---- 307

                  yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                             EPYR +L  vR  L  t +     + +G   ++  A
  gi|2607708   308 -----------HEPYRAVLKRVRSLLQETLDILDAKI-HG-QKLAVKAPL 344

                  tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                   ++ +  +PL  CY+sL eCG  viADGsLLD LR v  FG+ Lv+LDiR
  gi|2607708   345 QNISQLWDPLYACYQSLHECGMGVIADGSLLDTLRRVKAFGVHLVRLDIR 394

                  qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                  qEs R+ Dvl  +t+ L+iG Y  WsE+ +  +L  EL  KRPLl+ D
  gi|2607708   395 QESTRHSDVLSELTRYLGIGDYNHWSEQDKIAFLTNELASKRPLLPRDWE 444

                  ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                    E vk+vld+ +++A  P ++FGaY+isma + sDvLAv LL  E g
  gi|2607708   445 PSEPVKEVLDTCKIIAAQPREAFGAYVISMARTASDVLAVHLLLQESGCP 494

                  qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                    + v PLFE L DL+ A A + +L siD Y+  i+  q vm+GYsDs K
  gi|2607708   495 YRMDVCPLFETLDDLNNAEAVITQLMSIDLYRGFIQNHQMVMIGYSDSAK 544

                  DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                  DAG ++A W  Y A E +++vA + Gv L+lFHGRGGt+GRGG P H A+
  gi|2607708   545 DAGVMAAGWAQYHAMESLVRVAEEAGVELTLFHGRGGTIGRGGAPAHAAL 594

                  LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                  LsqPP  ++G lRvt qGE+i f  G  ++   s   ++ A L   + PP
  gi|2607708   595 LSQPPKSLKGGLRVTEQGEMIRFKLGLPEVAVNSFNLYASAVLQANLLPP 644

                  vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                    Pk EWR+Lm+ +  v  E YR+vv  EP Fv YFR AtPElE Gk+ +
  gi|2607708   645 PEPKQEWRDLMNVLSEVSCEAYRAVVRGEPDFVPYFRQATPELELGKLPL 694

                  GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                  GsRPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ idK
  gi|2607708   695 GSRPAKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSIDKGH 744

                  KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
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                  + l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv E L+P
  gi|2607708   745 QAL--LEEMCREWPFFSTRLGMLEMVYTKCSVDIARYYDERLVDEALRPL 792

                  GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                  G++LR++ +   + +L +     l+  DP+    +RLR+ Y+  Ln++qA
  gi|2607708   793 GQRLRAQLQKDIKTVLNVENNENLMQSDPWGHESIRLRNIYVEPLNMLQA 842

                  YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                    L R R                 +E+                aP LE+
  gi|2607708   843 ELLYRTRQ---------------SQEP----------------APELEEA 861

                  LiLtmKGiAAGmqntG<-*
                  L++t+ GiAAGm ntG
  gi|2607708   862 LMVTIAGIAAGMRNTG    877

gi|148549423|ref|YP_001269525.1|: domain 1 of 1, from 3 to 875: score 769.3, E = 2.7e-228
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      iD  LR      v           +L +   + +   HG+    +
  gi|1485494     3    DIDVRLRE----DVH----------VLGELLGETIRQQHGDA---FL 32

                  qECYElsAeYEGKkDtkKLeE.LGakLtsLdPaDailvAkailHmLnLAn
                  q   ++      K D +  +E+L + L  L+  D + vA+a+   LnLAn
  gi|1485494    33 QKIEDI--RHSAKADRRGPGEqLSSTLADLAEEDLLPVARAFNQFLNLAN 80

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  +AE  +l  RR   +        Ea+      + E l +L   +  s +
  gi|1485494    81 MAEQYQLIRRRDADQPE----PFEAQV-----LPELLGRLKQAG-HSNDA 120

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      L    + LvltAHPt  +RR L+qK   i   La    +D+t  ++
  gi|1485494   121 LARQLAKLDIQLVLTAHPTEVARRTLIQKYDAIAGQLAAQDHRDLTSAER 170

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  + + E L R i  A+ t+EiRR++PtP DE + G + i   +W+ +P  L
  gi|1485494   171 QQVRERLRRLIAEAWHTEEIRRTRPTPVDEAKWGFAVIEHSLWHAIPSHL 220

                  RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                  R+vD AL       RlP ++  i+F+sWmGGDRDG nP vt  vtR+v L
  gi|1485494   221 RKVDKALLE-ATGLRLPLEAAPIRFASWMGGDRDG-NPNVTAAVTREVLL 268

                  LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                  LaR mAa l++  ++ L  Elsm   nd LR
  gi|1485494   269 LARWMAADLFLRDIDALAAELSMQQANDALR------------------ 299

                  iEFWKqv.PPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vy
                      Kqv+   EPYR +L + RD+L  tR  a   L    s+ +  A+v
  gi|1485494   300 ----KQVgDSAEPYRAVLKQLRDRLRATRAWAHSALT---SNQPAGAdVL 342

                  tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                   +  e + PLELCY+sL eCG  viA+G LLD LR   tFGL L +LD+R
  gi|1485494   343 VDNRELIAPLELCYQSLHECGMGVIAEGPLLDCLRRAVTFGLFLGRLDVR 392

                  qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                  q++ R+ D l  it  L++G Y +W Ee+R  +L aELk +RPLl++
  gi|1485494   393 QDAARHRDALTEITDYLGLGRYADWDEEQRIAFLQAELKNRRPLLPAHFK 442

                  ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                     + ++vl + r +A  P  s G+Y+isma a sDvLAv LL +E g+
  gi|1485494   443 PQADTAEVLATCREVAAAPAASLGSYVISMAGAASDVLAVQLLLKEAGLT 492

                  qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                  +++rvvPLFE LADL+ A   +++L  +  Y+  + G qevm+GYsDs K
  gi|1485494   493 RPMRVVPLFETLADLDNAGPVMQRLLGLPGYRAGLRGPQEVMIGYSDSAK 542

                  DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                  DAG  +AAW  Y+AqE ++++  ++ v L lFHGRGGtvGRGGGP H Ai
  gi|1485494   543 DAGTTAAAWAQYRAQENLVRICAEHQVELLLFHGRGGTVGRGGGPAHAAI 592

                  LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                  LsqPP  + G  R t qGE+i f FG   +  + L  + AA LE  + PP
  gi|1485494   593 LSQPPGSVAGRFRTTEQGEMIRFKFGLPGIAEQNLNLYLAAVLEATLLPP 642
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                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      P+P WR++m+++A      YRsvv   P FvEYFR  tPE E G++ +
  gi|1485494   643 PPPQPAWREVMDQLAADGVQAYRSVVRENPDFVEYFRQSTPEQELGRLPL 692

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKR+ +GGiesLRAiPWiF WtqtR  LP WLG   A   A+ +
  gi|1485494   693 GSRPAKRR-AGGIESLRAIPWIFGWTQTRLMLPAWLGWETALTNALARGQ 741

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                      l  L  m ++WPFFR  +D+lEmv AK D  iA  yD+ Lv   L+P
  gi|1485494   742 GEL--LAQMREQWPFFRTRIDMLEMVLAKADAQIAEAYDERLVQPHLRPL 789

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G  LRd      + +L + G   lL   P     + LR+ Y+  L  +qA
  gi|1485494   790 GAHLRDLLSQSCQVVLGLTGQPVLLAHSPETLEFISLRNTYLDPLHRLQA 839

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R            s+E A +                   LE
  gi|1485494   840 ELLARSR------------SREAALDS------------------PLEQA 859

                    LiLtmKGiAAGmqntG<-*
                    L++t+ GiAAG+ ntG
  gi|1485494   860 LLVTVAGIAAGLRNTG    875

gi|269103968|ref|ZP_06156665.1|: domain 1 of 1, from 1 to 876: score 769.2, E = 2.9e-228
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  +  +L    vs           +l + L+  ++D HGe+L
  gi|2691039     1    -MNEKYSALK-SNVS-----------MLGHLLgNTIKDAHGEELLNK 34

                    vqECYEls.AeYEGKkDtkKLeELGakLtsLdPaDail.vAkailHmLnL
                    v     ls+    G  D +    L   L  L P D +l+vA+a++  LnL
  gi|2691039    35 VETIRKLSkSARAGNSDDR--AKLINELQNL-PDDELLpVARAFSQFLNL 81

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                     n+AE  +   R             E+s      i+  + +L  +++
  gi|2691039    82 TNIAEQYHTVSRHC-----------ETSVCSPDSIDGLFTQL-EQGDINQ 119

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                     +  +A++n  +DLvltAHPt  +RR ++ K   i  CL++L   ++
  gi|2691039   120 FDTINAIRNLKIDLVLTAHPTEIARRTMIHKLVQINKCLSKLELSELSSA 169

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    +++ ++  L   i  A+  D iR  +PtP DE + G + +   +W+ vP
  gi|2691039   170 ERQRIETRLEQLIAQAWHSDVIRQQRPTPLDEAKWGFAVVENSLWQAVPD 219

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    FLR  D  L    i E lP d+  + FssWmGGDRDG nP vt  vtR+v
  gi|2691039   220 FLRQFDDKLEA-HIGEGLPIDAAPVTFSSWMGGDRDG-NPFVTSQVTREV 267

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                     LL+R  Aa lY+  + +L+ Elsm +Cnd +R+ A +       +
  gi|2691039   268 LLLSRWKAADLYLKDIQELVSELSMVKCNDQVRALAGD-------E---- 306

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                                EPYR iL + R +L  tR+     + +G s ++   +
  gi|2691039   307 -----------HEPYRAILKNLRSQLTHTRDILDAQI-KGQS-VALLPII 343

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     +  +  +PL  CY+sL eCG  +iADG LLD LR +  FG+ Lv+LDiR
  gi|2691039   344 SDESQLWDPLYACYQSLHECGMGIIADGLLLDTLRRIKCFGIHLVRLDIR 393

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+ Dv+  +t+ L++G Y +WsE+ +  +L+ EL+ KRPLl+
  gi|2691039   394 QESTRHSDVISELTRYLGLGDYDQWSEQDKVAFLVRELSSKRPLLPRHWQ 443

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                       Ev++v+d+ + +A  P D+ GaY+isma + sDvLAv LL  E g
  gi|2691039   444 PSPEVQEVIDTCKTIAKQPKDALGAYVISMARTASDVLAVHLLLQEAGCP 493

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
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                     + v PLFE L DL+     +e+L  iDWY+  i+  q vm+GYsDs K
  gi|2691039   494 FRMDVCPLFETLDDLNNGADVIEQLLNIDWYRGFIQNHQMVMIGYSDSAK 543

                   DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                   DAG +sA W  Y A E ++ v  k Gv L+lFHGRGGt+GRGG P H A+
  gi|2691039   544 DAGVMSAGWAQYHAMEKLVDVCEKAGVELTLFHGRGGTIGRGGAPAHAAL 593

                   LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                   LsqPP  ++G lRvt qGE+i f  G  ++   sL  ++ AtL   + PP
  gi|2691039   594 LSQPPRSLKGGLRVTEQGEMIRFKLGLPEVAVNSLSLYASATLQANLLPP 643

                   vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                    +Pk EW +Lm+ +  v    YR vv   P Fv YFR AtPElE Gk+ +
  gi|2691039   644 PAPKQEWCELMDSLSEVSCKAYRDVVRGNPEFVPYFRAATPELELGKLPL 693

                   GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                   GsRPaKR P GG+esLRAiPWiFaW q R  LP WLG G A +  id+
  gi|2691039   694 GSRPAKRNPTGGVESLRAIPWIFAWSQNRLLLPAWLGAGEAIQNSIDQGH 743

                   KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                     l  L+Em +eWPFF   l +lEmvF K   GiA  yD+ L  E L+P
  gi|2691039   744 TEL--LEEMCREWPFFSTRLGMLEMVFTKTNVGIAQYYDQRLTDEALWPL 791

                   GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                   G++LRd+ +   + +L +     l+E DP+    +RLR+ Y+  Ln++qA
  gi|2691039   792 GQKLRDQLQQDIKTVLTVENNDHLMEQDPWGAEAIRLRNIYVEPLNMLQA 841

                   YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                     L R R                                 ++ +P +E+
  gi|2691039   842 ELLYRNRQ------------------------------QQESSPMMEEA 860

                   LiLtmKGiAAGmqntG<-*
                   L++t+ GiA Gm ntG
  gi|2691039   861 LMVTIAGIATGMRNTG    876

gi|206577729|ref|YP_002241183.1|: domain 1 of 1, from 1 to 883: score 769.2, E = 2.9e-228
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  q  +L    vs           +l k L+D ++D  Ge++ +
  gi|2065777     1    -MNEQYSALR-SNVS-----------MLGKVLgDTIKDALGENILDR 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls       ++ + +EL + L  L   + + vA+a++  LnLAn
  gi|2065777    35 VETIRKLSKSSRAGNEANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    AE  +      i+         Ea    E  i  tl+kL  + n   +
  gi|2065777    84 TAEQYH-----SISPNG------EAASNPEV-IARTLRKLKDQPNLNEDT 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   +  A+   s +LvltAHPt   RR L+ K   +  CL qL  KD+   +
  gi|2065777   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNSCLKQLDNKDIADYEH 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   + L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|2065777   172 HQLMRRLRQLIAQSWHTDEIRKYRPSPVDEAKWGFAVVENSLWEGVPNYL 221

                   RRvDtALK.niGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   R     L  n+G    lP d   ++F+sWmGGDRDG nP vt ++tR v
  gi|2065777   222 RELNEQLEaNLGY--QLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                   LL+R  A+ l++  v  L+ Elsm  C dELR+ A      a
  gi|2065777   269 LLSRWKATDLFLKDVQVLISELSMVECTDELRALA-----GAEGA----- 308

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                             +EPYR ++   R +L  t       L +G          t
  gi|2065777   309 ----------QEPYRYLMKKLRTQLMETQAWLEARL-KGQKLPKPAGLIT 347

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   + E+  EPL  CYksL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|2065777   348 QNEQLWEPLYACYKSLQACGMGIIANGELLDTLRRVKSFGVPLVRIDIRQ 397
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                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|2065777   398 ESTRHTEALGEMTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRQWEP 447

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     EE ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|2065777   448 SEETREVLDTCKVIAEAPRGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    +L+v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|2065777   498 ALPVAPLFETLDDLNNANDVMTQLLNIDWYRGFIQGKQMVMIGYSDSAKD 547

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|2065777   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2065777   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLSLYTSAILEANLLPPP 647

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk EWR++m e+  v    YR  v     Fv YFR+AtPE E Gk+ +G
  gi|2065777   648 EPKAEWRDIMAELSDVSCKMYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA +  ++   +
  gi|2065777   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQKVVEGGKQ 747

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        L+ m ++WPFF   l +lEmv+ K D  +A  yD+ Lv  eL+  G
  gi|2065777   748 S--ELEAMCRDWPFFSTRLGMLEMVYSKADLWLAEYYDQRLVKPELWALG 795

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                     +LR       + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|2065777   796 TELRKLLAADINVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 845

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R               A+E  k +d            P +E  L
  gi|2065777   846 LLHRSRQ---------------AEEAGKDPD------------PRVEQAL 868

                    iLtmKGiAAGmqntG<-*
                    ++t+ G+AAGm ntG
  gi|2065777   869 MVTIAGVAAGMRNTG    883

gi|59712915|ref|YP_205691.1|: domain 1 of 1, from 1 to 876: score 769.2, E = 2.9e-228
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  +  +L    vs           +l + L+  + D HGe+L
  gi|5971291     1    -MNEKYAALK-SNVS-----------MLGHLLgNTIRDAHGEELLAK 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDail.vAkailHmLnLA
                    v     ls       D  + + L   + sL P D + +vA+a++  LnL
  gi|5971291    35 VETIRKLSKTARAGSDEDR-NALIEEIKSL-PDDQLTpVARAFSQFLNLT 82

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE  +   R                   E D   tl    ++ n s
  gi|5971291    83 NMAEQYHTISRHCEAHVC------------EPDAISTLFSKLSQSNVSKL 120

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    +  +A++   ++LvltAHPt  +RR ++ K  +i  CL++L   D+   +
  gi|5971291   121 DTAQAVRELNIELVLTAHPTEIARRTMINKLVKINECLSKLELGDISFSE 170

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    +   +  L   i  A+  D iR  +PtP DE + G + +   +W+G+P F
  gi|5971291   171 RDKTERRLEQLIAQAWHSDVIRQERPTPLDEAKWGFAVVENSLWQGIPEF 220

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    LR  D  L    + E lP d+  ++ ssWmGGDRDG nP vt  +tR+v
  gi|5971291   221 LREFDQRLEG-HLGEGLPIDARPVHMSSWMGGDRDG-NPFVTHKITREVM 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
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                    LL+R  Aa lY+  + +L+ Elsm +C dE+R  A +      ++
  gi|5971291   269 LLSRWKAADLYLKDINELISELSMVKCTDEVRELAGD------QH----- 307

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei.sEeAvy
                               EPYR iL + R  L  t E    L A+   e+ +   +
  gi|5971291   308 -----------EPYRAILKQLRTLLGDTLES---LDAQMKGELaPNKVIL 343

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                    t+ ++   PL  CY+sL  CG  +iADGsLLD LR v  FG  Lv+LDiR
  gi|5971291   344 TDADQLWNPLYACYQSLHACGMGIIADGSLLDTLRRVKAFGAHLVRLDIR 393

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+ Dvl  +t+ L+iG Y +WsE+ +  +L+ EL+ KRPLl+
  gi|5971291   394 QESTRHSDVLSELTRYLGIGDYDQWSEQDKISFLVNELSSKRPLLPRKWE 443

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                       Ev++v+d+ +v+AE   ++ G+Y+isma + sDvLAv LL  E g
  gi|5971291   444 PSPEVQEVIDTCKVVAEQSKEALGSYVISMARTASDVLAVHLLLQEAGCP 493

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                      + v PLFE L DL+     +e+LFsiDWY+  i+  q vm+GYsDs K
  gi|5971291   494 FRMDVCPLFETLDDLNRSKEVMEQLFSIDWYRGFIQNHQMVMIGYSDSAK 543

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG +sA W  Y A E ++ v  k  + L+lFHGRGGt+GRGG P H A+
  gi|5971291   544 DAGVMSAGWAQYSAMEALVEVCEKESIELTLFHGRGGTIGRGGAPAHAAL 593

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|5971291   594 LSQPPKSLKGGLRVTEQGEMIRFKLGLPEVAVNSFNLYASAILEANLLPP 643

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      Pk EWR+Lme +  v  E YR vv  E  Fv YFR AtPElE Gk+ +
  gi|5971291   644 PEPKQEWRDLMEVLSEVSCEAYRNVVRGEKDFVPYFRAATPELELGKLPL 693

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ idK
  gi|5971291   694 GSRPAKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSIDKGH 743

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    + l  L+Em +eWPFF   l +lEmv+ K  P +   yD+ L    L+P
  gi|5971291   744 QAL--LEEMCREWPFFSTRLGMLEMVYTKCNPQMSEYYDQRLTDKSLWPL 791

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G++LR++ +   + +L +     l+E DP+    +RLR+ Y+  Ln++qA
  gi|5971291   792 GERLRNQLQADIKAVLNVENNDHLMERDPWGSESIRLRNIYVDPLNMLQA 841

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R                                  e+ +P LE+
  gi|5971291   842 ELLFRTRQ------------------------------QEETSPELEEA 860

                    LiLtmKGiAAGmqntG<-*
                    L++t+ GiAAGm ntG
  gi|5971291   861 LMVTIAGIAAGMRNTG    876

gi|66044566|ref|YP_234407.1|: domain 1 of 1, from 3 to 878: score 768.9, E = 3.5e-228
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        iDA LR      v           LL +     + +  G +  + +
  gi|6604456     3    DIDARLRE----DVH----------LLGELLGNTIREQRGAEFLDKI 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E     A    +  ++  e L + + +L   + + vA+a+   LnLAn+
  gi|6604456    36 -ERIRKGAKAGRRGSAEGAEQLSSSVDGLGDDELLPVARAFNQFLNLANI 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiE.EtlKkLvlklnKsPeE
                    AE  +l +RR  k+             Es + +E l +L   +  sP+
  gi|6604456    85 AEQYQLMHRRDDKQPL----------PFESRVLpELLDRLKAEG-HSPDA 123

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                        L    +DLvltAHPt  +RR L+qK   i   La L  +D+   ++
  gi|6604456   124 LARQLSKLEIDLVLTAHPTEVARRTLIQKYDAIAAQLAALDHRDLNSIER 173
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                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L R i  A+ t+EiRR +PtP DE + G + i   +W+ +P +L
  gi|6604456   174 TQITSRLQRLIAEAWHTEEIRRIRPTPVDEAKWGFAVIEHSLWHAIPNYL 223

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R+ D AL        lP ++  i+F+sWmGGDRDG nP vt  vtR+v L
  gi|6604456   224 RKADHALHA-ATGLHLPLEAAPIRFASWMGGDRDG-NPNVTAAVTREVLL 271

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    LaR mAa lY+  v+ L  Elsm    d LR+      +   +
  gi|6604456   272 LARWMAADLYLRDVDNLAAELSMQQASDALRA------SVGDSA------ 309

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR  L   R++L  tR  a   L   +   + eAv  +
  gi|6604456   310 ----------EPYRAELKRLRERLRATRNWANASLSETLP--APEAVLRD 347

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      e L+PL LC++sL eCG  viADG LLD LR   tFGL Lv+LD+Rq+
  gi|6604456   348 NRELLDPLLLCFQSLHECGMGVIADGPLLDCLRRAVTFGLFLVRLDVRQD 397

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+   +  it  L++G Y eW E+ R ++Ll EL  +RPLl+s
  gi|6604456   398 SSRHCAAMTEITDYLGLGRYEEWDEQTRIDFLLRELNNRRPLLPSYFKPA 447

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     + ++vl + r +A  P  s G+Y+isma + sDvLAv LL +E g++++
  gi|6604456   448 ADTAEVLATCREVAAAPAASLGSYVISMAGSASDVLAVQLLLKESGLQRP 497

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    +rvvPLFE LADL+ A   +e L  +  Y+ r+ G qevm+GYsDs KDA
  gi|6604456   498 MRVVPLFETLADLDNAGPVIETLLGLPGYRSRLHGPQEVMIGYSDSAKDA 547

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G  +AAW  Y+AqE ++ + ++  v L lFHGRGGtvGRGGGP H AiLs
  gi|6604456   548 GTTAAAWAQYRAQERLVEICREQQVELLLFHGRGGTVGRGGGPAHAAILS 597

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  + G  R t qGE+i f FG  ++  + L  + AA LE  + PP
  gi|6604456   598 QPPGSVAGRFRTTEQGEMIRFKFGLPDIAEQNLNLYLAAVLEATLLPPPP 647

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    P+P WR +m++mA      YR+vv   P FvEYFR AtPE E G++ +Gs
  gi|6604456   648 PQPAWRTMMDQMADDGVSAYRAVVRENPEFVEYFRQATPEQELGRLPLGS 697

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+  GG+esLRAiPWiFaWtqtR  LP WLG  AA   A+++
  gi|6604456   698 RPAKRR-EGGVESLRAIPWIFAWTQTRLMLPAWLGWEAALSKALERGEGE 746

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    +  L  m ++WPFFR  +D+lEmv AK D  iA LyD+ Lv+ eL+  G
  gi|6604456   747 V--LAQMREQWPFFRTRIDMLEMVLAKADADIARLYDERLVSAELQHLGA 794

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                     LRd      + +L + G   lL   P     + LR+ Y+  L  +qA
  gi|6604456   795 HLRDLLSQACNVVLGLTGQTQLLAHSPETLEFISLRNTYLDPLHLLQAEL 844

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                  E          L      +P LE  L+
  gi|6604456   845 LSRSRN----------------REA--------SLD-----SP-LELALL 864

                    LtmKGiAAGmqntG<-*
                    + + GiAAG+ ntG
  gi|6604456   865 VSVAGIAAGLRNTG    878

gi|161505390|ref|YP_001572502.1|: domain 1 of 1, from 1 to 883: score 768.2, E = 5.9e-228
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L++ ++D  Ge + +
  gi|1615053     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILDR 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
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                v     ls       ++ + +EL + L  L   + + vA+a++  LnLAn
gi|1615053    35 VETIRKLSKSSRAGNEANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                 AE  +      i+ k       Ea    E  i  tl+kL  + +   +
gi|1615053    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPDLNDAT 121

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                +  A+   s +LvltAHPt   RR L+ K + i nCL qL   D+   ++
gi|1615053   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMGEINNCLKQLDNTDIADYER 171

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                + +   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
gi|1615053   172 HQVMRRLRQLIAQSWHTDEIRKQRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                R     L+ n+G   +lP d   ++F+sWmGGDRDG nP vt ++tR v
gi|1615053   222 RELNEQLeENLGY--KLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                LL+R  A+ l++  +  L+ Elsm     EL +   E     a++
gi|1615053   269 LLSRWKATDLFLKDIHVLVSELSMVEATPELLALVGE---EGASE----- 310

                YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                            PYR ++   R +L  t       L +G      +   t
gi|1615053   311 ------------PYRYLMKKLRARLMATQSWLEARL-KGEKLPKPDGLLT 347

                kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                + E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
gi|1615053   348 QNEQLWEPLYACYQSLQACGMGIIANGELLDTLRRVKCFGVPLVRIDIRQ 397

                EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                Es R+t+ l  it+ L+iG Y +WsE  +q +L+ EL  KRPLl+
gi|1615053   398 ESTRHTEALGEITRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWEP 447

                tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                  + ++vl++ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
gi|1615053   448 SNDTREVLETCKVIAEAPKGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
gi|1615053   498 AMPVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 547

                AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
gi|1615053   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
gi|1615053   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEVTVSSLSLYTSAILEANLLPPP 647

                sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                 Pk  WR++m+e+ v+  E YR  v     Fv YFR+AtPE E Gk+ +G
gi|1615053   648 EPKDSWRHIMDELSVISCETYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
gi|1615053   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 746

                nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                    L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lva  L+P G
gi|1615053   747 Q-SELEAMCRDWPFFSTRLGMLEMVFSKADLWLADYYDQRLVAKTLWPLG 795

                ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                k+LRd  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
gi|1615053   796 KELRDLLEEDIKVVLAIANDSHLMADLPWIAESIQLRNVYTDPLNVLQAE 845

                tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                 L R R                 +E+ k +d            P +E  L
gi|1615053   846 LLYRSR---------------LTEEQGKSPD------------PRVEQAL 868
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                  iLtmKGiAAGmqntG<-*
                  ++t+ G+AAGm ntG
  gi|1615053   869 MVTIAGVAAGMRNTG    883

gi|16762323|ref|NP_457940.1|: domain 1 of 1, from 1 to 883: score 768.0, E = 6.5e-228
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      +  q  +L    vs           +l k L++ ++D  Ge + +
  gi|1676232     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILDR 34

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v     ls       ++ + +EL + L  L   + + vA+a++  LnLAn
  gi|1676232    35 VETIRKLSKSSRAGNEANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   AE  +      i+ k       Ea    E  i  tl+kL  + +   +
  gi|1676232    84 TAEQYH-----SISPKG------EAASNPEV-IAHTLRKLKNQPDLNDAT 121

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  +  A+   s +LvltAHPt   RR L+ K + i nCL qL   D+   ++
  gi|1676232   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMGEINNCLKQLDNTDIADYER 171

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  + +   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|1676232   172 HQVMRRLRQLIAQSWHTDEIRKQRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                  RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                  R     L+ n+G   +lP d   ++F+sWmGGDRDG nP vt E+tR v
  gi|1676232   222 RELNEQLeENLGY--KLPVDFVPVRFTSWMGGDRDG-NPNVTAEITRHVL 268

                  LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                  LL+R  A+ l++  +  L+ Elsm     EL +   E     a++
  gi|1676232   269 LLSRWKATDLFLKDIHVLVSELSMVDATPELLALVGE---EGASE----- 310

                  YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vy
                                PYR ++   R +L  t       L      ++  A+
  gi|1676232   311 ------------PYRYLMKKLRARLMATQSWLEARLKG--EKLPKPAgLL 346

                  tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                  t+ E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiR
  gi|1676232   347 TQNEQLWEPLYACYQSLQACGMGIIANGELLDTLRRVKCFGVPLVRIDIR 396

                  qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                  qEs R+t+ l  it+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|1676232   397 QESTRHTEALGEITRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWE 446

                  ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                     + ++vl++ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|1676232   447 PSNDTREVLETCKVIAEAPKGSIAAYVISMAKTPSDVLAVHLLLKEAGIG 496

                  qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                   +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs K
  gi|1676232   497 FAMPVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAK 546

                  DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                  DAG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+
  gi|1676232   547 DAGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAAL 596

                  LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                  LsqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|1676232   597 LSQPPGSLKGGLRVTEQGEMIRFKYGLPEVTVSSLSLYTSAILEANLLPP 646

                  vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                    Pk  WR++m+e+ v+  E YR  v     Fv YFR+AtPE E Gk+ +
  gi|1676232   647 PEPKDSWRHIMDELSVISCETYRGYVRENKDFVPYFRSATPEQELGKLPL 696

                  GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                  GsRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D
  gi|1676232   697 GSRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DG 745

                  KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                  K    L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lva  L+P
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  gi|1676232   746 KQ-SELEAMCRDWPFFSTRLGMLEMVFSKADLWLADYYDQRLVAKTLWPL 794

                   GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                   Gk+LRd  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|1676232   795 GKELRDLLEEDIKVVLAIANDSHLMADLPWIAESIQLRNVYTDPLNVLQA 844

                   YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                     L R R                +E+ k +d            P +E
  gi|1676232   845 ELLYRSR---------------LTEEQGKSPD------------PRVEQA 867

                   LiLtmKGiAAGmqntG<-*
                   L++t+ G+AAGm ntG
  gi|1676232   868 LMVTIAGVAAGMRNTG    883

gi|194737003|ref|YP_002117033.1|: domain 1 of 1, from 1 to 883: score 767.7, E = 8e-228
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  q  +L    vs           +l k L++ ++D  Ge + +
  gi|1947370     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILDR 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls       ++ + +EL + L  L   + + vA+a++  LnLAn
  gi|1947370    35 VETIRKLSKSSRAGNEANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    AE  +      i+ k       Ea    E  i  tl+kL  + +   +
  gi|1947370    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPDLNDAT 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   +  A+   s +LvltAHPt   RR L+ K + i nCL qL   D+   ++
  gi|1947370   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMGEINNCLKQLDNTDIADYER 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   + +   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|1947370   172 HQVMRRLRQLIAQSWHTDEIRKQRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                   RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   R     L+ n+G   +lP d   ++F+sWmGGDRDG nP vt ++tR v
  gi|1947370   222 RELNEQLeENLGY--KLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                   LL+R  A+ l++  +  L+ Elsm     EL +   E     a++
  gi|1947370   269 LLSRWKATDLFLKDIHVLVSELSMVDATPELLALVGE---EGASE----- 310

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               PYR ++   R +L  t       L +G      +   t
  gi|1947370   311 ------------PYRYLMKKLRARLMATQSWLEARL-KGEKLPKPDGLLT 347

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   + E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|1947370   348 QNEQLWEPLYACYQSLQACGMGIIANGELLDTLRRVKCFGVPLVRIDIRQ 397

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   Es R+t+ l  it+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|1947370   398 ESTRHTEALGEITRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWEP 447

                   tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     + ++vl++ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|1947370   448 SNDTREVLETCKVIAEAPKGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                   tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                   +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|1947370   498 AMPVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 547

                   AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                   AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|1947370   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                   sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                   sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|1947370   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEVTVSSLSLYTSAILEANLLPPP 647
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                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR++m+e+ v+  E YR  v     Fv YFR+AtPE E Gk+ +G
  gi|1947370   648 EPKDSWRHIMDELSVISCETYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
  gi|1947370   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lva  L+P G
  gi|1947370   747 Q-SELEAMCRDWPFFSTRLGMLEMVFSKADLWLADYYDQRLVAKTLWPLG 795

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    k+LRd  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|1947370   796 KELRDLLEEDIKVVLAIANDSHLMADLPWIAESIQLRNVYTDPLNVLQAE 845

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                +E+ k +d            P +E  L
  gi|1947370   846 LLYRSR---------------LTEEQGKSPD------------PRVEQAL 868

                    iLtmKGiAAGmqntG<-*
                    ++t+ G+AAGm ntG
  gi|1947370   869 MVTIAGVAAGMRNTG    883

gi|238921689|ref|YP_002935204.1|: domain 1 of 1, from 1 to 877: score 767.5, E = 9.1e-228
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  ++  G vs           +l k L+D ++D  Ge++ +
  gi|2389216     1    -MNEQYSAMR-GNVS-----------MLGKLLgDTIKDALGEEILDR 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++++ + L   L  L   + + vA+a++  LnLAn
  gi|2389216    35 VETIRRLSKSSRAGNEASR-QALLNTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +     Ri+   hG+ a   +A     +   + +L  k     +
  gi|2389216    84 VAEQYH-----RISP--HGEAASNPDA-----LYHLFTRLKNKN-LDEAQ 120

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + +A+ n s++LvltAHPt  +RR L+ K   +  CL+qL   D+   ++
  gi|2389216   121 IRQAVDNLSIELVLTAHPTEIARRTLIHKLVEVNTCLSQLDHDDLADYER 170

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + +   L   +   + tDEiR+ +PtP DE + G + +   +W+GvP FL
  gi|2389216   171 HQIMRRLRQLVAQSWHTDEIRKNRPTPIDEAKWGYAVVENSLWEGVPAFL 220

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+K +G    lP ++  ++F++WmGGDRDG nP vt EvtR
  gi|2389216   221 REFNEQLeKSLGY--QLPVEAVPVRFTAWMGGDRDG-NPNVTAEVTRRAL 267

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  Aa l++  v  L+ Elsm  C  ELR+ A E       +
  gi|2389216   268 LLSRWKAAELFLRDVQVLVSELSMTVCTPELRALAGE-----HTQ----- 307

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                              EPYR +L   R +L nt       L       + +
  gi|2389216   308 -----------EPYREVLKRLRQQLNNTLTYLDARLRGERLPRPADLLVS 346

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    + ++   PL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|2389216   347 N-DQLWQPLHTCYRSLKACGMGIIANGQLLDTLRRVHCFGVPLVRIDIRQ 395

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+t+ l  +t+ L++G Y  WsEe +q +Ll EL  KRPL++
  gi|2389216   396 ESTRHTEALAELTRYLGLGDYETWSEEDKQTFLLRELNSKRPLVPRHWTP 445

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E k+v d+ +v+AE P  +  aY+isma +PsDvLAv LL +E g
  gi|2389216   446 SPETKEVFDTCQVIAEAPAGAIAAYVISMARTPSDVLAVHLLLKEAGCPY 495

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                     L+vvPLFE L DL+ A A + +L siDWY+  i+GKq vm+GYsDs KD
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  gi|2389216   496 NLPVVPLFETLDDLNNAEAVMTQLLSIDWYRGFIQGKQMVMIGYSDSAKD 545

                   AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                   AG ++A W  Y+AqE +++v  + G+ L+lFHGRGG +GRGG P H A+L
  gi|2389216   546 AGVMAASWAQYRAQEALVRVCDNAGIALTLFHGRGGSIGRGGAPAHDALL 595

                   sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                   sqPP  ++  lRvt qGE+i f  G  ++   sL  +t A LE  + PP
  gi|2389216   596 SQPPGSLKSGLRVTEQGEMIRFKLGLPEIAVSSLTLYTSAILEANLLPPP 645

                   sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                   +Pk EWR++m+e+       YR  + K P Fv YFR+AtPElE Gk+ +G
  gi|2389216   646 APKQEWRDVMDELSQTSCALYRRYIRKNPDFVPYFRSATPELELGKLPLG 695

                   sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                   sRPaKR+PsGG+esLRAiPWiFaWtq R  LP WLG G A   A+    +
  gi|2389216   696 SRPAKRRPSGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALEEAMTEGHR 745

                   nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                       L+ mY+ WPFF   +D+lEmvFAK D  +A  yD+ Lv   L+P G
  gi|2389216   746 G--TLENMYRSWPFFTTRIDMLEMVFAKSDLWLAEYYDQRLVDPALWPLG 793

                   ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    +LR++ +   + +L iA    l+   P+    + LR+ Y   Lnv+qA
  gi|2389216   794 TELRQQVQRDIQAVLTIADTDHLMADLPWAAESIALRNVYTDPLNVLQAE 843

                   tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    L R R             +E  d n                  +E  L
  gi|2389216   844 LLYRSRH------------QEQPDAN------------------VEQAL 862

                   iLtmKGiAAGmqntG<-*
                   ++t+ G+AAGm ntG
  gi|2389216   863 MVTIAGVAAGMRNTG    877

gi|269140825|ref|YP_003297526.1|: domain 1 of 1, from 1 to 877: score 767.4, E = 1e-227
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  q  ++  G vs           +l k L+D ++D  Ged+ +
  gi|2691408     1    -MNEQYSAMR-GNVS----------MLGKLLgDTIKDALGEDILDR 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls       ++++ + L   L  L   + + vA+a++  LnLAn
  gi|2691408    35 VETIRRLSKSSRAGNEASR-QALLNTLQNLSNDELLPVARAFSQFLNLAN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +     Ri+   hG+ a   +A     +   + +L  k     +
  gi|2691408    84 VAEQYH-----RISP--HGEAASNPDA-----LSHLFTRLKNKN-LDEAQ 120

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   + +A+ n s++LvltAHPt  +RR L+ K   +  CL+qL   D+   ++
  gi|2691408   121 IRQAVDNLSIELVLTAHPTEIARRTLIHKLVEVNTCLSQLDHDDLADYER 170

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   + +   L   +   + tDEiR+ +PtP DE + G + +   +W+GvP FL
  gi|2691408   171 HQIMRRLRQLVAQSWHTDEIRKNRPTPIDEAKWGYAVVENSLWEGVPAFL 220

                   RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   R     L+K +G    lP ++  + F++WmGGDRDG nP vt EvtR
  gi|2691408   221 REFNEQLeKSLGY--QLPVEAVPVCFTAWMGGDRDG-NPNVTAEVTRRAL 267

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                   LL+R  Aa l++  v  L+ Elsm  C  ELR+ A E       +
  gi|2691408   268 LLSRWKAAELFLRDVQVLVSELSMTVCTPELRALAGE-----HAQ----- 307

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                             EPYR +L   R +L nt       L       + +
  gi|2691408   308 -----------EPYREVLKRLRQQLNNTLTYLDARLRGERLPRPTDLLVS 346

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   + ++   PL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|2691408   347 N-DQLWQPLHTCYRSLKACGMGIIANGQLLDTLRRVHCFGVPLVRIDIRQ 395
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                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+t+ l  +t+ L++G Y  WsEe +q +Ll EL  KRPL++
  gi|2691408   396 ESTRHTEALAELTRYLGLGDYETWSEEDKQTFLLRELNSKRPLVPRHWTP 445

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E k+v d+ +v+AE P  +  aY+isma +PsDvLAv LL +E g
  gi|2691408   446 SPETKEVFDTCQVIAEAPAGAIAAYVISMARTPSDVLAVHLLLKEAGCPY 495

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                     L+v PLFE L DL+ A A + +L siDWY+  i+GKq vm+GYsDs KD
  gi|2691408   496 NLPVAPLFETLDDLNNAEAVMTQLLSIDWYRGFIQGKQMVMIGYSDSAKD 545

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+AqE +++v    G+ L+lFHGRGG +GRGG P H A+L
  gi|2691408   546 AGVMAASWAQYRAQEALVRVCDGAGIALTLFHGRGGSIGRGGAPAHDALL 595

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f  G  ++   sL  +t A LE  + PP
  gi|2691408   596 SQPPGSLKGGLRVTEQGEMIRFKLGLPEIAVSSLTLYTSAILEANLLPPP 645

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                    +Pk EWR++m+e+       YR  v   P Fv YFR+AtPElE Gk+ +G
  gi|2691408   646 APKQEWRDVMDELSQTSCALYRRYVRENPDFVPYFRSATPELELGKLPLG 695

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+PsGG+esLRAiPWiFaWtq R  LP WLG GAA   A+    +
  gi|2691408   696 SRPAKRRPSGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALEEAMAEGRR 745

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        L+ mY+ WPFF   +D+lEmvFAK D  +A  yD+ Lv   L+P G
  gi|2691408   746 D--TLESMYRSWPFFTTRIDMLEMVFAKSDLWLAEYYDQRLVDPALWPLG 793

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                     +LR++ +   + +L iA    l+   P+    + LR+ Y   Lnv+qA
  gi|2691408   794 TELRQQVQRDIQAVLAIANTDHLMADLPWAAESIALRNVYTDPLNVLQAE 843

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R             +E  d n                   +E  L
  gi|2691408   844 LLYRSRH------------QEQPDAN-------------------VEQAL 862

                    iLtmKGiAAGmqntG<-*
                    ++t+ G+AAGm ntG
  gi|2691408   863 MVTIAGVAAGMRNTG    877

gi|194433218|ref|ZP_03065499.1|: domain 1 of 1, from 1 to 883: score 767.2, E = 1.2e-227
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L++ ++D  Ge + E
  gi|1944332     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILER 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       D+ + +EL + L  L   + + vA+a++  LnLAn
  gi|1944332    35 VETIRKLSKSSRAGNDANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+ k       Ea    E  i  tl+kL  + + s +
  gi|1944332    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPELSEDT 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K   +  CL qL  KD+   +
  gi|1944332   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNACLKQLDNKDIADYEH 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|1944332   172 NQLMRRLRQLIAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G   +lP +   ++F+sWmGGDRDG nP vt ++tR v
  gi|1944332   222 RELNEQLeENLGY--KLPVEFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  A+ l++  +  L+ Elsm     EL +   E       +
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  gi|1944332   269 LLSRWKATDLFLKDIQVLVSELSMVEATPELLALVGE-------E----- 306

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR ++ + R +L  t       L +G      e   t
  gi|1944332   307 --------GAAEPYRYLMKNLRSRLMATQAWLEARL-KGEELPKPEGLLT 347

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   + Ee  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|1944332   348 QNEELWEPLYACYQSLQACGMGIIANGDLLDTLRRVKCFGVPLVRIDIRQ 397

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|1944332   398 ESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWQP 447

                   tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     E ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|1944332   448 SAETREVLDTCQVIAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                   tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                   +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|1944332   498 AMPVAPLFETLDDLNNANDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 547

                   AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                   AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|1944332   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                   sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                   sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|1944332   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPP 647

                   sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                    Pk  WR++m+e+ v+  + YR  v     Fv YFR+AtPE E Gk+ +G
  gi|1944332   648 EPKESWRRIMDELSVISCDLYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                   sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                   sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
  gi|1944332   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 746

                   nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                       L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lv   L+P G
  gi|1944332   747 Q-SELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVDKALWPLG 795

                   ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                   k+LR+  +E  + +L iA    l+   P++ + + LR+ Y   Lnv+qA
  gi|1944332   796 KELRNLQEEDIKVVLAIANDSHLMADLPWIAKSIQLRNIYTDPLNVLQAE 845

                   tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    L R R                +E             +++  P +E  L
  gi|1944332   846 LLHRSRQ----------------AEK-----------EGQEPDPRVEQAL 868

                   iLtmKGiAAGmqntG<-*
                   ++t+ GiAAGm ntG
  gi|1944332   869 MVTIAGIAAGMRNTG    883

gi|24115246|ref|NP_709756.1|: domain 1 of 1, from 1 to 883: score 767.2, E = 1.2e-227
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  q  +L    vs          +l k L++ ++D  Ge + E
  gi|2411524     1    -MNEQYSALR-SNVS----------MLGKVLgETIKDALGEHILER 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls       D+ + +EL + L  L   + + vA+a++  LnLAn
  gi|2411524    35 VETIRKLSKSSRAGNDANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    AE  +      i+ k       Ea    E  i  tl+kL  + + s +
  gi|2411524    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPELSEDT 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   +  A+   s +LvltAHPt   RR L+ K   +  CL qL  KD+   ++
  gi|2411524   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNACLKQLDNKDIADYER 171
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                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|2411524   172 NQLMRRLRQLIAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G   +lP +   ++F+sWmGGDRDG nP vt ++tR v
  gi|2411524   222 RELNEQLeENLGY--KLPVEFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  A+ l++  +  L+ Elsm     EL +   E       +
  gi|2411524   269 LLSRWKATDLFLKDIQVLVSELSMVEATPELLALVGE-------E----- 306

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR ++ + R +L  t       L +G      e   t
  gi|2411524   307 --------GAAEPYRYLMKNLRSRLMATQAWLEARL-KGEELPKPEGLLT 347

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    + Ee  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|2411524   348 QNEELWEPLYACYQSLQACGMGIIANGDLLDTLRRVKCFGVPLVRIDIRQ 397

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|2411524   398 ESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWQP 447

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|2411524   448 SAETREVLDTCQVIAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|2411524   498 AMPVAPLFETLDDLNNANDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 547

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|2411524   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2411524   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPP 647

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR++m+e+ v+  + YR  v     Fv YFR+AtPE E Gk+ +G
  gi|2411524   648 EPKESWRRIMDELSVISCDLYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
  gi|2411524   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lv   L+P G
  gi|2411524   747 Q-SELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVDKALWPLG 795

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    k+LR+  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|2411524   796 KELRNLQEEDIKVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 845

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                +E             +++  P +E  L
  gi|2411524   846 LLHRSRQ----------------AEK-----------EGQEPDPRVEQAL 868

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|2411524   869 MVTIAGIAAGMRNTG    883

gi|254032062|gb|ACT54615.1|: domain 1 of 1, from 2 to 1051: score 767.1, E = 1.2e-227
                    *->siDAqLRlLvPGKvsedekLieYDA.LLlDkFLDiLqDLHGedLkEa
                               +   +s   +  e D +LL   F D+Lq   G d  E
  gi|2540320     2    ---TDTTDDIAEEIS--FQSFEDDCkLLGSLFNDVLQREVGSDFMEK 43

                    vqECYEl..sA...eYEGKkDtkKLeE..LGakLtsLdPaDailvAkail
                    +     l +sA +    G +Dt  L E++L + +  +   +a+ +A+a++
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gi|2540320    44 IERTRVLaqSAlnlRLAGIEDTAELLEtqLTSEISNMSLEEALTLARAFS 93

                 HmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlk
                 H LnL  +AE  +   R R+  +                  + +  L
gi|2540320    94 HFLNLMGIAETHHRVRRVRNLPQL------------SRSCNDVFSNLLQS 131

                 lnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK
                 +  sP+E ++ +  q v++vltAHPtq  RR L  K+ R+   L
gi|2540320   132 G-VSPDELYDTVCKQGVEIVLTAHPTQINRRTLQYKHIRMAHLLEYNDRP 180

                 DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvW
                 D+  eD++ + E + REi   + tDE+RR +PtP DE RaG+  +   +W
gi|2540320   181 DLGFEDRETVIEDMVREITSLWQTDELRRQKPTPVDEARAGLNIVEQSLW 230

                 kGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPE
                 k vP +L Rv   LK +     lP     ikF sWmGGDRDG nP vt
gi|2540320   231 KAVPHYLCRVSSSLKKL-TGKPLPLTCTPIKFGSWMGGDRDG-NPNVTAK 278

                 vtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEly.....
                 vt++v L++R mA  lYi  +  L FElsm RC d L   A+E+ +++
gi|2540320   279 VTKEVSLMSRWMAIDLYIREIGSLRFELSMNRCSDRLSRLADEILekeia 328

                 ........................................rtaardk
                  +++ +++ ++++++ +++++ + +++ +++ + +   + ++++ ++ +
gi|2540320   329 aqeswgtnvgrsqpkfpnqqglslptqlppradlplcaecgesQYPKLEV 378

                 vvKyYi.....................................
                  v  Yi+ ++++ ++ ++++ +++ + +++++++ ++++ +++ ++++++
gi|2540320   379 PVTDYIplsrqdvqgissdgygpnlqiktgnghsvnsngcqqsitprgss 428

                 .....................EFWKqvPPt.......EPYRviLGdvRDK
                 +++++   +++   +++ +++ F K + Pt++++ +  PYR++LG+v++K
gi|2540320   429 ssssqlllqkklladsqigrtSFQKLLEPTppkragiAPYRIVLGEVKEK 478

                 LYntRERaRHLLAtGi.seisEeAvytkvEeFLEPLELCYksLCeCGDkv
                 L  tR R   LL  G++ e      y   ++ LEPL LCY sL      v
gi|2540320   479 LLKTR-RLLELLLEGLpCEYDPWDYYETSDQLLEPLLLCYESLHASDSGV 527

                 iADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYRe
                 +ADG L Dl+R v tFG+ L+KLD+RqE+ ++ + lDAitt L++G Y e
gi|2540320   528 LADGRLADLIRRVATFGMVLMKLDLRQEAAKHSEALDAITTYLDMGTYSE 577

                 WsEeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFG
                 W EeK+ E+L  ELkGKRPL+++ +    Evk+vld+frv AEL ++s G
gi|2540320   578 WDEEKKLEFLTRELKGKRPLVPPNIEVGPEVKEVLDTFRVAAELGSESLG 627

                 aYiismataPsDvLAvELLqRECgvkq...........tLrvvPLFEkLA
                 aY+isma   sDvLAvELLq++  +  +++ +++ + +tLrvvPLFE +
gi|2540320   628 AYVISMASNASDVLAVELLQKDARLAVtgelgrpcpagTLRVVPLFETVK 677

                 DLeAAPAavekLFsiDWYinrid....GKqevmvGYsDsGKDAGRlsAAW
                 DL+ A   + kL siDWY+ +i+++++G qevmvGYsDsGKDAGR+ AAW
gi|2540320   678 DLRGAGSVIRKLLSIDWYREHIEknhtGHQEVMVGYSDSGKDAGRFTAAW 727

                 qLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtin
                  LYkAqE+++    ++G+K++lFHGRGG +GRGGGPt LAi sqPP  +
gi|2540320   728 ELYKAQEDVVAACNEFGIKVTLFHGRGGSIGRGGGPTYLAIQSQPPGSVM 777

                 GslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkP.EWR
                 G lR t qGE++   FG  +   r L  +t A L   ++PP  P+ + WR
gi|2540320   778 GTLRSTEQGEMVQAKFGIPQTAVRQLEIYTTAVLLATLEPPQPPREkKWR 827

                 kLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRk
                 +Lmee+  +    Y+  v+  P F+ YF  AtP  E G +niGsRPa+Rk
gi|2540320   828 NLMEEISTISSQNYKGTVYENPEFISYFHEATPQAELGYLNIGSRPARRK 877

                 PsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkE
                  s Gi  LRAiPW+FaWtqtRF LP WLGvGA  K   +K       ++E
gi|2540320   878 SSTGIGHLRAIPWVFAWTQTRFVLPAWLGVGAGLKGVSEKGYAD--DIQE 925

                 mYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkY
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                  mYkeWPFF  t+DL+Emv AK D  i  LyD+ Lv+E+ +  G+ LR +
  gi|2540320   926 MYKEWPFFQSTIDLIEMVLAKADIPITKLYDEQLVSENRRGLGDMLRKEL 975

                  vEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRD
                    t++++L i G   lLE    LK+ +  R +Y+  +n++q   LKR+R
  gi|2540320   976 MTTEKYVLVITGREKLLESNKSLKKLIESRLPYLNAMNMLQVEVLKRLR- 1024

                  PsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGi
                                  dE+          n        L D L++t+ Gi
  gi|2540320  1025 ---------------RDED----------N------NKLRDALLITINGI 1043

                  AAGmqntG<-*
                  AAGm ntG
  gi|2540320  1044 AAGMRNTG    1051

gi|16131794|ref|NP_418391.1|: domain 1 of 1, from 1 to 883: score 767.0, E = 1.3e-227
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      +  q  +L    vs           +l k L++ ++D  Ge + E
  gi|1613179     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILER 34

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v     ls       D+ + +EL + L  L   + + vA+a++  LnLAn
  gi|1613179    35 VETIRKLSKSSRAGNDANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   AE  +      i+ k       Ea    E  i  tl+kL  + + s +
  gi|1613179    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPELSEDT 121

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  +  A+   s +LvltAHPt   RR L+ K   +  CL qL  KD+   +
  gi|1613179   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNACLKQLDNKDIADYEH 171

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|1613179   172 NQLMRRLRQLIAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                  RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                  R     L+ n+G   +lP +   ++F+sWmGGDRDG nP vt ++tR v
  gi|1613179   222 RELNEQLeENLGY--KLPVEFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                  LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                  LL+R  A+ l++  +  L+ Elsm     EL +   E       +
  gi|1613179   269 LLSRWKATDLFLKDIQVLVSELSMVEATPELLALVGE-------E----- 306

                  YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                             EPYR ++ + R +L  t       L +G      e   t
  gi|1613179   307 --------GAAEPYRYLMKNLRSRLMATQAWLEARL-KGEELPKPEGLLT 347

                  kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                  + Ee  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|1613179   348 QNEELWEPLYACYQSLQACGMGIIANGDLLDTLRRVKCFGVPLVRIDIRQ 397

                  EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                  Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|1613179   398 ESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWQP 447

                  tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                    E ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|1613179   448 SAETREVLDTCQVIAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                  tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                  +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|1613179   498 AMPVAPLFETLDDLNNANDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 547

                  AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                  AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|1613179   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                  sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                  sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|1613179   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPP 647
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                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR++m+e+ v+  + YR  v     Fv YFR+AtPE E Gk+ +G
  gi|1613179   648 EPKESWRRIMDELSVISCDVYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
  gi|1613179   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lv   L+P G
  gi|1613179   747 Q-SELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVDKALWPLG 795

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    k+LR+  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|1613179   796 KELRNLQEEDIKVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 845

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                +E             +++  P +E  L
  gi|1613179   846 LLHRSRQ----------------AEK-----------EGQEPDPRVEQAL 868

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|1613179   869 MVTIAGIAAGMRNTG    883

gi|15834139|ref|NP_312912.1|: domain 1 of 1, from 1 to 883: score 766.7, E = 1.7e-227
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L++ ++D  Ge + E
  gi|1583413     1    -MNEQYSALR-SNVS----------MLGKVLgETIKDALGEHILER 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       D+ + +EL + L  L   + + vA+a++  LnLAn
  gi|1583413    35 VETIRKLSKSSRAGNDANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+ k       Ea    E  i  tl+kL  + + s +
  gi|1583413    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPELSEDT 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K   +  CL qL  KD+   +
  gi|1583413   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNACLKQLDNKDIADYEH 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|1583413   172 NQLMRRLRQLIAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G   +lP +   ++F+sWmGGDRDG nP vt ++tR v
  gi|1583413   222 RELNEQLeENLGY--KLPVEFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  A+ l++  +  L+ Elsm     EL +   E       +
  gi|1583413   269 LLSRWKATDLFLKDIQVLVSELSMVEATPELLALVGE-------E----- 306

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR ++ + R +L  t       L +G      e   t
  gi|1583413   307 --------GAAEPYRYLMKNLRSRLMATQAWLEARL-KGEELPKPEGLLT 347

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    + Ee  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|1583413   348 QNEELWEPLYACYQSLQACGMGIIANGDLLDTLRRVKCFGVPLVRIDIRQ 397

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|1583413   398 ESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWQP 447

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|1583413   448 SAETREVLDTCQVIAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
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                    +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|1583413   498 AMPVAPLFETLDDLNNANDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 547

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|1583413   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|1583413   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPP 647

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR++m+e+ v+  + YR  v     Fv YFR+AtPE E Gk+ +G
  gi|1583413   648 EPKESWRRIMDELSVISCDLYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
  gi|1583413   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lv   L+P G
  gi|1583413   747 Q-SELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVDKTLWPLG 795

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    k+LR+  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|1583413   796 KELRNLQEEDIKVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 845

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                +E             +++  P +E  L
  gi|1583413   846 LLHRSRQ----------------AEK-----------EGQEPDPRVEQAL 868

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|1583413   869 MVTIAGIAAGMRNTG    883

gi|26250729|ref|NP_756769.1|: domain 1 of 1, from 1 to 883: score 766.6, E = 1.7e-227
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L++ ++D  Ge + E
  gi|2625072     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILER 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       D+ + +EL + L  L   + + vA+a++  LnLAn
  gi|2625072    35 VETIRKLSKSSRAGNDANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+ k       Ea    E  i  tl+kL  + + s +
  gi|2625072    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPELSEDT 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K   +  CL qL  KD+   +
  gi|2625072   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNACLKQLDNKDIADYEH 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|2625072   172 NQLMRRLRQLIAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G   +lP +   ++F+sWmGGDRDG nP vt ++tR v
  gi|2625072   222 RELNEQLeENLGY--KLPVEFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  A+ l++  +  L+ Elsm     EL +   E       +
  gi|2625072   269 LLSRWKATDLFLKDIQVLVSELSMVEATPELLALVGE-------E----- 306

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR ++ + R +L  t       L +G      e   t
  gi|2625072   307 --------GAAEPYRYLMKNLRSRLMATQAWLEARL-KGEELPKPEGLLT 347

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    + Ee  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|2625072   348 QNEELWEPLYACYQSLQACGMGIIANGDLLDTLRRVKCFGVPLVRIDIRQ 397
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                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|2625072   398 ESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWQP 447

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|2625072   448 SAETREVLDTCQVIAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|2625072   498 AMPVAPLFETLDDLNNANDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 547

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|2625072   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2625072   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPP 647

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR++m+e+ v+  + YR  v     Fv YFR+AtPE E Gk+ +G
  gi|2625072   648 EPKESWRRIMDELSVISCDLYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
  gi|2625072   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lv   L+P G
  gi|2625072   747 Q-SELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVDKALWPLG 795

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    k+LR+  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|2625072   796 KELRNLQEEDIKVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 845

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                +E             +++  P +E  L
  gi|2625072   846 LLHRSRQ----------------AEK-----------EGQEPDPRVEQAL 868

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|2625072   869 MVTIAGIAAGMRNTG    883

gi|110807812|ref|YP_691332.1|: domain 1 of 1, from 1 to 883: score 766.5, E = 1.8e-227
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L++ ++D  Ge + E
  gi|1108078     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILER 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       D+ + +EL + L  L   + + vA+a++  LnLAn
  gi|1108078    35 VETIRKLSKSSRAGNDANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+ k       Ea    E  i  tl+kL  + + s +
  gi|1108078    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPELSEDT 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K   +  CL qL  KD+   +
  gi|1108078   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNACLKQLDNKDIADYEH 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|1108078   172 NQLMRRLRQLIAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G   +lP +   ++F+sWmGGDRDG nP vt ++tR v
  gi|1108078   222 RELNEQLeENLGY--KLPVEFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
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                    LL+R  A+ l++  +  L+ Elsm     EL +   E       +
  gi|1108078   269 LLSRWKATDLFLKDIQVLVSELSMVEATPELLALVGE-------E----- 306

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR ++ + R +L  t       L +G      e   t
  gi|1108078   307 --------GAAEPYRYLMKNLRSRLMATQAWLEARL-KGEELPKPEGLLT 347

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    + Ee  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|1108078   348 QNEELWEPLYACYQSLQACGMGIIANGDLLDTLRHVKCFGVPLVRIDIRQ 397

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|1108078   398 ESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWQP 447

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|1108078   448 SAETREVLDTCQVIAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|1108078   498 AMPVAPLFETLDDLNNANDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 547

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|1108078   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|1108078   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPP 647

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR++m+e+ v+  + YR  v     Fv YFR+AtPE E Gk+ +G
  gi|1108078   648 EPKESWRRIMDELSVISCDLYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
  gi|1108078   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lv   L+P G
  gi|1108078   747 Q-SELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVDKALWPLG 795

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    k+LR+  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|1108078   796 KELRNLQEEDIKVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 845

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                 +E             +++  P +E  L
  gi|1108078   846 LLHRSRQ----------------AEK-----------EGQEPDPRVEQAL 868

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|1108078   869 MVTIAGIAAGMRNTG    883

gi|170683041|ref|YP_001746348.1|: domain 1 of 1, from 1 to 883: score 766.2, E = 2.3e-227
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L++ ++D  Ge + E
  gi|1706830     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILER 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       D+ + +EL + L  L   + + vA+a++  LnLAn
  gi|1706830    35 VETIRKLSKSSRAGNDANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+ k       Ea    E  i  tl+kL  + + s +
  gi|1706830    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPELSEDT 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K   +  CL qL  KD+   +
  gi|1706830   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNACLKQLDNKDIADYEH 171
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                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|1706830   172 NQLMRRLRQLIAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G   +lP +   ++F+sWmGGDRDG nP vt ++tR v
  gi|1706830   222 RELNEQLeENLGY--KLPVEFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  A+ l++  +  L+ Elsm     EL +   E       +
  gi|1706830   269 LLSRWKATDLFLKDIQVLVSELSMVEATPELLALVGE-------E----- 306

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR ++ + R +L  t       L +G      e   t
  gi|1706830   307 --------GAAEPYRYLMKNLRSRLMATQAWLEARL-KGEELPKPEGLLT 347

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    + Ee  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|1706830   348 QNEELWEPLYACYQSLQACGMGIIANGDLLDTLRRVKCFGVPLVRIDIRQ 397

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|1706830   398 ESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWQP 447

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|1706830   448 SAETREVLDTCQVIAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|1706830   498 AMPVAPLFETLDDLNNANDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 547

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|1706830   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|1706830   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPP 647

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR++m+e+ v+  + YR  v     Fv YFR+AtPE E Gk+ +G
  gi|1706830   648 EPKESWRRIMDELSVISCDLYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
  gi|1706830   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lv   L+P G
  gi|1706830   747 Q-SELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVDKALWPLG 795

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    k+LR+  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|1706830   796 KELRNLQEEDIKVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 845

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                +E            + +  P +E  L
  gi|1706830   846 LLHRSRQ----------------AEK-----------EGHEPDPRVEQAL 868

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|1706830   869 MVTIAGIAAGMRNTG    883

gi|218692242|ref|YP_002400454.1|: domain 1 of 1, from 1 to 883: score 766.2, E = 2.4e-227
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L++ ++D  Ge + E
  gi|2186922     1    -MNEQYSALR-SNVS----------MLGKVLgETIKDALGEHILER 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
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                v     ls       D+ + +EL + L  L   + + vA+a++  LnLAn
gi|2186922    35 VETIRKLSKSSRAGNDANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                 AE  +      i+ k       Ea    E  i  tl+kL  + + s +
gi|2186922    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPELSEDT 121

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                +  A+   s +LvltAHPt   RR L+ K   +  CL qL  KD+   +
gi|2186922   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNACLKQLDNKDIADYEH 171

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
gi|2186922   172 NQLMRRLRQLIAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                R     L+ n+G   +lP +   ++F+sWmGGDRDG nP vt ++tR v
gi|2186922   222 RELNEQLeENLGY--KLPVEFAPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                LL+R  A+ l++  +  L+ Elsm     EL +   E       +
gi|2186922   269 LLSRWKATDLFLKDIQVLVSELSMVEATPELLALVGE-------E----- 306

                YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                           EPYR ++ + R +L  t       L +G      e   t
gi|2186922   307 --------GAAEPYRYLMKNLRSRLMATQAWLEARL-KGEELPKPEGLLT 347

                kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                + Ee  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
gi|2186922   348 QNEELWEPLYACYQSLQACGMGIIANGDLLDTLRRVKCFGVPLVRIDIRQ 397

                EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
gi|2186922   398 ESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWQP 447

                tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                  E ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
gi|2186922   448 SAETREVLDTCQVIAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
gi|2186922   498 AMPVAPLFETLDDLNNANDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 547

                AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
gi|2186922   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
gi|2186922   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPP 647

                sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                 Pk  WR +m+e+ v+  + YR  v     Fv YFR+AtPE E Gk+ +G
gi|2186922   648 EPKESWRCIMDELSVISCDVYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
gi|2186922   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 746

                nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                    L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lv   L+P G
gi|2186922   747 Q-SELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVDKALWPLG 795

                ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                k+LR+  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
gi|2186922   796 KELRNLQEEDIKVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 845

                tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                 L R R                 +E             +++  P +E  L
gi|2186922   846 LLHRSRQ----------------AEK-----------EGQEPDPRVEQAL 868
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                  iLtmKGiAAGmqntG<-*
                  ++t+ GiAAGm ntG
  gi|2186922   869 MVTIAGIAAGMRNTG    883

gi|291092305|gb|EFE24866.1|: domain 1 of 1, from 1 to 877: score 766.0, E = 2.7e-227
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      +  q  ++  G vs           +l k L+D ++D  Ge++ +
  gi|2910923     1    -MNEQYSAMR-GNVS-----------MLGKLLgDTIKDALGEQILDR 34

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v     ls       ++++ + L   L  L   + + vA+a++  LnLAn
  gi|2910923    35 VETIRRLSKSSRAGNEASR-QALLNTLQNLSNDELLPVARAFSQFLNLAN 83

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  +AE  +     Ri+   hG+ a   +A   s +   lKk  l
  gi|2910923    84 VAEQYH-----RISP--HGEAASNPDAL--SQLFTRLKKKNLDE----TQ 120

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  + +A+ n s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
  gi|2910923   121 IRQAVDNLSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHDDLADYER 170

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +   L   +   + tDEiR+ +PtP DE + G + +   +W+GvP FL
  gi|2910923   171 NQIMRRLRQLVAQSWHTDEIRKNRPTPIDEAKWGYAVVENSLWEGVPAFL 220

                  RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                  R     L+K +G    lP ++  ++F++WmGGDRDG nP vt EvtR
  gi|2910923   221 REFNEQLeKALGY--QLPVEAVPVRFTAWMGGDRDG-NPNVTAEVTRRAL 267

                  LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                  LL+R  Aa l++  v  L+ Elsm  C  ELRv A E       +
  gi|2910923   268 LLSRWKAAELFLRDVQVLVSELSMTVCTPELRVLAGE-----EAQ----- 307

                  YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                                EPYR +L   R +L  t       L       + +
  gi|2910923   308 -----------EPYREVLKRLRRQLIDTQTYLDARLRGEHPPRPNDLLIS 346

                  kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                  + ++   PL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|2910923   347 N-DQLWQPLHTCYRSLMACGMGIIANGQLLDTLRRVHCFGVPLVRIDIRQ 395

                  EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                  Es R+t+ +  +t+ L++G Y  WsE  +q +Ll EL  KRPL++
  gi|2910923   396 ESTRHTEAIAELTRYLGLGDYETWSEADKQAFLLRELNSKRPLVPRHWTP 445

                  tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                    E k+v d+ +v+AE P  +  aY+isma +PsDvLAv LL +E g
  gi|2910923   446 SPETKEVFDTCQVIAEAPAGAIAAYVISMARTPSDVLAVHLLLKEAGCPF 495

                  tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                   L+v PLFE L DL+ A A + +L siDWY+  i+GKq vm+GYsDs KD
  gi|2910923   496 NLPVAPLFETLDDLNNAEAVMSQLLSIDWYRGFIQGKQMVMIGYSDSAKD 545

                  AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                  AG ++A W  Y+AqE +++v  + G+ L+lFHGRGG +GRGG P H A+L
  gi|2910923   546 AGVMAASWAQYRAQEALVRVCDQAGIALTLFHGRGGSIGRGGAPAHDALL 595

                  sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                  sqPP  ++G lRvt qGE+i f  G  ++   sL  +t A LE  + PP
  gi|2910923   596 SQPPGSLKGGLRVTEQGEMIRFKLGLPEIAVSSLTLYTSAILEANLLPPP 645

                  sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                  +Pk  WR++m+e+       YR  v   P Fv YFR+AtPElE Gk+ +G
  gi|2910923   646 APKQAWRDIMDELSQTSCALYRRYVRENPDFVPYFRSATPELELGKLPLG 695

                  sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                  sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA   A+d+  +
  gi|2910923   696 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALSEAMDQGKR 745

                  nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                      L+ mY++WPFF   +D+lEmvFAK D  +A  yD+ Lv   L+P G
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  gi|2910923   746 D--TLENMYRDWPFFTTRIDMLEMVFAKSDLWLAEYYDQRLVDPALWPLG 793

                   ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                   ++LR++ +   + +L iA    l+   P+    + LR+ Y   Lnv+qA
  gi|2910923   794 NDLRQQVQRDIQAVLAIANTDHLMADLPWAAESIALRNVYTDPLNVLQAE 843

                   tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    L R R             +E  d n                  +E  L
  gi|2910923   844 LLHRSRQ------------QETPDAN------------------VEQAL 862

                   iLtmKGiAAGmqntG<-*
                   ++t+ G+AAGm ntG
  gi|2910923   863 MVTIAGVAAGMRNTG    877

gi|218710807|ref|YP_002418428.1|: domain 1 of 1, from 1 to 876: score 766.0, E = 2.7e-227
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  +  +L    vs           +l + L+  +qD HG+ + E
  gi|2187108     1    -MNEKYAALK-SNVS-----------MLGRLLgNTIQDAHGDVILEK 34

                   vqECYEl..sAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                   v     l++sA    K D   L E    +  L       vA+a+   LnL
  gi|2187108    35 VETIRKLskSARAGNKADRDSLVE---EIKNLPNEQLTPVARAFNQFLNL 81

                   AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                    n+AE  +   R   +               E D+   l     + + s
  gi|2187108    82 TNMAEQYHTISRHCEEHVC------------EPDVLQSLFSKLNQNDISK 119

                   eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    +  +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+
  gi|2187108   120 LDAAQAVRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSHK 169

                   DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                   ++   +  L   i   +  D iR  +PtP DE + G + +   +W+ vP
  gi|2187108   170 ERAKTERRLEQLIAQGWHSDVIRQQRPTPLDEAKWGFAVVENSLWEAVPD 219

                   FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                   FLR +D  LK   + E lP d+  ++FssWmGGDRDG nP vt  +t++v
  gi|2187108   220 FLREMDGRLKGY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITKEV 267

                   CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                     L+R  Aa lY+  v +L+ Elsm +Cnd +R         a  +
  gi|2187108   268 LRLSRWKAADLYLGDVNELITELSMTKCNDAVR-------ELAGDE---- 306

                   yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                              E YR iL   R  L nt E     L    +e++
  gi|2187108   307 -----------HEAYRAILKSLRTLLNNTLEVLDAKLHD--AEVPKKETL 343

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                    ++++   PL  CY+sL eCG  viADGsLLD LR    FG+ Lv+LD+R
  gi|2187108   344 QNIDQLWTPLYACYQSLHECGMGVIADGSLLDTLRRLKAFGVHLVRLDVR 393

                   qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                   qEs R+ Dvl  +t+ L+iG Y +WsE+ +  +L  EL+ KRPLl+ D
  gi|2187108   394 QESTRHSDVLSELTRYLGIGDYDQWSEQDKVAFLTNELSSKRPLLPRDWE 443

                   ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                     E vk+vld+ +v+A  P ++FGaY+isma + sDvLAv LL  ECg
  gi|2187108   444 PSEQVKEVLDTCKVVAAQPREAFGAYVISMARTASDVLAVHLLLQECGCP 493

                   qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                     + v PLFE L DL+   A +++L siD Y+  i+  q vm+GYsDs K
  gi|2187108   494 YRMDVCPLFETLDDLNNSEAVMKQLMSIDLYRGFIQNHQMVMIGYSDSAK 543

                   DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                   DAG +sA W  Y A + ++K   + G+ L+lFHGRGGtvGRGG P H A+
  gi|2187108   544 DAGVMSAGWAQYDAMDKLVKACEEEGIELTLFHGRGGTVGRGGAPAHAAL 593

                   LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                   LsqPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|2187108   594 LSQPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNLYASAILEANLLPP 643
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                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      Pk EWR+Lme +  v  E YR vv  E +Fv YFR AtPElE Gk+ +
  gi|2187108   644 PEPKQEWRDLMEVLSEVSCEAYRNVVRGEEKFVPYFRQATPELELGKLPL 693

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ +d+
  gi|2187108   694 GSRPAKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSVDQGH 743

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    + l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv EeL P
  gi|2187108   744 QAL--LEEMCREWPFFSTRLGMLEMVYSKCNMEIAKYYDQRLVDEELLPL 791

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G+ LR++ +   + +L +     l+  DP+    +RLR+ Y+  Ln++qA
  gi|2187108   792 GELLREQLQKDIKAVLNVENNENLMQSDPWGLESIRLRNIYVEPLNMLQA 841

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R                  E   +++e             LE+
  gi|2187108   842 ELLYRTRKC----------------ET--PPAE-------------LEEA 860

                    LiLtmKGiAAGmqntG<-*
                    L++t+ GiAAGm ntG
  gi|2187108   861 LMVTIAGIAAGMRNTG    876

gi|15804552|ref|NP_290593.1|: domain 1 of 1, from 1 to 883: score 765.9, E = 2.8e-227
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L++ ++D  Ge + E
  gi|1580455     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILER 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       D+ + +EL + L  L   + + vA+a++  LnLAn
  gi|1580455    35 VETIRKLSKSSRAGNDANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+ k       Ea    E  i  tl+kL  + + s +
  gi|1580455    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPELSEDT 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K   +  CL qL  KD+   +
  gi|1580455   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNACLKQLDNKDIADYEH 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|1580455   172 NQLMRRLRQLIAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G   +lP +   ++F+sWmGGDRDG nP vt ++tR v
  gi|1580455   222 RELNEQLeENLGY--KLPVEFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  A+ l++  +  L+ Elsm     EL +   E       +
  gi|1580455   269 LLSRWKATDLFLKDIQVLVSELSMVEATPELLALVGE-------E----- 306

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR ++ + R +L  t       L +G      e   t
  gi|1580455   307 --------GAAEPYRYLMKNLRSRLMATQAWLEARL-KGEELPKPEGXLT 347

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    + Ee  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|1580455   348 QNEELWEPLYACYQSLQACGMGIIANGDLLDTLRRVKCFGVPLVRIDIRQ 397

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|1580455   398 ESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWQP 447

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|1580455   448 SAETREVLDTCQVIAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
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  gi|1580455   498 AMPVAPLFETLDDLNNANDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 547

                   AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                   AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|1580455   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                   sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                   sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|1580455   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPP 647

                   sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                    Pk  WR++m+e+ v+  + YR  v     Fv YFR+AtPE E Gk+ +G
  gi|1580455   648 EPKESWRRIMDELSVISCDLYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                   sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                   sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
  gi|1580455   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 746

                   nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                       L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lv   L+P G
  gi|1580455   747 Q-SELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVDKTLWPLG 795

                   ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                   k+LR+  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|1580455   796 KELRNLQEEDIKVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 845

                   tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    L R R                +E            +++  P +E  L
  gi|1580455   846 LLHRSRQ----------------AEK-----------EGQEPDPRVEQAL 868

                   iLtmKGiAAGmqntG<-*
                   ++t+ GiAAGm ntG
  gi|1580455   869 MVTIAGIAAGMRNTG    883

gi|167551379|ref|ZP_02345134.1|: domain 1 of 1, from 1 to 883: score 765.9, E = 2.9e-227
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  q  +L    vs           +l k L++ ++D  Ge + +
  gi|1675513     1    -MNEQYSALR-SNVS----------MLGKVLgETIKDALGEHILDR 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls       ++ + +EL + L  L   + + vA+a++  LnLAn
  gi|1675513    35 VETIRKLSKSSRAGNEANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    AE  +      i+ k       Ea    E  i  tl+kL  + +   +
  gi|1675513    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPDLNDAT 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   +  A+   s +LvltAHPt   RR L+ K + i nCL qL   D+   ++
  gi|1675513   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMGEINNCLKQLDNTDIADYER 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   + +   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|1675513   172 HQVMRRLRQLIAQSWHTDEIRKQRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                   RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   R     L+ n+G   +lP d   ++F+sWmGGDRDG nP vt ++tR v
  gi|1675513   222 RELNEQLeENLGY--KLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                   LL+R  A+ l++  +  L+ Elsm     EL +   E     a++
  gi|1675513   269 LLSRWKATDLFLKDIHVLVSELSMVNATPELLALVGE---EGASE----- 310

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vy
                              PYR ++   R +L  t       L      ++  A+
  gi|1675513   311 ------------PYRYLMKKLRARLMATQSWLEARLKG--EKLPKPAgLL 346

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                   t+ E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiR
  gi|1675513   347 TQNEQLWEPLYACYQSLQACGMGIIANGELLDTLRRVKCFGVPLVRIDIR 396
```

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                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+t+ l  it+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|1675513   397 QESTRHTEALGEITRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWE 446

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                       + ++vl++ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|1675513   447 PSNDTREVLETCKVIAEAPKGSIAAYVISMAKTPSDVLAVHLLLKEAGIG 496

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                     +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs K
  gi|1675513   497 FAMPVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAK 546

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+
  gi|1675513   547 DAGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAAL 596

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|1675513   597 LSQPPGSLKGGLRVTEQGEMIRFKYGLPEVTVSSLSLYTSAILEANLLPP 646

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      Pk  WR++m+e+ v+  E YR  v     Fv YFR+AtPE E Gk+ +
  gi|1675513   647 PEPKDSWRHIMDELSVISCETYRGYVRENKDFVPYFRSATPEQELGKLPL 696

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D
  gi|1675513   697 GSRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DG 745

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    K    L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lva  L+P
  gi|1675513   746 KQ-SELEAMCRDWPFFSTRLGMLEMVFSKADLWLADYYDQRLVAKTLWPL 794

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    Gk+LRd  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|1675513   795 GKELRDLLEEDIKVVLAIANDSHLMADLPWIAESIQLRNVYTDPLNVLQA 844

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R                +E+ k +d            P +E
  gi|1675513   845 ELLYRSR---------------LTEEQGKSPD------------PRVEQA 867

                    LiLtmKGiAAGmqntG<-*
                    L++t+ G+AAGm ntG
  gi|1675513   868 LMVTIAGVAAGMRNTG    883

gi|56415957|ref|YP_153032.1|: domain 1 of 1, from 1 to 883: score 765.8, E = 3e-227
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L++ ++D  Ge + +
  gi|5641595     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILDR 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++ +  EL + L  L   + + vA+a++  LnLAn
  gi|5641595    35 VETIRKLSKSSRAGNEANR-RELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+ k       Ea    E  i  tl+kL  + +   +
  gi|5641595    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPDLNDAT 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K + i nCL qL   D+   ++
  gi|5641595   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMGEINNCLKQLDNTDIADYER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + +   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|5641595   172 HQVMRRLRQLIAQSWHTDEIRKQRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G   +lP d   ++F+sWmGGDRDG nP vt ++tR v
  gi|5641595   222 RELNEQLeENLGY--KLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  A+ l++  +  L+ Elsm     EL +   E     a++
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  gi|5641595   269 LLSRWKATDLFLKDIHVLVSELSMVDATPELLALVGE---EGASE----- 310

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vy
                                PYR ++   R +L  t       L     e++  A+
  gi|5641595   311 ------------PYRYLMKKLRARLMATQSWLEARLKG--EELPKPAgLL 346

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                   t+ E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiR
  gi|5641595   347 TQNEQLWEPLYACYQSLQACGMGIIANGELLDTLRRVKCFGVPLVRIDIR 396

                   qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                   qEs R+t+ l  it+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|5641595   397 QESTRHTEALGEITRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWE 446

                   ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                      + ++vl++ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|5641595   447 PSNDTREVLETCKVIAEAPKGSIAAYVISMAKTPSDVLAVHLLLKEAGIG 496

                   qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                    +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs K
  gi|5641595   497 FAMPVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAK 546

                   DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                   DAG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+
  gi|5641595   547 DAGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAAL 596

                   LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                   LsqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|5641595   597 LSQPPGSLEGGLRVTEQGEMIRFKYGLPEVTVSSLSLYTSAILEANLLPP 646

                   vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                     Pk  WR++m+e+ v+  E YR  v     Fv YFR+AtPE E Gk+ +
  gi|5641595   647 PEPKDSWRHIMDELSVISCETYRGYVRENKDFVPYFRSATPEQELGKLPL 696

                   GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                   GsRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D
  gi|5641595   697 GSRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DG 745

                   KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                   K    L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lva  L+P
  gi|5641595   746 KQ-SELEAMCRDWPFFSTRLGMLEMVFSKADLWLADYYDQRLVAKTLWPL 794

                   GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                   Gk+LRd  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|5641595   795 GKELRDLLEEDIKVVLAIANDSHLMADLPWIAESIQLRNVYTDPLNVLQA 844

                   YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                     L R R                +E+ k +d            P +E
  gi|5641595   845 ELLYRSR---------------LTEEQGKSPD------------PRVEQA 867

                   LiLtmKGiAAGmqntG<-*
                   L++t+ G+AAGm ntG
  gi|5641595   868 LMVTIAGVAAGMRNTG    883

gi|149200328|ref|ZP_01877347.1|: domain 1 of 1, from 1 to 882: score 765.7, E = 3.2e-227
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           ++   P K       i+    Ll    D ++   G++  +
  gi|1492003     1    -----MKQKSPLKQD-----IKMLGALLG---DTIKTQVGQEFFDKL 34

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        ls       D     EL   + +L   +   + +a+   LnLAnL
  gi|1492003    35 ENIRLLSKRARKNDDEAADKELKDLIRGLSNEELKNLVRAFGQFLNLANL 84

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AE  +      ++  k  DF + a       +   +  L   + +s eE+
  gi|1492003    85 AEAHHF-----MSDMK--DFEEGALTKHLTKLTQIIPELLANG-RSKEEI 126

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    + +    ++Lv+tAHPt   RR  L K+a i   L q     +t+ ++k
  gi|1492003   127 INTIAGMNIELVMTAHPTEVKRRTWLHKHAQINTLLDQKENYRMTPSEQK 176
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                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    +    +   i   +  DEiRR +PtP +E + G++ i +tvW+ vP+F+
  gi|1492003   177 DNINRIAVLITSLWESDEIRRVRPTPFEEAKWGLAIIEDTVWDAVPRFML 226

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                      D  +      E+lP  +  ikF+sWmGGDRDG nP vt E t  vCL
  gi|1492003   227 ELDAIVESF-TGEKLPTWAAPIKFASWMGGDRDG-NPNVTHETTEQVCLR 274

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                     R  A+ lY   v   +  +s   C  ELR+   +++
  gi|1492003   275 NRWTASDLYHKEVNKAIQRISETDCSAELRAIVGDVH------------- 311

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             EPYRv L   R +   t+  +   L  G s  +      ++
  gi|1492003   312 ---------EPYRVFLRPFRARFLETKKWTQAQL-EGKSYEPQLPLMEDI 351

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                     eFL+ L +C +sL eC  k +AD s+L ++R  s FGL + KLD+RqEs
  gi|1492003   352 NEFLDALHICHRSLVECSGKDLADASVLKIIRRASCFGLNILKLDVRQES 401

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     R+ Dv+ Ait+HLe+GsY eW E K+qE+L+ ELk KRPLl+ D+
  gi|1492003   402 TRHSDVINAITEHLELGSYDEWDEAKKQEFLVRELKSKRPLLPRDIQFDA 451

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    + ++v+d+++ +A  P ++ GaY+ism+ a sDvLAv LLq+ECgvk++L
  gi|1492003   452 DCQEVVDTVKTIAKQPEEALGAYVISMSRAASDVLAVHLLQKECGVKKPL 501

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rv PLFE L DLe     ++ LF iDWY+    G qevm+GYsDsGKDAG
  gi|1492003   502 RVAPLFETLEDLENSGEIMDTLFGIDWYKGASHGEQEVMIGYSDSGKDAG 551

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    +l+A W  Y AqE + +v  k+G+KL+lFHGRGG vGRGGGP   A++sq
  gi|1492003   552 KLAASWAQYTAQEALHQVSEKHGIKLTLFHGRGGSVGRGGGPVEHALMSQ 601

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP t++G +Rvt qGEv+   +   ++  + L  +  A L   +  P  P
  gi|1492003   602 PPGTVDGRMRVTEQGEVLQAKYSTIDVACHNLLLYVTAVLQATLAKPPVP 651

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR+Lm++m v+  + YR +v     Fv YFR  tPE E G++ iGsR
  gi|1492003   652 KPEWRELMDKMSVISCDAYRDIVRGRENFVKYFRQVTPEQELGRLHIGSR 701

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRk sGGiesLRAiPWiFaWtq R  LP WLGvG A K A++ D K
  gi|1492003   702 PAKRKKSGGIESLRAIPWIFAWTQIRLMLPSWLGVGEALKVALE-DGKHD 750

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q L+Em ++WPFF   +D+++mv  K D  +A  yD++L  +++k  G +
  gi|1492003   751 Q-LQEMIQDWPFFYFLMDMIDMVMVKTDHRVAKYYDEILADDDVKELGLE 799

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR k + t +   k+       E    L+  +++R++Y  tLn +q   +
  gi|1492003   800 LRTKLKQTLETSQKVVAGLSTQEERVALRASIKVRNPYADTLNYLQGECM 849

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    +R             l KE  d +                 P LED ++
  gi|1492003   850 RR-------------LYKENQDGD-----------------PVLEDAVMA 869

                    tmKGiAAGmqntG<-*
                    t+ GiAA m+ntG
  gi|1492003   870 TIAGIAAAMKNTG    882

gi|84390835|ref|ZP_00991527.1|: domain 1 of 1, from 1 to 876: score 765.6, E = 3.5e-227
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  +  +L    vs           +l + L+  +qD HG+ + E
  gi|8439083     1    -MNEKYAALK-SNVS-----------MLGRLLgNTIQDAHGDVILEK 34

                    vqECYEl..sAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    v     l++sA    K D   L E    +  L       vA+a+   LnL
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gi|8439083    35 VETIRKLskSARAGNKADRDSLVE---EIKNLPNEQLTPVARAFNQFLNL 81

                 AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                  n+AE  +   R   +               E D+   l     + + s
gi|8439083    82 TNMAEQYHTISRHCEEHVC-----------EPDVLQSLFSKLNQNDISK 119

                 eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                  +  +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+
gi|8439083   120 LDAAQAVRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSHK 169

                 DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                 ++   +  L   i   +  D iR  +PtP DE + G + +   +W+ vP
gi|8439083   170 ERVKTERRLEQLIAQGWHSDVIRQQRPTPLDEAKWGFAVVENSLWEAVPD 219

                 FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                 FLR +D  LK   + E lP d+  ++FssWmGGDRDG nP vt  +t++v
gi|8439083   220 FLRDMDGRLKGY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITKEV 267

                 CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                   L+R  Aa lY+  v +L+ Elsm +Cnd +R         a  +
gi|8439083   268 LRLSRWKAADLYLGDVNELITELSMTKCNDAVR-------ELAGDE---- 306

                 yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                             E YR iL   R  L nt E     L    +e++
gi|8439083   307 -----------HEAYRAILKSLRTLLNNTLEVLDAKLHD--AEVPKKETL 343

                 tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                  ++++   PL  CY+sL eCG  viADGsLLD LR    FG+ Lv+LD+R
gi|8439083   344 QNIDQLWTPLYACYQSLHECGMGVIADGSLLDTLRRLKAFGVHLVRLDVR 393

                 qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                 qEs R+ Dvl  +t+ L+iG Y +WsE+ +  +L  EL+ KRPLl+ D
gi|8439083   394 QESTRHSDVLSELTRYLGIGDYDQWSEQDKIAFLTNELSSKRPLLPRDWE 443

                 ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                   E vk+vld+ +v+A  P ++FGaY+isma + sDvLAv LL  ECg
gi|8439083   444 PSEQVKEVLDTCKVVAAQPREAFGAYVISMARTASDVLAVHLLLQECGCP 493

                 qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                   + v PLFE L DL+   A +++L siD Y+  i+  q vm+GYsDs K
gi|8439083   494 YRMDVCPLFETLDDLNNSEAVMKQLMSIDLYRGFIQNHQMVMIGYSDSAK 543

                 DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                 DAG +sA W  Y A + ++Kv  + G+ L+lFHGRGGtvGRGG P H A+
gi|8439083   544 DAGVMSAGWAQYDAMDKLVKVCEEEGIELTLFHGRGGTVGRGGAPAHAAL 593

                 LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                 LsqPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
gi|8439083   594 LSQPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNLYASAILEANLLPP 643

                 vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                   Pk EWR+Lme +  v  E YR vv  E +Fv YFR AtPElE Gk+ +
gi|8439083   644 PEPKQEWRDLMEVLSQVSCEAYRNVVRGEEKFVPYFRQATPELELGKLPL 693

                 GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                 GsRPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ +d+
gi|8439083   694 GSRPAKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSVDQGH 743

                 KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                 + l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv  eL P
gi|8439083   744 QAL--LEEMCREWPFFSTRLGMLEMVYSKCNMEIAKYYDQRLVDKELLPL 791

                 GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                 G+ LR++ +   + +L +     l+  DP+    +RLR+ Y+  Ln++qA
gi|8439083   792 GELLREQLQKDIKAVLNVENNENLMQSDPWGLESIRLRNIYVEPLNMLQA 841

                 YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                   L R R                  E   +++e             LE+
gi|8439083   842 ELLYRTRKC----------------ET--PPAE-------------LEEA 860

                 LiLtmKGiAAGmqntG<-*
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                  L++t+ GiAAGm ntG
  gi|8439083   861 LMVTIAGIAAGMRNTG    876

gi|283787363|ref|YP_003367228.1|: domain 1 of 1, from 1 to 883: score 765.5, E = 3.9e-227
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      +  q  +L    vs           +l k L++ ++D  Ge++ +
  gi|2837873     1    -MNEQYSALR-SNVS----------MLGKVLgETIKDALGENILDR 34

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v     ls       ++ + +EL + L  L   + + vA+a++  LnLAn
  gi|2837873    35 VETIRKLSKSSRAGNEANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   AE  +      i+ k       Ea    E  i  tl+kL  + n   +
  gi|2837873    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPNLNEAT 121

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  +  A+   s +LvltAHPt   RR L+ K   +  CL qL  KD+   ++
  gi|2837873   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNACLKQLDNKDIVDYER 171

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  + L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|2837873   172 HQLMRRLRQLIAQSWHTDEIRKQRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                  RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                  R     L+ n+G    lP d   ++F+sWmGGDRDG nP vt ++tR v
  gi|2837873   222 RELNEQLeENLGY--QLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                  LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                  LL+R  A+ l++  +  L+ Elsm     EL +   E     a++
  gi|2837873   269 LLSRWKATDLFLKDIQVLVSELSMVDATPELLAMVGE---EGASE----- 310

                  YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vy
                             PYR ++ + R +L  t       L      ++  A+
  gi|2837873   311 ------------PYRYLMKNLRSRLMATQAWLEARLKG--EKLPKPAgLL 346

                  tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                  t+ E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiR
  gi|2837873   347 TQNEQLWEPLYACYQSLQACGMGIIANGELLDTLRRVKCFGVPLVRIDIR 396

                  qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                  qEs R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|2837873   397 QESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRHWE 446

                  ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                     + ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|2837873   447 PSNDTREVLDTCKVIAEAPKGSIAAYVISMAKTPSDVLAVHLLLKEAGIG 496

                  qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                   +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs K
  gi|2837873   497 FAMPVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAK 546

                  DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                  DAG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+
  gi|2837873   547 DAGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAAL 596

                  LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                  LsqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2837873   597 LSQPPGSLKGGLRVTEQGEMIRFKYGLPEVTVSSLSLYTSAILEANLLPP 646

                  vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                    Pk  WR++m+e+ v+  + YR  v     Fv YFR+AtPE E Gk+ +
  gi|2837873   647 PEPKDAWRHIMDELSVISCDLYRGYVRENKDFVPYFRSATPEQELGKLPL 696

                  GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                  GsRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D
  gi|2837873   697 GSRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DG 745

                  KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                  K    L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lva eL+P
  gi|2837873   746 KQ-SELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVAKELWPL 794
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                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    Gk+LR+   E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|2837873   795 GKELRNLLAEDIKVVLDIANDSHLMADLPWIAESIQLRNIYTDPLNVLQA 844

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R          l  E   E+                P +E
  gi|2837873   845 ELLHRSR-----------LTEEQGKEP----------------DPRVEQA 867

                    LiLtmKGiAAGmqntG<-*
                    L++t+ G+AAGm ntG
  gi|2837873   868 LMVTIAGVAAGMRNTG    883

gi|260595982|ref|YP_003208553.1|: domain 1 of 1, from 1 to 883: score 765.2, E = 4.8e-227
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L+D ++D  Ge++ +
  gi|2605959     1    -MNEQYSALR-SNVS-----------MLGKLLgDTIKDALGENILDR 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++ + + L + L   L   + + vA+a++  LnLAn
  gi|2605959    35 VETIRKLSKSSRAGNEADR-QALLTTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+ k       Ea    E  i  tl+kL  + +
  gi|2605959    84 TAEQYH-----SISPKG------EAASNPEI-IARTLRKLKDQPDINETA 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + +A+   s +LvltAHPt   RR L+ K   + nCL qL  KD+   ++
  gi|2605959   122 IRQAVESLSLELVLTAHPTEITRRTLIHKMVEVNNCLKQLDHKDIADYER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|2605959   172 NQITRRLRQLIAQSWHTDEIRKNRPSPVDEAKWGFAVVENSLWEGVPNYL 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R     L    +  +lP d   ++F+sWmGGDRDG nP vt ++tR v L
  gi|2605959   222 RELNEQLEA-HLDYKLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVLL 269

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  A+ l++  +  L+ Elsm  C d LR    +   t   +
  gi|2605959   270 LSRWKATDLFLKDIQVLISELSMVECSDALR----DYVGTEGAQ------ 309

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR +L   R +L  t       L +G      +   t+
  gi|2605959   310 ----------EPYRYLLKGLRAQLLATQAWLEARL-KGQKLPKPQGLLTQ 348

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     E+  EPL  CY sL  CG  +iA G LLD LR v  FG+ Lv++DiRqE
  gi|2605959   349 NEQLWEPLYACYESLVACGLGIIANGELLDTLRRVKAFGVPLVRIDIRQE 398

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+ + l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|2605959   399 STRHAEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRQWEPS 448

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    +  ++vl++ +v+AE P  s  aY+isma +PsDvLAv LL +E g+  +
  gi|2605959   449 DNTREVLETCKVIAEAPKGSIAAYVISMAKTPSDVLAVHLLLKEAGIGFA 498

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    L+v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDA
  gi|2605959   499 LPVAPLFETLDDLNNANDVMTQLLNIDWYRGFIQGKQMVMIGYSDSAKDA 548

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Ls
  gi|2605959   549 GVMAASWAQYQAQDALIKTCEKAGIALTLFHGRGGSIGRGGAPAHAALLS 598

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2605959   599 QPPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLSLYTSAILEANLLPPPE 648

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
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                    Pk  WR++m+e+  +    YR  v     Fv YFR+AtPE E Gk+ +Gs
  gi|2605959   649 PKAAWRHIMDELSDISCAMYRGYVRENKDFVPYFRSATPEQELGKLPLGS 698

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA +  ++ D K
  gi|2605959   699 RPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQKVVE-DGKQ 747

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                       L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lv  eL+P G+
  gi|2605959   748 -DELETMCRDWPFFSTRLGMLEMVFAKADLWLADYYDQRLVKKELWPLGQ 796

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR+  +   + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|2605959   797 ELRQLLEADIKVVLDIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAEL 846

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R               A+E+ k+ad            P +E  L+
  gi|2605959   847 LHRSRQ---------------AEEEGKPAD------------PCVEQALM 869

                    LtmKGiAAGmqntG<-*
                    +t+ G+AAGm ntG
  gi|2605959   870 VTIAGVAAGMRNTG    883

gi|86147311|ref|ZP_01065625.1|: domain 1 of 1, from 1 to 876: score 765.1, E = 4.9e-227
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  +  +L    vs           +l + L+  +qD HG+ + E
  gi|8614731     1    -MNEKYAALK-SNVS-----------MLGRLLgNTIQDAHGDVILEK 34

                    vqECYEl..sAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    v     l++sA    K D   L E    +  L       vA+a+   LnL
  gi|8614731    35 VETIRKLskSARAGNKADRDSLVE---EIKNLPNEQLTPVARAFNQFLNL 81

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                     n+AE  +   R   +               E D+   l     + + s
  gi|8614731    82 TNMAEQYHTISRHCEEHVC-----------EPDVLQSLFSKLNQNDISK 119

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                     +  +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+
  gi|8614731   120 LDAAQAVRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSHK 169

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++   +  L   i   +  D iR  +PtP DE + G + +   +W+ vP
  gi|8614731   170 ERVKTERRLEQLIAQGWHSDVIRQQRPTPLDEAKWGFAVVENSLWEAVPD 219

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    FLR +D  LK   + E lP d+  ++FssWmGGDRDG nP vt  +t++v
  gi|8614731   220 FLREMDGRLKGY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITKEV 267

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      L+R  Aa lY+  v +L+ Elsm +Cnd +R         a  +
  gi|8614731   268 LRLSRWKAADLYLGDVNELITELSMTKCNDAVR-------ELAGDE---- 306

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                                E YR iL   R  L nt E     L    +e++
  gi|8614731   307 -----------HEAYRAILKSLRTLLNNTLEVLDAKLHD--AEVPKKETL 343

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     ++++   PL  CY+sL eCG  viADGsLLD LR    FG+ Lv+LD+R
  gi|8614731   344 QNIDQLWTPLYACYQSLHECGMGVIADGSLLDTLRRLKAFGVHLVRLDVR 393

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+ Dvl  +t+ L+iG Y +WsE+ +  +L  EL+ KRPLl+ D
  gi|8614731   394 QESTRHSDVLSELTRYLGIGDYDQWSEQDKVAFLTNELSSKRPLLPRDWE 443

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                      E vk+vld+ +v+A  P ++FGaY+isma + sDvLAv LL  ECg
  gi|8614731   444 PSEQVKEVLDTCKVVAAQPREAFGAYVISMARTASDVLAVHLLLQECGCP 493

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                      + v PLFE L DL+   A +++L siD Y+  i+  q vm+GYsDs K
  gi|8614731   494 YRMDVCPLFETLDDLNNSEAVMKQLMSIDLYRGFIQNHQMVMIGYSDSAK 543
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                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG +sA W  Y A + ++K   + G+ L+lFHGRGGtvGRGG P H A+
  gi|8614731   544 DAGVMSAGWAQYDAMDKLVKACEEEGIELTLFHGRGGTVGRGGAPAHAAL 593

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|8614731   594 LSQPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNLYASAILEANLLPP 643

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      Pk EWR+Lme +  v  E YR vv  E +Fv YFR AtPElE Gk+ +
  gi|8614731   644 PEPKQEWRDLMEVLSEVSCEAYRNVVRGEEKFVPYFRQATPELELGKLPL 693

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ +d+
  gi|8614731   694 GSRPAKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSVDQGH 743

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    + l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv EeL P
  gi|8614731   744 QAL--LEEMCREWPFFSTRLGMLEMVYSKCNMEIAKYYDQRLVDEELLPL 791

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G+ LR++ +   + +L +     l+  DP+    +RLR+ Y+  Ln++qA
  gi|8614731   792 GELLREQLQKDIKAVLNVENNENLMQSDPWGLESIRLRNIYVEPLNMLQA 841

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R                  E   +++e             LE+
  gi|8614731   842 ELLYRTRKC----------------ET--PPAE-------------LEEA 860

                    LiLtmKGiAAGmqntG<-*
                    L++t+ GiAAGm ntG
  gi|8614731   861 LMVTIAGIAAGMRNTG    876

gi|290477219|ref|YP_003470136.1|: domain 1 of 1, from 1 to 878: score 765.0, E = 5.2e-227
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  ++    vs           +l k L+  +++  Ge++ +
  gi|2904772     1    -MNQQYSAMR-SNVS-----------MLGKLLgNTIKEALGESILDK 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++ + + L + L  L   + + vA+a+   LnLAn
  gi|2904772    35 VETIRKLSKSSRAGNEADR-QQLLSTLQNLSNDELLPVARAFNQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +       +   hG+ a    A     +E  + +L  k   s ++
  gi|2904772    84 VAEQYH-------SISPHGEAASNPVA-----LEALFNRLKDKK-FSNDD 120

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      +A+   +++LvltAHPt  +RR L+ K   +  CL+qL   D+   ++
  gi|2904772   121 LINAVNELAIELVLTAHPTEIARRTLIHKLVEVNACLSQLDHDDLADYER 170

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L   i   + tDEiR+ +PtP DE + G + +   +W+GvP FL
  gi|2904772   171 INIMRRLRQLIAQSWHTDEIRKIRPTPIDEAKWGFAVVENSLWEGVPAFL 220

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R     L    i   lP ++  i+F+sWmGGDRDG nP vt E+tR v L
  gi|2904772   221 REFNEQLEE-SIGYSLPVEAVPIRFTSWMGGDRDG-NPNVTAEITRHVLL 268

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa l++  +  L+ Elsm  C  ELR       + a  d
  gi|2904772   269 LSRWKAADLFLKDIQVLVSELSMSECTPELR-------QLAGGD------ 305

                    iEFWKqvPPtEPYRviLGdvRDKLYntRER.aRHLLAtGiseisEeAvyt
                              EPYR i  + R +L  t     +HL  +G   ++
  gi|2904772   306 -------GVLEPYREIAKQLRTQLNSTLTYlEKHL--KGERVLPPVGLLL 346

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    + E+   PL  CY+sL  CG  +iA G LLD LR +  FGLsLv++DiRq
  gi|2904772   347 HNEQLWQPLYACYQSLKTCGMEIIANGQLLDTLRRIRCFGLSLVRIDIRQ 396

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
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                    Es R+tD +  +t+ Le+G Y +WsE  +q +Ll EL  KRPL++
  gi|2904772   397 ESTRHTDAIAELTQYLELGDYASWSETEKQTFLLRELNSKRPLIPHCWQP 446

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     EE  +v ++ +v+AE P D+  aY+isma  PsDvLAv LL +E g
  gi|2904772   447 SEETLEVFETCKVIAESPQDAIAAYVISMAKVPSDVLAVKLLLKEAGCSL 496

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                     L+v PLFE L DL+ A   +++L  i WY+  i+ Kq vm+GYsDs KD
  gi|2904772   497 KLPVAPLFETLDDLNNAESVIQQLLGIGWYRELIQDKQMVMIGYSDSAKD 546

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+Aq+ +iKv  +  v L+lFHGRGGt+GRGG P H A+L
  gi|2904772   547 AGVMAASWAQYRAQDALIKVCEQESVTLTLFHGRGGTIGRGGAPAHSALL 596

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP
  gi|2904772   597 SQPPGSLKGGLRVTEQGEMIRFKFGLPQVTISSLALYASAILEANLLPPP 646

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     PkPEW+++m+ +  v  + YR  v   P Fv YFR AtPE E  k+ +G
  gi|2904772   647 EPKPEWKQVMDTLSDVSCDMYRDYVREQPEFVPYFRAATPEQELAKLPLG 696

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA +h i  D
  gi|2904772   697 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQHVI--DAG 744

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     l  L +m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P G
  gi|2904772   745 KLSVLADMCRDWPFFNTRIAMLEMVFAKADLWLAEYYDQRLVDKKLWPLG 794

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                      LR++  E  + +L i     l+   P++   + LR+ Y   Lnv+qA
  gi|2904772   795 ITLRNQLAEDIKTVLTISQDEQLMADLPWIAESIALRNVYTDPLNVLQAE 844

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L+R R                 +E+   +d            P LE  L
  gi|2904772   845 LLQRSRQ----------------QEQ---PD-----------PHLEQAL 863

                    iLtmKGiAAGmqntG<-*
                    ++t+ G+AAGm ntG
  gi|2904772   864 MVTIAGVAAGMRNTG    878

gi|16767384|ref|NP_462999.1|: domain 1 of 1, from 1 to 883: score 764.9, E = 5.7e-227
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L++ ++D  Ge + +
  gi|1676738     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILDR 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++ + +EL + L  L   + + vA+a++  LnLAn
  gi|1676738    35 VETIRKLSKSSRAGNEANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+ k       Ea    E  i  tl+kL  + +   +
  gi|1676738    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPDLNDAT 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K + i nCL qL   D+   ++
  gi|1676738   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMGEINNCLKQLDNTDIADYER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + +   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|1676738   172 HQVMRRLRQLIAQSWHTDEIRKQRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G   +lP d   ++F+sWmGGDRDG nP vt ++tR v
  gi|1676738   222 RELNEQLeENLGY--KLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  A+ l++  +  L+ Elsm     EL +   E     a++
  gi|1676738   269 LLSRWKATDLFLKDIHVLVSELSMVDATPELLALVGE---EGASE----- 310
```

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                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vy
                               PYR ++   R +L  t       L      ++  A+
  gi|1676738   311 ------------PYRYLMKKLRARLMATQSWLEARLKG--EKLPKPAgLL 346

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                    t+ E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiR
  gi|1676738   347 TQNEQLWEPLYACYQSLQACGMGIIANGELLDTLRRVKCFGVPLVRIDIR 396

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+t+ l  it+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|1676738   397 QESTRHTEALGEITRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWE 446

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                       + ++vl++ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|1676738   447 PSNDTREVLETCKVIAEAPKGSIAAYVISMAKTPSDVLAVHLLLKEAGIG 496

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                     +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs K
  gi|1676738   497 FAMPVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAK 546

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+
  gi|1676738   547 DAGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAAL 596

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|1676738   597 LSQPPGSLKGGLRVTEQGEMIRFKYGLPEVTVSSLSLYTSAILEANLLPP 646

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      Pk  WR++m+e+ v+  E YR  v     Fv YFR+AtPE E Gk+ +
  gi|1676738   647 PEPKDSWRHIMDELSVISCETYRGYVRENKDFVPYFRSATPEQELGKLPL 696

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D
  gi|1676738   697 GSRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DG 745

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    K    L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lva  L+P
  gi|1676738   746 KQ-SELEAMCRDWPFFSTRLGMLEMVFSKADLWLADYYDQRLVAKTLWPL 794

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    Gk+LRd  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|1676738   795 GKELRDLLEEDIKVVLAIANDSHLMADLPWIAESIQLRNVYTDPLNVLQA 844

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R                +E+ k +d            P +E
  gi|1676738   845 ELLYRSR---------------LTEEQGKSPD------------PRVEQA 867

                    LiLtmKGiAAGmqntG<-*
                    L++t+ G+AAGm ntG
  gi|1676738   868 LMVTIAGVAAGMRNTG    883

gi|162420514|ref|YP_001608201.1|: domain 1 of 1, from 8 to 898: score 764.5, E = 7.4e-227
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +        v G + e+   ++    +l   L+D +++  Ge + +
  gi|1624205     8    AASNTKDKWVRGHMNEQYSAMRSNVSMLGTLLgDTIKEALGEHILDR 54

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++++ +EL + L  L   + + vA+a++  LnL n
  gi|1624205    55 VETIRKLSKSSRAGNEASR-QELLTTLQNLSNDELLPVARAFSQFLNLTN 103

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +       +   hG+ a   +A     +   + +L  k   s ++
  gi|1624205   104 TAEQYH-------SISPHGEAASNPEA-----LAQLFTRLKDKK-LSDQD 140

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
  gi|1624205   141 MRSAVDDLSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHNDLADYER 190

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
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                     +   L   +   + tDEiR+ +P P DE + G + +   +W+GvP FL
  gi|1624205   191 NKIMRRLRQLVAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWEGVPAFL 240

                     RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                     R     L n  +  RlP ++  i+F+sWmGGDRDG nP vt E+tR v L
  gi|1624205   241 REFNEQLEN-SLDYRLPVEAVPIRFTSWMGGDRDG-NPNVTAEITRHVLL 288

                     LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                     L+R  A+ l++  +  L+ Elsm  C  ELR    El
  gi|1624205   289 LSRWKATDLFLRDIQVLVSELSMSECTPELR----ELAGGEEVL------ 328

                     iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                               EPYR ++ +vR +L nt       L +G   ++
  gi|1624205   329 ----------EPYRQLMKNVRTQLTNTQAYLEARL-KGERVLPPHDLLVS 367

                     vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      ++  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+RqE
  gi|1624205   368 NDQLWEPLYACYQSLKACGMEIIANGQLLDTLRRVRCFGVPLVRIDVRQE 417

                     seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                     s R+tD +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
  gi|1624205   418 STRHTDAIAELTRYLGLGDYESWSESDKQAFLVRELNSKRPLVPLKWEPS 467

                     EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                      E ++vl++ rv+AE P  s  aY+isma  PsDvLAv LL +E g   t
  gi|1624205   468 AETQEVLETCRVIAEAPQGSIAAYVISMAKVPSDVLAVHLLLKEAGCPFT 517

                     LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                     L+v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDA
  gi|1624205   518 LPVAPLFETLDDLNNADDVMTQLLGIDWYRGLIQGKQMVMIGYSDSAKDA 567

                     GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                     G ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Ls
  gi|1624205   568 GVMAASWAQYRAQDALIKTCEKAGITLTLFHGRGGSIGRGGAPAHAALLS 617

                     qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                     qPP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP
  gi|1624205   618 QPPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLALYAGAILEANLLPPPE 667

                     PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                     Pk EW ++m+ +     + YRs v   P Fv YFR AtPElE Gk+ +Gs
  gi|1624205   668 PKKEWIEVMDLLSDASCDMYRSYVRENPEFVRYFRAATPELELGKLPLGS 717

                     RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                     RPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GA  + Aid   +
  gi|1624205   718 RPAKRRPDGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQRAIDAGKQD 767

                     lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                     +  L  m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P G+
  gi|1624205   768 V--LATMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVDKSLWPLGQ 815

                     sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                     +LRd+     + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|1624205   816 QLRDQLAADIKVVLAIANDDHLMADLPWIAESIALRNVYTDPLNVLQAEL 865

                     LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                     L R R             +E+ d                   +E  L+
  gi|1624205   866 LHRSRQ------------QEHPDAC------------------VEQALM 884

                     LtmKGiAAGmqntG<-*
                     +t+ G+AAGm ntG
  gi|1624205   885 VTIAGVAAGMRNTG    898

gi|121587916|ref|ZP_01677671.1|: domain 1 of 1, from 3 to 887: score 764.3, E = 8.5e-227
                     *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                         i  q R+    K +     ++    +l + L+  +q   G+ +
  gi|1215879     3    VIFFQGRMTMNEKYA----ALKSNVSMLGRLLgQTIQAADGDVILAK 45

                     vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                     v     ls        + + e L   +  L       vA+a+   LnL n
  gi|1215879    46 VETIRKLSKSARAGNQADR-ELLIEEIKNLPNHQLTPVARAFNQFLNLTN 94
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                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                +AE  +   R   +         E +A     i   + kL  k   s  +
gi|1215879     95 IAEQYHTISRHCESHVN------ELDA-----IGSLFAKLAQKS-VSKFD 132

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+ + ++
gi|1215879    133 TAQAIRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSPKER 182

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                +  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
gi|1215879    183 HKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWHAVPEFL 232

                RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                R  D  +K   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
gi|1215879    233 RELDEQVKSY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITREVLL 280

                LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                L+R  Aa lY+  + +L+ Elsm +Cn+ +R+ A E       +
gi|1215879    281 LSRWKAADLYLTDINELVSELSMTKCNEAVRALAGE-------E------ 317

                iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                           EPYR iL  +R  L  t E     L      ++  A
gi|1215879    318 ---------HEPYRAILKPIRSLLQETIEILDAKLNG--QKLAVKAPLQT 356

                vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                 ++  EPL  CY+sL eCG  viADGsLLD LR +  FG+ Lv+LD+RqE
gi|1215879    357 ADQLWEPLYACYQSLHECGMGVIADGSLLDTLRRIKAFGVHLVRLDVRQE 406

                seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                s R+ +v+  +t+HL+iG Y +WsE+ +  +L +EL  KRPLl+ D
gi|1215879    407 SSRHAEVISELTRHLGIGDYNQWSEQDKIAFLTTELNSKRPLLPRDWQPS 456

                EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                  vk+vld+ +++A    D+FGaY+isma + sDvLAv LL  E g
gi|1215879    457 PQVKEVLDTCKIIAAQSKDAFGAYVISMARTASDVLAVHLLLQEAGCPYR 506

                LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                + v PLFE L DL+ A   + +L  iD Y+  i+  q vm+GYsDs KDA
gi|1215879    507 MDVCPLFETLDDLNNAESVIRQLMNIDLYRGFIQNHQMVMIGYSDSAKDA 556

                GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                G ++A W  Y+A E ++Kv  + G+ L+lFHGRGGt+GRGG P H A+Ls
gi|1215879    557 GVMAAGWAQYRAMEALVKVGEEAGIELTLFHGRGGTIGRGGAPAHAALLS 606

                qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
gi|1215879    607 QPPKSLKGGLRVTEQGEMIRFKLGLPEVAVNSFNMYASAILEANLLPPPE 656

                PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                Pk EWR Lm+ +  +    YR vv  EP Fv YFR AtPElE Gk+ +Gs
gi|1215879    657 PKNEWRALMDILSEISCNAYRKVVRGEPDFVPYFRQATPELELGKLPLGS 706

                RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                RPaKR P GG+esLRAiPWiF+W q R  LP WLG G A + Ai+   +
gi|1215879    707 RPAKRNPTGGVESLRAIPWIFSWSQNRLILPAWLGAGEAIQIAINEGHQA 756

                lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv   L+P G+
gi|1215879    757 L--LEEMCREWPFFSTRLGMLEMVYTKCSVSIACHYDERLVEPTLRPLGE 804

                sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                +LR++ +   + +L +     l+  DP+ +  +RLR+ Yi  Ln++qA
gi|1215879    805 KLRAQLQQDIKVVLNVENNENLMQSDPWGQESIRLRNIYIEPLNMLQAEL 854

                LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                L R R  +                +                aP LE+ L+
gi|1215879    855 LYRTRQSEL---------------P----------------APELEEALM 873

                LtmKGiAAGmqntG<-*
                +t+ GiAAGm ntG
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  gi|1215879   874 VTIAGIAAGMRNTG    887

gi|197287040|ref|YP_002152912.1|: domain 1 of 1, from 1 to 878: score 764.0, E = 1e-226
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      +  q  ++    vs           +l k L+D +++  Ge++ +
  gi|1972870     1    -MNQQYSAMR-SNVS-----------MLGKLLgDTIKEALGEEILDK 34

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v     ls       + ++ + L   L  L   + + vA+a+   LnL n
  gi|1972870    35 VESIRKLSKSSRAGNEVQR-QKLLLTLQNLSNDELLPVARAFNQFLNLTN 83

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  +AE  +       +   hG+ a    A     +   + +L  k   + +
  gi|1972870    84 VAEQYH-------SISPHGEAASNPVA-----LAKLIERLKDKN-FTNQQ 120

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +A+   s++LvltAHPt  +RR L+ K   +  CL+qL   D+   ++
  gi|1972870   121 LKQAVEQISIELVLTAHPTEIARRTLIHKLVEVNTCLSQLDHDDLADYER 170

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +   L   +   + tDEiR+ +PtP DE + G + +   +W+GvP FL
  gi|1972870   171 TNIMRRLRQLVAQSWHTDEIRKIRPTPIDEAKWGFAVVENSLWEGVPAFL 220

                  RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                  R     L    i   lP ++  i+F+sWmGGDRDG nP vt E+tR   L
  gi|1972870   221 REFNEQLEE-SIDYNLPVEASPIRFTSWMGGDRDG-NPNVTAEITRHALL 268

                  LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                  L+R  Aa l+++ +  L+ Elsm     ELR    El   a
  gi|1972870   269 LSRWKAADLFLNDIQVLVSELSMTESTPELR----ELAGGADVA------ 308

                  iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                            EPYR i  + R +L  tR+     + +G   ++ e    +
  gi|1972870   309 ----------EPYREIAKQLRTRLQVTRDYLEQRI-KGQQSLPPEGLLID 347

                  vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                       EPL  CY+sL +CG ++iA G LLD LR +  FGL Lv+LDiRqE
  gi|1972870   348 NSALWEPLYACYQSLHQCGMRIIANGQLLDTLRRIRCFGLQLVRLDIRQE 397

                  seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                  s  +t+ l  +t+ Le+G Y +WsEe++q +Ll+EL  KRPL++
  gi|1972870   398 STNHTEALSELTQYLELGDYASWSEEQKQTFLLTELNSKRPLIPTHWQPS 447

                  EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                  E  k+v ++ rv+AE P Ds  +Y+isma  PsDvLAv LL +E g
  gi|1972870   448 EATKEVFETCRVIAESPKDSIASYVISMAKVPSDVLAVKLLLKEAGADIR 497

                  LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                  L+v PLFE L DL+ A   + +LF i WY+  id Kq vm+GYsDs KDA
  gi|1972870   498 LPVAPLFETLEDLNNAESVMTRLFDIPWYRDLIDNKQMVMIGYSDSAKDA 547

                  GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                  G ++A W  Y+Aq+ +iK   k Gv L+lFHGRGGt+GRGG P H A+Ls
  gi|1972870   548 GVMAASWAQYRAQDALIKLCEKSGVTLTLFHGRGGTIGRGGAPAHAALLS 597

                  qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                  qPP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP
  gi|1972870   598 QPPGSLKGGLRVTEQGEMIRFKFGLPQVTISSLAHYAGAILEANLLPPPE 647

                  PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                  Pk  W ++m+ +  v  E YR  v  E  Fv YFR AtPE E Gk+ +Gs
  gi|1972870   648 PKTAWIEVMDALSDVSCEMYRGYVRGEKDFVPYFRAATPEGELGKLPLGS 697

                  RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                  RPaKR+P GG+e+LRAiPWiFaWtq R  LP WLG GAA +h id   +
  gi|1972870   698 RPAKRRPTGGVETLRAIPWIFAWTQNRLMLPAWLGAGAALQHEIDNGKQA 747

                  lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                  +  L +m ++WPFF   + +lEmv+AK D  +A  yD+ Lv E+L+P G
  gi|1972870   748 V--LDDMCENWPFFNTRIAMLEMVYAKADLWLAEYYDQRLVEENLWPLGA 795
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                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR++  +  + +L i     l+   P++   + LR+ Y   Lnv+qA
  gi|1972870   796 KLRQQLSDDIKSVLAISKDEHLMADLPWVAESIALRNVYTDPLNVLQAEL 845

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L+R R                                 ++  P +E  L+
  gi|1972870   846 LQRSR-------------------------------THSESDPRIEQALM 864

                    LtmKGiAAGmqntG<-*
                    +t+ GiAAGm ntG
  gi|1972870   865 VTIAGIAAGMRNTG    878

gi|123440516|ref|YP_001004510.1|: domain 1 of 1, from 1 to 879: score 763.6, E = 1.4e-226
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +  q  ++    vs          +L     D +++  Ge + E v
  gi|1234405     1    -MNEQYSAMR-SNVS----------MLGTLLGDTIKEALGEHILEKV 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       ++++ +EL + L  L   + + vA+a++  LnL n
  gi|1234405    36 ETIRKLSKSSRAGNEASR-QELLTTLQNLSNDELLPVARAFSQFLNLTNT 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +       +   hG+ a   +A     +   + +L  k   s +++
  gi|1234405    85 AEQYH-------SISPHGEAASNPEA-----LAQLFTRLKDKK-LSEQDM 121

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
  gi|1234405   122 RSAVDELSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHNDLADYERN 171

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +   L   +   + tDEiR+ +P P DE + G + +   +W+GvP FLR
  gi|1234405   172 KIMRRLRQLVAQSWHTDEIRKIRPSPVDEAKWGFAVVENSLWEGVPAFLR 221

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         L+n  +  RlP ++  i+F+sWmGGDRDG nP vt E+tR v LL
  gi|1234405   222 EFNEQLQN-SLDYRLPVEAVPIRFTSWMGGDRDG-NPNVTAEITRHVLLL 269

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    +R  A+ l++  +  L+ Elsm  C  ELR    El
  gi|1234405   270 SRWKATDLFLRDIQVLVSELSMSECTPELR----ELAGGEEVL------- 308

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             EPYR ++  vR +L nt       L +G   ++
  gi|1234405   309 ---------EPYRELMKRVRTQLTNTQAYLEARL-KGERVLPPTDLLVSN 348

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    ++  +PL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+RqEs
  gi|1234405   349 DQLWDPLYACYQSLKACGMEIIANGQLLDTLRRVRCFGVPLVRIDVRQES 398

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     R+tD +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
  gi|1234405   399 TRHTDAIAELTRYLGLGDYESWSEADKQAFLIRELNSKRPLVPLKWEPSA 448

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    + ++vl++ rv+AE P  s  aY+isma  PsDvLAv LL +E g   tL
  gi|1234405   449 DTQEVLETCRVIAEAPQGSIAAYVISMAKVPSDVLAVHLLLKEAGCPFTL 498

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDAG
  gi|1234405   499 PVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKDAG 548

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Lsq
  gi|1234405   549 VMAASWAQYRAQDALIKTCEKAGISLTLFHGRGGSIGRGGAPAHAALLSQ 598

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP  P
  gi|1234405   599 PPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLALYASAVLEANLLPPPEP 648

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    k EW ++m+ +     E YR  v   P Fv YFR AtPElE Gk+ +GsR
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  gi|1234405   649 KKEWNEVMDILSDASCEMYRGYVRENPQFVPYFRAATPELELGKLPLGSR 698

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKR+P GG+esLRAiPWiFaWtq R  LP WLG GA  + Aid   K +
  gi|1234405   699 PAKRRPNGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQKAIDAGKKEV 748

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L  m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P G++
  gi|1234405   749 --LATMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVDKSLWPLGQQ 796

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LRd+ +   + +L iA    l+   P++   + LR+ Y   Lnv+qA  L
  gi|1234405   797 LRDQLEADIKVVLAIANDDHLMADLPWIAESIALRNVYTDPLNVLQAELL 846

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    R R             +E A++                  +E  L++
  gi|1234405   847 HRSRQ------------QENAADA------------------CVEQALMV 866

                   tmKGiAAGmqntG<-*
                   t+ G+AAGm ntG
  gi|1234405   867 TIAGVAAGMRNTG    879

gi|62182579|ref|YP_218996.1|: domain 1 of 1, from 1 to 883: score 763.1, E = 2e-226
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  q  +L    vs           +l k L++ ++D  Ge + +
  gi|6218257     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILDR 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls       ++ + +EL + L  L   + + vA+a++  LnLAn
  gi|6218257    35 VETIRKLSKSSRAGNEANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    AE  +      i+ k       Ea    E  i  tl+kL  + +   +
  gi|6218257    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPDLNDAT 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   +  A+   s +LvltAHPt   RR L+ K + i nCL qL   D+   ++
  gi|6218257   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMGEINNCLKQLDNTDIADYER 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   + +   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|6218257   172 HQVMRRLRQLIAQSWHTDEIRKQRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                   RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   R     L+ n+G   +lP d   ++F+sWmGGDRDG nP vt ++tR v
  gi|6218257   222 RELNEQLeENLGY--KLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                   LL+R  A+ l++  +  L+ Elsm     EL +   E     a++
  gi|6218257   269 LLSRWKATDLFLKDIHVLVSELSMVDATPELLALVGE---EGASE----- 310

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vy
                              PYR ++   R +L  t       L      ++  A+
  gi|6218257   311 ------------PYRYLMKKLRARLMATQSWLEARLKG--EKLPKPAgLL 346

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                   t+ E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiR
  gi|6218257   347 TQNEQLWEPLYACYQSLQACGMGIIANGELLDTLRRVKCFGVPLVRIDIR 396

                   qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                   qEs R+t+ l  it+ L+iG Y +WsE  +q  L+ EL  KRPLl+
  gi|6218257   397 QESTRHTEALGEITRYLGIGDYESWSEADKQALLIRELNSKRPLLPRNWE 446

                   ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                      + ++vl++ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|6218257   447 PSNDTREVLETCKVIAEAPKGSIAAYVISMAKTPSDVLAVHLLLKEAGIG 496

                   qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                    +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs K
  gi|6218257   497 FAMPVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAK 546
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                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+
  gi|6218257   547 DAGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAAL 596

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|6218257   597 LSQPPGSLKGGLRVTEQGEMIRFKYGLPEVTVSSLSLYTSAILEANLLPP 646

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      Pk  WR++m+e+ v+  E YR  v     Fv YFR+AtPE E Gk+ +
  gi|6218257   647 PEPKDSWRHIMDELSVISCETYRGYVRENKDFVPYFRSATPEQELGKLPL 696

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D
  gi|6218257   697 GSRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DG 745

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    K    L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lva  L+P
  gi|6218257   746 KQ-SELEAMCRDWPFFSTRLGMLEMVFSKADLWLADYYDQRLVAKTLWPL 794

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    Gk+LRd  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|6218257   795 GKELRDLLEEDIKVVLAIANDSHLMADLPWIAESIQLRNVYTDPLNVLQA 844

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R                +E+ k +d            P +E
  gi|6218257   845 ELLYRSR---------------LTEEQGKSPD------------PRVEQA 867

                    LiLtmKGiAAGmqntG<-*
                    L++t+ G+AAGm ntG
  gi|6218257   868 LMVTIAGVAAGMRNTG    883

gi|121727604|ref|ZP_01680712.1|: domain 1 of 1, from 3 to 887: score 763.0, E = 2.1e-226
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        i  q R+    K +     ++    +l + L+  +q   G+ +
  gi|1217276     3    VIFFQGRMTMNEKYA----ALKSNVSMLGRLLgQTIQAADGDVILAK 45

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls        + + e L   +  L       vA+a+   LnL n
  gi|1217276    46 VETIRKLSKSARAGNQADR-ELLIEEIKNLPNHQLTPVARAFNQFLNLTN 94

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R   +         E +A     i   + kL  k   s  +
  gi|1217276    95 IAEQYHTISRHCESHVN------ELDA-----IGSLFAKLAQKS-VSKFD 132

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+ + ++
  gi|1217276   133 TAQAIRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSPKER 182

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
  gi|1217276   183 HKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWHAVPEFL 232

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R  D  +K   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
  gi|1217276   233 RELDEQVKSY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITREVLL 280

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa lY+  + +L+ Elsm +Cn+ +R+ A E       +
  gi|1217276   281 LSRWKAADLYLTDINELVSELSMTKCNEAVRALAGE-------E------ 317

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                                EPYR iL  +R  L  t E     L      ++  A
  gi|1217276   318 ---------HEPYRAILKPIRSLLQETIEILDAKLNG--QKLAVKAPLQT 356

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     ++  EPL  CY+sL eCG  viADGsLLD LR +  FG+ Lv+LD+RqE
  gi|1217276   357 ADQLWEPLYACYQSLHECGMGVIADGSLLDTLRRIKAFGVHLVRLDVRQE 406

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+ +v+  +t+HL+iG Y +WsE+ +  +L +EL  KRPLl+ D
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  gi|1217276   407 SSRHAEVISELTRHLGIGDYNQWSEQDKIAFLTTELNSKRPLLPRDWQPS 456

                   EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     vk+vld+ +++A    D+FGaY+isma + sDvLAv LL  E g
  gi|1217276   457 PQVKEVLDTCKIIAAQSKDAFGAYVISMARTASDVLAVHLLLQEAGCPYR 506

                   LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                   + v PLFE L DL+ A   + +L  iD Y+  i+  q vm+GYsDs KDA
  gi|1217276   507 MDVCPLFETLDDLNNAESVIRQLMNIDLYRGFIQNHQMVMIGYSDSAKDA 556

                   GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                   G ++A W  Y+A E ++Kv  + G+ L+lFHGRGGt+GRGG P H A+Ls
  gi|1217276   557 GVMAAGWAQYRAMEALVKVGEEAGIELTLFHGRGGTIGRGGAPAHAALLS 606

                   qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                   qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|1217276   607 QPPKSLKGGLRVTEQGEMIRFKLGLPEVAVNSFNMYASAILEANLLPPPE 656

                   PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                   Pk EWR Lm+ +  +    YR vv  EP Fv YFR AtPElE Gk+ +Gs
  gi|1217276   657 PKNEWRALMDILSEISCNAYRKVVRGEPDFVPYFRQATPELELGKLPLGS 706

                   RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                   RPaKR P GG+esLRAiPWiF+W q R  LP WLG G A + Ai+   +
  gi|1217276   707 RPAKRNPTGGVESLRAIPWIFSWSQNRLILPAWLGAGEAIQIAINEGHQA 756

                   lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                   l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv   L+P G+
  gi|1217276   757 L--LEEMCREWPFFSTRLGMLEMVYTKCSVSIARHYDERLVEPTLRPLGE 804

                   sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                   +LR++ +   + +L +     l+  DP+ +  +RLR+ Yi  Ln++qA
  gi|1217276   805 KLRAQLQQDIKVVLNVENNENLMQSDPWGQESIRLRNIYIEPLNMLQAEL 854

                   LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                   L R R  +               +                aP LE+ L+
  gi|1217276   855 LYRTRQSEL---------------P----------------APELEEALM 873

                   LtmKGiAAGmqntG<-*
                   +t+ GiAAGm ntG
  gi|1217276   874 VTIAGIAAGMRNTG    887

gi|183597325|ref|ZP_02958818.1|: domain 1 of 1, from 1 to 879: score 762.9, E = 2.3e-226
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  q  ++    vs           +l k L+D +++  Ged+ +
  gi|1835973     1    -MNQQYSAMR-SNVS-----------MLGKLLgDTIKEALGEDILDK 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls       + ++ + L   L  L   + + vA+a+   LnL n
  gi|1835973    35 VESIRKLSKSSRAGNEVQR-QKLLMTLQNLSNDELLPVARAFNQFLNLTN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +       +   hG+ a    A     +   + +L  k   +  +
  gi|1835973    84 VAEQYH-------SISPHGEAASNPVA-----LKKLFSRLKEKN-FTDSD 120

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     +A+   s++LvltAHPt  +RR L+ K   +  CL+qL   D+   ++
  gi|1835973   121 LRQAVNQLSIELVLTAHPTEIARRTLIHKLVEVNTCLSQLDHDDLADYER 170

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     +   L   +   + tDEiR+ +PtP DE + G + +   +W+ vP FL
  gi|1835973   171 NNIMRRLRQLVAQSWHTDEIRKIRPTPIDEAKWGFAVVENSLWEAVPAFL 220

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   R     L    i   lP ++  i+F+sWmGGDRDG nP vt EvtR v L
  gi|1835973   221 REFNEQLED-SIGAELPVEANPIRFTSWMGGDRDG-NPNVTAEVTRHVLL 268

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   L+R  Aa l++  +  L+ Elsm     ELR+    l      d
  gi|1835973   269 LSRWKAADLFLKDIQVLVSELSMTEATPELRA----LAGGDEVD------ 308
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                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR i  + R +L+ t E     + +G   ++     t+
  gi|1835973   309 ----------EPYRQIAKNLRSQLFSTLEYLERKV-KGEQALPPADLLTD 347

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      +  +PL  CY+sL  CG  +iA G LLD LR +  FGL Lv++D+RqE
  gi|1835973   348 NAQLWDPLYACYQSLMACGMSIIANGQLLDTLRRIRSFGLQLVRIDVRQE 397

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+t+ l  +t+ L++G Y  WsEe +q +Ll+EL+ +RPL++
  gi|1835973   398 STRHTEALAELTQYLGLGDYAAWSEEEKQAFLLSELQSRRPLIPRHWQPS 447

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     E ++v ++ rv+AE   Ds  aY+isma  PsDvLAv LL +E g
  gi|1835973   448 PETAEVFETCRVIAESKNDSIAAYVISMAKVPSDVLAVKLLLKEAGASVR 497

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    L+v PLFE L DL+ A   ++kL si+WY+  id +q vm+GYsDs KDA
  gi|1835973   498 LPVAPLFETLEDLNNAESVMQKLLSIEWYRELIDDRQMVMIGYSDSAKDA 547

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y+Aq+ +iK   k Gv L+lFHGRGGt+GRGG P H A+Ls
  gi|1835973   548 GVMAASWAQYRAQDALIKLCDKEGVTLTLFHGRGGTIGRGGAPAHSALLS 597

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP
  gi|1835973   598 QPPGSLKGGLRVTEQGEMIRFKFGLPQVAISSLALYASAILEANLLPPPE 647

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EW+ +m+ +  v    YR  v   P Fv YFR AtPElE Gk+ +Gs
  gi|1835973   648 PKQEWKSVMDTLSDVSCAMYRDYVREQPDFVPYFRAATPELELGKLPLGS 697

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+P GG+e+LRAiPWiFaWtq R  LP WLG GAA K+ i+K+ K
  gi|1835973   698 RPAKRRPTGGVETLRAIPWIFAWTQNRLMLPAWLGAGAALKYVIEKEGKQ 747

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                       L Em+++WPFF   + +lEmv+AK D  +A  yD+ Lv E L+P G
  gi|1835973   748 -AILDEMWQQWPFFNTRIAMLEMVYAKADLWLAEYYDHRLVEERLWPLGV 796

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR++  E  + +L +     l+   P++   + LR+ Y   Lnv+qA
  gi|1835973   797 KLREQLSEDIKSVLAVSKDEALMADLPWIAESIALRNVYTDPLNVLQAEL 846

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                 +E    +d            P +E  L+
  gi|1835973   847 LHRSRQ----------------QEH---PD------------PRVEQALM 865

                    LtmKGiAAGmqntG<-*
                    +t+ G+AAGm ntG
  gi|1835973   866 VTIAGVAAGMRNTG    879

gi|237800119|ref|ZP_04588580.1|: domain 1 of 1, from 3 to 878: score 762.1, E = 3.9e-226
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        iDA LR      v           LL +     + +  G +  + +
  gi|2378001     3    DIDARLRE----DVH----------LLGELLGNTIREQRGAEFLDKI 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E     A    +  ++  e L + + +L+  + + vA+a+   LnLAn+
  gi|2378001    36 -ERIRKGAKAGRRGSAEGAEQLSSSVDGLEDDELLPVARAFNQFLNLANI 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiE.EtlKkLvlklnKsPeE
                    AE  +l +RR   +             Es + +E l +L   +  +P+
  gi|2378001    85 AEQYQLMHRRDDTQPL----------PFESRVLpELLDRLKTEG-HAPDA 123

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                        L    ++LvltAHPt  +RR L+qK   i   La L  +D+   ++
  gi|2378001   124 LARQLSTLQIELVLTAHPTEVARRTLIQKYDAIAAQLAALDHRDLSSAER 173

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L R i  A+ t+EiRR +PtP DE + G + i   +W+ +P +L
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  gi|2378001   174 SQITSRLQRLIAEAWHTEEIRRIRPTPVDEAKWGFAVIEHSLWHAIPNYL 223

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R+ D AL        lP d+  i+F+sWmGGDRDG nP vt  vtR+v L
  gi|2378001   224 RKADHALFS-ATGTHLPLDAAPIRFASWMGGDRDG-NPNVTAAVTREVLL 271

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    LaR mAa lY+  v+ L  Elsm      LR+      +   +
  gi|2378001   272 LARWMAADLYLRDVDNLAAELSMQQASTALRA------SVGDSA------ 309

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR  L   R++L  tR  a   L    s+ + eAv  +
  gi|2378001   310 ----------EPYRAELKRLRERLRATRNWANASLTA--SQPAPEAVLHD 347

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      + L PL LC++sL eCG  viADG LLD LR   tFGL Lv+LD+Rq+
  gi|2378001   348 NQDLLAPLLLCFQSLHECGMGVIADGPLLDCLRRAVTFGLFLVRLDVRQD 397

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+   +  it  L++G Y +W E+ R ++Ll EL  +RPLl+s
  gi|2378001   398 STRHCAAMTEITDYLGLGRYEDWDEQARIDFLLRELDNRRPLLPSYFKPA 447

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     + ++vl + r +A  P  s G+Y+isma + sDvLAv LL +E g++++
  gi|2378001   448 ADTAEVLATCREVAAAPAASLGSYVISMAGSASDVLAVQLLLKESGLQRP 497

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    +rvvPLFE LADL+ A   +e L  +  Y+ r+ G qevm+GYsDs KDA
  gi|2378001   498 MRVVPLFETLADLDNAGPVIETLLGLPGYRSRLHGPQEVMIGYSDSAKDA 547

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G  +AAW  Y+AqE ++ + ++  v L lFHGRGGtvGRGGGP H AiLs
  gi|2378001   548 GTTAAAWAQYRAQERLVEICREQQVELLLFHGRGGTVGRGGGPAHAAILS 597

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  + G  R t qGE+i f FG  ++  + L  + AA LE  + PP
  gi|2378001   598 QPPGSVAGRFRTTEQGEMIRFKFGLPDIAEQNLNLYLAAVLEATLLPPPP 647

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    P+P WR +m++mA      YR+vv   P FvEYFR AtPE E G++ +Gs
  gi|2378001   648 PQPAWRTMMDQMASDGVSAYRAVVRENPEFVEYFRQATPEQELGRLPLGS 697

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+  GG+esLRAiPWiFaWtqtR  LP WLG  AA   A+ +
  gi|2378001   698 RPAKRR-EGGVESLRAIPWIFAWTQTRLMLPAWLGWEAALSKALARGEGD 746

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    +  L  m ++WPFFR  +D+lEmv AK D  iA LyD+ Lv+ eL+  G
  gi|2378001   747 V--LAQMREQWPFFRTRIDMLEMVLAKADADIARLYDERLVSAELQHLGA 794

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                     LRd      + +L + G   lL   P     + LR++Y+  L  +qA
  gi|2378001   795 HLRDLLSQACKVVLGLTGQARLLAHSPETLEFISLRNAYLDPLHLLQAEL 844

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                  E          L      +P LE  L+
  gi|2378001   845 LSRSRN----------------REA--------NLD-----SP-LELALL 864

                    LtmKGiAAGmqntG<-*
                    + + GiAAG+ ntG
  gi|2378001   865 VSVAGIAAGLRNTG    878

gi|157373015|ref|YP_001481004.1|: domain 1 of 1, from 1 to 878: score 762.1, E = 3.9e-226
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  ++    vs           +l k L+D +++  Ge + +
  gi|1573730     1    -MNEQYSAMR-SNVS-----------MLGKLLgDTIKEALGEHILDR 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++++ +EL + L  L   + + vA+a++  LnL n
  gi|1573730    35 VETIRKLSKSSRAGNEAHR-QELLSTLQNLSNDELLPVARAFSQFLNLTN 83
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                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                +AE  +       +    G+ a   +A     +   + +L  k   s +E
gi|1573730    84 VAEQYH-------SISPNGEAASNPEA-----LAQLFTRLKDKK-LSTKE 120

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  +A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
gi|1573730   121 LQNAVSQLSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHNDLADYER 170

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  +   L   +   + tDEiR+ +P P DE + G + +   +W+GvP FL
gi|1573730   171 NKIMRRLRQLVAQSWHTDEIRKHRPSPIDEAKWGFAVVENSLWEGVPAFL 220

                RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                R     L n  i   lP ++  ++F+sWmGGDRDG nP vt E+tR v L
gi|1573730   221 REFNEQLEN-SIDYSLPAEAVPVRFTSWMGGDRDG-NPNVTAEITRHVLL 268

                LaRmmAanlYisqvEDLmFElsmWRCndELRvRA..EElyrtaardkvvK
                L+R  A  l+   +  L+ Elsm  C  ELR+RA+++E++
gi|1573730   269 LSRWKACDLFTRDIQVLVSELSMTECTPELRARAggDEVQ---------- 308

                yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                           EPYR i+ + R +L          L +G   +
gi|1573730   309 ------------EPYREIMKQLRSQLMSSQAYLEGRL-KGERVLKPHDLL 345

                tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                 + E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+R
gi|1573730   346 VNNEQLWEPLFACYQSLQACGMSIIANGQLLDTLRRVRCFGVPLVRIDVR 395

                qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                qEs R+t+ +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
gi|1573730   396 QESTRHTEAIAELTRYLGLGDYESWSEADKQAFLIRELNSKRPLVPLKWE 445

                ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                   + ++vl++ rv+AE P  s  aY+isma +PsDvLAv LL +E g
gi|1573730   446 PSADTQEVLETCRVIAEAPQGSIAAYVISMARTPSDVLAVHLLLKEAGCP 495

                qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                 +L+v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs K
gi|1573730   496 FALPVAPLFETLDDLNNADDVMTQLLNIDWYRGFIQGKQMVMIGYSDSAK 545

                DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                DAG ++A W  Y+Aq+ +iK   k Gv L+lFHGRGG +GRGG P H A+
gi|1573730   546 DAGVMAASWAQYRAQDALIKTCEKAGVALTLFHGRGGSIGRGGAPAHAAL 595

                LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                LsqPP  ++G lRvt qGE+i f FG  ++   sL  +t A LE  + PP
gi|1573730   596 LSQPPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLALYTGAILEANLLPP 645

                vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                  Pk EWR Lm+++       YR  v   P Fv YFR AtPElE Gk+ +
gi|1573730   646 PEPKKEWRALMDDLSDTSCKMYRGYVRENPEFVPYFRAATPELELGKLPL 695

                GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                GsRPaKRkP GG+esLRAiPWiFaWtq R  LP WLG GA  + A++
gi|1573730   696 GSRPAKRKPNGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQEAVKAGK 745

                KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                +   +L+ m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P
gi|1573730   746 QD--QLEAMCRDWPFFSTRIAMLEMVFAKADLWLAEYYDQRLVDKSLWPL 793

                GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                G++LRd+     + +L iA    l+E  P++   + LR+ Y   Lnv+qA
gi|1573730   794 GQQLRDQLASDIKVVLTIANDAHLMEDLPWIAESIALRNVYTDPLNVLQA 843

                YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                  L R R                +E+           p  rv    E
gi|1573730   844 ELLHRSRQ----------------QEQ-----------PDARV----EQA 862

                LiLtmKGiAAGmqntG<-*
                L++t+ G+AAGm ntG
gi|1573730   863 LMVTIAGVAAGMRNTG    878
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gi|153830201|ref|ZP_01982868.1|: domain 1 of 1, from 3 to 887: score 761.8, E = 4.9e-226
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      i  q R+    K +     ++    +l + L+  +q   G+ +
  gi|1538302     3    VIFFQGRMTMNEKYA----ALKSNVSMLGRLLgQTIQAADGDVILAK 45

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v     ls        + + e L   +  L       vA+a+   LnL n
  gi|1538302    46 VETIRKLSKSARAGNQADR-ELLIEEIKNLPNHQLTPVARAFNQFLNLTN 94

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  +AE  +   R   +         E +A     i   + kL  k   s  +
  gi|1538302    95 IAEQYHTISRHCESHVN------ELDA-----IGSLFAKLAQKS-VSKFD 132

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+ + ++
  gi|1538302   133 TAQAIRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSPKER 182

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  +  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
  gi|1538302   183 HKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWHAVPEFL 232

                  RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                  R  D  +K   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
  gi|1538302   233 RELDEQVKSY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITREVLL 280

                  LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                  L+R  Aa lY+  + +L+ Elsm +Cn+ +R+ A E       +
  gi|1538302   281 LSRWKAADLYLTDINELVSELSMTKCNETVRALAGE-------E------ 317

                  iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                           EPYR iL  +R  L  t E     L      ++  A
  gi|1538302   318 ---------HEPYRAILKPIRSLLQETIEILDAKLNG--QKLAVKAPLQT 356

                  vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                   ++  EPL  CY+sL eCG  viADGsLLD LR +  FG+ Lv+LD+RqE
  gi|1538302   357 ADQLWEPLYACYQSLHECGMGVIADGSLLDTLRRIKAFGVHLVRLDVRQE 406

                  seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                  s R+ +v+  +t+HL+iG Y +WsE+ +  +L +EL  KRPLl+ D
  gi|1538302   407 SSRHAEVISELTRHLGIGDYNQWSEQDKIAFLTTELNSKRPLLPRDWQPS 456

                  EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    vk+vld+ +++A    D+FGaY+isma + sDvLAv LL  E g
  gi|1538302   457 PQVKEVLDTCKIIAAQSKDAFGAYVISMARTASDVLAVHLLLQEAGCPYR 506

                  LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                  + v PLFE L DL+ A   + +L  iD Y+  i+  q vm+GYsDs KDA
  gi|1538302   507 MDVCPLFETLDDLNNAESVIRQLMNIDLYRGFIQNHQMVMIGYSDSAKDA 556

                  GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                  G ++A W  Y+A E ++Kv  + G+ L+lFHGRGGt+GRGG P H A+Ls
  gi|1538302   557 GVMAAGWAQYRAMEALVKVGEEAGIELTLFHGRGGTIGRGGAPAHAALLS 606

                  qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                  qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|1538302   607 QPPKSLKGGLRVTEQGEMIRFKLGLPEVAVNSFNMYASAILEANLLPPPE 656

                  PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                  Pk EWR Lm+ +  +    YR vv  EP Fv YFR AtPElE Gk+ +Gs
  gi|1538302   657 PKNEWRALMDILSEISCNAYRKVVRGEPDFVPYFRQATPELELGKLPLGS 706

                  RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                  RPaKR P GG+esLRAiPWiF+W q R  LP WLG G A + Ai+   +
  gi|1538302   707 RPAKRNPTGGVESLRAIPWIFSWSQNRLILPAWLGAGEAIQIAINEGHQA 756

                  lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                  l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv   L+P G+
  gi|1538302   757 L--LEEMCREWPFFSTRLGMLEMVYTKCSVSIARHYDERLVEPTLRPLGE 804

                  sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
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                    +LR + +   + +L +     l+  DP+ +  +RLR+ Yi  Ln++qA
  gi|1538302   805 KLRSQLQQDIKVVLNVENNENLMQSDPWGQESIRLRNIYIEPLNMLQAEL 854

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R  +                +                aP LE+ L+
  gi|1538302   855 LYRTRQSEL---------------P----------------APELEEALM 873

                    LtmKGiAAGmqntG<-*
                    +t+ GiAAGm ntG
  gi|1538302   874 VTIAGIAAGMRNTG    887

gi|283834724|ref|ZP_06354465.1|: domain 1 of 1, from 1 to 883: score 761.4, E = 6.7e-226
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L++ ++D  Ge + +
  gi|2838347     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILDR 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       +  + +EL + L  L   + + vA+a++  LnLAn
  gi|2838347    35 VETIRKLSKSSRAGNEVNR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+ k       Ea    E  i  tl+kL  + n   +
  gi|2838347    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKDQPNLDEAT 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K + +  CL qL  KD+   ++
  gi|2838347   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMGEVNACLKQLDNKDLVDYER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|2838347   172 HQLMRRLRQLIAQSWHTDEIRKIRPSPVDEAKWGFAVVENSLWEGVPNYL 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G   +lP d   ++F+sWmGGDRDG nP vt ++tR v
  gi|2838347   222 RELNEQLeENLGY--KLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  A+ l++  +  L+ Elsm     EL +   E       +
  gi|2838347   269 LLSRWKATDLFLKDIQFLISELSMVDATPELMAMVGE-------E----- 306

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vy
                               EPYR ++   R +L  t       L      ++  A+
  gi|2838347   307 --------GAAEPYRYLMKTLRSRLMATQAWLEARLKG--EKLPKPAgLL 346

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                    t+ E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiR
  gi|2838347   347 TQNEQLWEPLYACYQSLQACGMGIIANGELLDTLRRVKCFGVPLVRIDIR 396

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|2838347   397 QESTRHTEALGELTRYLGIGDYENWSEADKQAFLIRELNSKRPLLPRNWE 446

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                       + ++vld+ rv+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|2838347   447 PSNDTREVLDTCRVIAEAPYGSIAAYVISMAKTPSDVLAVHLLLKEAGIG 496

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                     +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs K
  gi|2838347   497 FAMPVAPLFETLDDLNNADDVMSQLLNIDWYRGFIQGKQMVMIGYSDSAK 546

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+
  gi|2838347   547 DAGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAAL 596

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPP  ++G lRvt qGE+i f +G  ++   sL  +tAA LE  + PP
  gi|2838347   597 LSQPPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLSLYTAAILEANLLPP 646

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      Pk  WR++m+e+  +  E YR  v     Fv YFR+AtPE E Gk+ +
  gi|2838347   647 PEPKDNWRHIMDELSDISCELYRGYVRENKDFVPYFRSATPEQELGKLPL 696
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                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D
  gi|2838347   697 GSRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DG 745

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    K    L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lv  eL+P
  gi|2838347   746 KQ-SELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVKKELWPL 794

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G++LR++ +   + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|2838347   795 GEELRQRQEADINVVLAIANDSHLMADLPWIAESIQLRNVYTDPLNVLQA 844

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R               A+E+ k +d            P +E
  gi|2838347   845 ELLHRSR---------------LAEEQGKAPD------------PRVEQA 867

                    LiLtmKGiAAGmqntG<-*
                    L++t+ G+AAGm ntG
  gi|2838347   868 LMVTIAGVAAGMRNTG    883

gi|270265165|ref|ZP_06193427.1|: domain 1 of 1, from 1 to 878: score 761.3, E = 6.9e-226
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  ++    vs           +l k L+D ++D  Ge + +
  gi|2702651     1    -MNEQYSAMR-SNVS-----------MLGKLLgDTIKDALGEHILDR 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++++ +EL + L  L   + + vA+a++  LnL n
  gi|2702651    35 VETIRKLSKSSRAGNEAHR-QELLSTLQNLSNDELLPVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +       +    G+ a   +A     +   + +L  k   s +E
  gi|2702651    84 VAEQYH-------SISPNGEAASNPEA-----LAQLFTRLKDKK-LSTKE 120

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      +A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
  gi|2702651   121 LQNAVSQLSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHNDLADYER 170

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L   +   + tDEiR+ +P P DE + G + +   +W+GvP FL
  gi|2702651   171 NKIMRRLRQLVAQSWHTDEIRKNRPSPIDEAKWGFAVVENSLWEGVPAFL 220

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R     L n  i   lP ++  ++F+sWmGGDRDG nP vt E+tR v L
  gi|2702651   221 REFNEQLEN-SIDYSLPAEAVPVRFTSWMGGDRDG-NPNVTAEITRHVLL 268

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRA..EElyrtaardkvvK
                    L+R  A  l+   +  L+ Elsm  C  ELR+ A+++E++
  gi|2702651   269 LSRWKACDLFTRDIQVLVSELSMTECTPELRALAggDEVQ---------- 308

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                                EPYR i+ + R +L          L       + +
  gi|2702651   309 ------------EPYREIMKQLRGQLMRSQAYLEGRLKGERVLKPNDLLV 346

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     + ++  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+R
  gi|2702651   347 SN-DQLWEPLFACYQSLQACGMSIIANGQLLDTLRRVRCFGVPLVRIDVR 395

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs+R+t+ +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
  gi|2702651   396 QESNRHTEAIAELTRYLGLGDYESWSEADKQAFLIRELNSKRPLVPLKWE 445

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                       + ++vl++ rv+AE P  s  aY+isma +PsDvLAv LL +E g
  gi|2702651   446 PSADTQEVLETCRVIAEAPQGSIAAYVISMARTPSDVLAVHLLLKEAGCP 495

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                     +L+v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs K
  gi|2702651   496 FALPVAPLFETLDDLNNADDVMTQLLNIDWYRGFIQGKQMVMIGYSDSAK 545

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
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                    DAG ++A W  Y+Aq+ +iK   k Gv L+lFHGRGG +GRGG P H A+
  gi|2702651   546 DAGVMAASWAQYRAQDALIKTCEKAGVALTLFHGRGGSIGRGGAPAHAAL 595

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP
  gi|2702651   596 LSQPPGSLKGGLRVTEQGEMIRFKFGLPEVAISSLALYAGAVLEANLLPP 645

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      Pk EWR Lm+++       YR  v   P Fv YFR AtPElE Gk+ +
  gi|2702651   646 PEPKKEWRSLMDDLSETSCKMYRGYVRENPDFVPYFRAATPELELGKLPL 695

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKRkP GG+esLRAiPWiFaWtq R  LP WLG GA  + A++
  gi|2702651   696 GSRPAKRKPNGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQEAVKAGK 745

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    +n  +L+ m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P
  gi|2702651   746 QN--QLEAMCRDWPFFSTRIAMLEMVFAKADLWLAEYYDQRLVDKSLWPL 793

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G++LRd+ +   + +L iA    l+E  P++   + LR+ Y   Lnv+qA
  gi|2702651   794 GQQLRDQLESDIKVVLTIANDAHLMEDLPWIAESIALRNVYTDPLNVLQA 843

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R             +E+ d                    +E
  gi|2702651   844 ELLHRSRQ------------QEHPDTR------------------VEQA 862

                    LiLtmKGiAAGmqntG<-*
                    L++t+ G+AAGm ntG
  gi|2702651   863 LMVTIAGVAAGMRNTG    878

gi|45437741|gb|AAS63291.1|: domain 1 of 1, from 8 to 898: score 761.2, E = 7.5e-226
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +        v G + e+   ++    +l   L+D +++  Ge + +
  gi|4543774     8    AASNTKDKWVRGHMNEQYSAMRSNVSMLGTLLgDTIKEALGEHILDR 54

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++++ +EL + L  L   + + vA+a++  LnL n
  gi|4543774    55 VETIRKLSKSSRAGNEASR-QELLTTLQNLSNDELLPVARAFSQFLNLTN 103

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +       +   hG+ a   +A     +   + +L  k   s ++
  gi|4543774   104 TAEQYH-------SISPHGEAASNPEA-----LAQLFTRLKDKK-LSDQD 140

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
  gi|4543774   141 MRSAVDDLSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHNDLADYER 190

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L   +   + tDEiR+ +P P DE + G + +   +W+GvP FL
  gi|4543774   191 NKIMRRLRQLVAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWEGVPAFL 240

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R     L n  +  RlP ++  i+F+sWmGGDRDG nP vt E+tR v L
  gi|4543774   241 REFNEQLEN-SLDYRLPVEAVPIRFTSWMGGDRDG-NPNVTAEITRHVLL 288

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  A+ l++  +  L+ Elsm  C  ELR    El
  gi|4543774   289 LSRWKATDLFLRDIQVLVSELSMSECTPELR----ELAGGEEVL------ 328

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR ++ +vR +L nt       L +G   ++
  gi|4543774   329 ----------EPYRQLMKNVRTQLTNTQAYLEARL-KGERVLPPHDLLVS 367

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     ++  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+RqE
  gi|4543774   368 NDQLWEPLYACYQSLKACGMEIIANGQLLDTLRRVRCFGVPLVRIDVRQE 417

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+tD +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
  gi|4543774   418 STRHTDAIAELTRYLGLGDYESWSESDKQAFLVRELNSKRPLVPLKWEPS 467
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                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     E ++vl++ rv+AE P  s  aY+isma  PsDvLAv LL +E g   t
  gi|4543774   468 AETQEVLETCRVIAEAPQGSIAAYVISMAKVPSDVLAVHLLLKEAGCPFT 517

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    L+v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDA
  gi|4543774   518 LPVAPLFETLDDLNNADDVMTQLLGIDWYRGLIQGKQMVMIGYSDSAKDA 567

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Ls
  gi|4543774   568 GVMAASWAQYRAQDALIKTCEKAGITLTLFHGRGGSIGRGGAPAHAALLS 617

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP
  gi|4543774   618 QPPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLALYAGAILEANLLPPPE 667

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EW ++m+ +     + YR  v   P Fv YFR AtPElE Gk+ +Gs
  gi|4543774   668 PKKEWIEVMDLLSDASCDMYRNYVRENPEFVRYFRAATPELELGKLPLGS 717

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GA  + Aid   +
  gi|4543774   718 RPAKRRPDGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQRAIDAGKQD 767

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    +  L  m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P G+
  gi|4543774   768 V--LATMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVDKSLWPLGQ 815

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LRd+     + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|4543774   816 QLRDQLAADIKVVLAIANDDHLMADLPWIAESIALRNVYTDPLNVLQAEL 865

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R             +E+ d                    +E  L+
  gi|4543774   866 LHRSRQ------------QEHPDAC-------------------VEQALM 884

                    LtmKGiAAGmqntG<-*
                    +t+ G+AAGm ntG
  gi|4543774   885 VTIAGVAAGMRNTG    898

gi|82546307|ref|YP_410254.1|: domain 1 of 1, from 1 to 883: score 761.0, E = 8.3e-226
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L++ ++D  Ge + E
  gi|8254630     1    -MNEQYSALR-SNVS----------MLGKVLgETIKDALGEHILER 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       D+ + +EL + L  L   + + vA+a++  LnLAn
  gi|8254630    35 VETIRKLSKSSRAGNDANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+ k       Ea    E  i  tl+kL  + + s +
  gi|8254630    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPELSEDT 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K   +  CL qL  KD+   +
  gi|8254630   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNACLKQLDNKDIADYEH 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|8254630   172 NQLMRRLRQLIAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G   +lP +   ++F+sWmGGDRDG nP vt ++tR v
  gi|8254630   222 RELNEQLeENLGY--KLPVEFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  A+ l++  +  L+ Elsm     EL +   E       +
  gi|8254630   269 LLSRWKATDLFLKDIQVLVSELSMVEAPPELLALVGE-------E----- 306

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
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                            EPYR ++ + R +L  t       L +G      e   t
  gi|8254630   307 --------GAAEPYRYLMKNLRSRLMATQAWLEARL-KGEELPKPEGLLT 347

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    + Ee  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|8254630   348 QNEELWEPLYACYQSLQACGMGIIANGDLLDTLRRVKCFGVPLVRIDIRQ 397

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+t+ l  +t+ L+iG Y++WsE  +q +L+ EL  KRPLl+
  gi|8254630   398 ESTRHTEALGELTRYLGIGDYKSWSEADKQAFLIRELNSKRPLLPRNWQP 447

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|8254630   448 SAETREVLDTCQVIAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|8254630   498 AMPVAPLFETLDDLNNANDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 547

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+Aq+ +i+   k G+ L+lFHGRGG +GRGG P H A+L
  gi|8254630   548 AGVMAASWAQYQAQDALIRTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|8254630   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPP 647

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR++m+e+ v+  + YR  v     Fv Y R+AtPE E Gk+ +G
  gi|8254630   648 EPKESWRRIMDELSVISCDVYRGYVRENKDFVPYLRSATPEQELGKLPLG 697

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
  gi|8254630   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lv   L+P G
  gi|8254630   747 Q-SELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVDKALWPLG 795

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    k+LR+  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|8254630   796 KELRNLQEEDIKVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 845

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                 +E             +++  P +E  L
  gi|8254630   846 LLHRSRQ----------------AEK-----------EGQEPDPRVEQAL 868

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|8254630   869 MVTIAGIAAGMRNTG    883

gi|262041721|ref|ZP_06014913.1|: domain 1 of 1, from 1 to 870: score 760.8, E = 1e-225
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                GKv                   D ++D  Ge++ + v
  gi|2620417     1    ---------MLGKVL----------------GDTIKDALGENILDRV 22

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       ++ + +EL + L  L   + + vA+a++  LnLAn
  gi|2620417    23 ETIRKLSKSSRAGNEANR-QELLTTLQNLSNDELLPVARAFSQFLNLANT 71

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +      i+         Ea    E  i  tl+kL  + n   e +
  gi|2620417    72 AEQYH-----SISANG------EAASNPEV-IARTLRKLKDQPNLNEETI 109

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     +A+   s +LvltAHPt   RR L+ K   + nCL qL  KD+   + +
  gi|2620417   110 KQAVESLSLELVLTAHPTEITRRTLIHKMVEVNNCLKQLDNKDIADYEHH 159

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +LR
  gi|2620417   160 QLMRRLRQLIAQSWHTDEIRKHRPSPVDEAKWGFAVVENSLWEGVPNYLR 209
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                    RvDtALK.niGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                         L  n+G    lP d   ++F+sWmGGDRDG nP vt ++tR v L
  gi|2620417   210 ELNEQLEaNLGY--QLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVLL 256

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  A+ l++  v  L+ Elsm  C dELR+ A      a
  gi|2620417   257 LSRWKATDLFLKDVQVLISELSMVECTDELRALA-----GAEGA------ 295

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                             +EPYR ++   R +L  t       L +G          t+
  gi|2620417   296 ---------QEPYRYLMKKLRSQLMETQAWLEARL-KGQKLPKPAGLITQ 335

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     E+  EPL  CYksL  CG  +iA G LLD LR +  FG+ Lv++DiRqE
  gi|2620417   336 NEQLWEPLYACYKSLQACGMGIIANGELLDTLRRMKSFGVPLVRIDIRQE 385

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|2620417   386 STRHTEALGEMTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRQWEPS 435

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    EE ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+  +
  gi|2620417   436 EETREVLDTCKVIAEAPRGSISAYVISMAKTPSDVLAVHLLLKEAGIGFA 485

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    L+v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDA
  gi|2620417   486 LPVAPLFETLDDLNNANDVMTQLLNIDWYRGFIQGKQMVMIGYSDSAKDA 535

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Ls
  gi|2620417   536 GVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALLS 585

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2620417   586 QPPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLSLYTSAILEANLLPPPE 635

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EWR++m e+  v    YR  v     Fv YFR+AtPE E Gk+ +Gs
  gi|2620417   636 PKAEWRDIMAELSDVSCKMYRGYVRENKDFVPYFRSATPEQELGKLPLGS 685

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA +  ++   +
  gi|2620417   686 RPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQKVVEGGKQS 735

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                       L+ m ++WPFF   l +lEmv+ K D  +A  yD+ Lv  eL+  G
  gi|2620417   736 --ELEAMCRDWPFFSTRLGMLEMVYSKADLWLAEYYDQRLVKPELWALGS 783

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR       + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|2620417   784 ELRKLLAADINVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAEL 833

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R               A+E+ k +d            P +E  L+
  gi|2620417   834 LHRSRQ--------------AEEEGKDPD-----------PRVEQALM 856

                    LtmKGiAAGmqntG<-*
                    +t+ G+AAGm ntG
  gi|2620417   857 VTIAGVAAGMRNTG    870

gi|193063946|ref|ZP_03045032.1|: domain 1 of 1, from 1 to 883: score 760.6, E = 1.1e-225
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L++ ++D  Ge + E
  gi|1930639     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILER 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       D+ + +EL + L  L   + + vA+a++  LnLAn
  gi|1930639    35 VETIRKLSKSSRAGNDANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
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                 AE  +      i+ k       Ea    E  i  tl+kL  + + s +
gi|1930639    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPELSEDT 121

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                +  A+   s +LvltAHPt   RR L+ K   +  CL qL  KD+   +
gi|1930639   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNACLKQLDNKDIADYEH 171

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
gi|1930639   172 NQLMRRLRQLIAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                R     L+ n+G   +lP +   ++F+sWmGGDRDG nP vt ++tR v
gi|1930639   222 RELNEQLeENLGY--KLPVEFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                LL+R  A+ l++  +  L+ Elsm     EL +   E       +
gi|1930639   269 LLSRWKATDLFLKDIQVLVSELSMVEATPELLALVGE-------E----- 306

                YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                           EPYR ++ + R +L  t       L +G      e   t
gi|1930639   307 --------GAAEPYRYLMKNLRSRLMATQAWLEARL-KGEELPKPEGLLT 347

                kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                + Ee  EPL  CY+sL   G  +iA G LLD LR v  FG+ Lv++DiRq
gi|1930639   348 QNEELWEPLYACYQSLQASGMGIIANGDLLDTLRRVKCFGVPLVRIDIRQ 397

                EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
gi|1930639   398 ESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWQP 447

                tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                  E ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
gi|1930639   448 SAETREVLDTCQVIAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
gi|1930639   498 AMPVAPLFETLDDLNNANDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 547

                AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
gi|1930639   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
gi|1930639   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPP 647

                sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                 Pk  WR++m+e+ v+  + YR  v     Fv YFR+AtPE E Gk+ +G
gi|1930639   648 EPKESWRRIMDELSVISCDLYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
gi|1930639   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 746

                nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                    L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lv   L+P G
gi|1930639   747 Q-SELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVDKALWPLG 795

                ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                k+LR+  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
gi|1930639   796 KELRNLQEEDIKVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 845

                tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                 L R R                 +E             +++  P +E  L
gi|1930639   846 LLHRSRQ----------------AEK-----------EGQEPDPRVEQAL 868

                iLtmKGiAAGmqntG<-*
                ++t+ GiAAGm ntG
gi|1930639   869 MVTIAGIAAGMRNTG    883
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gi|254285840|ref|ZP_04960802.1|: domain 1 of 1, from 3 to 887: score 760.4, E = 1.3e-225
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      i  q R+    K +     ++    +l + L+  +q   G+ +
  gi|2542858     3    VIFFQGRMTMNEKYA----ALKSNVSMLGRLLgQTIQAADGDVILAK 45

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v     ls        + + e L   +  L       vA+a+   LnL n
  gi|2542858    46 VETIRKLSKSARAGNQADR-ELLIEEIKNLPNHQLTPVARAFNQFLNLTN 94

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  +AE  +   R   +         E +A     i   + kL  k   s  +
  gi|2542858    95 IAEQYHTISRHCESHVN------ELDA-----IGSLFAKLAQKS-VSKFD 132

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+ + ++
  gi|2542858   133 TAQAIRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSPKER 182

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  +  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
  gi|2542858   183 HKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWHAVPEFL 232

                  RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                  R  D  +K   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
  gi|2542858   233 RELDEQVKSY-LGESLPIDARPVHFSSWMGGDRDG-NPFVTHTITREVLL 280

                  LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                  L+R  Aa lY+  + +L+ Elsm +Cn+ +R+ A E       +
  gi|2542858   281 LSRWKAADLYLTDINELVSELSMTKCNEAVRALAGE-------E------ 317

                  iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                            EPYR iL  +R  L  t E     L      ++  A
  gi|2542858   318 ---------HEPYRAILKPIRSLLQETIEILDAKLNG--QKLAVKAPLQT 356

                  vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                   ++  EPL  CY+sL eCG  viADGsLLD LR +  FG+ Lv+LD+RqE
  gi|2542858   357 ADQLWEPLYACYQSLHECGMGVIADGSLLDTLRRIKAFGVHLVRLDVRQE 406

                  seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                  s R+ +v+  +t+HL+iG Y +WsE+ +  +L +EL  KRPLl+ D
  gi|2542858   407 SSRHAEVISELTRHLGIGDYNQWSEQDKIAFLTTELNSKRPLLPRDWQPS 456

                  EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    vk+vld+ +++A    ++FGaY+isma + sDvLAv LL  E g
  gi|2542858   457 PQVKEVLDTCKIIAAQSKEAFGAYVISMARTASDVLAVHLLLQEAGCPYR 506

                  LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                  + v PLFE L DL+ A   + +L  iD Y+  i+  q vm+GYsDs KDA
  gi|2542858   507 MDVCPLFETLDDLNNAESVIRQLMNIDLYRGFIQNHQMVMIGYSDSAKDA 556

                  GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                  G ++A W  Y+A E ++Kv  + G+ L+lFHGRGGt+GRGG P H A+Ls
  gi|2542858   557 GVMAAGWAQYRAMEALVKVGEEAGIELTLFHGRGGTIGRGGAPAHAALLS 606

                  qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                  qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|2542858   607 QPPKSLKGGLRVTEQGEMIRFKLGLPEVAVNSFNMYASAILEANLLPPPE 656

                  PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                  Pk EWR Lm+ +  +    YR vv  EP Fv YFR AtPElE Gk+ +Gs
  gi|2542858   657 PKNEWRALMDILSEISCNAYRKVVRGEPDFVPYFRQATPELELGKLPLGS 706

                  RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                  RPaKR P GG+esLRAiPWiF+W q R  LP WLG G A + Ai+   +
  gi|2542858   707 RPAKRNPTGGVESLRAIPWIFSWSQNRLILPAWLGAGEAIQIAINEGHQA 756

                  lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                  l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv   L+P G+
  gi|2542858   757 L--LEEMCREWPFFSTRLGMLEMVYTKCSVSIARHYDERLVEPTLRPLGE 804

                  sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                  +LR++ +   + +L +     l+  DP+ +  +RLR+ Yi  Ln++qA
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  gi|2542858   805 KLRAQLQQDIKVVLNVENNENLMQSDPWGQESIRLRNIYIEPLNMLQAEL 854

                   LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                   L R R  +                +                 aP LE+ L+
  gi|2542858   855 LYRTRQSEL---------------P----------------APELEEALM 873

                   LtmKGiAAGmqntG<-*
                   +t+ GiAAGm ntG
  gi|2542858   874 VTIAGIAAGMRNTG    887

gi|82778878|ref|YP_405227.1|: domain 1 of 1, from 1 to 883: score 760.3, E = 1.3e-225
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  q  +L    vs           +l k L++ ++D  Ge + E
  gi|8277887     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILER 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls       D+ + +EL + L  L   + + vA+a++  LnLAn
  gi|8277887    35 VETIRKLSKSSRAGNDANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    AE  +      i+ k       Ea    E  i  tl+kL  + + s +
  gi|8277887    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPELSEDT 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   +  A+   s +LvltAHPt   RR L+ K   +  CL qL  KD+   +
  gi|8277887   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNACLKQLDNKDIADYEH 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|8277887   172 NQLMRRLRQLIAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                   RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   R     L+ n+G   +lP +   ++F+sWmGGDRDG nP vt ++tR v
  gi|8277887   222 RELNEQLeENLGY--KLPVEFVPVRFTSWMGGDRDG-NPNVTADITRHVL 268

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                   LL+R  A+ l++  +  L+ Elsm     EL +   E       +
  gi|8277887   269 LLSRWKATDLFLKDIQVLVSELSMVEATPELLALVGE-------E----- 306

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                             EPYR ++ + R +L  t       L +G      e   t
  gi|8277887   307 --------GAAEPYRYLMKNLRSRLMATQAWLEARL-KGEELPKPEGLLT 347

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   + Ee  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|8277887   348 QNEELWEPLYACYQSLQACGMGIIANGDLLDTLRRVKCFGVPLVRIDIRQ 397

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|8277887   398 ESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWQP 447

                   tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     E ++vld+ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|8277887   448 SAETREVLDTCQVIAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                   tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                   +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|8277887   498 AMPVAPLFETLDDLNNANDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 547

                   AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                   AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|8277887   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                   sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                   sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|8277887   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPP 647

                   sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     k  WR++m+e+ v+  + YR  v     Fv YFR+AtPE E Gk+ +G
  gi|8277887   648 ELKESWRRIMDELSVISCDLYRGYVRENKDFVPYFRSATPEQELGKLPLG 697
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                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
  gi|8277887   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lv   L+P G
  gi|8277887   747 Q-SELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVDKALWPLG 795

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    k+LR+  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|8277887   796 KELRNLQEEDIKVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 845

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                +E             +++  P +E  L
  gi|8277887   846 LLHRSRQ----------------AEK-----------EGQEPDPRVEQAL 868

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|8277887   869 MVTIAGIAAGMRNTG    883

gi|205354304|ref|YP_002228105.1|: domain 1 of 1, from 1 to 883: score 760.3, E = 1.4e-225
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L++ ++D  Ge + +
  gi|2053543     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILDR 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++ + +EL + L  L   + + vA+a++  LnLAn
  gi|2053543    35 VETIRKLSKSSRAGNEANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+ k       Ea    E  i  tl+kL  + +   +
  gi|2053543    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKNQPDLNDAT 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K + i nCL qL   D+   ++
  gi|2053543   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMGEINNCLKQLDNTDIADYER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + +   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|2053543   172 HQVMRRLRQLIAQSWHTDEIRKQRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G    + + vP ++F+sWmGGDRDG nP vt ++tR v
  gi|2053543   222 RELNEQLeENLGYKLTVDF-VP-VRFTSWMGGDRDG-NPNVTADITRHVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  A+ l++  +  L+ Elsm     EL +   E     a++
  gi|2053543   269 LLSRWKATDLFLKDIHILVSELSMVDATPELLALVGE---EGASE----- 310

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vy
                                PYR ++   R +L  t       L      ++  A+
  gi|2053543   311 ------------PYRYLMKKLRARLMATQSWLEARLKG--EKLPKPAgLL 346

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                    t+ E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiR
  gi|2053543   347 TQNEQLWEPLYACYQSLQACGMGIIANGELLDTLRRVKCFGVPLVRIDIR 396

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+t+ l  it+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|2053543   397 QESTRHTEALGEITRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWE 446

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                       + ++vl++ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|2053543   447 PSNDTREVLETCKVIAEAPKGSIAAYVISMAKTPSDVLAVHLLLKEAGIG 496

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                     +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs K
  gi|2053543   497 FAMPVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAK 546

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+
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  gi|2053543   547 DAGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAAL 596

                   LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                   LsqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2053543   597 LSQPPGSLKGGLRVTEQGEMIRFKYGLPEVTVSSLSLYTSAILEANLLPP 646

                   vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                     Pk  WR++m+e+ v+  E YR  v     Fv YFR+AtPE E Gk+ +
  gi|2053543   647 PEPKDSWRHIMDELSVISCETYRGYVRENKDFVPYFRSATPEQELGKLPL 696

                   GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                   GsRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D
  gi|2053543   697 GSRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DG 745

                   KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                   K    L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lva  L+P
  gi|2053543   746 KQ-SELEAMCRDWPFFSTRLGMLEMVFSKADLWLADYYDQRLVAKTLWPL 794

                   GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                   Gk+LRd  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|2053543   795 GKELRDLLEEDIKVVLAIANDSHLMADLPWIAESIQLRNVYTDPLNVLQA 844

                   YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                     L R R                 +E+ k +d            P +E
  gi|2053543   845 ELLYRSR---------------LTEEQGKSPD------------PRVEQA 867

                   LiLtmKGiAAGmqntG<-*
                   L++t+ G+AAGm ntG
  gi|2053543   868 LMVTIAGVAAGMRNTG    883

gi|262170418|ref|ZP_06038096.1|: domain 1 of 1, from 1 to 876: score 760.3, E = 1.4e-225
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  +  +L    vs           +l + L+  +q   G+ + E
  gi|2621704     1    -MNEKYAALK-SNVS-----------MLGRLLgQTIQAADGDVILEK 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls        + + e L   +  L       vA+a+   LnL n
  gi|2621704    35 VETIRKLSKSARTGNQADR-ELLIEEIKNLPNHQLTPVARAFNQFLNLTN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +   R   +         E +A     i   + kL      s  +
  gi|2621704    84 IAEQYHTISRHCESHVN------ELDA-----IGSLFAKLAQNS-VSKFD 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+   ++
  gi|2621704   122 TAQAIRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSSKER 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   +  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
  gi|2621704   172 HKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWHAVPEFL 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   R  D  +K   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
  gi|2621704   222 RELDEQVKS-HLGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITREVLL 269

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   L+R  Aa lY+  + +L+ Elsm +Cn+ +R+ A +       +
  gi|2621704   270 LSRWKAADLYLTDINELVSELSMTKCNEAVRALAGD-------E------ 306

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                             EPYR iL + R  L  t +     L      ++  A   +
  gi|2621704   307 ---------HEPYRAILKQLRSLLQETIDILEAKLNG--QKLAVKAPLQN 345

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                   v++  EPL  CY+sL eCG  viADGsLLD LR +  FG+ Lv+LDiRqE
  gi|2621704   346 VDQLWEPLYACYQSLHECGMGVIADGSLLDTLRRIKAFGVHLVRLDIRQE 395

                   seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                   s R+ +v+  +t+ L+iG Y +WsE+ +  +L +EL  KRPLl+ D
  gi|2621704   396 SSRHAEVISELTRYLGIGDYNQWSEQDKIAFLTTELNSKRPLLPRDWQPS 445
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                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                      vk+vld+ +++A    D+FGaY+isma + sDvLAv LL  E g
  gi|2621704   446 AQVKEVLDTCKIIAAQSRDAFGAYVISMARTASDVLAVHLLLQEAGCPYR 495

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    + v PLFE L DL+ A   + +L siD Y+  i+  q vm+GYsDs KDA
  gi|2621704   496 MDVCPLFETLDDLNNAESVIRQLMSIDLYRGFIQNHQMVMIGYSDSAKDA 545

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y+A + ++Kv  + G+ L+lFHGRGGt+GRGG P H A+Ls
  gi|2621704   546 GVMAAGWAQYRAMDALVKVSEEAGIELTLFHGRGGTIGRGGAPAHAALLS 595

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|2621704   596 QPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNMYASAILEANLLPPPE 645

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EWR+Lm+ +  v  E YR vv  EP Fv YFR AtPElE Gk+ +Gs
  gi|2621704   646 PKQEWRDLMDVLSEVSCEAYRHVVRGEPDFVPYFRQATPELELGKLPLGS 695

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RP+KR P GG+esLRAiPWiF+W q R  LP WLG G A ++ idK  +
  gi|2621704   696 RPSKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQFSIDKGHQA 745

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv   L+P G+
  gi|2621704   746 L--LEEMCREWPFFSTRLGMLEMVYTKCSAEIARYYDERLVEPALRPLGE 793

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR++ +   + +L +     l+  DP+ +  +RLR+ Y+  Ln++qA
  gi|2621704   794 KLRAQLQKDIKTVLNVENNENLMQSDPWGQESIRLRNIYVEPLNMLQAEL 843

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                 d +                +P LE+ L+
  gi|2621704   844 LYRTRQ---------------SDLP----------------SPELEEALM 862

                    LtmKGiAAGmqntG<-*
                    +t+ GiAAGm ntG
  gi|2621704   863 VTIAGIAAGMRNTG    876

gi|254225390|ref|ZP_04919001.1|: domain 1 of 1, from 3 to 887: score 760.3, E = 1.4e-225
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        i  q R+    K +     ++    +l + L+  +q   G+ + E
  gi|2542253     3    VIFFQGRMTMNEKYA----ALKSNVSMLGRLLgQTIQAADGDVILEK 45

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls        + + e L   +  L       vA+a+   LnL n
  gi|2542253    46 VETIRKLSKSARTGNQADR-ELLIEEIKNLPNHQLTPVARAFNQFLNLTN 94

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R   +         E +A     i   + kL  k   s  +
  gi|2542253    95 IAEQYHTISRHCESHVN------ELDA-----IGSLFAKLAQKS-VSKFD 132

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+ + ++
  gi|2542253   133 TAQAIRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSPKER 182

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
  gi|2542253   183 HKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWHAVPEFL 232

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R  D  +K   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
  gi|2542253   233 RELDEQVKSY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITREVLL 280

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa lY+  + +L+ Elsm +Cn+ +R+ A E       +
  gi|2542253   281 LSRWKAADLYLTDINELVSELSMTKCNEAVRALAGE-------E------ 317

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR iL  +R  L  t E     L      ++  A
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  gi|2542253   318 ---------HEPYRAILKPIRSLLQETIEILDAKLNG--QKLAVKAPLQT 356

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     ++   PL  CY+sL eCG  viADGsLLD LR +  FG+ Lv+LD+RqE
  gi|2542253   357 ADQLWAPLYACYQSLHECGMGVIADGSLLDTLRRIKAFGVHLVRLDVRQE 406

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+ +v+  +t+HL+iG Y +WsE+ +  +L +EL  KRPLl+ D
  gi|2542253   407 SSRHAEVISELTRHLGIGDYNQWSEQDKIAFLTTELNSKRPLLPRDWQPS 456

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                      vk+vld+ +++A    D+FGaY+isma + sDvLAv LL  E g
  gi|2542253   457 PQVKEVLDTCKIIAAQSKDAFGAYVISMARTASDVLAVHLLLQEAGCPYR 506

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    + v PLFE L DL+ A   + +L  iD Y+  i+  q vm+GYsDs KDA
  gi|2542253   507 MDVCPLFETLDDLNNAESVIRQLMNIDLYRGFIQNHQMVMIGYSDSAKDA 556

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y+A E ++Kv  + G+ L+lFHGRGGt+GRGG P H A+Ls
  gi|2542253   557 GVMAAGWAQYRAMEALVKVGEEAGIELTLFHGRGGTIGRGGAPAHAALLS 606

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|2542253   607 QPPKSLKGGLRVTEQGEMIRFKLGLPEVAVNSFNMYASAILEANLLPPPE 656

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EWR Lm+ +  +    YR vv  EP Fv YFR AtPElE Gk+ +Gs
  gi|2542253   657 PKNEWRALMDILSEISCNAYRKVVRGEPDFVPYFRQATPELELGKLPLGS 706

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR P GG+esLRAiPWiF+W q R  LP WLG G A + Ai+   +
  gi|2542253   707 RPAKRNPTGGVESLRAIPWIFSWSQNRLILPAWLGAGEAIQIAINEGHQA 756

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l  L++m +eWPFF   l +lEmv+ K    iA  yD+ Lv   L+P G+
  gi|2542253   757 L--LEDMCREWPFFSTRLGMLEMVYTKCSVSIARHYDERLVEPTLRPLGE 804

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR++ +   + +L +     l+  DP+ +  +RLR+ Yi  Ln++qA
  gi|2542253   805 KLRAQLQQDIKVVLNVENNENLMQSDPWGQESIRLRNIYIEPLNMLQAEL 854

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R  +               +                aP LE+ L+
  gi|2542253   855 LYRTRQSEL---------------P----------------APELEEALM 873

                    LtmKGiAAGmqntG<-*
                    +t+ GiAAGm ntG
  gi|2542253   874 VTIAGIAAGMRNTG    887

gi|28868714|ref|NP_791333.1|: domain 1 of 1, from 3 to 878: score 760.2, E = 1.5e-225
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        iDA LR      v           LL +     + +  G +  + +
  gi|2886871     3    DIDARLRE----DVH----------LLGELLGNTIREQRGAEFLDKI 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E     A    +  ++  e L + + +L+  + + vA+a+   LnLAn+
  gi|2886871    36 -ERIRKGAKAGRRGSAEGAEQLSSSVDGLEDDELLPVARAFNQFLNLANI 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDi.EEtlKkLvlklnKsPeE
                    AE  +l +RR   +              Es +  E l +L   +   Pe
  gi|2886871    85 AEQYQLMHRRDDAQPL----------PFESRVlSELLDRLKAEG-HQPET 123

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                        L    ++LvltAHPt  +RR L+qK   i   La L  +D+   ++
  gi|2886871   124 LARQLSKLEIELVLTAHPTEVARRTLIQKYDAIATQLAALDHRDLNSAER 173

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L R i  A+ t+EiRR +PtP DE + G + i   +W+ +P +L
  gi|2886871   174 AQITSRLQRLIAEAWHTEEIRRIRPTPVDEAKWGFAVIEHSLWHAIPNYL 223
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                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R+ D  L        lP +   i+F+sWmGGDRDG nP vt  vtR+v L
  gi|2886871   224 RKADHVLHA-ATGLHLPLESAPIRFASWMGGDRDG-NPNVTAAVTREVLL 271

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    LaR mAa lY+  v+ L  Elsm    d LR+      +   +
  gi|2886871   272 LARWMAADLYLRDVDNLAAELSMQQASDALRA------SVGDSA------ 309

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                             EPYR  L   R++L  tR  a   L   +   + eAv  +
  gi|2886871   310 ----------EPYRAELKRLRERLRATRNWANASLTETLP--APEAVLRD 347

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      e L+PL LC++sL eCG  viADG LLD LR   tFGL Lv+LD+Rq+
  gi|2886871   348 NRELLDPLLLCFQSLHECGMGVIADGPLLDCLRRAVTFGLFLVRLDVRQD 397

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+   +  it  L++G Y eW E+ R ++Ll EL  +RPLl+s
  gi|2886871   398 STRHCAAMTEITDYLGLGRYEEWDEQTRIDFLLRELNNRRPLLPSYFKPA 447

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     + ++vl + r +A  P  s G+Y+isma + sDvLAv LL +E g++++
  gi|2886871   448 ADTAEVLATCREVAAAPAASLGSYVISMAGSASDVLAVQLLLKESGLQRP 497

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    +rvvPLFE LADL+ A   +e L  +  Y+ r++G qevm+GYsDs KDA
  gi|2886871   498 MRVVPLFETLADLDNAGPVIETLLGLPGYRSRLQGPQEVMIGYSDSAKDA 547

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G  +AAW  Y+AqE ++ + ++  v L lFHGRGGtvGRGGGP H AiLs
  gi|2886871   548 GTTAAAWAQYRAQEKLVEICREQQVELLLFHGRGGTVGRGGGPAHAAILS 597

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  + G  R t qGE+i f FG  ++  + L  + AA LE  + PP
  gi|2886871   598 QPPGSVAGRFRTTEQGEMIRFKFGLPDIAEQNLNLYLAAVLEATLLPPPP 647

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    P+P WR +m++mA      YR+vv   P FvEYFR AtPE E G++ +Gs
  gi|2886871   648 PQPAWRTMMDQMASDGVSAYRAVVRENPEFVEYFRQATPEQELGRLPLGS 697

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+  GG+esLRAiPWiFaWtqtR  LP WLG  AA   A+++
  gi|2886871   698 RPAKRR-EGGVESLRAIPWIFAWTQTRLMLPAWLGWEAALSKALERGEGE 746

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    +  L  m ++WPFFR  +D+lEmv AK D  iA LyD+ Lv+ eL+  G
  gi|2886871   747 V--LAQMREQWPFFRTRIDMLEMVLAKADADIARLYDERLVTAELQHLGA 794

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                     LRd      + +L + G   lL   P     + LR++Y+  L  +qA
  gi|2886871   795 HLRDLLSQACNVVLGLTGQTQLLAHSPETLEFISLRNAYLDPLHLLQAEL 844

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                  E          L      +P LE  L+
  gi|2886871   845 LSRSRN----------------REA--------SLD-----SP-LELALL 864

                    LtmKGiAAGmqntG<-*
                    + + GiAAG+ ntG
  gi|2886871   865 VSVAGIAAGLRNTG    878

gi|91791616|ref|YP_561267.1|: domain 1 of 1, from 1 to 887: score 760.1, E = 1.6e-225
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +  q ++     v     L      L     D +    G+   E v
  gi|9179161     1    -MSVQSKAEDATDVY--ASLRANVGQLGQILGDTMRSHLGDAFLEKV 44

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E   + A    + D    e + a Lt+L   + i  Aka+   LnLAn+
  gi|9179161    45 -EQIRILAKKSRQGDDGAREQMLALLTALPDEELIPFAKAFNQFLNLANI 93

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +   R   ++                +E  l +L
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  gi|9179161    94 AEQFHTISRNCDELVC-----------VPDPVEQLLGRLLKHD-LDKSQL 131

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    + L    +DLvltAHPt   RR L+qK a +  CL+ L    +t  +
  gi|9179161   132 HQCLTELDIDLVLTAHPTEISRRTLIQKYASVVDCLTSLENPLLTEREHS 181

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    L   L   i   + t EiR  +PtP DE R G+s i   +W+ vP FLR
  gi|9179161   182 QLQLRLRQLIAQIWHTNEIRHERPTPVDEARWGLSTIETSLWQAVPDFLR 231

                   Rv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                     +D   +  G+   l  dv  ++FssWmGGDRDG nP vt  vt +v
  gi|9179161   232 QLnDQFEQKTGL--QLAKDVSPVRFSSWMGGDRDG-NPFVTARVTQEVLD 278

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                     R  Aa lY+  +  Lm Elsm   n EL++       t  ++
  gi|9179161   279 RNRHAAARLYLKDIVTLMNELSMEEANAELKA------LTNNSN------ 316

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                             EPYR +L   R KL nt +     L     +i  + +  +
  gi|9179161   317 ----------EPYRDVLKGLRQKLRNTIDYLNERLEGHQPDIDFNSIIWE 356

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     +   PLE  Y+sLC+ G + iA G LLD+LR    FG+ + KLDiRq+
  gi|9179161   357 QSDLQAPLECLYQSLCDSGMRLIAHGLLLDILRRLACFGIHMLKLDIRQD 406

                   seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                   +eR+ Dv+  +t+ L++G Y  W E+ +q +Ll EL  +RPLl++
  gi|9179161   407 AERHSDVIAELTRYLGLGDYHHWDEDEKQAFLLRELTNRRPLLPPNWKPS 456

                   EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    +v++vl +   +      + G+Y+isma  PsDvL v LL +E g   +
  gi|9179161   457 PDVAEVLSTCALISKQSPKALGSYVISMASKPSDVLTVLLLLKESGCTYP 506

                   LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                   +rvvPLFE L DL  A A ++ L  iDWY+    G qevm+GYsDs KDA
  gi|9179161   507 MRVVPLFETLKDLTGAAACIKELLQIDWYRGYTKGMQEVMIGYSDSAKDA 556

                   GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                   G ++AAW  Y+AqEE++ v K+ GvKL+lFHGRGGtvGRGGGP H AiLs
  gi|9179161   557 GVMAAAWAQYRAQEELVAVCKQAGVKLTLFHGRGGTVGRGGGPAHQAILS 606

                   qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                   qPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A +E  + PP
  gi|9179161   607 QPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVMEATLMPPPE 656

                   PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                   Pk  WR+ m+ +A      YR +v  EP Fv YFR AtPE+E Gk+ +Gs
  gi|9179161   657 PKKAWRECMQAIADESVLAYRGIVREEPDFVAYFRAATPEVELGKLPLGS 706

                   RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                   RPaKRk +GGiesLRAiPWiFaW q R  LP WLG G A   Ai++   n
  gi|9179161   707 RPAKRKVGGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALSSAIEQSQLN 756

                   lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                   l  L+Em +eWPFF   + +lEmv+ K +P +A  y++ Lv  eL+  G+
  gi|9179161   757 L--LQEMEREWPFFETRISMLEMVYTKAEPNLARYYERCLVPTELHHLGD 804

                   sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                   +LR++ +   d +L +    +l+   P+ +  ++LR++Yi  Ln +q
  gi|9179161   805 KLRARLQLGIDTVLSLTQSDELMSHTPWSRESVKLRNPYIDPLNFLQTEL 854

                   LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                   L R R                +E+  +a e v+L            L+
  gi|9179161   855 LARTR-----------------NED--QASEKVQLA------------LM 873

                   LtmKGiAAGmqntG<-*
                   Lt+ G+AAGm ntG
  gi|9179161   874 LTIAGVAAGMRNTG    887

gi|262166662|ref|ZP_06034399.1|: domain 1 of 1, from 1 to 876: score 759.9, E = 1.9e-225
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                *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                    +  +  +L    vs           +l + L+  +q   G+ + E
gi|2621666     1    -MNEKYAALK-SNVS-----------MLGRLLgQTIQAADGDVILEK 34

                vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                v     ls        + + e L   +  L       vA+a+   LnL n
gi|2621666    35 VETIRKLSKSARTGNQADR-ELLIEEIKNLPNHQLTPVARAFNQFLNLTN 83

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                +AE  +   R   +         E +A     i   + kL      s  +
gi|2621666    84 IAEQYHTISRHCESHVN------ELDA-----IGSLFAKLAQNS-VSKFD 121

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+   ++
gi|2621666   122 TAQAIRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSSKER 171

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                +  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
gi|2621666   172 HKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWHAVPEFL 221

                RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                R  D  +K   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
gi|2621666   222 RELDEQVKS-HLGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITREVLL 269

                LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                L+R  Aa lY+  + +L+ Elsm +Cn+ +R+ A +       +
gi|2621666   270 LSRWKAADLYLTDINELVSELSMTKCNEAVRALAGD-------E------ 306

                iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                          EPYR iL + R  L  t +     L      ++  A   +
gi|2621666   307 ---------HEPYRAILKQLRGLLQETIDILEAKLNG--QKLAVKAPLQN 345

                vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                v++  EPL  CY+sL eCG  viADGsLLD LR +  FG+ Lv+LDiRqE
gi|2621666   346 VDQLWEPLYACYQSLHECGMGVIADGSLLDTLRRIKAFGVHLVRLDIRQE 395

                seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaElkGKRPLlgsDLPkt
                s R+ +v+  +t+ L+iG Y +WsE+ +  +L +EL  KRPLl+ D
gi|2621666   396 SSRHAEVISELTRYLGIGDYNQWSEQDKIAFLTTELNSKRPLLPRDWQPS 445

                EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                  vk+vld+ +++A    D+FGaY+isma + sDvLAv LL  E g
gi|2621666   446 AQVKEVLDTCKIIAAQSRDAFGAYVISMARTASDVLAVHLLLQEAGCPYR 495

                LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                + v PLFE L DL+ A   + +L siD Y+  i+  q vm+GYsDs KDA
gi|2621666   496 MDVCPLFETLDDLNNAESVIRQLMSIDLYRGFIQNHQMVMIGYSDSAKDA 545

                GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                G ++A W  Y+A + ++Kv  + G+ L+lFHGRGGt+GRGG P H A+Ls
gi|2621666   546 GVMAAGWAQYRAMDALVKVSEEAGIELTLFHGRGGTIGRGGAPAHAALLS 595

                qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
gi|2621666   596 QPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNMYASAILEANLLPPPE 645

                PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                Pk EWR+Lm+ +  v  E YR vv  EP Fv YFR AtPElE Gk+ +Gs
gi|2621666   646 PKQEWRDLMDVLSEVSCEAYRHVVRGEPDFVPYFRQATPELELGKLPLGS 695

                RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                RP+KR P GG+esLRAiPWiF+W q R  LP WLG G A ++ idK  +
gi|2621666   696 RPSKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQFSIDKGHQA 745

                lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv   L+P G+
gi|2621666   746 L--LEEMCREWPFFSTRLGMLEMVYTKCSAEIARYYDERLVEPALRPLGE 793

                sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                +LR++ +   + +L +     l+  DP+ +  +RLR+ Y+  Ln++qA
gi|2621666   794 KLRAQLQKDIKTVLNVENNENLMQSDPWGQESIRLRNIYVEPLNMLQAEL 843
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                  LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                  L R R                 d +                +P LE+ L+
  gi|2621666   844 LYRTRQ---------------SDLP----------------SPELEEALM 862

                  LtmKGiAAGmqntG<-*
                  +t+ GiAAGm ntG
  gi|2621666   863 VTIAGIAAGMRNTG    876

gi|293393511|ref|ZP_06637821.1|: domain 1 of 1, from 19 to 907: score 759.4, E = 2.5e-225
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                          +   v G + e+   ++    +l k L++ +++  Ge + +
  gi|2933935    19    -----ISKWVRGYMNEQYSAMRSNVSMLGKLLgETIKEALGEHILDR 60

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v     ls       ++++ +EL   L  L   + + vA+a++  LnL n
  gi|2933935    61 VETIRKLSKSSRAGSEAHR-QELLNTLQNLSNDELLPVARAFSQFLNLTN 109

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  +AE  +       +    G+ a   +  t       + +L  k   s +
  gi|2933935   110 VAEQYH-------SISPNGEAASNPEVLT-----QLFSRLKDKK-LSNKA 146

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
  gi|2933935   147 LQDAVDQLSIELVLTAHPTEITRRTLIHKLVEVNSCLSQLDHNDLADYER 196

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +   L   +   + tDEiR  +PtP DE + G + +   +W+GvP FL
  gi|2933935   197 NKIMRRLRQLVAQSWHTDEIRHNRPTPIDEAKWGFAVVENSLWEGVPAFL 246

                  RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                  R     L n  i  RlP ++  ++F+sWmGGDRDG nP vt E+tR v L
  gi|2933935   247 RELNEQLENT-IDYRLPVEAVPVRFTSWMGGDRDG-NPNVTAEITRHVLL 294

                  LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                  L+R  A  l+   +  L+ Elsm  C  ELR    El    a +
  gi|2933935   295 LSRWKACDLFTRDIQVLVSELSMTECTPELR----ELAGGDAVQ------ 334

                  iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                            EPYR i+   R +L          L +G   +       +
  gi|2933935   335 ----------EPYREIMKRLRSQLMSSQAYLEGRL-KGERMLRPHDLLVN 373

                  vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                   E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+RqE
  gi|2933935   374 NEQLWEPLYACYQSLVACGMSIIANGQLLDTLRRVRCFGVPLVRIDVRQE 423

                  seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                  s R+t+ +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
  gi|2933935   424 STRHTEAIAELTRYLGLGDYESWSEADKQAFLIRELNSKRPLVPLKWQPS 473

                  EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                   + ++vl++ rv+AE P  s  aY+isma +PsDvLAv LL +E g   +
  gi|2933935   474 ADTQEVLETCRVIAEAPEGSIAAYVISMARTPSDVLAVHLLLKEAGCPFA 523

                  LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                  L+v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDA
  gi|2933935   524 LPVAPLFETLDDLNNADDVMTQLLNIDWYRGFIQGKQMVMIGYSDSAKDA 573

                  GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                  G ++A W  Y+Aq+ +iK   k Gv L+lFHGRGG +GRGG P H A+Ls
  gi|2933935   574 GVMAASWAQYRAQDALIKTCEKAGVALTLFHGRGGSIGRGGAPAHAALLS 623

                  qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                  qPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2933935   624 QPPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLALYTGAILEANLLPPPE 673

                  PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                  Pk EWR Lm+e+       YR  v   P Fv YFR AtPElE Gk+ +Gs
  gi|2933935   674 PKKEWRTLMDELSDTSCKMYRGYVRENPDFVPYFRAATPELELGKLPLGS 723

                  RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
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                    RPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GA  + A++   +
  gi|2933935   724 RPAKRRPNGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQEAVKAGKQD 773

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                      +L+ m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P Gk
  gi|2933935   774 --QLEAMCRDWPFFSTRIAMLEMVFAKADLWLAEYYDQRLVDKSLWPLGK 821

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LRd+     + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|2933935   822 QLRDQLDSDIKVVLTIANDDHLMADLPWIAESIALRNVYTDPLNVLQAEL 871

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                +E+          n +++ a  +E  L+
  gi|2933935   872 LHRSRQ----------------QEE----------N-GQQDAR-VEQALM 893

                    LtmKGiAAGmqntG<-*
                    +t+ G+AAGm ntG
  gi|2933935   894 VTIAGVAAGMRNTG    907

gi|109896934|ref|YP_660189.1|: domain 1 of 1, from 4 to 872: score 759.3, E = 2.8e-225
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +D qL+  v    s   ++i+  A L D +L  +     e ++
  gi|1098969     4    ILDSQLKETVRNLGSTLGDMIR--AQLGDEWLQRI-----ETIRLDG 43

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E Y        K D++  + L a    L+    ++v +a++  LnLAn+
  gi|1098969    44 RESY--------KGDSECSDKLKALFSELEDEQLLVVGRAFSQFLNLANI 85

                    AE.EvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    AE+E + A     + +      D  +        Et+ k v +l
  gi|1098969    86 AEqEFNSANHDQDSIQELFNHLDKDNVSA-----ETFEKAVNQL------ 124

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                            s++LvltAHPt   RR L+ K++ +  CL q+    +   ++
  gi|1098969   125 --------SIELVLTAHPTEVTRRTLIHKHSELAQCLRQIHQTSLSDIER 166

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   +   +  A+ t+EiR  +PtP DE R G s i   +W+ vP F+
  gi|1098969   167 DKIRTRIADLVAQAWHTEEIRTVRPTPVDEARWGFSVIENSLWEAVPDFV 216

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R    A      n  lP d+  +k ssWmGGDRDG nP vt  vt  v L
  gi|1098969   217 REL-SAKFEAKYNLALPLDAAPVKLSSWMGGDRDG-NPFVTSKVTQQVLL 264

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    LaR  Aa l+ + v+ L  Elsm  C d +R       +    +
  gi|1098969   265 LARKRAAKLFAQDVDMLQVELSMSDCDDTIR-------SMVGDE------ 301

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR +L    D L nt+      L  G s + +
  gi|1098969   302 ---------LEPYRALLRPLLDTLTNTKNGIAEFLS-GAS-VDDSKWIAS 340

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     +e L PL LCY sL  CG  viADG LLD +R v  FG+ L KLDiRq+
  gi|1098969   341 KDELLTPLMLCYNSLQACGMSVIADGRLLDTIRRVHCFGVHLLKLDIRQD 390

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    seR+ Dv   +t+HL++G Y +WsEe +q +Ll EL+ KRPL+++
  gi|1098969   391 SERHADVFSELTRHLGMGDYGNWSEEDKQAFLLKELSSKRPLFPAKWQPS 440

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     +v++v+d+ +v+A    + FG Yiisma  PsDvL v LL RE gv  +
  gi|1098969   441 ADVQEVIDTCKVVAQHSEEGFGIYIISMASLPSDVLSVHLLLREFGVTWP 490

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    ++v PLFE L DL+AA   ++ L  iDWY+  i+G q vm+GYsDs KDA
  gi|1098969   491 MPVAPLFETLDDLNAAATVIDALMNIDWYRGYIQGHQYVMIGYSDSAKDA 540

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y  qE ++ +A kyGv L+lFHGRGGt+GRGG P H AiLs
  gi|1098969   541 GAMAAGWAQYESQEALVGIAEKYGVELTLFHGRGGTIGRGGLPAHAAILS 590
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                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  + G  Rvt qGE i + FG  +L  rsL  ++ A LE  + PP +
  gi|1098969   591 QPPGSLSGGFRVTEQGETIRYKFGMPQLAQRSLALYASAILEALISPPPA 640

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EWR+L+ e+A  A + YR  v  +  Fv YFR+AtPE E Gk+ +Gs
  gi|1098969   641 PKQEWRDLITEVAANARDNYRNTVRHDENFVPYFRVATPEQELGKLPLGS 690

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKRkPsGGiesLRAiPWiFaW qtR  LP WLG   A + Aid   +
  gi|1098969   691 RPAKRKPSGGIESLRAIPWIFAWAQTRLVLPSWLGAMKAVQTAIDAGHRP 740

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l  + +m ++WPFF     +l+mvF K DP i a yDk Lv EeL+  G+
  gi|1098969   741 L--IDDMLQNWPFFHSRFSMLDMVFGKADPRISAEYDKRLVPEELRHLGD 788

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                     LRd+      lLL +   k+++E DP     + +R  Y+  L  +q
  gi|1098969   789 ALRDELNMSMSLLLDVLQQKEVMESDPKGNESMNIRAGYLQPLHFLQIEL 838

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L RiR                                 +e+  P LE  ++
  gi|1098969   839 LERIR------------------------------AKGEEADPTLERAMM 858

                    LtmKGiAAGmqntG<-*
                    +t+ GiA Gm ntG
  gi|1098969   859 VTIAGIAVGMRNTG    872

gi|225423837|ref|XP_002280842.1|: domain 1 of 1, from 16 to 1061: score 759.3, E = 2.8e-225
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s D   RlL  G     +++++ +  +   F++ +     e  +
  gi|2254238    16    SFDDDCRLL--GSLL--NEVLQRE--VGSNFMEKV-----ERNRILA 51

                    qECYElsAeYEGKkDtkKLeE..LGakLtsLdPaDailvAkailHmLnLA
                    q    + A   G +Dt  L E++L + +  ++  +a+ +A+a++H LnL
  gi|2254238    52 QSACNMRAS--GIEDTAELLEkqLISEISQMNLEEALTLARAFSHYLNLM 99

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                     +AE     +R R  +           A      ++ + +L   +  sPe
  gi|2254238   100 GIAET---HHRLRKARNV---------AHMSKSCDDIFNQLLQGG-VSPE 136

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    E ++ +  q v++vltAHPtq  RR L  K+ Ri   L       +  eD
  gi|2254238   137 ELYNTVCKQEVEIVLTAHPTQINRRTLQYKHIRIAHLLDYNDRPNLGHED 186

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    ++ L E L REi   + tDE+RR +Pt  DE RaG+  +   +W+ vP +
  gi|2254238   187 REMLIEDLVREITSIWQTDELRRQKPTVVDEARAGLNIVEQSLWRAVPHY 236

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    LRRv  ALK       lP     ikF sWmGGDRDG nP vt EvtRDv
  gi|2254238   237 LRRVSNALKK-HTGKSLPLTCTPIKFGSWMGGDRDG-NPNVTAEVTRDVS 284

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyr..........
                    LL+R mA  lYi  v+ L FElsm RC d L   A E+  +++++ ++++
  gi|2254238   285 LLSRWMAIDLYIREVDSLRFELSMNRCSDSLSRLAHEILEketssvdrne 334

                    .................................taardkvvKy......
                    +++++ ++++ ++ ++ +++ +++ + + + ++ t  +d   Ky++ + +
  gi|2254238   335 srnqplnrsqlkpysqlgptlprqlpagadlpscTECKDGESKYpklefp 384

                    ...Yi.....................EFWK...................
                    +++Y++ ++++ +  ++++++ ++++++F K+ ++++  +++++++  ++
  gi|2254238   385 gtdYMplnrqdvkaasssdtsfqdsnkDFGKtygngtvanssnsqsaatp 434

                    ..................................qvPPtEPYRviLGd
                    ++ + ++++  ++++  ++++ ++++ ++  +++ +q P   PYR++LG+
  gi|2254238   435 rtvsfssgqllsqrklfsesqlgrssfqkllepslpQRPGIAPYRIVLGN 484

                    vRDKLYntRERaRHLLAtGiseisEeAvytkvEeFLEPLELCYksLCeCG
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                    v+DKL  t  R   LL     e      y   +e LEPL LC  s+  CG
  gi|2254238   485 VKDKLMKTQRRLELLLEDLPCEHDPGDYYETADELLEPLLLCHESMQSCG 534

                    DkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs
                      ++ADG L Dl+R v tF + L+KLD+RqEs R+ + lDAit  L++G
  gi|2254238   535 SGILADGRLADLIRRVATFRMVLMKLDLRQESARHAETLDAITSYLDMGI 584

                    YReWsEeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiD
                    Y eW Ee++ ++L  ELkGKRPL+++ +    +vk+vld+frv AE+ +D
  gi|2254238   585 YSEWDEERKLDFLTRELKGKRPLVPPTIEVVADVKEVLDTFRVAAEIGSD 634

                    sFGaYiismataPsDvLAvELLqRECgvkq...........tLrvvPLFE
                    sFGaY+isma   sDvLAvELLq++  +   ++ +++ +++tLrvvPLFE
  gi|2254238   635 SFGAYVISMASNASDVLAVELLQKDARLAVcgelgrpcsggTLRVVPLFE 684

                    kLADLeAAPAavekLFsiDWYinri....dGKqevmvGYsDsGKDAGRls
                     + DL+ A A + kL siDWY+ +i ++++G qevmvGYsDsGKDAGR+
  gi|2254238   685 TVKDLRGAGAVIRKLLSIDWYREHIiknhNGHQEVMVGYSDSGKDAGRFT 734

                    AAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPD
                    AAW LYkAqE+++    +yG+K++lFHGRGG +GRGGGPt LAi sqPP
  gi|2254238   735 AAWELYKAQEDVVAACNEYGIKVTLFHGRGGSIGRGGGPTYLAIQSQPPG 784

                    tinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE
                     + G lR t qGE++   FG  +   r L  +t A L   m PP+ P+ E
  gi|2254238   785 SVMGTLRSTEQGEMVQAKFGLPHTAVRQLEIYTTAVLLATMRPPLPPREE 834

                    .WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPa
                    +WR+Lmee+  +    YRs v+  P F  YF  AtP  E G +niGsRP+
  gi|2254238   835 kWRNLMEEISKISGQCYRSTVYENPEFLAYFHEATPQAELGFLNIGSRPT 884

                    KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqk
                    +Rk s Gi  LRAiPW+FaWtqtRF LP WLGvG   K   +K  K
  gi|2254238   885 RRKSSTGIGHLRAIPWVFAWTQTRFVLPAWLGVGSGLKGVCEKGHKE--D 932

                    LkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLR
                    L  mYkeWPFF  t+DL+Emv  K D  iA  yD++Lv+   +  G +LR
  gi|2254238   933 LIAMYKEWPFFQSTIDLIEMVLGKADITIAKHYDEVLVSPSRQELGADLR 982

                    dkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKR
                     +   t +++L + GH  l      L+  +  R +++  +n++q   L+R
  gi|2254238   983 RELLTTGKFVLVVTGHDKLSQNNRSLRRLIESRLPFLNPMNMLQVEILRR 1032

                    iRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtm
                    +R                d+n          n        L D L++t+
  gi|2254238  1033 LRR---------------DDDN----------N-------KLRDALLITI 1050

                    KGiAAGmqntG<-*
                     GiAAGm ntG
  gi|2254238  1051 NGIAAGMRNTG    1061

gi|126667184|ref|ZP_01738158.1|: domain 1 of 1, from 1 to 876: score 759.1, E = 3.1e-225
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEa.
                                                      +L +L G++++  +
  gi|1266671     1    ---------------------------------MLGELLGQSIRQHp 14

                    vqECYElsAeYEGKkDtkKLeELGa.....kLtsLdPaDail.vAkailH
                     q C++   +      + +L+E G++++   L +    D il+v +a+
  gi|1266671    15 GQQCFDTIEQVRAAAKADRLQESGSgqrlvNLLGQLGDDEILpVTRAFNQ 64

                    mLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkl
                     LnLAnLAE  +    RR++          a+   Es   E +++L   +
  gi|1266671    65 FLNLANLAE--QYHGIRRNRGHS-------ADLMVES-FSEVFQRLLAGG 104

                    nKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKD
                        +E    + n  v+ vltAHPt   RR L+ K   +  CL qL  +D
  gi|1266671   105 -IRADELHRQVVNLRVEFVLTAHPTEVTRRTLIMKYDDMSDCLEQLDHQD 153

                    vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWk
                    + + ++  +   L R i  A+ tDEiR  +Pt  DE + G + i   +W
  gi|1266671   154 LMPSERDGIVRRLTRLIAEAWHTDEIRYDRPTAVDEAKWGFAVIENSLWS 203
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                    GvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEv
                      P+FL   DtAL        lP ++  ++ +sWmGGDRDG nP vt  v
  gi|1266671   204 ALPRFLESLDTALLE-ATGKGLPLQATPVRVASWMGGDRDG-NPNVTHRV 251

                    tRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaard
                    tR v LL R mAa lY+  +  L  ElsmW   dELR +  +
  gi|1266671   252 TRKVFLLGRWMAADLYMKDITALRAELSMWQASDELRSKVGDTR------ 295

                    kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                                    EPYR iLG+ RD+L  tR+ a   +    ++ s
  gi|1266671   296 ----------------EPYRQILGELRDQLSRTRDWAEASISGAAAD-SN 328

                    eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                       + + E F EPLELCY+sL eCG   iA G LLD +R   tFGL L +
  gi|1266671   329 GILFANSE-FTEPLELCYRSLVECGLEYIANGPLLDTIRRAHTFGLPLSR 377

                    LDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlg
                    LDiRqE+ R+ + +  i   L++G Y  WsE  Rq +L+ ELkG+RPL++
  gi|1266671   378 LDIRQEAARHAEAVAEIVGYLGLGDYQAWSEVERQAFLVRELKGRRPLIP 427

                    sDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRE
                          E v++vl + +v+AE    + G+Y+isma  PsDvL v LL RE
  gi|1266671   428 RNWQPSEAVEEVLATCKVVAEQTPQALGSYVISMASKPSDVLSVILLLRE 477

                    CgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYs
                     g++ ++ vvPLFE L DL  AP ++  L+ iDWY+   dGKqevm+GYs
  gi|1266671   478 AGMQYPMAVVPLFETLNDLSGAPQSMTELYQIDWYREYCDGKQEVMIGYS 527

                    DsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPt
                    Ds KDAG + AAW  Y+AqE + KvA +y ++L+lFHGRGGtvGRGGGP
  gi|1266671   528 DSSKDAGQMMAAWAQYQAQEALTKVAAEYDMRLTLFHGRGGTVGRGGGPA 577

                    HLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHG
                      AiLsqPP  +nGs R+t qGE+i f FG  +L  +sL  +t A +E
  gi|1266671   578 NRAILSQPPGSVNGSFRITEQGEMIRFKFGMPDLAVQSLTLYTTAVIEAT 627

                    mnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYG
                    + PP  P   WR+ m+ +       YR vv  +P Fv YFR  tPE   G
  gi|1266671   628 LAPPPQPEDSWRETMNWLTERSLKAYRDVVRDDPQFVLYFRQVTPEQALG 677

                    kmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAi
                    k+ +GsRPa+Rk +GG+esLRAiPWiFaWtq R  LP WLG   A   A
  gi|1266671   678 KLALGSRPARRKAGGGVESLRAIPWIFAWTQMRLMLPAWLGSDVALEAAA 727

                    dKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaE.
                    +   + + +L+Em   WPFFR  +D+lEmv AK D  iA+ y++ Lv ++
  gi|1266671   728 ED--QRIDQLREMMAGWPFFRTYIDMLEMVLAKADLRIASYYEQTLVDDp 775

                    eLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittL
                     L+  G++LR++       +L++     lL  +P     + +R++Y   L
  gi|1266671   776 ALRALGENLRQRLSRCIHRVLELKQQDHLLADEPVFAHSMNVRNPYTDPL 825

                    nvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaP
                      +qA  L+R R                  E   k       n   +v+
  gi|1266671   826 HYLQAELLRRERQ----------------SEG--KGGHNGDRN--GKVPE 855

                    GLEDtLiLtmKGiAAGmqntG<-*
                     +E  L +tm Gi AGm ntG
  gi|1266671   856 LVERALKVTMAGISAGMRNTG    876

gi|258625692|ref|ZP_05720571.1|: domain 1 of 1, from 1 to 876: score 759.1, E = 3.2e-225
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  +  +L    vs           +l + L+  +q   G+ + E
  gi|2586256     1    -MNEKYAALK-SNVS-----------MLGRLLgQTIQAADGDVILEK 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls        + + e L   +  L       vA+a+   LnL n
  gi|2586256    35 VETIRKLSKSARTGNQADR-ELLIEEIKNLPNHQLTPVARAFNQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
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                +AE  +   R   +         E +A     i   + kL      s  +
gi|2586256    84 IAEQYHTISRHCESHVN------ELDA-----IGSLFAKLAQNS-VSKFD 121

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+   ++
gi|2586256   122 TAQAIRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSSKER 171

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                +  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
gi|2586256   172 HKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWHAVPEFL 221

                RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                R  D  +K   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
gi|2586256   222 RELDEQVKS-HLGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITREVLL 269

                LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                L+R  Aa lY+  + +L+ Elsm +Cn+ +R+ A +       +
gi|2586256   270 LSRWKAADLYLTDINELVSELSMTKCNEAVRALAGD-------E------ 306

                iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                          EPYR iL + R  L  t +     L      ++  A   +
gi|2586256   307 ---------HEPYRAILKQLRSLLQETIDILEAKLNG--QKLAVKAPLQN 345

                vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                v++  EPL  CY+sL eCG  viADGsLLD LR +  FG+ Lv+LDiRqE
gi|2586256   346 VDQLWEPLYACYQSLHECGMGVIADGSLLDTLRRIKAFGVHLVRLDIRQE 395

                seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                s R+ +v+  +t+ L+iG Y +WsE+ +  +L +EL  KRPLl+ D
gi|2586256   396 SSRHEEVISELTRYLGIGDYNQWSEQDKIAFLTTELNSKRPLLPRDWQPS 445

                EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                  vk+vld+ +++A    D+FGaY+isma + sDvLAv LL  E g
gi|2586256   446 AQVKEVLDTCKIIAAQSRDAFGAYVISMARTASDVLAVHLLLQEAGCPYR 495

                LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                + v PLFE L DL+ A   + +L siD Y+  i+  q vm+GYsDs KDA
gi|2586256   496 MDVCPLFETLDDLNNAESVIRQLMSIDLYRGFIQNHQMVMIGYSDSAKDA 545

                GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                G ++A W  Y+A + ++Kv  + G+ L+lFHGRGGt+GRGG P H A+Ls
gi|2586256   546 GVMAAGWAQYRAMDALVKVSEEAGIELTLFHGRGGTIGRGGAPAHAALLS 595

                qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
gi|2586256   596 QPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNMYASAILEANLLPPPE 645

                PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                Pk EWR+Lm+ +  v  E YR vv  EP Fv YFR AtPElE Gk+ +Gs
gi|2586256   646 PKQEWRDLMDVLSEVSCEAYRHVVRGEPDFVPYFRQATPELELGKLPLGS 695

                RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                RP+KR P GG+esLRAiPWiF+W q R  LP WLG G A ++ idK  +
gi|2586256   696 RPSKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQFSIDKGHQA 745

                lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv   L+P G+
gi|2586256   746 L--LEEMCREWPFFSTRLGMLEMVYTKCSAEIARYYDERLVEPALRPLGE 793

                sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                +LR++ +   + +L +     l+  DP+ +  +RLR+ Y+  Ln++qA
gi|2586256   794 KLRAQLQKDIKTVLNVENNENLMQSDPWGQESIRLRNIYVEPLNMLQAEL 843

                LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                L R R                 d +                +P LE+ L+
gi|2586256   844 LYRTRQ---------------SDLP----------------SPELEEALM 862

                LtmKGiAAGmqntG<-*
                +t+ GiAAGm ntG
gi|2586256   863 VTIAGIAAGMRNTG    876
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gi|213969092|ref|ZP_03397231.1|: domain 1 of 1, from 3 to 878: score 758.9, E = 3.7e-225
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      iDA LR      v           LL +     + +  G +  + +
  gi|2139690     3    DIDARLRE----DVH----------LLGELLGNTIREQRGAEFLDKI 35

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   E     A    +  ++  e L + + +L+  + + vA+a+   LnLAn+
  gi|2139690    36 -ERIRKGAKAGRRGSAEGAEQLSSSVDGLEDDELLPVARAFNQFLNLANI 84

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDi.EEtlKkLvlklnKsPeE
                  AE  +l +RR   +              Es +  E l +L   +   Pe
  gi|2139690    85 AEQYQLMHRRDDAQPL----------PFESRVlSELLDRLKAEG-HQPET 123

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      L    ++LvltAHPt  +RR L+qK   i   La L  +D+   ++
  gi|2139690   124 LARQLSKLEIELVLTAHPTEVARRTLIQKYDAIAAQLAALDHRDLNSAER 173

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +   L R i  A+ t+EiRR +PtP DE + G + i   +W+ +P +L
  gi|2139690   174 AQITSRLQRLIAEAWHTEEIRRIRPTPVDEAKWGFAVIEHSLWHAIPNYL 223

                  RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                  R+ D  L        lP ++  i+F+sWmGGDRDG nP vt  vtR+v L
  gi|2139690   224 RKADHVLHA-ATGLHLPLEAAPIRFASWMGGDRDG-NPNVTAAVTREVLL 271

                  LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                  LaR mAa lY+  v+ L  Elsm    d LR+      +   +
  gi|2139690   272 LARWMAADLYLRDVDNLAAELSMQQASDALRA------SVGDSA------ 309

                  iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                            EPYR  L   R++L  tR  a   L   +   + eAv  +
  gi|2139690   310 ----------EPYRAELKRLRERLRATRNWANASLTETLP--APEAVLRD 347

                  vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    e L+PL LC++sL eCG  viADG LLD LR   tFGL Lv+LD+Rq+
  gi|2139690   348 NRELLDPLLLCFQSLHECGMGVIADGPLLDCLRRAVTFGLFLVRLDVRQD 397

                  seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                  s R+   +  it  L++G Y eW E+ R ++Ll EL  +RPLl+
  gi|2139690   398 STRHCAAMTEITDYLGLGRYEEWDEQTRIDFLLRELNNRRPLLPRYFKPA 447

                  EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                   + ++vl + r +A  P  s G+Y+isma + sDvLAv LL +E g++++
  gi|2139690   448 ADTAEVLATCREVAAAPAASLGSYVISMAGSASDVLAVQLLLKESGLQRP 497

                  LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                  +rvvPLFE LADL+ A   +e L  +  Y+ r++G qevm+GYsDs KDA
  gi|2139690   498 MRVVPLFETLADLDNAGPVIETLLGLPGYRSRLQGPQEVMIGYSDSAKDA 547

                  GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                  G  +AAW  Y+AqE ++ + ++  v L lFHGRGGtvGRGGGP H AiLs
  gi|2139690   548 GTTAAAWAQYRAQEKLVEICREQQVELLLFHGRGGTVGRGGGPAHAAILS 597

                  qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                  qPP  + G  R t qGE+i f FG  ++  + L  + AA LE  + PP
  gi|2139690   598 QPPGSVAGRFRTTEQGEMIRFKFGLPDIAEQNLNLYLAAVLEATLLPPPP 647

                  PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                  P+P WR +m++mA      YR+vv   P FvEYFR AtPE E G++ +Gs
  gi|2139690   648 PQPAWRTMMDQMASDGVSAYRAVVRENPEFVEYFRQATPEQELGRLPLGS 697

                  RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                  RPaKR+  GG+esLRAiPWiFaWtqtR  LP WLG  AA   A+++
  gi|2139690   698 RPAKRR-EGGVESLRAIPWIFAWTQTRLMLPAWLGWEAALSKALERGEGE 746

                  lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                  +  L  m ++WPFFR  +D+lEmv AK D  iA LyD+ Lv+ eL+  G
  gi|2139690   747 V--LAQMREQWPFFRTRIDMLEMVLAKADADIARLYDERLVTAELQHLGA 794

                  sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                   LRd      + +L + G   lL   P     + LR++Y+  L  +qA
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  gi|2139690   795 HLRDLLSQACNVVLGLTGQTQLLAHSPETLEFISLRNAYLDPLHLLQAEL 844

                   LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                   L R R                  E          L      +P LE  L+
  gi|2139690   845 LSRSRN----------------REA--------SLD-----SP-LELALL 864

                   LtmKGiAAGmqntG<-*
                   + + GiAAG+ ntG
  gi|2139690   865 VSVAGIAAGLRNTG    878

gi|52425072|ref|YP_088209.1|: domain 1 of 1, from 1 to 880: score 758.7, E = 4.2e-225
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                    + e+  +++    +l +FL++ +q+  G+d+ E
  gi|5242507     1    -------------MTEEYLMMRNNINMLGRFLgETIQEAQGDDILEL 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +     ls +     D  +   L + L  +     i vA+a++  LnL n
  gi|5242507    35 IENIRVLSRNSRSGDDKARAALLDT-LSTISADNIIPVARAFSQFLNLTN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +   R    k              E      + +L  +   s eE
  gi|5242507    84 VAEQYQTMSRSHEDKVS-----------AERSTAALFARLKEQH-VSQEE 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   +   ++   +++vltAHPt   RRsL+ K+  i  CLaqL   D+t e++
  gi|5242507   122 IIKTVQKLLIEIVLTAHPTEVTRRSLMHKQVEINKCLAQLDHTDLTAEEQ 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   k ++  L R i  A+ t EiR  +PtP +E + G + i   +W+G P F+
  gi|5242507   172 KNIEYKLLRLIAEAWHTNEIRTNRPTPLEEAKWGFAVIENSLWEGLPAFI 221

                   RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   R+ +D A+    +n  lP d   ++FssWmGGDRDG nP vt  +tR+
  gi|5242507   222 RKLnDAAVEH--LNYALPVDLTPVRFSSWMGGDRDG-NPFVTAKITREAL 268

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LaR  Aa l++  + +L  Elsm  C  E R            +k   +
  gi|5242507   269 QLARWKAADLFLTDIQELCDELSMTQCTAEFR-----------EKYGDH 306

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                             EPYRv++ d R KL nt +    +LA  i     + +
  gi|5242507   307 L----------EPYRVVVKDLRSKLKNTLDYYNDILAGRIPPFKQDEIIS 346

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   +  +   PL  CY+sL  CG ++iA G LLD LR v  FG+ L +LDiRq
  gi|5242507   347 EDQQLWQPLYDCYQSLTACGMRIIANGLLLDTLRRVRCFGVTLLRLDIRQ 396

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   Es R+ D +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|5242507   397 ESTRHSDAIGEITRYIGLGDYSQWTEDDKQAFLIRELSSRRPLIPHNWTP 446

                   tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                    E  +++ld+ +v+A  P      Yiisma + sDvLAv LL +E g+
  gi|5242507   447 SEHTREILDTCKVIAKQPEGVISCYIISMARTASDVLAVHLLLKEAGISY 496

                   tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    L+vvPLFE L DL+A    + +LF + WY+  i  +q +m+GYsDs KD
  gi|5242507   497 HLPVVPLFETLDDLDASKEVMTQLFNVGWYRGVIKNRQMIMIGYSDSAKD 546

                   AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                   AG ++A W  Y+Aq+ ++K   + G+ L+lFHGRGGtvGRGG P H A+L
  gi|5242507   547 AGMMAASWAQYRAQDALVKLCEQTGIELTLFHGRGGTVGRGGAPAHAALL 596

                   sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                   sqPP  ++   lRvt qGE+i f  G   +   sL  ++ A LE  + PP
  gi|5242507   597 SQPPRSLKNGLRVTEQGEMIRFKLGLPAIAAESLDLYASAILEANLLPPP 646

                   sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                    Pk  W ++m+e+Av   E YR vv  +  Fv YFR+AtPE E  k+ +G
  gi|5242507   647 EPKASWCRVMDELAVASCEIYRNVVRGDKDFVPYFRSATPEQELAKLPLG 696
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                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR P GG+esLRAiPWiFaW q R  LP WLG GA  + A++  +
  gi|5242507   697 SRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGASIRQAME--SG 744

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        ++Em + WPFF   + +lEmvF K D  +   yD+ Lv  eL+  G
  gi|5242507   745 KAAVIEEMCNHWPFFNTRIGMLEMVFSKTDSWLSEYYDQRLVKKELWYLG 794

                    ksLRdkYvEtkdlLLkiAGHkDlLEGD.PYLKqrlRLRdsYittLnvfqA
                    +sLR +  E    +L++ G  D L  D P++   + LR+ Y   Ln +q
  gi|5242507   795 ESLRKQLSEDIATVLRLSGKGDQLMSDlPWVAESIALRNVYTDPLNLLQV 844

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L+R+R               Ad +        + n      P +E
  gi|5242507   845 ELLRRLR----------------ADPE--------HPN------PDIEQA 864

                    LiLtmKGiAAGmqntG<-*
                    L++t+ GiAAGm ntG
  gi|5242507   865 LMITITGIAAGMRNTG    880

gi|258620479|ref|ZP_05715517.1|: domain 1 of 1, from 2 to 878: score 758.6, E = 4.4e-225
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  +  +L    vs           +l + L+  +q   G+ + E
  gi|2586204     2    TMNEKYAALK-SNVS-----------MLGRLLgQTIQAADGDVILEK 36

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls        + + e L   +  L       vA+a+   LnL n
  gi|2586204    37 VETIRKLSKSARTGNQADR-ELLIEEIKNLPNHQLTPVARAFNQFLNLTN 85

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R   +         E +A     i   + kL      s  +
  gi|2586204    86 IAEQYHTISRHCESHVN------ELDA-----IGSLFAKLAQNS-VSKFD 123

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                       A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+   ++
  gi|2586204   124 TALAIRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSSKER 173

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
  gi|2586204   174 HKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWHAVPEFL 223

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R  D  +K   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
  gi|2586204   224 RELDEQVKS-HLGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITREVLL 271

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa lY+  + +L+ Elsm +Cn+ +R+ A +       +
  gi|2586204   272 LSRWKAADLYLTDINELVSELSMTKCNEAVRALAGD-------E------ 308

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR iL + R  L  t +     L      ++  A   +
  gi|2586204   309 ---------HEPYRAILKQLRGLLQETIDILEAKLNG--QKLAVKAPLQN 347

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    v++  EPL  CY+sL eCG  viADGsLLD LR +  FG+ Lv+LDiRqE
  gi|2586204   348 VDQLWEPLYACYQSLHECGMGVIADGSLLDTLRRIKAFGVHLVRLDIRQE 397

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+ +v+  +t+ L+iG Y +WsE+ +  +L +EL  KRPLl+ D
  gi|2586204   398 SSRHAEVISELTRYLGIGDYNQWSEQDKIAFLTTELNSKRPLLPRDWQPS 447

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                      vk+vld+ +++A    D+FGaY+isma + sDvLAv LL  E g
  gi|2586204   448 AQVKEVLDTCKIIAAQSRDAFGAYVISMARTASDVLAVHLLLQEAGCPYR 497

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    + v PLFE L DL+ A   + +L siD Y+  i+  q vm+GYsDs KDA
  gi|2586204   498 MDVCPLFETLDDLNNAESVIRQLMSIDLYRGFIQNHQMVMIGYSDSAKDA 547

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y+A + ++Kv  + G+ L+lFHGRGGt+GRGG P H A+Ls
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  gi|2586204   548 GVMAAGWAQYRAMDALVKVSEEAGIELTLFHGRGGTIGRGGAPAHAALLS 597

                   qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                   qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|2586204   598 QPPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNMYASAILEANLLPPPE 647

                   PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                   Pk EWR+Lm+ +  v  E YR vv  EP Fv YFR AtPElE Gk+ +Gs
  gi|2586204   648 PKQEWRDLMDVLSEVSCEAYRHVVRGEPDFVPYFRQATPELELGKLPLGS 697

                   RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                   RP+KR P GG+esLRAiPWiF+W q R  LP WLG G A ++ idK  +
  gi|2586204   698 RPSKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQFSIDKGHQA 747

                   lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                   l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv   L+P G+
  gi|2586204   748 L--LEEMCREWPFFSTRLGMLEMVYTKCSAEIARYYDERLVEPALRPLGE 795

                   sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                   +LR++ +   + +L +     l+  DP+ +  +RLR+ Y+  Ln++qA
  gi|2586204   796 KLRAQLQKDIKTVLNVENNENLMQSDPWGQESIRLRNIYVEPLNMLQAEL 845

                   LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                   L R R                 d +                +P LE+ L+
  gi|2586204   846 LYRTRQ---------------SDLP----------------SPELEEALM 864

                   LtmKGiAAGmqntG<-*
                   +t+ GiAAGm ntG
  gi|2586204   865 VTIAGIAAGMRNTG    878

gi|157147246|ref|YP_001454565.1|: domain 1 of 1, from 1 to 883: score 758.6, E = 4.5e-225
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  q  +L    vs           +l k L++ ++D  Ge++ +
  gi|1571472     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGENILDR 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls       ++ + +EL + L  L   + + vA+a++  LnLAn
  gi|1571472    35 VETIRKLSKSSRAGNEANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    AE  +      i+ +       Ea    E  i  tl+kL  + n   +
  gi|1571472    84 TAEQYH-----SISPQG------EAASNPEV-IARTLRKLKDQPNLDEAT 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   + +A+   s +LvltAHPt   RR L+ K + +  CL qL  K++   ++
  gi|1571472   122 IKNAVESLSLELVLTAHPTEITRRTLIHKMGEVNACLKQLDNKEIADYER 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|1571472   172 NQLMRRLRQLIAQSWHTDEIRKNRPSPVDEAKWGFAVVENSLWEGVPNYL 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   R     L    +  +lP d   ++F+sWmGGDRDG nP vt +vtR v L
  gi|1571472   222 RELNEQLEE-HLGYKLPVDFVPVRFTSWMGGDRDG-NPNVTADVTRHVLL 269

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   L+R  A+ l++  +  L+ Elsm     EL +   E     a++
  gi|1571472   270 LSRWKATDLFLKDIQVLISELSMVDATPELLALVGE---EGASE------ 310

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vyt
                              PYR ++   R +L  t       L      ++  A+  t
  gi|1571472   311 -----------PYRYLMKSLRSRLMATQAWLEARLKG--EKLPKPAgLLT 347

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   + E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|1571472   348 QNEQLWEPLYACYQSLQACGMGIIANGELLDTLRRVKCFGVPLVRIDIRQ 397

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|1571472   398 ESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRQWEP 447
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                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     ++ ++vl++ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|1571472   448 SDDTREVLETCQVIAEAPLGSIAAYVISMAKTPSDVLAVHLLLKEAGISF 497

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    +++v PLFE L DL+ A A + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|1571472   498 AMPVAPLFETLDDLNNADAVMTQLLNIDWYRGFIQGKQMVMIGYSDSAKD 547

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|1571472   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|1571472   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLSLYTGAILEANLLPPP 647

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR++m+e+ v+  + YR  v     Fv YFR+AtPE E Gk+ +G
  gi|1571472   648 EPKNSWRHIMDELSVISCDLYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
  gi|1571472   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lv   L+P G
  gi|1571472   747 Q-SELEAMCRDWPFFSTRLGMLEMVFSKADLWLAEYYDQRLVKKALWPLG 795

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    ++LR+   E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|1571472   796 EELRNLLAEDIKVVLAIANDSHLMADLPWIAESIQLRNVYTDPLNVLQAE 845

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R               A+E+ k +d            P +E  L
  gi|1571472   846 LLHRSR---------------LAEEQGKDPD------------PRVEQAL 868

                    iLtmKGiAAGmqntG<-*
                    ++t+ G+AAGm ntG
  gi|1571472   869 MVTIAGVAAGMRNTG    883

gi|262373873|ref|ZP_06067151.1|: domain 1 of 1, from 4 to 893: score 758.1, E = 6.3e-225
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLH.GedLkEa
                        i A LR               D  Ll   L     LH G+dL
  gi|2623738     4    QITAPLRE---------------DVRLLGNLLGETLKLHaGQDLFNQ 35

                    vqECYEls.AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    +     l++   +G+ +++K   L     +L   + + + +a++H Ln A
  gi|2623738    36 IEQIRALAkGARDGQIEAEK--QLEQLFLGLKDEEILPLTRAFSHFLNFA 83

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE  ++   RR       + a   +  t   + E +K          +
  gi|2623738    84 NIAEQYHVVRSRRHAEFD--EHAPSPNPLTH--LFEKFKNQQISE----Q 125

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                      F+ +    ++LvltAHPt   RR L+qK   i  CL+qL  K +t+ +
  gi|2623738   126 QLFQQICDLKIELVLTAHPTEVSRRTLIQKYDDITDCLSQLDQKKLTPRE 175

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    ++     L   +  A+ tDEiR  +PtP DE + G + i  t+W+ vPKF
  gi|2623738   176 RQQTIATLKQLVTSAWQTDEIRQHRPTPVDEAKWGFATIEQTLWNAVPKF 225

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    +R     L        lP  +  i+F+sWmGGDRDG nP vt  vt +v
  gi|2623738   226 IRELNE-LTQQHCLQALPLSIAPIRFASWMGGDRDG-NPNVTHQVTQEVL 273

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     L+R  Aa lY+  +E L +Els+  C  EL        + a
  gi|2623738   274 WLSRWQAADLYLRDIENLRWELSIQNCSKEL--------SEALGY----- 310

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                              EPYR  L   R++L  tR      L +G+ +  +  +
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  gi|2623738   311 --------EHPEPYREYLRITRERLKATRYCLGQRL-QGL-DADDSNIIR 350

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   + +e L PL LCY+sL +     iA G LLD++  v  FG+ L KLDiRq
  gi|2623738   351 NKDELLAPLLLCYRSLVDSNLAEIANGQLLDFIYRVNCFGIELLKLDIRQ 400

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   Es R+   + Ait+ L++G + +W E+ Rq +L+ EL+ KRPLl+  L
  gi|2623738   401 ESGRHRQAISAITEYLGLGNFESWTEQARQNFLIQELQSKRPLLPKYLNE 450

                   tE.......EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLq
                    E++  ++++v +v  ++r LAE P +s GaYiisma  PsDvLAv LLq
  gi|2623738   451 PEgsliqhpDVLEVFATMRTLAEQPAESLGAYIISMAEYPSDVLAVLLLQ 500

                   RECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvG
                   +E g++++LrvvPLFE L DL+ A  +++ LF + WY+ +i GK evm+G
  gi|2623738   501 KEAGIQHPLRVVPLFETLKDLDGAAKTMDTLFNMHWYKQHIHGKHEVMIG 550

                   YsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGG
                   YsDs KDAG +sA W  Y+AqEE+  vAKk+ v+L+lFHGRGG + RGG
  gi|2623738   551 YSDSAKDAGFMSANWAQYRAQEELTAVAKKHDVQLTLFHGRGGSISRGGA 600

                   PtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLE
                   Pt  A+ sqPP  i G++Rvt qGE+i f FG E +  + L  +tAAtLE
  gi|2623738   601 PTQQALFSQPPGSISGAIRVTEQGEMIRFKFGLEGIALQNLEIYTAATLE 650

                   HGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElE
                     + PP  Pk EWR+Lm++m       YR  v   P Fv Y R  tPElE
  gi|2623738   651 ATLLPPPEPKKEWRDLMNQMTDLSVKVYRQTVRENPNFVSYLRTVTPELE 700

                   YGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKh
                      + +GsRPaKRk sGGiesLRAiPW+FaWtq R  LP WLG G A
  gi|2623738   701 LQMLPLGSRPAKRKVSGGIESLRAIPWVFAWTQIRLMLPAWLGTGTAINQ 750

                   AidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva
                    ++   Kn   L +m ++WP+F   +D+lEmv  K D  iA  y+  L
  gi|2623738   751 -VHEQHKN--TLNDMLDQWPYFQTLIDMLEMVLSKSDADIALYYESHLTD 797

                   E.eLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYit
                   +++Lk  G +LR++ +   d LL + G   lL     L q + +R +Y+
  gi|2623738   798 DqDLKALGIELRQRLQNAVDTLLNLKGESKLLSNNEVLDQSMQVRKPYLL 847

                   tLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpterv
                    L  +qA  +KR R               y +E             te+
  gi|2623738   848 PLHLLQAELMKRRR--------------LYLAEH-----------QTEHT 872

                   aPGLEDtLiLtmKGiAAGmqntG<-*
                   +  ++  L++ + GiAAG+ ntG
  gi|2623738   873 P--VDHALMVSIAGIAAGLRNTG    893

gi|291619398|ref|YP_003522140.1|: domain 1 of 1, from 1 to 882: score 757.4, E = 1e-224
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  q  ++    vs           +l k L+D ++D  Ge++ +
  gi|2916193     1    -MNEQYSAMR-SNVS-----------MLGKLLgDTIKDALGENILDQ 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls       Dt++   L   L  L   + + vA+a++  LnL n
  gi|2916193    35 VETIRKLSKSSRAGNDTHR-KALLNTLQNLSNDELLPVARAFSQFLNLTN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +          + GD a   +      +  t+  L      s
  gi|2916193    84 VAEQYQ-------TISRSGDGANHPEL-----LKKTFETLKQNN-LSESA 120

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   +  A+   s +LvltAHPt   RR L+ K + +  CL qL   D+   ++
  gi|2916193   121 IHAAIESLSLELVLTAHPTEITRRTLIHKLGEVNSCLEQLDHSDISDYER 170

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     +   L   +  A+ tDEiR+ +PtP DE + G + +   +W+GvP FL
  gi|2916193   171 NQIMRRLRQLVAQAWHTDEIRKYRPTPVDEAKWGFAVVENSLWEGVPAFL 220
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                    RRvDtALKn.iGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     +  + Gi  +lP d   ++F+sWmGGDRDG nP vt  +tR v
  gi|2916193   221 RELNEQVEEtFGI--KLPVDFVPVQFTSWMGGDRDG-NPNVTASITRHVM 267

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     L+R  A+ l++  +  L+ Elsm  C +E+     +l   +
  gi|2916193   268 QLSRWKATDLFLRDIGVLISELSMSECSQEV----ADLSGDPEAL----- 308

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                                EPYRviL   R +L  t       L       + +
  gi|2916193   309 -----------EPYRVILKRLRSQLMSTQAYLERRLKGERLPRPADLLVS 347

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  +  +PL   Y+sL +CG  +iA G LLD LR v  FG+ Lv++D+Rq
  gi|2916193   348 NA-QLWDPLYAIYQSLQQCGMSIIANGQLLDTLRRVKCFGVPLVRIDVRQ 396

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+t+ +  it+ L++G Y +WsE  +q +L+ EL  KRPLl+
  gi|2916193   397 ESTRHTEAIAEITRYLGLGDYESWSEADKQAFLIRELNSKRPLLPRSWEP 446

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     +E ++vl++ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|2916193   447 SDETREVLETCKVVAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIPF 496

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    +++v PLFE L DL+ A   + kL  iDWY+  i+GKq vm+GYsDs KD
  gi|2916193   497 AMPVAPLFETLDDLNNANDVMSKLLNIDWYRGFIQGKQMVMIGYSDSAKD 546

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+Aq+ +iK   k Gv L+lFHGRGGt+GRGG P H A+L
  gi|2916193   547 AGVMAASWAQYQAQDALIKTCEKAGVSLTLFHGRGGTIGRGGAPAHAALL 596

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2916193   597 SQPPGSLKGGLRVTEQGEMIRFKYGLPEVTIASLSLYTGAILEANLMPPP 646

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     PkPEWR +m+++       YR  v     Fv YFR+AtPE E Gk+ +G
  gi|2916193   647 EPKPEWRSIMNQLSADSCAMYRGYVRENADFVPYFRSATPEQELGKLPLG 696

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA + A+    +
  gi|2916193   697 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQQAMLAGHQ 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                       +L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lv   L+P G
  gi|2916193   747 D--QLEAMCRDWPFFSTRLGMLEMVFSKADLWLAEYYDQRLVDKSLWPLG 794

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    ++LRd+     + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|2916193   795 QQLRDQLDADIKAVLTIANDSHLMADQPWIAESIALRNVYTDPLNVLQAE 844

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R               A+E             +++    +E  L
  gi|2916193   845 LLHRSR----------------AQEA-----------RGDEPDARVEQAL 867

                    iLtmKGiAAGmqntG<-*
                    ++t+ G+AAGm ntG
  gi|2916193   868 MVTIAGVAAGMRNTG    882

gi|251792638|ref|YP_003007364.1|: domain 1 of 1, from 6 to 879: score 756.9, E = 1.5e-224
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                          Aq+R      +s           +l +FL++ + D  G+ +
  gi|2517926     6    ---AQMRQ----NIS-----------MLGHFLgETICDAQGDAILQL 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls +     D  + + L   L  +     i vA+a++  LnL n
  gi|2517926    35 IENIRVLSKNSRNGDDQAR-QQLLQTLSTISDDNIIPVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R                     iE  +K+L  +   + e+
```

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  gi|2517926    84 IAEQYQTISRHHHDEVS-----------SNRSIEALFKRLQGQN-LAQED 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   +   +    ++LvltAHPt   RRsL+ Kn  i  CL+qL   D+t  ++
  gi|2517926   122 IIKTVEKLLIELVLTAHPTEVTRRSLVHKNVEINKCLSQLEHSDLTEKER 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   k ++  L   i  A+ t EiR  +PtP +E + G + i   +W+ vP FL
  gi|2517926   172 KAIERRLLQLIAEAWHTNEIRTKRPTPFEEAKWGFAVIENSLWQAVPEFL 221

                   RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   R  ++ A+K +Gi   lP +   ++FssWmGGDRDG nP vt  vtR v
  gi|2517926   222 RQFnESAVKYLGIS--LPVELAPVQFSSWMGGDRDG-NPFVTANVTRQVL 268

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LaR  Aa l++  +  L+ Elsm  C +  R++          d
  gi|2517926   269 QLARWKAADLFLKDIQLLVDELSMQQCTEAFRAK--------YGD----- 305

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                              EPYRv+    R KL  t      LLA        e + t
  gi|2517926   306 ---------HPEPYRVVAKTLRTKLSATLTYYDDLLANRPPRATKEDIIT 346

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                     E+  EPL  CY+sL  CG ++iA G LLD+LR +  FG+ L +LDiRq
  gi|2517926   347 TNEQLWEPLYDCYQSLMACGMRIIANGLLLDYLRRIRCFGVTLSRLDIRQ 396

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   Es R+t+ l  it+ +++G Y +WsE  +q +L+ EL+ +RPL++ D
  gi|2517926   397 ESTRHTEALAEITRYIGLGDYAQWSEADKQAFLIRELSSRRPLIPLDWTP 446

                   tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     E +++ld+ +v+AE P      Yiisma + sDvLAv LL +ECgv
  gi|2517926   447 SAETQEILDTCKVIAEQPQGVISCYIISMARTTSDVLAVHLLLKECGVPY 496

                   tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    L+vvPLFE L DL+A    +  LF i WY+  i+ Kq vm+GYsDs KD
  gi|2517926   497 HLPVVPLFETLDDLDASEQVMTELFNIGWYRGVINNKQMVMIGYSDSAKD 546

                   AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                   AG ++A W  Y+AqE ++K   +  + L+lFHGRGGt GRGG P H A+L
  gi|2517926   547 AGMMAASWAQYRAQEALVKLCEQQHIELTLFHGRGGTTGRGGAPAHAALL 596

                   sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                   sqPP  ++  lRvt qGE+i f  G   +   sL  ++ A LE  + PP
  gi|2517926   597 SQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVESLDLYASAVLEANLLPPP 646

                   sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                    Pk EWR++m+e+       YR +v  +  Fv YFR+AtPE E  k+ +G
  gi|2517926   647 EPKTEWREIMDELSDSSCAIYRNIVRGDKDFVPYFRSATPEQELAKLPLG 696

                   sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                   sRPaKR P GG+esLRAiPWiFaW q R  LP WLG GA  + Ai++
  gi|2517926   697 SRPAKRNPHGGVESLRAIPWIFAWMQNRLMLPSWLGAGASVQEAIKRG-- 744

                   nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                    l  ++Em + WPFF   + +lEmvF K D  +   yD+ Lv  eL+  G
  gi|2517926   745 KLALIEEMCQHWPFFSTRIGMLEMVFSKTDMWLSEHYDQHLVKPELWYLG 794

                   ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                   +sLR + ++  + +L +     l+   P++   + LR+ Y   Ln +q
  gi|2517926   795 ESLRKQLQDDIKTILSLSHKDQLMSNLPWIAESIALRNVYTDPLNLLQVE 844

                   tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    L+R+R        +P       + +          n      P +E  L
  gi|2517926   845 LLRRLRG-------QP-------NNP----------N------PDVEQAL 864

                   iLtmKGiAAGmqntG<-*
                   ++t+ GiAAGm ntG
  gi|2517926   865 MITITGIAAGMRNTG    879

gi|229521712|ref|ZP_04411130.1|: domain 1 of 1, from 2 to 878: score 756.7, E = 1.7e-224
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                *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                    +  +  +L    vs           +l + L+  +q   G+ +
gi|2295217     2    TMNEKYAALK-SNVS-----------MLGRLLgQTIQAADGDVILAK 36

                vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                v     ls        + + e L   +  L       vA+a+   LnL n
gi|2295217    37 VETIRKLSKSARAGNQADR-ELLIEEIKNLPNHQLTPVARAFNQFLNLTN 85

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                +AE  +   R   +         E +A     i   + kL  k   s  +
gi|2295217    86 IAEQYHTISRHCESHVN------ELDA-----IGSLFAKLAQKS-VSKFD 123

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+ + ++
gi|2295217   124 TAQAIRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSPKER 173

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                +  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
gi|2295217   174 HKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWHAVPEFL 223

                RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                R  D  +K   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
gi|2295217   224 RELDEQVKSY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITREVLL 271

                LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                L+R  Aa lY+  + +L+ Elsm +Cn+ +R+ A E       +
gi|2295217   272 LSRWKAADLYLTDINELVSELSMTKCNEAVRALAGE-------E------ 308

                iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                          EPYR iL  vR  L  t E     L      ++  A
gi|2295217   309 ---------HEPYRAILKPVRSLLQETIEILDAKLNG--QKLAVKAPLQT 347

                vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                 ++  EPL  CY+sL eCG  viADGsLLD LR +  FG+ Lv+LD+RqE
gi|2295217   348 ADQLWEPLYACYQSLHECGMGVIADGSLLDTLRRIKAFGVHLVRLDVRQE 397

                seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                s R+ +v+  +t+HL+iG Y +WsE+ +  +L +EL  KRPLl+ D
gi|2295217   398 SSRHAEVISELTRHLGIGDYNQWSEQDKIAFLTTELNSKRPLLPRDWQPS 447

                EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                  vk+vld+ +++A    D+FGaY+isma + sDvLAv LL  E g
gi|2295217   448 PQVKEVLDTCKIIAAQSKDAFGAYVISMARTASDVLAVHLLLQEAGCPYR 497

                LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                + v PLFE L DL+ A   + +L  iD Y+  i+  q vm+GYsDs KDA
gi|2295217   498 MDVCPLFETLDDLNNAESVIRQLMNIDLYRGFIQNHQMVMIGYSDSAKDA 547

                GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                G ++A W  Y+A E ++Kv  + G+ L+lFHGRGGt+GRGG P H A+Ls
gi|2295217   548 GVMAAGWAQYRAMEALVKVGEEAGIELTLFHGRGGTIGRGGAPAHAALLS 597

                qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
gi|2295217   598 QPPKSLKGGLRVTEQGEMIRFKLGLPEVAVNSFNMYASAILEANLLPPPE 647

                PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                Pk EWR Lm+ +  +    YR vv  EP Fv YFR AtPElE Gk+ +Gs
gi|2295217   648 PKNEWRALMDILSEISCNAYRKVVRGEPDFVPYFRQATPELELGKLPLGS 697

                RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                RPaKR P GG+esLRAiPWiF+W q R  LP WLG G A + Ai+   +
gi|2295217   698 RPAKRNPTGGVESLRAIPWIFSWSQNRLILPAWLGAGEAIQIAINEGHQA 747

                lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv   L+P G+
gi|2295217   748 L--LEEMCREWPFFSTRLGMLEMVYTKCSVSIARHYDERLVEPTLRPLGE 795

                sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                +LR++ +   + +L +     l+  DP+ +  +RLR+ Yi  Ln++qA
gi|2295217   796 KLRAQLQQDIKVVLNVENNENLMQSDPWGQESIRLRNIYIEPLNMLQAEL 845
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                  LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                  L R R  +               +                aP LE+ L+
  gi|2295217   846 LYRTRQSEL--------------P----------------APELEEALM 864

                  LtmKGiAAGmqntG<-*
                  +t+ GiAAGm ntG
  gi|2295217   865 VTIAGIAAGMRNTG    878

gi|51594466|ref|YP_068657.1|: domain 1 of 1, from 1 to 878: score 756.5, E = 1.9e-224
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      +  q  ++    vs          +L     D +++  Ge + + v
  gi|5159446     1    -MNEQYSAMR-SNVS----------MLGTLLGDTIKEALGEHILDRV 35

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       ls       ++++ +EL + L  L   + + vA+a++  LnL n
  gi|5159446    36 ETIRKLSKSSRAGNEASR-QELLTTLQNLSNDELLPVARAFSQFLNLTNT 84

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AE  +       +   hG+ a   +A     +   + +L  k   s +++
  gi|5159446    85 AEQYH-------SISPHGEAASNPEA-----LAQLFTRLKDKK-LSDQDM 121

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
  gi|5159446   122 RSAVDDLSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHNDLADYERN 171

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   +   L   +   + tDEiR+ +P P DE + G + +   +W+GvP FLR
  gi|5159446   172 KIMRRLRQLVAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWEGVPAFLR 221

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                       L n  +  RlP ++  i+F+sWmGGDRDG nP vt E+tR v LL
  gi|5159446   222 EFNEQLEN-SLDYRLPVEAVPIRFTSWMGGDRDG-NPNVTAEITRHVLLL 269

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                  +R  A+ l++  +  L+ Elsm  C  ELR    El
  gi|5159446   270 SRWKATDLFLRDIQVLVSELSMSECTPELR----ELAGGEEVL------- 308

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                           EPYR ++ +vR +L nt       L +G   ++
  gi|5159446   309 ---------EPYRQLMKNVRTQLTNTQAYLEARL-KGERVLPPHDLLVSN 348

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                  ++  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+RqEs
  gi|5159446   349 DQLWEPLYACYQSLKACGMEIIANGQLLDTLRRVRCFGVPLVRIDVRQES 398

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   R+tD +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
  gi|5159446   399 TRHTDAIAELTRYLGLGDYESWSESDKQAFLVRELNSKRPLVPLKWEPSA 448

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E ++vl++ rv+AE P  s  aY+isma  PsDvLAv LL +E g   tL
  gi|5159446   449 ETQEVLETCRVIAEAPQGSIAAYVISMAKVPSDVLAVHLLLKEAGCPFTL 498

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDAG
  gi|5159446   499 PVAPLFETLDDLNNADDVMTQLLGIDWYRGLIQGKQMVMIGYSDSAKDAG 548

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Lsq
  gi|5159446   549 VMAASWAQYRAQDALIKTCEKAGITLTLFHGRGGSIGRGGAPAHAALLSQ 598

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP  P
  gi|5159446   599 PPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLALYAGAILEANLLPPPEP 648

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  k EW ++m+ +     + YRs v   P Fv YFR AtPElE Gk+ +GsR
  gi|5159446   649 KKEWIEVMDLLSDASCDMYRSYVRENPEFVRYFRAATPELELGKLPLGSR 698

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
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                    PaKR+P GG+esLRAiPWiFaWtq R  LP WLG GA  + Aid   + +
  gi|5159446   699 PAKRRPDGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQRAIDAGKRDV 748

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L  m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P G++
  gi|5159446   749 --LATMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVDKSLWPLGQQ 796

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRd+     + +L iA    l+   P++   + LR+ Y   Lnv+qA  L
  gi|5159446   797 LRDQLAADIKVVLAIANDDHLMADLPWIAESIALRNVYTDPLNVLQAELL 846

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     R R             +E+ d                    +E  L++
  gi|5159446   847 HRSRQ------------QEHPDAC-------------------VEQALMV 865

                    tmKGiAAGmqntG<-*
                    t+ G+AAGm ntG
  gi|5159446   866 TIAGVAAGMRNTG    878

gi|108806093|ref|YP_650009.1|: domain 1 of 1, from 1 to 878: score 756.3, E = 2.3e-224
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +  q  ++    vs          +L     D +++  Ge + + v
  gi|1088060     1    -MNEQYSAMR-SNVS----------MLGTLLGDTIKEALGEHILDRV 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       ++++ +EL + L  L   + + vA+a++  LnL n
  gi|1088060    36 ETIRKLSKSSRAGNEASR-QELLTTLQNLSNDELLPVARAFSQFLNLTNT 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +       +   hG+ a   +A     +   + +L  k   s +++
  gi|1088060    85 AEQYH-------SISPHGEAASNPEA-----LAQLFTRLKDKK-LSDQDM 121

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
  gi|1088060   122 RSAVDDLSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHNDLADYERN 171

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +   L   +   + tDEiR+ +P P DE + G + +   +W+GvP FLR
  gi|1088060   172 KIMRRLRQLVAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWEGVPAFLR 221

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         L n  +  RlP ++  i+F+sWmGGDRDG nP vt E+tR v LL
  gi|1088060   222 EFNEQLEN-SLDYRLPVEAVPIRFTSWMGGDRDG-NPNVTAEITRHVLLL 269

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    +R  A+ l++  +  L+ Elsm  C  ELR    El
  gi|1088060   270 SRWKATDLFLRDIQVLVSELSMSECTPELR----ELAGGEEVL------- 308

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             EPYR ++ +vR +L nt       L +G   ++
  gi|1088060   309 ---------EPYRQLMKNVRTQLTNTQAYLEARL-KGERVLPPHDLLVSN 348

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    ++  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+RqEs
  gi|1088060   349 DQLWEPLYACYQSLKACGMEIIANGQLLDTLRRVRCFGVPLVRIDVRQES 398

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     R+tD +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
  gi|1088060   399 TRHTDAIAELTRYLGLGDYESWSESDKQAFLVRELNSKRPLVPLKWEPSA 448

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E ++vl++ rv+AE P  s  aY+isma  PsDvLAv LL +E g   tL
  gi|1088060   449 ETQEVLETCRVIAEAPQGSIAAYVISMAKVPSDVLAVHLLLKEAGCPFTL 498

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDAG
  gi|1088060   499 PVAPLFETLDDLNNADDVMTQLLGIDWYRGLIQGKQMVMIGYSDSAKDAG 548

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Lsq
  gi|1088060   549 VMAASWAQYRAQDALIKTCEKAGITLTLFHGRGGSIGRGGAPAHAALLSQ 598
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                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP  P
  gi|1088060   599 PPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLALYAGAILEANLLPPPEP 648

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    k EW ++m+ +     + YRs v   P Fv YFR AtPElE Gk+ +GsR
  gi|1088060   649 KKEWIEVMDLLSDASCDMYRSYVRENPEFVRYFRAATPELELGKLPLGSR 698

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+P GG+esLRAiPWiFaWtq R  LP WLG GA  + Aid   + +
  gi|1088060   699 PAKRRPDGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQRAIDAGKQDV 748

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L  m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P G++
  gi|1088060   749 --LATMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVDKSLWPLGQQ 796

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRd+     + +L iA    l+   P++   + LR+ Y   Lnv+qA  L
  gi|1088060   797 LRDQLAADIKVVLAIANDDHLMADLPWIAESIALRNVYTDPLNVLQAELL 846

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     R R             +E+ d                    +E  L++
  gi|1088060   847 HRSRQ------------QEHPDAC-------------------VEQALMV 865

                    tmKGiAAGmqntG<-*
                    t+ G+AAGm ntG
  gi|1088060   866 TIAGVAAGMRNTG    878

gi|229507302|ref|ZP_04396807.1|: domain 1 of 1, from 2 to 878: score 756.2, E = 2.4e-224
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  +  +L    vs          +l + L+  +q   G+ +
  gi|2295073     2    TMNEKYAALK-SNVS----------MLGRLLgQTIQAADGDVILAK 36

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls        + + e L   +  L       vA+a+   LnL n
  gi|2295073    37 VETIRKLSKSARAGNQADR-ELLIEEIKNLPNHQLTPVARAFNQFLNLTN 85

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R   +         E +A     i   + kL  k   s  +
  gi|2295073    86 IAEQYHTISRHCESHVN------ELDA-----IGSLFAKLAQKS-VSKFD 123

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+ + ++
  gi|2295073   124 TAQAIRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSPKER 173

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
  gi|2295073   174 HKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWHAVPEFL 223

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R  D  +K   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
  gi|2295073   224 RELDEQVKSY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITREVLL 271

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa lY+  + +L+ Elsm +Cn+ +R+ A E       +
  gi|2295073   272 LSRWKAADLYLTDINELVSELSMTKCNEAVRALAGE-------E------ 308

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR iL  +R  L  t E     L      ++  A
  gi|2295073   309 ---------HEPYRAILKPIRSLLQETIEILDAKLNG--QKLAVKAPLQT 347

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     ++  EPL  CY+sL eCG  viADGsLLD LR +  FG+ Lv+LD+RqE
  gi|2295073   348 ADQLWEPLYACYQSLHECGMGVIADGSLLDTLRRIKAFGVHLVRLDVRQE 397

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+ +v+  +t+HL+iG Y +WsE+ +  +L +EL  KRPLl+ D
  gi|2295073   398 SSRHAEVISELTRHLGIGDYNQWSEQDKIAFLTTELNSKRPLLPRDWQPS 447

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
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                     vk+vld+ +++A    D+FGaY+isma + sDvLAv LL  E g
  gi|2295073   448 PQVKEVLDTCKIIAAQSKDAFGAYVISMARTASDVLAVHLLLQEAGCPYR 497

                     LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                     + v PLFE L DL+ A   + +L  iD Y+  i+  q vm+GYsDs KDA
  gi|2295073   498 MDVCPLFETLDDLNNAESVIRQLMNIDLYRGFIQNHQMVMIGYSDSAKDA 547

                     GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                     G ++A W  Y+A E ++Kv  + G+ L+lFHGRGGt+GRGG P H A+Ls
  gi|2295073   548 GVMAAGWAQYRAMEALVKVGEEAGIELTLFHGRGGTIGRGGAPAHAALLS 597

                     qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                     qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|2295073   598 QPPKSLKGGLRVTEQGEMIRFKLGLPEVAVNSFNMYASAILEANLLPPPE 647

                     PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                     Pk EWR Lm+ +  +    YR vv  EP Fv YFR AtPElE Gk+ +Gs
  gi|2295073   648 PKNEWRALMDILSEISCNAYRKVVRGEPDFVPYFRQATPELELGKLPLGS 697

                     RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                     RPaKR P GG+esLRAiPWiF+W q R  LP WLG G A + Ai+   +
  gi|2295073   698 RPAKRNPTGGVESLRAIPWIFSWSQNRLILPAWLGAGEAIQIAINEGHQA 747

                     lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                     l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv   L+P G+
  gi|2295073   748 L--LEEMCREWPFFSTRLGMLEMVYTKCSVSIACHYDERLVEPTLRPLGE 795

                     sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                     +LR++ +   + +L +     l+  DP+ +  +RLR+ Yi  Ln++qA
  gi|2295073   796 KLRAQLQQDIKVVLNVENNENLMQSDPWGQESIRLRNIYIEPLNMLQAEL 845

                     LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                     L R R  +               +                aP LE+ L+
  gi|2295073   846 LYRTRQSEL---------------P----------------APELEEALM 864

                     LtmKGiAAGmqntG<-*
                     +t+ GiAAGm ntG
  gi|2295073   865 VTIAGIAAGMRNTG    878

gi|107103201|ref|ZP_01367119.1|: domain 1 of 1, from 3 to 878: score 756.0, E = 2.7e-224
                     *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         iDA LR          e++ +   LL D     + +  G+   + +
  gi|1071032     3    EIDARLR----------EDVHQLGELLGDT----IREQYGPRFLDKI 35

                     qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                      E     A    +  ++  + L a L +L+  + + vA+a+   LnLAn+
  gi|1071032    36 -ELIRKGAKAARRGSAEGAQQLTATLDGLEEDELLPVARAFNQFLNLANI 84

                     AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     AE  +     Ri++++      E +      +EE l +L   +  +P
  gi|1071032    85 AEQYH-----RIRRRR----PNEPEPFENLVLEELLGRLKDAG-HAPGQL 124

                     FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                        L    ++LvltAHPt  +RR L+qK   i   La     D+ +e++
  gi|1071032   125 ARQLAGLEIELVLTAHPTEVARRTLIQKYDAITAQLAAKDHADLLPEERS 174

                     ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                      +   L R +  A+ tDEiR+ +PtP DE + G + i   +W+  P  LR
  gi|1071032   175 RIQQRLQRLVAEAWHTDEIRKVRPTPVDEAKWGFAVIEHSLWQALPNVLR 224

                     RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                      vD  L      ERlP  +  ++F+sWmGGDRDG nP vt  vtR+v LL
  gi|1071032   225 HVDEVLLR-STGERLPLTAAPLRFASWMGGDRDG-NPNVTASVTREVLLL 272

                     aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                     aR mAa lY+  ++ L  Elsm      L +R  +      +
  gi|1071032   273 ARWMAADLYLRDIDRLAAELSMQQASPQLLARVGD------SA------- 309

                     EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                              EPYR +L + R++L  tR  +   LA  +   + e v  +
  gi|1071032   310 ---------EPYRALLKQLRERLRVTRNWTHQALAGEVP--AAEGVLEHN 348
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                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                     + +EPL LC  sL  CG  viADG+LLD LR   tFGL Lv+LD+Rq+s
  gi|1071032   349 RDLVEPLQLCHESLHACGMGVIADGALLDCLRRAATFGLFLVRLDVRQDS 398

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     R+   l  it+ Le+GsY eW E  R E+Ll EL  +RPLl++
  gi|1071032   399 ARHAAALSEITEYLELGSYDEWDEKTRLEFLLEELNSRRPLLPAHYQPSA 448

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    + ++vl + r +A  P  s G+Y+isma  PsDvLAv LL +E gv  ++
  gi|1071032   449 DTAEVLATCRAIAAAPPASLGSYVISMAGQPSDVLAVQLLLKESGVDWPM 498

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFE L DL+ A   +e+L  +  Y+ r+ G qevm+GYsDs KDAG
  gi|1071032   499 RVVPLFETLDDLDNAGPCMERLLTLPGYRSRLSGVQEVMIGYSDSAKDAG 548

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     l AAW  Y+AqE ++ + +++ v L lFHGRGGtvGRGGGP H AiLsq
  gi|1071032   549 TLTAAWAQYRAQEKLVEICRQHEVELLLFHGRGGTVGRGGGPAHAAILSQ 598

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  + G  Rvt qGE+i f FG  ++  + L  + AA LE  + PP +P
  gi|1071032   599 PPGSVAGRFRVTEQGEMIRFKFGLPDIAEQNLNLYLAAVLEATLMPPPAP 648

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                     P WR  m+++A  A   YR vv  +P FvEYFRlAtPE E G++ +GsR
  gi|1071032   649 EPAWRAQMDRLAKDALLAYRRVVRDDPQFVEYFRLATPEQELGRLPLGSR 698

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+  GG+esLRAiPWiFaWtqtR  LP WLG   A   Ai++    l
  gi|1071032   699 PAKRR-EGGVESLRAIPWIFAWTQTRLMLPAWLGWETALLNAIERGEGAL 747

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L  m + WPFF   +D+lEmv AK D  iA LyD+ Lv  +L+P G++
  gi|1071032   748 --LGQMRERWPFFTTRIDMLEMVLAKADADIARLYDERLVPLDLRPLGRR 795

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRd        +L + G   lL      +  + +R+sY+  L  +qA  L
  gi|1071032   796 LRDLLSQAVRVVLGLTGQSLLLAHASETRESISVRNSYLDPLHLLQAELL 845

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     R              s+    +                   GLE  L++
  gi|1071032   846 AR--------------SRRCQGDA----------------CGGLEQALLV 865

                    tmKGiAAGmqntG<-*
                    t+ G+AAG+ ntG
  gi|1071032   866 TVAGVAAGLRNTG    878

gi|15598883|ref|NP_252377.1|: domain 1 of 1, from 3 to 878: score 756.0, E = 2.8e-224
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        iDA LR          e++ +   LL D     + +  G+   + +
  gi|1559888     3    EIDARLR----------EDVHQLGELLGDT----IREQYGPRFLDKI 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E     A    +  ++  + L a L +L+  + + vA+a+   LnLAn+
  gi|1559888    36 -ELIRKGAKAARRGSAEGAQQLTATLDGLEEDELLPVARAFNQFLNLANI 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +     Ri++++      E +      +EE l +L   +  +P
  gi|1559888    85 AEQYH-----RIRRRR----PNEPEPFENLVLEELLGRLKDAG-HAPGQL 124

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L    ++LvltAHPt  +RR L+qK   i   La     D+ +e++
  gi|1559888   125 ARQLAGLEIELVLTAHPTEVARRTLIQKYDAITAQLAAKDHADLLPEERS 174

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +   L R +  A+ tDEiR+ +PtP DE + G + i   +W+  P  LR
  gi|1559888   175 RIQQRLQRLVAEAWHTDEIRKVRPTPVDEAKWGFAVIEHSLWQALPNVLR 224

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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                    vD  L      ERlP  +  ++F+sWmGGDRDG nP vt  vtR+v LL
  gi|1559888   225 HVDEVLLR-STGERLPLTAAPLRFASWMGGDRDG-NPNVTASVTREVLLL 272

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aR mAa lY+  ++ L  Elsm      L +R  +      +
  gi|1559888   273 ARWMAADLYLRDIDRLAAELSMQQASPQLLARVGD------SA------- 309

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             EPYR +L + R++L  tR  +   LA  +   + e v  +
  gi|1559888   310 ---------EPYRALLKQLRERLRVTRNWTHQALAGEVP--AAEGVLEHN 348

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                     + +EPL LC  sL  CG  viADG+LLD LR   tFGL Lv+LD+Rq+s
  gi|1559888   349 RDLVEPLQLCHESLHACGMGVIADGALLDCLRRAATFGLFLVRLDVRQDS 398

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     R+   l  it+ Le+GsY eW E  R E+Ll EL  +RPLl++
  gi|1559888   399 ARHAAALSEITEYLELGSYDEWDEKTRLEFLLEELNSRRPLLPAHYQPSA 448

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    + ++vl + r +A  P  s G+Y+isma  PsDvLAv LL +E gv  ++
  gi|1559888   449 DTAEVLATCRAIAAAPPASLGSYVISMAGQPSDVLAVQLLLKESGVDWPM 498

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFE L DL+ A   +e+L  +  Y+ r+ G qevm+GYsDs KDAG
  gi|1559888   499 RVVPLFETLDDLDNAGPCMERLLTLPGYRSRLSGVQEVMIGYSDSAKDAG 548

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     l AAW  Y+AqE ++ + +++ v L lFHGRGGtvGRGGGP H AiLsq
  gi|1559888   549 TLTAAWAQYRAQEKLVEICRQHEVELLLFHGRGGTVGRGGGPAHAAILSQ 598

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  + G  Rvt qGE+i f FG  ++  + L  + AA LE  + PP +P
  gi|1559888   599 PPGSVAGRFRVTEQGEMIRFKFGLPDIAEQNLNLYLAAVLEATLMPPPAP 648

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                     P WR  m+++A  A   YR vv  +P FvEYFRlAtPE E G++ +GsR
  gi|1559888   649 EPAWRAQMDRLAKDALLAYRRVVRDDPQFVEYFRLATPEQELGRLPLGSR 698

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+  GG+esLRAiPWiFaWtqtR  LP WLG   A   Ai++    l
  gi|1559888   699 PAKRR-EGGVESLRAIPWIFAWTQTRLMLPAWLGWETALLNAIERGEGAL 747

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L  m ++WPFF   +D+lEmv AK D  iA LyD+ Lv  eL+P G++
  gi|1559888   748 --LGQMREQWPFFTTRIDMLEMVLAKADADIARLYDERLVPLELRPLGRR 795

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRd        +L + G   lL      +  + +R+sY+  L  +qA  L
  gi|1559888   796 LRDLLSQAVRVVLGLTGQSLLLAHASETRESISVRNSYLDPLHLLQAELL 845

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     R              s+    +                  GLE  L++
  gi|1559888   846 AR--------------SRRCRGDA----------------CGGLEQALLV 865

                    tmKGiAAGmqntG<-*
                    t+ G+AAG+ ntG
  gi|1559888   866 TVAGVAAGLRNTG    878

gi|253991711|ref|YP_003043067.1|: domain 1 of 1, from 1 to 878: score 756.0, E = 2.8e-224
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  ++    vs           +l k L+D +++  Ge++ +
  gi|2539917     1    -MNQQYSAMR-SNVS-----------MLGKLLgDTIKEALGEEILDK 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++++ + L + L  L   + + vA+a+   LnL n
  gi|2539917    35 VETIRKLSKSSRAGNEAHR-QQLLSTLQNLSNDELLPVARAFNQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +       +   hG+ a    A     +   + +L  k   s ++
  gi|2539917    84 VAEQYH-------SISPHGEAASNPVA-----LAKLFTHLKEKN-FSNND 120
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                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                       A+   s++LvltAHPt  +RR L+ K   +  CL+qL   D+   +
  gi|2539917   121 LKKAVNELSIELVLTAHPTEIARRTLIHKLVAVNTCLSQLDHDDLADYEH 170

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L   +   + tDEiR+ +PtP DE + G + +   +W+GvP FL
  gi|2539917   171 NNIMRRLRQLVAQSWHTDEIRKIRPTPIDEAKWGFAMVENSLWDGVPAFL 220

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R     L    i   lP ++  i+F+sWmGGDRDG nP vt EvtR v L
  gi|2539917   221 REFNEQLEE-SIDYSLPVEAVPIRFTSWMGGDRDG-NPNVTAEVTRHVLL 268

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa l++  +  L+ Elsm  C  E+R       + a  d +
  gi|2539917   269 LSRWKAADLFLKDIQVLVSELSMSECTPEVR-------KLAGGDEIL--- 308

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR i    R +L nt       L +G   ++      +
  gi|2539917   309 ----------EPYREIAKKLRVQLNNTLAYLEKRL-KGEQVLPPTDLLLD 347

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     E+   PL  CY+sL  CG  +iA G LLD+LR +  FGLsLv++D+RqE
  gi|2539917   348 NEQLWQPLYACYQSLKICGMEIIANGQLLDILRRIRCFGLSLVRIDVRQE 397

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+t  +  +t+ Le+G Y +WsEeK+q +Ll EL+ KRPL++
  gi|2539917   398 STRHTTAISELTQYLELGDYASWSEEKKQAFLLYELHSKRPLIPHNWQPS 447

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     E ++v  + +v+AE P D+  aY+isma aPsDvLAv LL +E     t
  gi|2539917   448 AETQEVFATCKVIAESPQDAIAAYVISMAKAPSDVLAVHLLLKEASCPFT 497

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    L+v PLFE L DL+ A   +++L  i WY+  i+ Kq vm+GYsDs KDA
  gi|2539917   498 LPVAPLFETLDDLNNADNVIQQLMNIKWYRALIQDKQMVMIGYSDSAKDA 547

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++AAW  Y+Aq+ +iKv    Gv L+lFHGRGGt+GRGG P H A+Ls
  gi|2539917   548 GVMAAAWAQYRAQDALIKVCETEGVALTLFHGRGGTIGRGGAPAHAALLS 597

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP
  gi|2539917   598 QPPGSLKGGLRVTEQGEMIRFKFGLPQVTISSLALYASAILEANLLPPPE 647

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    PkPEW ++m+ +  v    YR  v   P Fv YFR AtPE E  k+ +Gs
  gi|2539917   648 PKPEWHQVMDTLSDVSCKMYRDYVREQPDFVPYFRAATPEQELAKLPLGS 697

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA +  ++ D K
  gi|2539917   698 RPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQKVVN-DGKQ 746

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                       L Em ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P G+
  gi|2539917   747 -DVLAEMCRNWPFFTTRIGMLEMVFAKADLWLAKYYDHRLVDKSLWPLGQ 795

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR +     + +L i     l+   P++   + LR+ Y   Lnv+qA
  gi|2539917   796 KLRKQLSADIKTVLAISKDEHLMADLPWIAESIALRNVYTDPLNVLQAEL 845

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R  +y               +                P +E  L+
  gi|2539917   846 LLRSRQQQY---------------P----------------DPQVEQALM 864

                    LtmKGiAAGmqntG<-*
                    +t+ GiAAGm ntG
  gi|2539917   865 VTIAGIAAGMRNTG    878

gi|160877316|ref|YP_001556632.1|: domain 1 of 1, from 11 to 889: score 755.0, E = 5.3e-224
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
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                  + A LR      vs           +l + L+D +    G++  E
gi|1608773    11    DMYASLRS----NVS-----------MLGQILgDTMRTHLGDSFLEK 42

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v     l+ +   + D    e +   Lt+L   + +  Aka+   LnLAn
gi|1608773    43 VEQIRKLAKDSR-RGDQAAREQMLELLTALPDEELVPFAKAFNQFLNLAN 91

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  L E  +   R   ++                +E  l ++
gi|1608773    92 LSEQFHTISRNCDELVC-----------VPDPVEQLLGRMLNGR-VDQTK 129

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  + + LK   +DLvltAHPt   RR L+qK a i  CL+      +   ++
gi|1608773   130 MLDCLKTLDIDLVLTAHPTEISRRTLIQKYAAIVDCLTEQENDQLSDRER 179

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  + +   L   i   + t EiRR +PtP DE R G+s i E +W+ vP FL
gi|1608773   180 QQISLRLRQLIAQIWHTNEIRRERPTPVDEARWGLSTIEESLWHAVPDFL 229

                  RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                  R  +D   +  G    lP d+  ++FssWmGGDRDG nP vt  vt +v
gi|1608773   230 RQLnDQVQQRTG--QQLPIDIAPVRFSSWMGGDRDG-NPFVTAKVTQEVL 276

                  LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     R  Aa l+++ +  L+ Elsm   ndEL++       t  +
gi|1608773   277 DRNRHAAARLFLEDIVLLVGELSMEEANDELKA------YTNNSC----- 315

                  YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                                EPYR +L  +R +L  t +     +     e+
gi|1608773   316 -----------EPYRHVLRSIRQRLRDTIDYLNARIEGHNPEVDKSSLIW 354

                  kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                  +  +   PLE+ YksL +CG + iA G LLD+LR    FG+ + +LDiRq
gi|1608773   355 QESDLKAPLEMLYKSLTDCGMRLIANGLLLDILRRLACFGIHMLRLDIRQ 404

                  EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                  ++ R+ Dvl  +t+ L++G +  W E  +q +Ll EL+ +RPL++s
gi|1608773   405 DASRHSDVLAELTRYLGMGDFNHWDETEKQAFLLRELSNRRPLIPSNWQP 454

                  tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                    +v++vl++ r +A  P  + G+Y+isma  PsDvL v LL +E g  +
gi|1608773   455 SADVAEVLNTCRLIAKHPAKALGSYVISMAGKPSDVLTVLLLLKETGCSH 504

                  tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                  ++rvvPLFE L DL+ A A +  L  iDWY+    G qevm+GYsDs KD
gi|1608773   505 PMRVVPLFETLSDLNNAAACITDLLDIDWYRGYTKGMQEVMIGYSDSAKD 554

                  AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                  AG ++AAW  Y AqE ++ v K+ GvKL+lFHGRGG +GRGGGP H AiL
gi|1608773   555 AGVMAAAWAQYHAQEQLVAVCKQAGVKLTLFHGRGGSIGRGGGPAHKAIL 604

                  sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                  sqPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A LE  + PP
gi|1608773   605 SQPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVLEATLLPPP 654

                  sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                   Pk EWR+ m+++A      YR +v  EP Fv YFR AtPE+E Gk+ +G
gi|1608773   655 EPKQEWRDCMQRIAEESVGAYRGIVRDEPDFVAYFRAATPEVELGKLPLG 704

                  sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                  sRPaKR+  GGiesLRAiPWiFaW q R  LP WLG G A + A ++  +
gi|1608773   705 SRPAKRRVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALQAACER--R 752

                  nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                   +  L+Em +eWPFF   + +lEmv+AK +P +A  y+  Lv  +L+  G
gi|1608773   753 EMGLLQEMEREWPFFSTRISMLEMVYAKAEPNLARYYETCLVPKDLHHLG 802

                  ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                  + LR++     + +L++     l+   P+ +  ++LR++Yi  Ln +q
gi|1608773   803 ETLRQRLDLGIKVVLELTKSDSLMAHTPWNRESVKLRNPYIDPLNFLQTE 852
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                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R             KE  + +   a e v+L             L
  gi|1608773   853 LLARTR-------------KETTETP---ASEHVQLA------------L 874

                    iLtmKGiAAGmqntG<-*
                    +Lt+ G+AAGm ntG
  gi|1608773   875 MLTIAGVAAGMRNTG    889

gi|238750857|ref|ZP_04612355.1|: domain 1 of 1, from 1 to 878: score 755.0, E = 5.6e-224
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +  q  ++    vs          +L     D +++  Ge + + v
  gi|2387508     1    -MNEQYSAMR-SNVS----------MLGTLLGDTIKEALGEHILDRV 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       ++++ +EL + L  L   + + vA+a++  LnL n
  gi|2387508    36 ETIRKLSKSSRAGNEASR-QELLTTLQNLSNDELLPVARAFSQFLNLTNT 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +       +   hG+ a   +A     +   + +L  k   s +++
  gi|2387508    85 AEQYH-------SISPHGEAASNPEA-----LAQLFTRLKDKK-LSEQDM 121

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     +A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
  gi|2387508   122 RNAVDELSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHNDLADYERN 171

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +   L   +   + tDEiR+ +P P DE + G + +   +W+GvP FLR
  gi|2387508   172 KIMRRLRQLVAQSWHTDEIRKIRPSPIDEAKWGFAVVENSLWEGVPAFLR 221

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         L+n  +  RlP ++  i+F+sWmGGDRDG nP vt E+tR v LL
  gi|2387508   222 EFNEQLQN-SLDYRLPVEAVPIRFTSWMGGDRDG-NPNVTAEITRHVLLL 269

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRA..EElyrtaardkvvKy
                    +R  A+ l++  +  L+ Elsm  C  ELR  A++EE+
  gi|2387508   270 SRWKATDLFLRDIQVLVSELSMSECTPELRKLAggEEVL----------- 308

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR ++  vR +L nt       L +G   ++
  gi|2387508   309 -----------EPYRELMKRVRTQLTNTQTYLESRL-KGERVLPPTDLLV 346

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                      ++  +PL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+Rq
  gi|2387508   347 SNDQLWDPLYACYQSLKSCGMEIIANGQLLDTLRRVRCFGVPLVRIDVRQ 396

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+tD +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
  gi|2387508   397 ESTRHTDAIAELTRYLGLGDYESWSEADKQAFLIRELNSKRPLVPLKWEP 446

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      + ++vl++ rv+AE P  s  aY+isma  PsDvLAv LL +E g
  gi|2387508   447 SADTQEVLETCRVIAEAPQGSIAAYVISMAKVPSDVLAVHLLLKEAGCPF 496

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    tL+v PLFE L DL+ A   + +L siDWY+  i+GKq vm+GYsDs KD
  gi|2387508   497 TLPVAPLFETLDDLNNADEVMTQLLSIDWYRGLIQGKQMVMIGYSDSAKD 546

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|2387508   547 AGVMAASWAQYRAQDALIKTCEKAGISLTLFHGRGGSIGRGGAPAHAALL 596

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP
  gi|2387508   597 SQPPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLALYAGAILEANLLPPP 646

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk EW ++m+       E YR  v   P Fv YFR AtPlE Gk+ +G
  gi|2387508   647 EPKKEWIEVMDLQSEASCEMYRGYVRENPEFVPYFRAATPELELGKLPLG 696

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GA  + Aid   K
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  gi|2387508   697 SRPAKRRPNGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQKAIDAGKK 746

                   nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                    +  L  m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P G
  gi|2387508   747 DV--LATMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVDKSLWPLG 794

                   ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                   ++LRd+     + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|2387508   795 QQLRDQLAADIKVVLAIANDDHLMADLPWIAESIALRNVYTDPLNVLQAE 844

                   tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    L R R             +E+ d                     +E  L
  gi|2387508   845 LLHRSRQ------------QEHPDAR------------------VEQAL 863

                   iLtmKGiAAGmqntG<-*
                   ++t+ G+AAGm ntG
  gi|2387508   864 MVTIAGVAAGMRNTG    878

gi|229513569|ref|ZP_04403033.1|: domain 1 of 1, from 2 to 878: score 754.9, E = 5.8e-224
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  +  +L    vs           +l + L+  +q   G+ +
  gi|2295135     2    TMNEKYAALK-SNVS-----------MLGRLLgQTIQAADGDVILAK 36

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls        + + e L   +  L       vA+a+   LnL n
  gi|2295135    37 VETIRKLSKSARAGNQADR-ELLIEEIKNLPNHQLTPVARAFNQFLNLTN 85

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +   R   +         E +A     i   + kL  k   s  +
  gi|2295135    86 IAEQYHTISRHCESHVN------ELDA-----IGSLFAKLAQKS-VSKFD 123

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+ + ++
  gi|2295135   124 TAQAIRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSPKER 173

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   +  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
  gi|2295135   174 HKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWHAVPEFL 223

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   R  D  +K   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
  gi|2295135   224 RELDEQVKSY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITREVLL 271

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   L+R  Aa lY+  + +L+ Elsm +Cn+ +R+ A E       +
  gi|2295135   272 LSRWKAADLYLTDINELVSELSMTKCNEAVRALAGE-------E------ 308

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                             EPYR iL  +R  L  t E     L      ++  A
  gi|2295135   309 ---------HEPYRAILKPIRSLLQETIEILDAKLNG--QKLAVKAPLQT 347

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    ++  EPL  CY+sL eCG  viADGsLLD LR +  FG+ Lv+LD+RqE
  gi|2295135   348 ADQLWEPLYACYQSLHECGMGVIADGSLLDTLRRIKAFGVHLVRLDVRQE 397

                   seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                   s R+ +v+  +t+HL+iG Y +WsE+ +  +L +EL  KRPLl+ D
  gi|2295135   398 SSRHAEVISELTRHLGIGDYNQWSEQDKIAFLTTELNSKRPLLPRDWQPS 447

                   EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     vk+vld+ +++A    D+FGaY+isma + sDvLAv LL  E g
  gi|2295135   448 PQVKEVLDTCKIIAAQSKDAFGAYVISMARTASDVLAVHLLLQEAGCPYR 497

                   LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                   + v PLFE L DL+ A   + +L  iD Y+  i+  q vm+GYsDs KDA
  gi|2295135   498 MDVCPLFETLDDLNNAESVIRQLMNIDLYRGFIQNHQMVMIGYSDSAKDA 547

                   GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                   G ++A W  Y+A E ++Kv  + G+ L+lFHGRGGt+GRGG P H A+Ls
  gi|2295135   548 GVMAAGWAQYRAMEALVKVGEEAGIELTLFHGRGGTIGRGGAPAHAALLS 597
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                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|2295135   598 QPPKSLKGGLRVTEQGEMIRFKLGLPEVAVNSFNMYASAILEANLLPPPE 647

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EWR Lm+ +  +    YR vv  EP Fv YFR AtPElE Gk+ +Gs
  gi|2295135   648 PKNEWRALMDILSEISCNAYRKVVRGEPDFVPYFRQATPELELGKLPLGS 697

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR P GG+esLRAiPWiF+W q R  LP WLG G A + Ai+   +
  gi|2295135   698 RPAKRNPTGGVESLRAIPWIFSWSQNRLILPAWLGAGEAIQIAINEGHQA 747

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv   L+P G+
  gi|2295135   748 L--LEEMCREWPFFSTRLGMLEMVYTKCSVSIARHYDERLVEPTLRPLGE 795

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR++ +   + +L +     l+  DP+ +  +RLR+ Yi  Ln++qA
  gi|2295135   796 KLRAQLQQDIKVVLNVENNENLMQSDPWGQESIRLRNIYIEPLNMLQAEL 845

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R  +                +                aP LE+ L+
  gi|2295135   846 LYRTRQSEL---------------P----------------APELEEALM 864

                    LtmKGiAAGmqntG<-*
                    +t+ GiAAGm ntG
  gi|2295135   865 VTIAGIAAGMRNTG    878

gi|218890036|ref|YP_002438900.1|: domain 1 of 1, from 3 to 878: score 754.8, E = 6.1e-224
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        iDA LR          e++ +   LL D     + +  G+   + +
  gi|2188900     3    EIDARLR----------EDVHQLGELLGDT----IREQYGPRFLDKI 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E     A    +  ++  + L a L +L+  + + vA+a+   LnLAn+
  gi|2188900    36 -ELIRKGAKAARRGSAEGAQQLTATLDGLEEDELLPVARAFNQFLNLANI 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +     Ri++++      E +      +EE l +L   +  +P
  gi|2188900    85 AEQYH-----RIRRRR----PNEPEPFENLVLEELLGRLKDAG-HAPGQL 124

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L    ++LvltAHPt  +RR L+qK   i   La     D+ +e++
  gi|2188900   125 ARQLAGLEIELVLTAHPTEVARRTLIQKYDAITAQLAAKDHADLLPEERS 174

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +   L R +  A+ tDEiR+ +PtP DE + G + i   +W+  P  LR
  gi|2188900   175 RIQQRLQRLVAEAWHTDEIRKVRPTPVDEAKWGFAVIEHSLWQALPNVLR 224

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     vD  L      ERlP  +  ++F+sWmGGDRDG nP vt  vtR+v LL
  gi|2188900   225 HVDEVLLR-STGERLPLTAAPLRFASWMGGDRDG-NPNVTASVTREVLLL 272

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aR mAa lY+  ++ L  Elsm      L +R          d
  gi|2188900   273 ARWMAADLYLRDIDRLAAELSMQQASPQLLARV--------GD------- 307

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             EPYR +L + R++L  tR  +   LA  +   + e v  +
  gi|2188900   308 -------NAEPYRALLKQLRERLRVTRNWTHQALAGEVP--AAEGVLEHN 348

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                     + +EPL LC  sL  CG  viADG+LLD LR   tFGL Lv+LD+Rq+s
  gi|2188900   349 RDLVEPLQLCHESLHACGMGVIADGALLDCLRRAATFGLFLVRLDVRQDS 398

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     R+   l  it+ Le+GsY eW E  R E+Ll EL  +RPLl++
  gi|2188900   399 ARHAAALSEITEYLELGSYDEWDEKTRLEFLLEELNSRRPLLPAHYQPSA 448

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    + ++vl + r +A  P  s G+Y+isma  PsDvLAv LL +E gv  ++
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  gi|2188900   449 DTAEVLATCRAIAAAPPASLGSYVISMAGQPSDVLAVQLLLKESGVDWPM 498

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFE L DL+ A   +e+L  +  Y+ r+ G qevm+GYsDs KDAG
  gi|2188900   499 RVVPLFETLDDLDNAGPCMERLLTLPGYRSRLSGVQEVMIGYSDSAKDAG 548

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    l AAW  Y+AqE ++ + +++ v L lFHGRGGtvGRGGGP H AiLsq
  gi|2188900   549 TLTAAWAQYRAQEKLVEICRQHEVELLLFHGRGGTVGRGGGPAHAAILSQ 598

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP  + G  Rvt qGE+i f FG  ++  + L  + AA LE  + PP +P
  gi|2188900   599 PPGSVAGRFRVTEQGEMIRFKFGLPDIAEQNLNLYLAAVLEATLMPPPAP 648

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    P WR  m+++A  A   YR vv  +P FvEYFRlAtPE E G++ +GsR
  gi|2188900   649 EPAWRAQMDRLAKDALLAYRRVVRDDPQFVEYFRLATPEQELGRLPLGSR 698

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKR+  GG+esLRAiPWiFaWtqtR  LP WLG   A   Ai++    l
  gi|2188900   699 PAKRR-EGGVESLRAIPWIFAWTQTRLMLPAWLGWETALLNAIERGEGAL 747

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L  m + WPFF   +D+lEmv AK D  iA LyD+ Lv  eL+P G++
  gi|2188900   748 --LGQMRERWPFFTTRIDMLEMVLAKADADIARLYDERLVPLELRPLGRR 795

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LRd        +L + G   lL      +  + +R+sY+  L  +qA  L
  gi|2188900   796 LRDLLSQAVRVVLGLTGQSLLLAHASETRESISVRNSYLDPLHLLQAELL 845

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    R              s+    +                  GLE  L++
  gi|2188900   846 AR--------------SRRCRGDA----------------CGGLEQALLV 865

                   tmKGiAAGmqntG<-*
                   t+ G+AAG+ ntG
  gi|2188900   866 TVAGVAAGLRNTG    878

gi|161581981|ref|NP_232274.2|: domain 1 of 1, from 1 to 876: score 754.6, E = 7.1e-224
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  +  +L    vs           +l + L+  +q   G+ +
  gi|1615819     1    -MNEKYAALK-SNVS-----------MLGRLLgQTIQAADGDVILAK 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls        + + e L   +  L       vA+a+   LnL n
  gi|1615819    35 VETIRKLSKSARAGNQADR-ELLIEEIKNLPNHQLTPVARAFNQFLNLTN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +   R   +         E +A     i   + kL  k   s  +
  gi|1615819    84 IAEQYHTISRHCESHVN------ELDA-----IGSLFAKLAQKS-VSKFD 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+ + ++
  gi|1615819   122 TAQAIRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSPKER 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   +  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
  gi|1615819   172 HKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWHAVPEFL 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   R  D  +K   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
  gi|1615819   222 RELDEQVKSY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITREVLL 269

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   L+R  Aa lY+  + +L+ Elsm +Cn+ +R+ A E       +
  gi|1615819   270 LSRWKAADLYLTDINELVSELSMTKCNEAVRALAGE-------E------ 306

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                             EPYR iL  +R  L  t E     L      ++  A
  gi|1615819   307 ---------HEPYRAILKPIRSLLQETIEILDAKLNG--QKLAVKAPLQT 345
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                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     ++  EPL  CY+sL eCG  viADGsLLD LR +  FG+ Lv+LD+RqE
  gi|1615819   346 ADQLWEPLYACYQSLHECGMGVIADGSLLDTLRRIKAFGVHLVRLDVRQE 395

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+ +v+  +t+HL+iG Y +WsE+ +  +L +EL  KRPLl+ D
  gi|1615819   396 SSRHAEVISELTRHLGIGDYNQWSEQDKIAFLTTELNSKRPLLPRDWQPS 445

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                      vk+vld+ +++A    D+FGaY+isma + sDvLAv LL  E g
  gi|1615819   446 PQVKEVLDTCKIIAAQSKDAFGAYVISMARTASDVLAVHLLLQEAGCPYR 495

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    + v PLFE L DL+ A   + +L  iD Y+  i+  q vm+GYsDs KDA
  gi|1615819   496 MDVCPLFETLDDLNNAESVIRQLMNIDLYRGFIQNHQMVMIGYSDSAKDA 545

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y+A E ++Kv  + G+ L+lFHGRGGt+GRGG P H A+Ls
  gi|1615819   546 GVMAAGWAQYRAMEALVKVGEEAGIELTLFHGRGGTIGRGGAPAHAALLS 595

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|1615819   596 QPPKSLKGGLRVTEQGEMIRFKLGLPEVAVNSFNMYASAILEANLLPPPE 645

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EWR Lm+ +  +    YR vv  EP Fv YFR AtPElE Gk+ +Gs
  gi|1615819   646 PKNEWRALMDILSEISCNAYRKVVRGEPDFVPYFRQATPELELGKLPLGS 695

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR P GG+esLRAiPWiF+W q R  LP WLG G A + Ai+   +
  gi|1615819   696 RPAKRNPTGGVESLRAIPWIFSWSQNRLILPAWLGAGEAIQIAINEGHQA 745

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv   L+P G+
  gi|1615819   746 L--LEEMCREWPFFSTRLGMLEMVYTKCSVSIACHYDERLVEPTLRPLGE 793

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR++ +   + +L +     l+  DP+ +  +RLR+ Yi  Ln++qA
  gi|1615819   794 KLRAQLQQDIKVVLNVENNENLMQSDPWGQESIRLRNIYIEPLNMLQAEL 843

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R  +                +                aP LE+ L+
  gi|1615819   844 LYRTRQSEL---------------P----------------APELEEALM 862

                    LtmKGiAAGmqntG<-*
                    +t+ GiAAGm ntG
  gi|1615819   863 VTIAGIAAGMRNTG    876

gi|262401934|ref|ZP_06078499.1|: domain 1 of 1, from 1 to 876: score 754.2, E = 9.7e-224
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  +  +L    vs           +l + L+  +q   G+ + E
  gi|2624019     1    -MNEKYAALK-SNVS-----------MLGRLLgQTIQAADGDVILEK 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls        + + e L   +  L       vA+a+   LnL n
  gi|2624019    35 VETIRKLSKSARTGNQADR-ELLIEEIKNLPNHQLTPVARAFNQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R   +         E +A     i   + kL      s  +
  gi|2624019    84 IAEQYHTISRHCESHVN------ELDA-----IGSLFAKLTQNS-VSKFD 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvteDK
                      +A++   ++LvltAHPt   RR ++ K  +i  CL++L   ++   ++
  gi|2624019   122 TAQAIRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSELSSKER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
  gi|2624019   172 HKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWHAVPEFL 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R  D  +K   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
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  gi|2624019   222 RELDEQVKS-HLGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITREVLL 269

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   L+R  Aa lY+  + +L+ Elsm +Cn+ +R  A E       +
  gi|2624019   270 LSRWKAADLYLTDINELVSELSMTKCNEAVRTLAGE-------E------ 306

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                             EPYR iL + R  L  t +     L      ++  A   +
  gi|2624019   307 ---------HEPYRAILKQLRSLLQETIDILEAKLNG--QKLAVKAPLQN 345

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                   v++  EPL  CY+sL eCG  viADGsLLD LR +  FG+ Lv+LD+RqE
  gi|2624019   346 VDQLWEPLYACYQSLHECGMGVIADGSLLDTLRRIKAFGVHLVRLDVRQE 395

                   seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                   s R+ +v+  +t+HL+iG Y +WsE+ +  +L +EL  KRPLl+ D
  gi|2624019   396 SSRHAEVISELTRHLGIGDYNQWSEQDKIAFLTTELNSKRPLLPRDWQPS 445

                   EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     vk+vld+ +++A    D+FGaY+isma + sDvLAv LL  E g
  gi|2624019   446 AQVKEVLDTCKIIAAQSKDAFGAYVISMARTASDVLAVHLLLQEAGCPYR 495

                   LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                   + v PLFE L DL+ A   + +L siD Y+  i+  q vm+GYsDs KDA
  gi|2624019   496 MDVCPLFETLDDLNNAESVIRQLMSIDLYRGFIQNHQMVMIGYSDSAKDA 545

                   GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                   G ++A W  Y+A + ++Kv  + G+ L+lFHGRGGt+GRGG P H A+Ls
  gi|2624019   546 GVMAAGWAQYRAMDALVKVSEEAGIELTLFHGRGGTIGRGGAPAHAALLS 595

                   qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                   qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|2624019   596 QPPKSLKGGLRVTEQGEMIRFKLGLPEVAVNSFNMYASAILEANLLPPPE 645

                   PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                   Pk EWR+Lm+ +  v  E YR vv  EP Fv YFR AtPElE Gk+ +Gs
  gi|2624019   646 PKQEWRDLMNVLSEVSCEAYRHVVRGEPDFVPYFRQATPELELGKLPLGS 695

                   RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                   RP+KR P GG+esLRAiPWiF+W q R  LP WLG G A ++ id+  +
  gi|2624019   696 RPSKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQFSIDQGHQS 745

                   lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                   l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv   L+  G+
  gi|2624019   746 L--LEEMCREWPFFSTRLGMLEMVYTKCSAEIARYYDERLVEPALRSLGE 793

                   sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                   +LR++ +   + +L +     l+  DP+ +  +RLR+ Y+  Ln++qA
  gi|2624019   794 KLRAQLQKDIKTVLNVENNENLMQSDPWGQESIRLRNIYVEPLNMLQAEL 843

                   LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                   L R R                                +e  aP LE+ L+
  gi|2624019   844 LYRTRQ------------------------------SELLAPELEEALM 862

                   LtmKGiAAGmqntG<-*
                   +t+ GiAAGm ntG
  gi|2624019   863 VTIAGIAAGMRNTG    876

gi|157377410|ref|YP_001476010.1|: domain 1 of 1, from 3 to 878: score 754.1, E = 1e-223
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       + A LR  v G             +L +     L D   e +  +
  gi|1573774     3    DMYASLRSNV-GTLG---------QILGETIRTNLDDAFLEKIEQIR 39

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   q      A    + D    +E+   Lt+L   + +  Aka+   LnLAn+
  gi|1573774    40 Q-----LAKSSRQGDEAARDEMLKLLTALPDNELVPFAKAFNQFLNLANI 84

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AE  +   R   ++               D  E l   vl  n   e +
  gi|1573774    85 AEQFHTISRNCDELVC------------VPDPVEQLLGRVLSSNIDQEKM 122
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                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     + L n  +DLvltAHPt   RR L+qK a +   La L    +t  +Kk
  gi|1573774   123 LDCLENLDIDLVLTAHPTEISRRTLIQKYASVIDILAALENPQLTEREKK 172

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                         L   i   + t EiR  +PtP DE R G+s i   +W+ +P FLR
  gi|1573774   173 QQHLRLRQLIAQIWHTNEIRNERPTPVDEARWGLSTIEVSLWQAIPDFLR 222

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         +        lP d+  ++FssWmGGDRDG nP vt  vt +v
  gi|1573774   223 QLNEQVEE-RTGKQLPTDIAPVRFSSWMGGDRDG-NPFVTAKVTQEVLDR 270

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                     R  Aa lY+  +  L+ +ls+   n EL      l  t  +
  gi|1573774   271 NRHTAARLYLKDIVVLVNDLSVEEANAEL------LEYTNNSL------- 307

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             EPYR +L d R KL nt +     L     ei    +  +
  gi|1573774   308 ---------EPYRDVLKDLRQKLRNTVDYLNARLEGHSPEIDLSSIIWHE 348

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                     +  EPL + Y+sL + G   iA G LLD+LR +  FG+ + +LDiRq++
  gi|1573774   349 SDLKEPLLMLYRSLTDSGMSLIAHGLLLDILRRIACFGIHMLRLDIRQDA 398

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+ Dv+  +t+ L++G Y  W E  +q +Ll EL GKRPL++s     +
  gi|1573774   399 ERHSDVIAELTRYLGMGDYNHWDESEKQAFLLRELTGKRPLIPSNWQPSD 448

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    +v++v+ + r +A  P  + G+Y+isma  PsDvL v LL +E g  +++
  gi|1573774   449 DVAEVVSTCRLIATQPARALGSYVISMASKPSDVLTVLLLLKETGCPHPM 498

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFE L DL+ A   +  LF+iDWY+    G qevm+GYsDs KDAG
  gi|1573774   499 RVVPLFETLDDLNNASSCMTALFAIDWYRGYTKGHQEVMIGYSDSAKDAG 548

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     ++AAW  Y AqEE++ v ++  vKL+lFHGRGGt+GRGGGP H AiLsq
  gi|1573774   549 VMAAAWAQYHAQEELVEVSRQAEVKLTLFHGRGGTIGRGGGPAHEAILSQ 598

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  ++G +Rvt qGE+i f FG  +L  +sL  +t A +E  + PP  P
  gi|1573774   599 PPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVMEATLLPPPEP 648

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR  m+++A    + YRs+v  EP Fv YFR AtPE+E Gk+ +GsR
  gi|1573774   649 KPEWRACMQKLAEESVDAYRSIVRDEPDFVAYFRAATPEVELGKLPLGSR 698

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+  GGiesLRAiPWiFaW q R  LP WLG G A + A   D   +
  gi|1573774   699 PAKRRVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALQAA--SDRGEM 746

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+Em ++WPFF+  + +lEmv+AK +P +A  y+  Lv E+L+  G+
  gi|1573774   747 ALLQEMEQDWPFFKTRISMLEMVYAKAEPNLAKYYETCLVPENLHHLGEA 796

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +     + +L++     l+E  P+ +  + LR++Yi  Ln +qA  L
  gi|1573774   797 LRTRLATGIKAVLELTQSNALMEHTPWNRESVTLRNPYIDPLNFVQAELL 846

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     R R                  E+  +a   v+L             L++
  gi|1573774   847 ARTR-----------------KEE--EASTNVELA------------LMI 865

                    tmKGiAAGmqntG<-*
                    t+ G+AAGm ntG
  gi|1573774   866 TIAGVAAGMRNTG    878

gi|238789607|ref|ZP_04633391.1|: domain 1 of 1, from 1 to 878: score 753.9, E = 1.2e-223
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  ++    vs           +l k L+D +++  Ge + +
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gi|2387896     1    -MNEQYSAMR-SNVS-----------MLGKLLgDTIKEALGEHILDR 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++++ +EL + L  L   + + vA+a++  LnL n
gi|2387896    35 VETIRKLSKSSRAGNEASR-QELLTTLQNLSNDELLPVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +       +   hG+ a   +A     +   + +L  k   s ++
gi|2387896    84 TAEQYH-------SISPHGEAASNPEA-----LAQLFTRLKDKN-LSEKD 120

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
gi|2387896   121 MRSAVDELSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHNDLADYER 170

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L   +   + tDEiR+ +P P DE + G + +   +W+GvP FL
gi|2387896   171 NKIMRRLRQLVAQSWHTDEIRKIRPSPVDEAKWGFAVVENSLWEGVPAFL 220

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R     L+n  +  RlP ++  i+F+sWmGGDRDG nP vt E+tR v L
gi|2387896   221 REFNEQLQN-SLDYRLPVEAVPIRFTSWMGGDRDG-NPNVTAEITRHVLL 268

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  A+ l++  +  L+ Elsm  C  ELR    El
gi|2387896   269 LSRWKATDLFLRDIQVLVSELSMSECTPELR----ELAGGEEVL------ 308

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR ++  vR +L nt       L +G   ++
gi|2387896   309 ----------EPYRELMKRVRTQLTNTQAYLESRL-KGERVLPPTDLLVS 347

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     ++  +PL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+RqE
gi|2387896   348 NDQLWDPLYACYQSLKTCGMEIIANGQLLDTLRRVRCFGVPLVRIDVRQE 397

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+tD +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
gi|2387896   398 STRHTDAIAELTRYLGLGDYESWSEADKQAFLIRELNSKRPLVPLKWEPS 447

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     + ++vl++ rv+AE P  s  aY+isma  PsDvLAv LL +E g   t
gi|2387896   448 ADTQEVLETCRVIAEAPQGSIAAYVISMAKVPSDVLAVHLLLKEAGCPFT 497

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    L+v PLFE L DL+ A   + +L siDWY+  i+GKq vm+GYsDs KDA
gi|2387896   498 LPVAPLFETLDDLNNADDVMTQLLSIDWYRGLIQGKQMVMIGYSDSAKDA 547

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Ls
gi|2387896   548 GVMAASWAQYRAQDALIKTCEKAGISLTLFHGRGGSIGRGGAPAHAALLS 597

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP
gi|2387896   598 QPPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLALYAGAILEANLLPPPE 647

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EW ++m+ +     + YR  v   P Fv YFR AtPElE Gk+ +Gs
gi|2387896   648 PKKEWVEVMDLLSDASCDMYRGYVRENPEFVPYFRAATPELELGKLPLGS 697

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GA  + Aid   K
gi|2387896   698 RPAKRRPNGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQKAIDAGKKE 747

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                       L  m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P G+
gi|2387896   748 --ALATMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVDKSLWPLGQ 795

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LRd+ +   + +L iA    l+   P++   + LR+ Y   Lnv+qA
gi|2387896   796 QLRDQLEADIKVVLAIANDDHLMADLPWIAESIALRNVYTDPLNVLQAEL 845

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
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                  L R R   +                            p  rv    E  L+
  gi|2387896   846 LHRSRQQAH--------------------------PDARV----EQALM 864

                  LtmKGiAAGmqntG<-*
                  +t+ G+AAGm ntG
  gi|2387896   865 VTIAGVAAGMRNTG    878

gi|119773395|ref|YP_926135.1|: domain 1 of 1, from 12 to 887: score 753.9, E = 1.2e-223
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      + AqLR+     v            ++ + L+D +++  Ge   +
  gi|1197733    12    DMYAQLRA----NVG-----------MMGQILgDTMKEHLGEAFLDK 43

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v     l+       D  +   L a L  L   + +  Aka+   LnLAn
  gi|1197733    44 VEQIRLLAKGSRSGDDEARAKML-ALLGQLPDEELVPFAKAFNQFLNLAN 92

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  +AE  +   R   ++                 +E  l ++        +E
  gi|1197733    93 IAEQFHTISRNCDELVC-----------VPDPVEQLLGRMLGSQ-VDKKE 130

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  +   LK   +DLvltAHPt   RR L+qK + i  CL  L    +t  +
  gi|1197733   131 MLATLKTLDIDLVLTAHPTEISRRTLIQKYSAIVDCLHDLENPQLTEREH 180

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  k     L   i   + t EiRR +PtP DE R G+s i   +W+ vP FL
  gi|1197733   181 KSQTLRLRQLIAQIWHTNEIRRERPTPVDEARWGLSTIETSLWHAVPDFL 230

                  RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                  R     +        +P d   ++FssWmGGDRDG nP vt  vt +v
  gi|1197733   231 RQLNDQVEE-ATGTQIPTDMAPVRFSSWMGGDRDG-NPFVTARVTAEVLD 278

                  LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    R  Aa lY+  v +L+ Elsm   n EL +     y+    +
  gi|1197733   279 RNRHTAARLYLKDVVELVGELSMEEANAELMA-----YSNNSCE------ 317

                  iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                             PYR +L   R KL nt +     L     e++ + +  +
  gi|1197733   318 -----------PYRDVLRSLRSKLRNTIDFLNARLEGHNPEVARDEIIWE 356

                  vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    +   PL L YksLC+ G + iA G LLD+LR    FG+ + +LDiRq+
  gi|1197733   357 QQDLETPLKLLYKSLCDSGMRLIANGRLLDMLRRLACFGIHMLRLDIRQD 406

                  seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                  + R+   +  +t+ L++G Y  WsE  +q +Ll EL+G+RPL++
  gi|1197733   407 AGRHEAAIAELTRYLGLGDYAHWSEAEKQAFLLKELSGRRPLIPGNWKPS 456

                  EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                  +Ev++vl + r +   P  + G+Y+isma  PsDvLAv LL +E g   +
  gi|1197733   457 DEVAEVLATCRLVGTQPQQALGSYVISMASLPSDVLAVLLLLKESGCNYP 506

                  LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                  +rvvPLFE L DL+ A A +  L  iDWY+    G qevm+GYsDs KDA
  gi|1197733   507 IRVVPLFETLDDLNNAAACITALLDIDWYRGYTKGMQEVMIGYSDSAKDA 556

                  GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                  G ++AAW  Y+AqE ++Kv  k GvKL+lFHGRGGt+GRGGGP H AiLs
  gi|1197733   557 GVMAAAWAQYRAQEQLVKVCNKAGVKLTLFHGRGGTIGRGGGPAHKAILS 606

                  qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                  qPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A LE  + PP
  gi|1197733   607 QPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVLEATLLPPPE 656

                  PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                  Pk EWR+ m+++A    E YR +v +EP Fv YFR AtPE+E Gk+ +Gs
  gi|1197733   657 PKQEWRNAMQRIADESVEAYRGIVRQEPDFVPYFRAATPEVELGKLPLGS 706

                  RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                  RPaKR+  GGiesLRAiPWiFaW q R  LP WLG G A K A d+
  gi|1197733   707 RPAKRRVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALKAAADRG--E 754
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                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l  L+Em ++WPFF   + +lEmv+ K +P +A  y++ Lv E L+  G
  gi|1197733   755 LGLLREMEQDWPFFNTRISMLEMVYSKAEPNLARYYEQCLVPEALHHLGV 804

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                     LR++     + +L + G   l+   P+ +  +RLR++Yi  Ln +qA
  gi|1197733   805 TLRERLALGVEAVLALTGEDSLMAHTPWNRESVRLRNPYIDPLNFLQAEL 854

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                  E+   + e v+L             L+
  gi|1197733   855 LGRTR-----------------REE--TPSESVQLA------------LM 873

                    LtmKGiAAGmqntG<-*
                    Lt+ G+AAGm ntG
  gi|1197733   874 LTIAGVAAGMRNTG    887

gi|262170106|ref|ZP_06037795.1|: domain 1 of 1, from 1 to 876: score 753.3, E = 1.7e-223
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  +  +L    vs           +l + L+  +q   G+ +
  gi|2621701     1    -MNEKYAALK-SNVS-----------MLGRLLgQTIQAADGDVILAK 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls        + + e L   +  L       vA+a+   LnL n
  gi|2621701    35 VETIRKLSKSARAGNQADR-ELLIEEIKNLPNHQLTPVARAFNQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R   +         E +A     i   + kL  k   s  +
  gi|2621701    84 IAEQYHTISRHCESHVN------ELDA-----IGSLFAKLAQKS-VSKFD 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      +A++   ++LvltAHPt   RR ++ K  +i  CL++L   D+ + ++
  gi|2621701   122 TAQAIRDLNIELVLTAHPTEITRRTMINKLVKINECLSKLELSDLSPKER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +  +  L   i   +  D iR  +PtP DE + G + +   +W+ vP FL
  gi|2621701   172 HKTERRLEQLIAQSWHSDVIRQQRPTPLDEAKWGFAVVENSLWHAVPEFL 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R  D  +K   + E lP d+  ++FssWmGGDRDG nP vt  +tR+v L
  gi|2621701   222 RELDEQVKSY-LGEGLPIDARPVHFSSWMGGDRDG-NPFVTHTITREVLL 269

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa lY+  + +L+ Elsm +Cn+ +R+ A E       +
  gi|2621701   270 LSRWKAADLYLTDINELVSELSMTKCNEAVRALAGE-------E------ 306

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR iL  +R  L  t E     L      ++  A
  gi|2621701   307 ---------HEPYRAILKPIRSLLQETIEILDAKLNG--QKLAVKAPLQT 345

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     ++  EPL  CY+sL eCG  viADGsLLD LR +  FG+ Lv+LD+RqE
  gi|2621701   346 ADQLWEPLYACYQSLHECGMGVIADGSLLDTLRRIKAFGVHLVRLDVRQE 395

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+ +v+  +t+HL+iG Y +WsE+ +  +L +EL  KRPLl+ D
  gi|2621701   396 SSRHAEVISELTRHLGIGDYNQWSEQDKIAFLTTELNSKRPLLPRDWQPS 445

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                      vk+vld+ +++A    D+FGaY+isma + sDvLAv LL  E g
  gi|2621701   446 PQVKEVLDTCKIIAAQSKDAFGAYVISMARTASDVLAVHLLLQEAGCPYR 495

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    + v PLFE L DL+ A   + +L  iD Y+  i+  q vm+GYsDs KDA
  gi|2621701   496 MDVCPLFETLDDLNNAESVIRQLMNIDLYRGFIQNHQMVMIGYSDSAKDA 545

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y+A E ++Kv  + G+ L+lFHGRGGt+GRGG P H A+Ls
  gi|2621701   546 GVMAAGWAQYRAMEALVKVGEEAGIELTLFHGRGGTIGRGGAPAHAALLS 595

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
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                    qPP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP
  gi|2621701   596 QPPKSLKGGLRVTEQGEMIRFKLGLPEVAVNSFNMYASAILEANLLPPPE 645

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EWR Lm+ +  +    YR vv  EP Fv YFR AtPElE Gk+ +Gs
  gi|2621701   646 PKNEWRALMDILSEISCNAYRKVVRGEPDFVPYFRQATPELELGKLPLGS 695

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR P GG+esLRAiPWiF+W q R  LP WLG G A + Ai+   +
  gi|2621701   696 RPAKRNPTGGVESLRAIPWIFSWSQNRLILPAWLGAGEAIQIAINEGHQA 745

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv   L+P G+
  gi|2621701   746 L--LEEMCREWPFFSTRLGMLEMVYTKCSVSIARHYDERLVEPTLRPLGE 793

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR++ +   + +L +     l+  DP+ +  +RLR+ Yi  Ln++qA
  gi|2621701   794 KLRAQLQQDIKVVLNVENNENLMQSDPWGQESIRLRNIYIEPLNMLQAEL 843

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R  +                +                aP LE+ L+
  gi|2621701   844 LYRTRQSEL---------------P----------------APELEEALM 862

                    LtmKGiAAGmqntG<-*
                    +t+ GiAAGm ntG
  gi|2621701   863 VTIAGIAAGMRNTG    876

gi|153002595|ref|YP_001368276.1|: domain 1 of 1, from 11 to 889: score 753.3, E = 1.8e-223
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        + A LR      vs           +l + L+D +    G++  E
  gi|1530025    11    DMYASLRS----NVS-----------MLGQILgDTMRTHLGDSFLEK 42

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     l+ +   + D    e +   Lt+L   + +  Aka+   LnLAn
  gi|1530025    43 VEQIRKLAKDSR-RGDQAAREQMLELLTALPDEELVPFAKAFNQFLNLAN 91

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    L E  +   R   ++                  +E  l ++
  gi|1530025    92 LSEQFHTISRNCDELVC----------VPDPVEQLLGRMLNGR-VDQTK 129

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + + LK   +DLvltAHPt   RR L+qK a i  CL+      +   ++
  gi|1530025   130 MLDCLKTLDIDLVLTAHPTEISRRTLIQKYAAIVDCLTEQENDQLSDRER 179

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + +   L   i   + t EiRR +PtP DE R G+s i E +W+ vP FL
  gi|1530025   180 QQISLRLRQLIAQIWHTNEIRRERPTPVDEARWGLSTIEESLWHAVPDFL 229

                    RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R  +D   +  G    lP d+  ++FssWmGGDRDG nP vt  vt +v
  gi|1530025   230 RQLnDQVQQRTG--QQLPIDIAPVRFSSWMGGDRDG-NPFVTAKVTQEVL 276

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                       R  Aa l++  +  L+ Elsm   ndEL++       t  +
  gi|1530025   277 DRNRHAAARLFLKDIVLLVGELSMEEANDELKA------YTNNSC----- 315

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                              EPYR +L  +R +L  t +     +     e+
  gi|1530025   316 -----------EPYRHVLRSIRQRLRDTIDYLNARIEGHNPEVDKSSLIW 354

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  +   PLE+ YksL +CG + iA G LLD+LR    FG+ + +LDiRq
  gi|1530025   355 QESDLKAPLEMLYKSLTDCGMRLIANGLLLDILRRLACFGIHMLRLDIRQ 404

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    ++ R+ Dvl  +t+ L++G +  W E  +q +Ll EL+ +RPL++s
  gi|1530025   405 DASRHSDVLAELTRYLGMGDFNHWDETEKQAFLLRELSNRRPLIPSNWQP 454

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      +v++vl++ r +A  P  + G+Y+isma  PsDvL v LL +E g  +
  gi|1530025   455 SADVAEVLNTCRLIAKHPAKALGSYVISMAGKPSDVLTVLLLLKETGCSH 504
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                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    ++rvvPLFE L DL+ A A +  L  iDWY+    G qevm+GYsDs KD
  gi|1530025   505 PMRVVPLFETLSDLNNAAACITDLLDIDWYRGYTKGMQEVMIGYSDSAKD 554

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++AAW  Y AqE ++ v K+ GvKL+lFHGRGG +GRGGGP H AiL
  gi|1530025   555 AGVMAAAWAQYHAQEQLVAVCKQAGVKLTLFHGRGGSIGRGGGPAHKAIL 604

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A LE  + PP
  gi|1530025   605 SQPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVLEATLLPPP 654

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk EWR+ m+++A      YR +v  EP Fv YFR AtPE+E Gk+ +G
  gi|1530025   655 EPKQEWRDCMQRIAEESVGAYRGIVRDEPDFVAYFRAATPEVELGKLPLG 704

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+  GGiesLRAiPWiFaW q R  LP WLG G A + A ++
  gi|1530025   705 SRPAKRRVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALQAACERG-- 752

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     +  L+Em +eWPFF   + +lEmv+AK +P +A  y+  Lv  +L+  G
  gi|1530025   753 EMGLLQEMEREWPFFSTRISMLEMVYAKAEPNLARYYETCLVPKDLHHLG 802

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    + LR++     + +L++     l+   P+ +  ++LR++Yi  Ln +q
  gi|1530025   803 ETLRQRLDLGIKVVLELTKSDSLMAHTPWNRESVKLRNPYIDPLNFLQTE 852

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R             KE  + +   a e v+L             L
  gi|1530025   853 LLARTR-------------KETTETP---ASEHVQLA------------L 874

                    iLtmKGiAAGmqntG<-*
                    +Lt+ G+AAGm ntG
  gi|1530025   875 MLTIAGVAAGMRNTG    889

gi|161511331|ref|NP_994414.2|: domain 1 of 1, from 1 to 878: score 752.9, E = 2.3e-223
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +  q  ++    vs          +L     D +++  Ge + + v
  gi|1615113     1    -MNEQYSAMR-SNVS----------MLGTLLGDTIKEALGEHILDRV 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       ++++ +EL + L  L   + + vA+a++  LnL n
  gi|1615113    36 ETIRKLSKSSRAGNEASR-QELLTTLQNLSNDELLPVARAFSQFLNLTNT 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +       +   hG+ a   +A     +   + +L  k   s +++
  gi|1615113    85 AEQYH-------SISPHGEAASNPEA-----LAQLFTRLKDKK-LSDQDM 121

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
  gi|1615113   122 RSAVDDLSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHNDLADYERN 171

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +   L   +   + tDEiR+ +P P DE + G + +   +W+GvP FLR
  gi|1615113   172 KIMRRLRQLVAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWEGVPAFLR 221

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         L n  +  RlP ++  i+F+sWmGGDRDG nP vt E+tR v LL
  gi|1615113   222 EFNEQLEN-SLDYRLPVEAVPIRFTSWMGGDRDG-NPNVTAEITRHVLLL 269

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    +R  A+ l++  +  L+ Elsm  C  ELR    El
  gi|1615113   270 SRWKATDLFLRDIQVLVSELSMSECTPELR----ELAGGEEVL------- 308

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             EPYR ++ +vR +L nt       L +G   ++
  gi|1615113   309 ---------EPYRQLMKNVRTQLTNTQAYLEARL-KGERVLPPHDLLVSN 348

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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                    ++  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+RqEs
  gi|1615113   349 DQLWEPLYACYQSLKACGMEIIANGQLLDTLRRVRCFGVPLVRIDVRQES 398

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     R+tD +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
  gi|1615113   399 TRHTDAIAELTRYLGLGDYESWSESDKQAFLVRELNSKRPLVPLKWEPSA 448

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E ++vl++ rv+AE P  s  aY+isma  PsDvLAv LL +E g   tL
  gi|1615113   449 ETQEVLETCRVIAEAPQGSIAAYVISMAKVPSDVLAVHLLLKEAGCPFTL 498

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDAG
  gi|1615113   499 PVAPLFETLDDLNNADDVMTQLLGIDWYRGLIQGKQMVMIGYSDSAKDAG 548

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Lsq
  gi|1615113   549 VMAASWAQYRAQDALIKTCEKAGITLTLFHGRGGSIGRGGAPAHAALLSQ 598

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP  P
  gi|1615113   599 PPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLALYAGAILEANLLPPPEP 648

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    k EW ++m+ +     + YR  v   P Fv YFR AtPElE Gk+ +GsR
  gi|1615113   649 KKEWIEVMDLLSDASCDMYRNYVRENPEFVRYFRAATPELELGKLPLGSR 698

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+P GG+esLRAiPWiFaWtq R  LP WLG GA  + Aid   + +
  gi|1615113   699 PAKRRPDGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQRAIDAGKQDV 748

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L  m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P G++
  gi|1615113   749 --LATMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVDKSLWPLGQQ 796

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRd+     + +L iA    l+   P++   + LR+ Y   Lnv+qA  L
  gi|1615113   797 LRDQLAADIKVVLAIANDDHLMADLPWIAESIALRNVYTDPLNVLQAELL 846

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     R R             +E+ d                    +E  L++
  gi|1615113   847 HRSRQ------------QEHPDAC-------------------VEQALMV 865

                    tmKGiAAGmqntG<-*
                    t+ G+AAGm ntG
  gi|1615113   866 TIAGVAAGMRNTG    878

gi|152987651|ref|YP_001346835.1|: domain 1 of 1, from 3 to 878: score 752.8, E = 2.4e-223
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        iDA LR          e++ +   LL D     + +  G+   + +
  gi|1529876     3    EIDARLR----------EDVHQLGELLGDT----IREQYGPAFLDKI 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E     A    +  ++  + L a L +L+ ++ + vA+a+   LnLAn+
  gi|1529876    36 -ERIRKGAKAARRGSAEGAQQLTATLDGLEESELLPVARAFNQFLNLANI 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +   RRR        F   a       +EE l +L   +  +P
  gi|1529876    85 AEQYHRIRRRRPNEPE--PFENLA-------LEELLGRLKDAG-HAPGQL 124

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L    ++LvltAHPt  +RR L+qK   i   La     D+ +e++
  gi|1529876   125 ARQLAGLEIELVLTAHPTEVARRTLIQKYDAITAQLATKDHADLLPEERS 174

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +   L R +   + tDEiR+ +PtP DE + G + i   +W+  P  LR
  gi|1529876   175 RIQRRLQRLVAEVWHTDEIRKVRPTPVDEAKWGFAVIEHSLWEALPNVLR 224

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     vD  L      ERlP  +  ++F+sWmGGDRDG nP vt  vtR+v LL
  gi|1529876   225 HVDEVLLR-STGERLPLSAAPLRFASWMGGDRDG-NPNVTAGVTREVLLL 272
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                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aR mAa lY+  ++ L  Elsm      L +R  +      +
  gi|1529876   273 ARWMAADLYLRDIDRLAAELSMQEASPALLARVGD------SA------- 309

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             EPYR +L + R++L  tR  +   LA  +   + e v  +
  gi|1529876   310 ---------EPYRALLKQLRERLRLTRSWTHQALAGEVP--AAEGVLEHN 348

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                     + +EPL LC  sL  CG  viADG+LLD LR   tFGL Lv+LD+Rq++
  gi|1529876   349 RDLVEPLQLCHESLHACGMGVIADGALLDCLRRAATFGLFLVRLDVRQDA 398

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     R+   l  it+ Le+GsY eW E  R E+Ll EL  +RPLl++
  gi|1529876   399 GRHAAALSEITEYLELGSYAEWDEKTRLEFLLEELNSRRPLLPAHYQPSA 448

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E ++vl + r +A  P  s G+Y+isma  PsDvLAv LL +E gv  ++
  gi|1529876   449 ETAEVLATCRAIAAAPPASLGSYVISMAGQPSDVLAVQLLLKESGVDWPM 498

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFE L DL+ A   +e+L  +  Y+ r+ G qevm+GYsDs KDAG
  gi|1529876   499 RVVPLFETLDDLDNAGPCMERLLTLPGYRSRLSGVQEVMIGYSDSAKDAG 548

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     l AAW  Y+AqE ++ + +++ v L lFHGRGGtvGRGGGP H AiLsq
  gi|1529876   549 TLTAAWAQYRAQEKLVEICRHHEVELLLFHGRGGTVGRGGGPAHAAILSQ 598

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  + G  Rvt qGE+i f FG  ++  + L  + AA LE  + PP +P
  gi|1529876   599 PPGSVAGRFRVTEQGEMIRFKFGLPDIAEQNLNLYLAAVLEATLMPPPAP 648

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                     P WR  m+++A  A   YR vv  +P FvEYFRlAtPE E G++ +GsR
  gi|1529876   649 EPAWRAQMDRLAKDALHAYRRVVRDDPQFVEYFRLATPEQELGRLPLGSR 698

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+  GG+esLRAiPWiFaWtqtR  LP WLG   A   Ai++    l
  gi|1529876   699 PAKRR-EGGVESLRAIPWIFAWTQTRLMLPAWLGWETALLNAIERGEGAL 747

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L  m + WPFF   +D+lEmv AK D  iA LyD+ Lv  eL+P G++
  gi|1529876   748 --LGQMRERWPFFTTRIDMLEMVLAKADADIARLYDERLVPLELRPLGRR 795

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRd        +L + G   lL      +  + +R+sY+  L  +qA  L
  gi|1529876   796 LRDLLSQAVRVVLGLTGQSLLLAHASETRESISVRNSYLDPLHLLQAELL 845

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     R              s+    +                   GLE  L++
  gi|1529876   846 AR--------------SRRCRGDA----------------CGGLEQALLV 865

                    tmKGiAAGmqntG<-*
                    t+ GiAAG+ ntG
  gi|1529876   866 TVAGIAAGLRNTG    878

gi|156935917|ref|YP_001439833.1|: domain 1 of 1, from 1 to 870: score 752.7, E = 2.7e-223
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                              GK                    D ++D  Ge++ + v
  gi|1569359     1    ---------MLGKLL----------------GDTIKDALGENILDRV 22

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       ++ + + L + L  L   + + vA+a++  LnLAn
  gi|1569359    23 ETIRKLSKSSRAGNEADR-QALLTTLQNLSNDELLPVARAFSQFLNLANT 71

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +      i+ k       Ea    E  i  tl+kL  + +     +
  gi|1569359    72 AEQYH-----SISPKG------EAASNPEI-IARTLRKLKDQPDINETAI 109

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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                    +A+   s +LvltAHPt   RR L+ K   + nCL qL  KD+   ++
  gi|1569359   110 RQAVESLSLELVLTAHPTEITRRTLIHKMVEVNNCLKQLDHKDIADYERN 159

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +LR
  gi|1569359   160 QIMRRLRQLIAQSWHTDEIRKNRPSPVDEAKWGFAVVENSLWEGVPNYLR 209

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         L    +  +lP d   ++F+sWmGGDRDG nP vt ++tR v LL
  gi|1569359   210 ELNEQLEA-HLDYKLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVLLL 257

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    +R  A+ l++  +  L+ Elsm  C d LR    E   t   +
  gi|1569359   258 SRWKATDLFLKDIQVLISELSMVECSDALR----EYVGTEGAQ------- 296

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                              EPYR +L   R +L  t       L +G      +   t+
  gi|1569359   297 ---------EPYRYLLKGLRAQLLATQAWLEARL-KGQKLPKPQGLLTQN 336

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+  EPL  CY sL  CG  +iA G LLD LR v  FG+ Lv++DiRqEs
  gi|1569359   337 EQLWEPLYACYESLVACGLGIIANGELLDTLRRVKAFGVPLVRIDIRQES 386

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+      +
  gi|1569359   387 TRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRQWEPSD 436

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                      ++vl++ +v+AE P  s  aY+isma +PsDvLAv LL +E g+  +L
  gi|1569359   437 NTREVLETCKVIAEAPKGSIAAYVISMAKTPSDVLAVHLLLKEAGIGFAL 486

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDAG
  gi|1569359   487 PVAPLFETLDDLNNANDVMTQLLNIDWYRGFIQGKQMVMIGYSDSAKDAG 536

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Lsq
  gi|1569359   537 VMAASWAQYQAQDALIKTCEKAGIALTLFHGRGGSIGRGGAPAHAALLSQ 586

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP  P
  gi|1569359   587 PPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLSLYTSAILEANLLPPPEP 636

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    k  WR++m+e+  +    YR  v     Fv YFR+AtPE E Gk+ +GsR
  gi|1569359   637 KAAWRHIMDELSDISCTMYRGYVRENNDFVPYFRSATPEQELGKLPLGSR 686

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA +  ++ D K
  gi|1569359   687 PAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQKVVE-DGKQ- 734

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lv  eL+P G++
  gi|1569359   735 DELETMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVKKELWPLGRE 784

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR+  +   + +L iA    l+   P++   + LR+ Y   Lnv+qA  L
  gi|1569359   785 LRQLLEADIKVVLDIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAELL 834

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     R R                A+E+ k+ad            P +E  L++
  gi|1569359   835 HRSR---------------LAEEEGKPAD------------PCVEQALMV 857

                    tmKGiAAGmqntG<-*
                    t+ G+AAGm ntG
  gi|1569359   858 TIAGVAAGMRNTG    870

gi|292825460|gb|EFF84201.1|: domain 1 of 1, from 4 to 893: score 752.6, E = 2.9e-223
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        i A LR               D  Ll   L++ L+   G+dL
  gi|2928254     4    QITAPLRE---------------DVRLLGNLLgETLKQHAGQDLFNQ 35
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                vqECYEls.AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                +     l++   +G+ +++K   L     +L   + + + +a++H Ln A
gi|2928254    36 IEQIRALAkGARDGQIEAEK--QLEQLFLGLKDEEILPLTRAFSHFLNFA 83

                nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                n+AE  ++   RR             +    + + E +K          +
gi|2928254    84 NIAEQYHVVRNRRQAEFD----EQVPNPNPLAPLFEKFKTQQISA----Q 125

                EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                  F+ +    ++LvltAHPt   RR L+qK   i  CL+ L  + +t+ +
gi|2928254   126 QLFQQICDLNIELVLTAHPTEVSRRTLIQKYDDITDCLSRLDQQKLTPRE 175

                KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                ++     L   i  A+ tDEiR  +PtP DE + G + i   +W+ vPKF
gi|2928254   176 RQQAIAVLKQLISSAWQTDEIRQHRPTPVDEAKWGFATIEQSLWNAVPKF 225

                LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                +R     L        lP d+  i+F+sWmGGDRDG nP vt  vt +v
gi|2928254   226 IRELNE-LTQQHCQKELPLDIAPIRFASWMGGDRDG-NPNVTHQVTQEVL 273

                LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                 L+R  Aa lY+  +E L +Els+  C +EL         t a
gi|2928254   274 WLSRWQAADLYLRDIENLRWELSIQSCSQEL---------TDALG----- 309

                YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                Y+         EPYR  L d R++L  tR      L +Gi     + + t
gi|2928254   310 YVH-------PEPYREYLRDTRERLKATRTWLGQRL-QGIEADDSNIIRT 351

                kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                k +e L PL LCY+sL +     iA G LLD++  v  FG+ L KLDiRq
gi|2928254   352 K-DELLAPLLLCYRSLMDRNLAEIANGQLLDFIYRVNCFGIELLKLDIRQ 400

                EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                Es R+   + Ait+ L++G + +W E+ Rq +L+ EL+ KRPLl+
gi|2928254   401 ESGRHRQAVSAITEYLGLGNFESWTEQARQNFLIQELQSKRPLLPKFFNE 450

                tE.......EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLq
                 E++  ++++v +v  ++r LAE P +s GaYiisma  PsDvLAv LLq
gi|2928254   451 PEgsliqhpDVLEVFATMRTLAEQPAESLGAYIISMAEYPSDVLAVLLLQ 500

                RECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvG
                +E g++++LrvvPLFE L DL+ A  +++ LF + WY+ +i+ K evm+G
gi|2928254   501 KEAGIQHPLRVVPLFETLKDLDGAAKTMDTLFNMHWYKQHIQAKHEVMIG 550

                YsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGG
                YsDs KDAG +sA W  Y+AqEE+  +AKk+G++L+lFHGRGG + RGG
gi|2928254   551 YSDSAKDAGFMSANWAQYRAQEELTAIAKKHGIQLTLFHGRGGSISRGGA 600

                PtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLE
                Pt  A+ sqPP  i G++Rvt qGE+i f FG E +  + L  +tAAtLE
gi|2928254   601 PTQQALFSQPPGSISGAIRVTEQGEMIRFKFGLEGIALQNLEIYTAATLE 650

                HGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElE
                  + PP  Pk EWR Lm++m       YR  v   P Fv Y R  tPElE
gi|2928254   651 ATLLPPPVPKQEWRALMNQMTDLSVQVYRQTVRENPNFVRYLRTVTPELE 700

                YGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKh
                   + +GsRPaKRk sGGiesLRAiPW+FaWtq R  LP WLG G A
gi|2928254   701 LQMLPLGSRPAKRKVSGGIESLRAIPWVFAWTQIRLMLPAWLGTGTAINQ 750

                AidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva
                  ++  K    L Em ++WP+F   +D+lEmv  K D  iA  y+  L
gi|2928254   751 VHEQHKK---TLDEMLEQWPYFQTLIDMLEMVLSKSDADIALYYESHLTQ 797

                E.eLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYit
                +++Lk  G +LR++ +   d LL++ G   lL     L q + +R +Y+
gi|2928254   798 DqDLKVLGVELRQRLQNAVDTLLRLKGESKLLSNNEVLDQSMQVRKPYLL 847

                tLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpterv
                 L  +qA  +KR R               y +E               +
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  gi|2928254   848 PLHLLQAELMKRRR--------------VYLAEH------------QTEH 871

                   aPGLEDtLiLtmKGiAAGmqntG<-*
                   +P ++  L++ + GiAAG+ ntG
  gi|2928254   872 SP-VDHALMVSIAGIAAGLRNTG    893

gi|24371872|ref|NP_715914.1|: domain 1 of 1, from 3 to 881: score 752.5, E = 3e-223
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       + A LR      vs           +l + L+D +    G++  E
  gi|2437187     3    DMYASLRS----NVS-----------MLGQILgDTMRTHLGDSFLEK 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     l+ +   + D    e +   Lt+L   + +  Aka+   LnLAn
  gi|2437187    35 VEQIRKLAKDSR-RGDEAAREQMLELLTALPDEELVPFAKAFNQFLNLAN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   L E  +   R   ++                 +E  l ++
  gi|2437187    84 LSEQFHTISRNCDELVC-----------VPDPVEQLLGRMLNGR-VDQTK 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   + + LK   +DLvltAHPt   RR L+qK a i  CLa      +   ++
  gi|2437187   122 MLDCLKTLDIDLVLTAHPTEISRRTLIQKYAAIVDCLAEQENNQLSDRER 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   + +   L   i   + t EiRR +PtP DE R G+s i E +W+ vP FL
  gi|2437187   172 QQINLRLRQLIAQIWHTNEIRRERPTPVDEARWGLSTIEESLWHAVPDFL 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   R     ++       lP d+  ++FssWmGGDRDG nP vt  vt +v
  gi|2437187   222 RQLNDQVQE-RTGQQLPIDIAPVRFSSWMGGDRDG-NPFVTAKVTQEVLD 269

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                     R  Aa l++  +  L+ Elsm   ndEL++       t  +
  gi|2437187   270 RNRHAAARLFLKDIVLLVGELSMEEANDELKA------YTNNSC------ 307

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                             EPYR +L   R KL  t +     +     e+       +
  gi|2437187   308 ----------EPYRFVLRSLRQKLRDTIDYLNARIEGHNPEVDKSTLIWQ 347

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     +   PLE+ YksL +CG + iA G LLD+LR    FG+ + +LDiRq+
  gi|2437187   348 ESDLKAPLEMLYKSLYDCGMRLIANGLLLDILRRLACFGIHMLRLDIRQD 397

                   seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                   + R+ Dvl  +t+ L++G +  W E  +q +Ll EL+ +RPL++s
  gi|2437187   398 AGRHCDVLAELTRYLGMGDFNHWDETEKQAFLLRELSNRRPLIPSNWQPS 447

                   EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    +v++vl++ r +A  P  + G+Y+isma  PsDvL v LL +E g  ++
  gi|2437187   448 ADVAEVLNTCRLIAKHPAKALGSYVISMASKPSDVLTVLLLLKETGCTHP 497

                   LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                   +rvvPLFE L DL+ A A +  L  iDWY+    G qevm+GYsDs KDA
  gi|2437187   498 MRVVPLFETLSDLNNAAACITDLLDIDWYRGYTKGMQEVMIGYSDSAKDA 547

                   GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                   G ++AAW  Y+AqE ++ v  + GvKL+lFHGRGG +GRGGGP H AiLs
  gi|2437187   548 GVMAAAWAQYRAQEQLVAVCNQAGVKLTLFHGRGGSIGRGGGPAHKAILS 597

                   qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                   qPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A LE  + PP
  gi|2437187   598 QPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVLEATLLPPPE 647

                   PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                   Pk EWR+ me++A      YR +v  EP Fv YFR AtPE+E Gk+ +Gs
  gi|2437187   648 PKQEWRNCMERIAEESVSAYRGIVREEPDFVAYFRAATPEVELGKLPLGS 697

                   RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                   RPaKR+  GGiesLRAiPWiFaW q R  LP WLG G A + A ++
  gi|2437187   698 RPAKRRVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALQAACQRG--E 745
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                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    +  L++m +eWPFF   + +lEmv+AK +P +A  y+  Lv+ +L+  G+
  gi|2437187   746 IGLLQDMEREWPFFSTRISMLEMVYAKAEPNLARYYETCLVSTNLHHLGE 795

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                     LR++     + +L++     l+   P+ +  ++LR++Yi  Ln +q
  gi|2437187   796 TLRQRLDLGIKVVLELTKSDTLMAHTPWNRESVKLRNPYIDPLNFLQTEL 845

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R             KE  + +   a e v+L            L+
  gi|2437187   846 LARTR-------------KETSETP---ASEHVQLA------------LM 867

                    LtmKGiAAGmqntG<-*
                    Lt+ G+AAGm ntG
  gi|2437187   868 LTIAGVAAGMRNTG    881

gi|117922338|ref|YP_871530.1|: domain 1 of 1, from 11 to 889: score 752.5, E = 3.1e-223
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        + A LR      vs           +l + L+D +    G++  E
  gi|1179223    11    DMYASLRS----NVS-----------MLGQILgDTMRTHLGDSFLEK 42

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     l+ +   + D    e +   Lt+L   + +  Aka+   LnLAn
  gi|1179223    43 VEQIRKLAKDSR-RGDEAAREQMLELLTALPDEELVPFAKAFNQFLNLAN 91

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    L E  +   R   ++                +E  l ++
  gi|1179223    92 LSEQFHTISRNCDELVC-----------VPDPVEQLLGRMLNSR-IDQTK 129

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + + LK   +DLvltAHPt   RR L+qK a i  CLa      +   ++
  gi|1179223   130 MLDCLKTLDIDLVLTAHPTEISRRTLIQKYAAIVDCLAEQENNQLSDRER 179

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + +   L   i   + t EiRR +PtP DE R G+s i E +W+ vP FL
  gi|1179223   180 RQINLRLRQLIAQIWHTNEIRRERPTPVDEARWGLSTIEESLWHAVPDFL 229

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R     ++       lP d+  ++FssWmGGDRDG nP vt  vt +v
  gi|1179223   230 RQLNDQVQD-RTGQQLPIDIAPVRFSSWMGGDRDG-NPFVTAKVTQEVLD 277

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                      R  Aa l++  +  L+ Elsm   n+EL +       t  +
  gi|1179223   278 RNRHAAARLFLKDIVLLVGELSMEEANSELMA------YTNNSC------ 315

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR +L   R KL  t +     +     e+       +
  gi|1179223   316 ----------EPYRFVLRSLRQKLRDTIDYLNARIEGHNPEVDKSTLIWQ 355

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      +   PLE+ YksLC+CG + iA G LLD+LR    FG+ + +LDiRq+
  gi|1179223   356 ESDLKAPLEMLYKSLCDCGMRLIANGLLLDILRRLACFGIHMLRLDIRQD 405

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    + R+ Dvl  +t+ L++G +  W E  +q +Ll EL+ +RPL++s
  gi|1179223   406 AGRHCDVLAELTRYLGMGDFNHWDETEKQAFLLRELSNRRPLIPSNWQPS 455

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     +v++vl++ r +A  P  + G+Y+isma  PsDvL v LL +E g  ++
  gi|1179223   456 ADVAEVLNTCRLIAKHPAKALGSYVISMASKPSDVLTVLLLLKETGCTHP 505

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    +rvvPLFE L DL+ A   +  L  iDWY+    G qevm+GYsDs KDA
  gi|1179223   506 MRVVPLFETLSDLNNAAECITALLDIDWYRGYTKGMQEVMIGYSDSAKDA 555

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++AAW  Y+AqE ++ v K+ GvKL+lFHGRGG +GRGGGP H AiLs
  gi|1179223   556 GVMAAAWAQYRAQEQLVAVCKQAGVKLTLFHGRGGSIGRGGGPAHKAILS 605

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A LE  + PP
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  gi|1179223   606 QPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVLEATLLPPPE 655

                   PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                   Pk EWR+ me++A      YR +v  EP Fv YFR AtPE+E Gk+ +Gs
  gi|1179223   656 PKQEWRNCMERIAEESVSAYRGIVREEPDFVPYFRAATPEVELGKLPLGS 705

                   RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                   RPaKR+  GGiesLRAiPWiFaW q R  LP WLG G A + A ++
  gi|1179223   706 RPAKRRVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALQAACQRG--E 753

                   lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                   +  L++m +eWPFF   + +lEmv+AK +P +A  y+  Lv  +L+  G+
  gi|1179223   754 MGLLQDMEREWPFFSTRISMLEMVYAKAEPNLARYYETCLVPTNLHHLGE 803

                   sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    LR++     + +L++     l+   P+ +  ++LR++Yi  Ln +q
  gi|1179223   804 TLRQRLDLGIKVVLELTKSDTLMAHTPWNRESVKLRNPYIDPLNFLQTEL 853

                   LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                   L R R             KE  + +   a e v+L             L+
  gi|1179223   854 LARTR-------------KETTEAP---ASEHVQLA------------LM 875

                   LtmKGiAAGmqntG<-*
                   Lt+ G+AAGm ntG
  gi|1179223   876 LTIAGVAAGMRNTG    889

gi|170724697|ref|YP_001758723.1|: domain 1 of 1, from 3 to 878: score 752.4, E = 3.4e-223
                   *->siDAqLRlLvP..GKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                       + A LR  v + G++    + i+    L D FLD +     e+++
  gi|1707246     3    DMYASLRSNVGtlGQIL--GETIRTN--LDDPFLDKI-----EQIRQ 40

                   avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                            A    + D    eE+   L +L   + +  Aka+   LnLA
  gi|1707246    41 L--------AKSSRQGDEASREEMLKLLAALPDDELVPFAKAFNQFLNLA 82

                   nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                   n+AE  +   R   ++                D  E l   vl  n   +
  gi|1707246    83 NIAEQFHTISRNCDELVC------------VPDPVEQLLGRVLSSNIEQD 120

                   EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    + + L+n  +DLvltAHPt   RR L+qK a +   La L    +t  +
  gi|1707246   121 KMLDCLQNLDIDLVLTAHPTEISRRTLIQKYASVVDSLAALENPLLTERE 170

                   KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                   Kk     L   i   + t EiR  +PtP DE R G+s i   +W+ +P F
  gi|1707246   171 KKQQHLRLRQLIAQIWHTNEIRHERPTPVDEARWGLSTIEVSLWQAIPDF 220

                   LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   LR     +        lP d+  ++FssWmGGDRDG nP vt  vt +v
  gi|1707246   221 LRQLNEQVEE-RTGKQLPIDIAPVRFSSWMGGDRDG-NPFVTAQVTQEVL 268

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                      R  Aa lY+  v  L+ +lsm   ndEL      l  t  ++
  gi|1707246   269 DRNRHTAARLYLKDVVLLVNDLSMEEANDEL------LALTNNSH----- 307

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                                EPYR +L  +R KL nt +     L     e+  + +
  gi|1707246   308 -----------EPYRDVLRGIRQKLRNTIDYLNERLEGHQPEVDKNSIIW 346

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   + ++   PL + YksL + G   iA G LLD+LR +  FG+ + +LDiRq
  gi|1707246   347 NEDDLKAPLMMLYKSLSDSGMSLIANGLLLDMLRRIACFGIHMLRLDIRQ 396

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   +++R+ Dv+  +t+ L++G +  W E+ +q +Ll EL+ KRPL++s
  gi|1707246   397 DAQRHCDVVAELTRYLGMGDFNHWDENEKQAFLLRELSSKRPLIPSNWQP 446

                   tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                    E+v++v+ + r +A  P  + G+Y+isma  PsDvL v LL +E g  +
  gi|1707246   447 SEDVAEVVSTCRLIATQPARALGSYVISMASKPSDVLTVLLLLKETGCPH 496
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                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    ++rvvPLFE L DL+ A   +  LF+iDWY+    G qevm+GYsDs KD
  gi|1707246   497 PMRVVPLFETLDDLNNASSCMSALFAIDWYRGYTKGHQEVMIGYSDSAKD 546

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++AAW  Y AqE ++ v ++  vKL+lFHGRGGt+GRGGGP H AiL
  gi|1707246   547 AGVMAAAWAQYHAQEQLVEVSRQADVKLTLFHGRGGTIGRGGGPAHEAIL 596

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A +E  + PP
  gi|1707246   597 SQPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVMEATLLPPP 646

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                    +PkPEWR  m+++A      YRs+v  EP Fv YFR AtPE+E Gk+ +G
  gi|1707246   647 APKPEWRACMQRLAEESVAAYRSIVREEPDFVAYFRAATPEVELGKLPLG 696

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+  GGiesLRAiPWiFaW q R  LP WLG G A + A   D
  gi|1707246   697 SRPAKRRVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALQAA--SDRG 744

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     +  L+Em ++WPFF+  + +lEmv+AK +P +A  y+  Lv E+L+  G
  gi|1707246   745 EMELLQEMEQKWPFFKTRISMLEMVYAKAEPNLAKYYETCLVPENLHHLG 794

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    + LR +     + +L +   + l+E  P+ +  + LR++Yi  Ln +qA
  gi|1707246   795 DALRGRLATGVKAVLALTQSQALMEHTPWNRESVTLRNPYIDPLNFMQAE 844

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R  + + t            n       v+L             L
  gi|1707246   845 LLARTRKDEVQST------------N-------VELA------------L 863

                    iLtmKGiAAGmqntG<-*
                    +Lt+ G+AAGm ntG
  gi|1707246   864 MLTIAGVAAGMRNTG    878

gi|146313662|ref|YP_001178736.1|: domain 1 of 1, from 1 to 883: score 752.1, E = 4e-223
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L+D ++D  Ge + +
  gi|1463136     1    -MNEQYSALR-SNVS-----------MLGKVLgDTIKDALGETILDR 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++ + +EL + L  L   + + vA+a++  LnLAn
  gi|1463136    35 VETIRKLSKSSRAGNEANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+ k       E+    E  i  tl+kL  + +   e
  gi|1463136    84 TAEQYH-----SISPKG------EGASNPEV-IARTLRKLKDQPELNEET 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K + +  CL qL  KD+   ++
  gi|1463136   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMGEVNSCLKQLDNKDIVDYER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|1463136   172 NQLMRRLRQLIAQSWHTDEIRKYRPSPVDEAKWGFAVVENSLWEGVPNYL 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G   RlP d   ++F+sWmGGDRDG nP vt E+tR v
  gi|1463136   222 RELNEQLeENLGY--RLPVDFVPVRFTSWMGGDRDG-NPNVTAEITRHVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  A+ l++  +  L+ Elsm             +  t+
  gi|1463136   269 LLSRWKATDLFLKDIQILISELSM-------------VEATPELL----- 300

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                      E       tEPYR +L   R +L  t       L +G
  gi|1463136   301 --ELVGEAGATEPYRFLLKGLRGQLMATQAWLEARL-KGQRLPKPAGLLS 347

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    + E+  +PL  CYksL  CG  +iA G LLD LR v  FG+ Lv++D+Rq
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  gi|1463136   348 QNEQLWDPLYACYKSLQACGMGIIANGELLDTLRRVKCFGVPLVRIDVRQ 397

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|1463136   398 ESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRSWEP 447

                   tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                    EE  +vl++ + + + P  s  aY+isma +PsDvLAv LL +E g+
  gi|1463136   448 SEETSEVLNTCKAIVDAPKGSVAAYVISMAKTPSDVLAVHLLLKEAGISF 497

                   tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                   +L+v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|1463136   498 ALPVAPLFETLDDLNNANDVMTQLLNIDWYRGFIQGKQMVMIGYSDSAKD 547

                   AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                   AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|1463136   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                   sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                   sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|1463136   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLSLYTSAILEANLLPPP 647

                   sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                    Pk  WR++m+e+  +  + YR  v     Fv YFR+AtPE E Gk+ +G
  gi|1463136   648 EPKDAWRHIMDELSDISCDLYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                   sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                   sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA +  ++ D K
  gi|1463136   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQKVVE-DGK 746

                   nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                       L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lv  eL+  G
  gi|1463136   747 Q-TELETMCRDWPFFSTRLGMLEMVFSKVDLWLAEYYDQRLVKPELWALG 795

                   ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                   k+LR+  +   +++L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|1463136   796 KELRELLEGDIKIVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 845

                   tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    L R R               A+E+           +++  P +E  L
  gi|1463136   846 LLHRSRK--------------AEEE-----------GKEADPRVEQAL 868

                   iLtmKGiAAGmqntG<-*
                   ++t+ G+AAGm ntG
  gi|1463136   869 MVTIAGVAAGMRNTG    883

gi|226953287|ref|ZP_03823751.1|: domain 1 of 1, from 4 to 893: score 752.1, E = 4.1e-223
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       i A LR               D  Ll   L++ L+   G+dL
  gi|2269532     4    QITAPLRE--------------DVRLLGNLLgETLKQHAGQDLFNQ 35

                   vqECYEls.AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                   +     l++   +G+ +++K   L     +L   + + + +a++H Ln A
  gi|2269532    36 IEQIRALAkGARDGQIEAEK--QLEQLFLGLKDEEILPLTRAFSHFLNFA 83

                   nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                   n+AE  ++   RR             +    + + E +K          +
  gi|2269532    84 NIAEQYHVVRNRRQAEFD----EQVPNPNPLAPLFEKFKTQQISA----Q 125

                   EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                     F+ +    ++LvltAHPt   RR L+qK   i  CL+ L  + +t+ +
  gi|2269532   126 QLFQQICDLNIELVLTAHPTEVSRRTLIQKYDDITDCLSRLDQQKLTPRE 175

                   KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                   ++     L   i  A+ tDEiR  +PtP DE + G + i   +W+ vPKF
  gi|2269532   176 RQQAIAVLKQLISSAWQTDEIRQHRPTPVDEAKWGFATIEQSLWNAVPKF 225

                   LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   +R     L        lP d+  i+F+sWmGGDRDG nP vt  vt +v
  gi|2269532   226 IRELNE-LTQQHCQKALPLDIAPIRFASWMGGDRDG-NPNVTHQVTQEVL 273
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                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     L+R  Aa lY+  +E L +Els+  C +EL         t a
  gi|2269532   274 WLSRWQAADLYLRDIENLRWELSIQSCSQEL---------TDALG----- 309

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                    Y          EPYR  L d R++L  tR      L +Gi     + + t
  gi|2269532   310 YAH-------PEPYREYLRDTRERLKATRTWLGQRL-QGIEADDSNIIRT 351

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    k +e L PL LCY+sL +     iA G LLD++  v  FG+ L KLDiRq
  gi|2269532   352 K-DELLAPLLLCYRSLMDRNLAEIANGQLLDFIYRVNCFGIELLKLDIRQ 400

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+   + Ait+ L++G + +W E+ Rq +L+ EL+ KRPLl+
  gi|2269532   401 ESGRHRQAVSAITEYLGLGNFESWTEQARQNFLIQELQSKRPLLPKFFNE 450

                    tE.......EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLq
                     E++  ++++v +v  ++r LAE P +s GaYiisma  PsDvLAv LLq
  gi|2269532   451 PEgsliqhpDVLEVFATMRTLAEQPAESLGAYIISMAEYPSDVLAVLLLQ 500

                    RECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvG
                    +E g++++LrvvPLFE L DL+ A  +++ LF + WY+ +i+ K evm+G
  gi|2269532   501 KEAGIQHPLRVVPLFETLKDLDGAAKTMDTLFNMHWYKQHIQAKHEVMIG 550

                    YsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGG
                    YsDs KDAG +sA W  Y+AqEE+  +AKk+Gv+L+lFHGRGG + RGG
  gi|2269532   551 YSDSAKDAGFMSANWAQYRAQEELTAIAKKHGVQLTLFHGRGGSISRGGA 600

                    PtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLE
                    Pt  A+ sqPP  i G++Rvt qGE+i f FG E +  + L  +tAAtLE
  gi|2269532   601 PTQQALFSQPPGSISGAIRVTEQGEMIRFKFGLEGIALQNLEIYTAATLE 650

                    HGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElE
                      + PP  Pk EWR Lm++m       YR  v   P Fv Y R  tPElE
  gi|2269532   651 ATLLPPPVPKQEWRALMNQMTDLSVQVYRQTVRENPNFVRYLRTVTPELE 700

                    YGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKh
                       + +GsRPaKRk sGGiesLRAiPW+FaWtq R  LP WLG G A
  gi|2269532   701 LQMLPLGSRPAKRKVSGGIESLRAIPWVFAWTQIRLMLPAWLGTGTAINQ 750

                    AidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva
                      ++  K    L Em ++WP+F   +D+lEmv  K D  iA  y+  L
  gi|2269532   751 VHEQHKK---TLDEMLEQWPYFQTLIDMLEMVLSKSDADIALYYESHLTQ 797

                    E.eLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYit
                    +++Lk  G +LR++ +   d LL++ G   lL     L q + +R +Y+
  gi|2269532   798 DqDLKVLGVELRQRLQNAVDTLLRLKGESKLLSNNEVLDQSMQVRKPYLL 847

                    tLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpterv
                     L  +qA  +KR R               y +E               +
  gi|2269532   848 PLHLLQAELMKRRR--------------VYLAEH------------QTEH 871

                    aPGLEDtLiLtmKGiAAGmqntG<-*
                    +P ++  L++ + GiAAG+ ntG
  gi|2269532   872 SP-VDHALMVSIAGIAAGLRNTG    893

gi|116051684|ref|YP_789477.1|: domain 1 of 1, from 3 to 878: score 751.8, E = 5.1e-223
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        iDA LR          e++ +   LL D     + +  G+   + +
  gi|1160516     3    EIDARLR----------EDVHQLGELLGDT----IREQYGPRFLDKI 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E     A    +  ++  + L a L +L+  + + vA+a+   LnLAn+
  gi|1160516    36 -ELIRKGAKAARRGSAEGAQQLTATLDGLEEDELLPVARAFNQFLNLANI 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +     Ri++++      E +      +EE l +L   +  +P
  gi|1160516    85 AEQYH-----RIRRRR----PNEPEPFENLVLEELLGRLKDAG-HAPGQL 124

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L    ++LvltAHPt  +RR L+qK   i   La     D+ +e++
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  gi|1160516   125 ARQLAGLEIELVLTAHPTEVARRTLIQKYDAITAQLAAKDHADLLPEERS 174

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +   L R +  A+ tDEiR+ +PtP DE + G + i   +W+  P  LR
  gi|1160516   175 RIQQRLQRLVAEAWHTDEIRKVRPTPVDEAKWGFAVIEHSLWQALPNVLR 224

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     vD  L      ERlP  +  ++F+sWmGGDRDG nP vt  vtR+v LL
  gi|1160516   225 HVDEVLLR-STGERLPLTAAPLRFASWMGGDRDG-NPNVTASVTREVLLL 272

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aR mAa lY+  ++ L  Elsm      L +R  +      +
  gi|1160516   273 ARWMAADLYLRDIDRLAAELSMQQASPQLLARVGD------SA------- 309

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             EPYR +L + R++L  tR  +   LA  +   + e v  +
  gi|1160516   310 ---------EPYRALLKQLRERLRVTRNWTHQALAGEVP--AAEGVLEHN 348

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                     + +EPL LC  sL  CG  viADG+LLD LR   tFGL Lv+LD+Rq+s
  gi|1160516   349 RDLVEPLQLCHESLHACGMGVIADGALLDCLRRAATFGLFLVRLDVRQDS 398

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     R+   l  it+ Le+GsY eW E  R E+Ll EL  +RPLl++
  gi|1160516   399 ARHAAALSEITEYLELGSYDEWDEKTRLEFLLEELNSRRPLLPAHYQPSA 448

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    + ++vl + r +A  P  s G+Y+isma  PsDvLAv LL +E gv  ++
  gi|1160516   449 DTAEVLATCRAIAAAPPASLGSYVISMAGQPSDVLAVQLLLKESGVDWPM 498

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFE L DL+ A   +e+L  +  Y+ r+ G qevm+GYsDs +DAG
  gi|1160516   499 RVVPLFETLDDLDNAGPCMERLLTLPGYRSRLSGVQEVMIGYSDSARDAG 548

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     l AAW  Y+AqE ++ + ++  v L lFHGRGGtvGRGGGP H AiLsq
  gi|1160516   549 TLTAAWAQYRAQEKLVEICRQQEVELLLFHGRGGTVGRGGGPAHAAILSQ 598

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  + G  Rvt qGE+i f FG  ++  + L  + AA LE  + PP +P
  gi|1160516   599 PPGSVAGRFRVTEQGEMIRFKFGLPDIAEQNLNLYLAAVLEATLMPPPAP 648

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                     P WR  m+++A  A   YR vv  +P FvEYFRlAtPE E G++ +GsR
  gi|1160516   649 EPAWRAQMDRLAKDALLAYRRVVRDDPQFVEYFRLATPEQELGRLPLGSR 698

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+  GG+esLRAiPWiFaWtqtR  LP WLG   A   Ai++    l
  gi|1160516   699 PAKRR-EGGVESLRAIPWIFAWTQTRLMLPAWLGWETALLNAIERGEGAL 747

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L  m ++WPFF   +D+lEmv AK D  iA LyD+ Lv  eL+P G++
  gi|1160516   748 --LGQMREQWPFFTTRIDMLEMVLAKADADIARLYDERLVPLELRPLGRR 795

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRd        +L + G   lL      +  + +R+sY+  L  +qA  L
  gi|1160516   796 LRDLLSQAVRVVLGLTGQSLLLAHASETRESISVRNSYLDPLHLLQAELL 845

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     R             s+    +                    GLE  L++
  gi|1160516   846 AR--------------SRRCQGDA----------------CGGLEQALLV 865

                    tmKGiAAGmqntG<-*
                    t+ G+AAG+ ntG
  gi|1160516   866 TVAGVAAGLRNTG    878

gi|124548514|ref|ZP_01707155.1|: domain 1 of 1, from 11 to 889: score 751.6, E = 5.7e-223
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        + A LR      vs           +l + L+D +    G++  E
  gi|1245485    11    DMYASLRS----NVS-----------MLGQILgDTMRTHLGDSFLEK 42
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                vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                v     l+ +   + D    e +   Lt+L   + +  Aka+   LnLAn
gi|1245485    43 VEQIRKLAKDSR-RGDQAAREQMLELLTALPDEELVPFAKAFNQFLNLAN 91

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                L E  +   R   ++                 +E  l ++        +
gi|1245485    92 LSEQFHTISRNCDELVC-----------VPDPVEQLLGRMLNGR-VDQAK 129

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                + + LK   +DLvltAHPt   RR L+qK a i  CL+      +   ++
gi|1245485   130 MLDCLKTLDIDLVLTAHPTEISRRTLIQKYAAIVDCLTEQENDQLSDRER 179

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                + +   L   i   + t EiRR +PtP DE R G+s i E +W+ vP FL
gi|1245485   180 QQISLRLRQLIAQIWHTNEIRRERPTPVDEARWGLSTIEESLWHAVPDFL 229

                RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                R  +D   +  G    lP d+  ++FssWmGGDRDG nP vt  vt +v
gi|1245485   230 RQLnDQVQQRTG--QQLPIDIAPVRFSSWMGGDRDG-NPFVTAKVTQEVL 276

                LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                   R  Aa l++  +  L+ Elsm   ndEL++       t  +
gi|1245485   277 DRNRHAAARLFLKDIVLLVGELSMEEANDELKA------YTNNSC----- 315

                YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                           EPYR +L  +R +L  t +     +     e+
gi|1245485   316 -----------EPYRHVLRSIRQRLRDTIDYLNARIEGHNPEVDKSSLIW 354

                kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                +  +   PLE+ YksL +CG + iA G LLD+LR    FG+ + +LDiRq
gi|1245485   355 QESDLKAPLEMLYKSLTDCGMRLIANGLLLDILRRLACFGIHMLRLDIRQ 404

                EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                ++ R+ Dvl  +t+ L++G +  W E  +q +Ll EL+ +RPL++s
gi|1245485   405 DASRHSDVLAELTRYLGMGDFNHWDETEKQAFLLRELSNRRPLIPSNWQP 454

                tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                  +v++vl++ r +A  P  + G+Y+isma  PsDvL v LL +E g  +
gi|1245485   455 SADVAEVLNTCRLIAKHPAKALGSYVISMAGKPSDVLTVLLLLKETGCSH 504

                tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                ++rvvPLFE L DL+ A A +  L  iDWY+    G qevm+GYsDs KD
gi|1245485   505 PMRVVPLFETLSDLNNAAACITDLLDIDWYRGYTKGMQEVMIGYSDSAKD 554

                AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                AG ++AAW  Y AqE ++ v K+ GvKL+lFHGRGG +GRGGGP H AiL
gi|1245485   555 AGVMAAAWAQYHAQEQLVAVCKQAGVKLTLFHGRGGSIGRGGGPAHKAIL 604

                sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                sqPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A LE  + PP
gi|1245485   605 SQPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVLEATLLPPP 654

                sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                 Pk EWR+ m+++A      YR +v  EP Fv YFR AtPE+E Gk+ +G
gi|1245485   655 EPKQEWRNCMQRIAEESVGAYRGIVRDEPDFVAYFRAATPEVELGKLPLG 704

                sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                sRPaKR+  GGiesLRAiPWiFaW q R  LP WLG G A + A ++
gi|1245485   705 SRPAKRRVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALQAASERG-- 752

                nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                 +  L++m +eWPFF   + +lEmv+AK +P +A  y+  Lv  +L+  G
gi|1245485   753 EMGLLQDMEREWPFFSTRISMLEMVYAKAEPNLARYYETCLVPKDLHHLG 802

                ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                + LR++     + +L++     l+   P+ +  ++LR++Yi  Ln +q
gi|1245485   803 ETLRQRLDLGIKVVLELTKSDSLMAHTPWNRESVKLRNPYIDPLNFLQTE 852

                tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                 L R R             KE  + +   a e v+L             L
gi|1245485   853 LLARTR-------------KETTETP---ASEHVQLA------------L 874
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                  iLtmKGiAAGmqntG<-*
                  +Lt+ G+AAGm ntG
  gi|1245485   875 MLTIAGVAAGMRNTG    889

gi|223670909|dbj|BAH22704.1|: domain 1 of 1, from 73 to 1011: score 751.5, E = 6.4e-223
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                     s +    l +       e+    +  +    LD L  L   ++ E+
  gi|2236709    73    SSEPEGHLPAGSPLGRPEQQPALERAMSSVMLDGLPRL-PASVTEML 118

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   E   l  +      ++ L  +  +   +d +  +  A+ +  ++  AnL
  gi|2236709   119 TEVGSLPQD-----AAESLRVMSERAGNMDASTLLSSAQLLGELMSQANL 163

                  AEEvelAyRRRikkkkhGDFaDE...asAttEsDiEEtlKkLvlklnKsP
                  A   +     R  ++     +++++++           +  L   + ++
  gi|2236709   164 ALAQQTVRAWRANLRADAGCTEDtstGAVVGNQTFRMAFDALLASG-RAA 212

                  eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv.tv
                  +E+ +A+  q +++vltAHPt + RR +L+K+  i   L q     v t+
  gi|2236709   213 AEIRDAISEQEIEIVLTAHPTEAQRRTILKKHQQIVALLGQHDKGTVlTP 262

                  eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                   +  EL+EA+ RE  AA+Rt  +RR++Pt   E R G+  i Et W+ vP
  gi|2236709   263 GEVTELEEAISREQLAAWRTSNVRRSKPTAEGEARNGLMVIEETCWDAVP 312

                  KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                     RR D AL+ iG    +PYd  ++k s WmGGDRDG nP vt   t
  gi|2236709   313 EHYRRLDRALRRIG-QPPVPYDKAIVKVSTWMGGDRDG-NPNVTAVTTGH 360

                  vCLLaRmmAanlYisqvEDLmFElsmWR.CndELRvRAEEl...yrtaar
                  v  L R  Aa lY   vE L++Els   +   E+R+  E ++++ +
  gi|2236709   361 VLCLQRARAAELYHKEVEKLLYELSHTGpVSAEMRAAVEQItgpRQPGVH 410

                  dkvvKy...YiEFWKq...vPPtEPYRviLGdvRDKLYntRERaRHLLAt
                   kv  ++++Y   W  +++    EPYRv+L + R +LY tR +   +
  gi|2236709   411 RKVFPHedgYGLAWTFqtgCQEDEPYRVLLMALRRRLYRTRVKMEEVYLG 460

                  GiseisEeA.vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvs
                    s   E+A+v t   + L PLEL Y+sL   GD+v+A G LLDlLR v
  gi|2236709   461 HDSGADEDAdVLTSQAQLLAPLELMYRSLVTVGDRVLANGTLLDLLRRVR 510

                  tFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaEL
                  tFG+ L K+DiRqEs+R+ + +DAit+ L++G Y eW Ee R  WL aEL
  gi|2236709   511 TFGICLAKMDIRQESDRHSEAIDAITRALGLGRYLEWDEEARIAWLSAEL 560

                  kGKRPLlgsD..LPktEEvkDvldafrvLAELPiDsFGaYiismataPsD
                     RPL++  ++L   E vk+vl +f  LA LP ++ GaY isma + sD
  gi|2236709   561 VSPRPLIPDSgtLAADERVKEVLATFALLATLPPECLGAYCISMARSASD 610

                  vLAvELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                  vLAv LLq   gvk ++rv PLFE   DL+ AP  v++LFs+  Y+  i
  gi|2236709   611 VLAVRLLQVKSGVKSPMRVAPLFETREDLQNAPRVVARLFSVAAYKGAIG 660

                  GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRG
                  G  evm+GYsDs KDAG+++  W L +A E i    +  Gv++  FHGRG
  gi|2236709   661 GFHEVMLGYSDSSKDAGKFASLWELHVAMEKILEAGRAAGVRINFFHGRG 710

                  GtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLq
                  G +GRGGGP HLA+LsqP   i G+ RvtvqGE i       +L  ++ q
  gi|2236709   711 GSIGRGGGPLHLALLSQPAGSIAGAYRVTVQGEQIQAFLASTELAVHTFQ 760

                  RFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvK..EPRFvE
                   ++   LEH + PP  P    R+Lm+++A      + + v+++++  F
  gi|2236709   761 SYAISVLEHTISPPKLPTDAQRELMQQLADASAKAFQAQVYQseDGIFSR 810

                  YFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPv
                  YF  AtP      mn+GsRPaKRk +GGie+LRAiPW+FaWtqtR HLPv
  gi|2236709   811 YFHAATPTSALASMNLGSRPAKRKAAGGIETLRAIPWVFAWTQTRLHLPV 860

                  WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
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                    WLG GAA    i      l  L++ Y +WPFFR  +DL+E+   K +P +
  gi|2236709   861 WLGCGAALAERIAGG--GLAELRDAYSTWPFFRGLVDLMELELSKAEPAV 908

                    AaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                       yD  L + +L+  G+ LR      k  ++++AGH  lLE  P  Kq
  gi|2236709   909 SEYYDGRLCTPDLRAVGDGLRSALAQAKAAVMEVAGHALLLENHPLAKQS 958

                    lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                      LR++Y+ tL  +q   + R             l KE  d +
  gi|2236709   959 FGLRQPYLLTLHAIQGEVMAR-------------LKKEPSDAE------- 988

                    vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     +L         L+D + +t++G+AAGmqntG
  gi|2236709   989 -RLA--------LDDAMTVTVQGVAAGMQNTG    1011

gi|237728069|ref|ZP_04558550.1|: domain 1 of 1, from 1 to 883: score 751.1, E = 8.3e-223
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L++ ++D  Ge++ +
  gi|2377280     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGENILDR 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       +  + +EL + L  L   + + vA+a++  LnLAn
  gi|2377280    35 VETIRKLSKSSRAGNEVNR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+ k       Ea    E  i  tl+kL  + n   +
  gi|2377280    84 TAEQYH-----SISPKG------EAASNPEV-IARTLRKLKEQPNLNDAT 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K + +  CL qL  KD+   ++
  gi|2377280   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMGEVNACLKQLDNKDLVDYER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|2377280   172 NQLMRRLRQLIAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWEGVPNYL 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R     L    +  +lP d   ++F+sWmGGDRDG nP vt ++tR v L
  gi|2377280   222 RELNEQLEE-HLGYKLPVDFVPVRFTSWMGGDRDG-NPNVTADITRHVLL 269

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  A+ l++  +  L+ Elsm     EL +   E       +
  gi|2377280   270 LSRWKATDLFLKDIQFLISELSMVDATPELMALVGE-------E------ 306

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vyt
                              EPYR ++   R +L  t       L      ++  A+  t
  gi|2377280   307 -------GAAEPYRYLMKTLRSRLMATQAWLEARLKG--EKLPKPAgLLT 347

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    + E+  +PL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|2377280   348 QNEQLWDPLYACYQSLQSCGMGIIANGELLDTLRRVKCFGVPLVRIDIRQ 397

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|2377280   398 ESTRHTEALGELTRYLGIGDYENWSEADKQAFLIRELNSKRPLLPRNWEP 447

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      + ++vld+ rv+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|2377280   448 SNDTREVLDTCRVIAEAPYGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 497

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|2377280   498 AMPVAPLFETLDDLNNADDVMSQLLNIDWYRGFIQGKQMVMIGYSDSAKD 547

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|2377280   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2377280   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLSLYTGAILEANLLPPP 647
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                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR++m+e+  +  E YR  v     Fv YFR+AtPE E Gk+ +G
  gi|2377280   648 EPKDSWRHIMDELSDISCELYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
  gi|2377280   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        L+ m ++WPFF   l +lEmvFAK D  +A  yD+ Lv  +L+P G
  gi|2377280   747 Q-SELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVKKDLWPLG 795

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                     +LR++     d +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|2377280   796 AELRQRLAADIDVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAE 845

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R               A+E+            ++   P +E  L
  gi|2377280   846 LLHRSR---------------LAEEQ-----------GNAPDPRVEQAL 868

                    iLtmKGiAAGmqntG<-*
                    ++t+ G+AAGm ntG
  gi|2377280   869 MVTIAGVAAGMRNTG    883

gi|145635078|ref|ZP_01790784.1|: domain 1 of 1, from 2 to 879: score 751.0, E = 8.7e-223
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           q        +s           +l +FL++ + D  Ged+ E
  gi|1456350     2    ---TQEYSTLRNNIS-----------MLGRFLgETINDAQGEDILEL 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls +     D  + + L   L s+     i vA+a++  LnL n
  gi|1456350    35 IENIRKLSRNSRAGDDKAR-QALLDTLGSISNENIIPVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R     +                + E +K+L  +   s eE
  gi|1456350    84 IAEQYQTISREHSLAQS-----------SSQSLSELFKRLKEQN-ASVEE 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v   +    ++LvltAHPt   RRsL+ K+  i  CL++L   D+t  ++
  gi|1456350   122 VHKTVEKLLIELVLTAHPTETTRRSLIHKHIEINKCLSKLEHHDLTEKER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      ++  L R i  A+ t EiR  +PtP DE + G + +   +W+ vP FL
  gi|1456350   172 NIIERLLLRLIAEAWHTNEIRTVRPTPFDEAKWGFAMLENSLWQAVPEFL 221

                    RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R  ++tA   +G    lP     ++ ssWmGGDRDG nP vt  +t+ v
  gi|1456350   222 RQLnETAREFLGYD--LPVGLKPVRISSWMGGDRDG-NPFVTAQITKKVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                      aR  Aa l+++ +  L  Elsm +C dE R++          d
  gi|1456350   269 YFARWKAADLFLQDISKLADELSMMKCSDEFRAK--------YGD----- 305

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR ++ + R +L  t       L      +sE  +
  gi|1456350   306 ---------HLEPYRFVVKNLRNQLTATLAYFDDHLSNRTPRVSESEIIL 346

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  +  EPL  CY+sL +CG ++iA GsLLD+L  +s FG+ L ++DiRq
  gi|1456350   347 EDNQLWEPLYDCYQSLIQCGMRIIANGSLLDILHRISCFGVTLSQMDIRQ 396

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+tDv+  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|1456350   397 ESTRHTDVIAEITRYIGLGDYAQWTEDDKQAFLIRELSSRRPLIPQNWTP 446

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E +++ld+ +v+A         Y+isma + sDvLAv LL +E gv
  gi|1456350   447 SPETQEILDTCKVIAQQKQGVIACYVISMARSASDVLAVHLLLKEAGVPY 496

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
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                    ++vvPLFE L DL+AA   + +LF + WY+  i+ +q vm+GYsDs KD
  gi|1456350   497 HIPVVPLFETLEDLDAAEKVMTQLFNVGWYRGVINNRQMVMIGYSDSAKD 546

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+AqE ++    k G+ L+lFHGRGGt+GRGG P H A+L
  gi|1456350   547 AGMMAASWAQYRAQEALVNLTEKLGIELTLFHGRGGTIGRGGAPAHAALL 596

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++  lRvt qGE+i f  G   +   +   ++ A LE  + PP
  gi|1456350   597 SQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVETFDLYASAILEANLLPPP 646

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     PkPEWR +m+e+  +  + YR vv  +  Fv YFR+AtPE E  k+ +G
  gi|1456350   647 EPKPEWRTIMDELSTISCDIYRGVVRGDKDFVPYFRSATPEQELSKLPLG 696

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR P GG+esLRAiPWiFaW q R  LP WLG GAA +  i++
  gi|1456350   697 SRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGAAIRQVIEQGKG 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     +  ++ m ++WPFF   + +lEmvF K D  +   yD+ Lv  eL+  G
  gi|1456350   747 DI--IHKMCENWPFFSTRIGMLEMVFSKSDTWLSQQYDQRLVKKELWYLG 794

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    ++LR + ++  + +L +    +l+   P++   + LR+ Y   Ln +q
  gi|1456350   795 ENLRKQLEDDIQTVLSLSHQSELMSDLPWIADSIALRNIYTDPLNLLQVE 844

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                  En            e+v P +E  L
  gi|1456350   845 LLHRFR-----------------EN-----------PEQVNPDVEQAL 864

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|1456350   865 MITITGIAAGMRNTG    879

gi|260914089|ref|ZP_05920562.1|: domain 1 of 1, from 2 to 879: score 750.9, E = 9.2e-223
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           q        +s           +l +FL++ + D  G d+ E
  gi|2609140     2    ---IQQYSTMRNNIS-----------MLGRFLgETISDAQGSDILEL 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls +  G  D  + + L + L  +     i vA+a++  LnL n
  gi|2609140    35 IENIRVLSRNSRGGDDKAR-NQLLSTLATISNDNIIPVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R  + +              E  i   +K+L  +     +
  gi|2609140    84 IAEQYQTISRHHNDQVA-----------SERSIPALFKRLKAQQ-VPQQK 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      eA+    ++LvltAHPt   RRsL+ K+  i  CL++L   D+  +++
  gi|2609140   122 LMEAVEKLLIELVLTAHPTEVTRRSLVHKHVEINKCLSKLEHSDLMDNER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    k ++  L   i  A+ t EiR  +PtP +E + G + i   +W+ vP FL
  gi|2609140   172 KMIERRLLQLIAQAWHTNEIRTQRPTPFEEAKWGFAVIENSLWQAVPEFL 221

                    RRvDt.ALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R    +A+   G n  +P +   i+FssWmGGDRDG nP vt +vt  v
  gi|2609140   222 RQLNAsAVEFFGFN--IPVELNPIRFSSWMGGDRDG-NPFVTADVTCQVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     LaR  Aa l++  +  L  Elsm +C +E R      ++
  gi|2609140   269 RLARWKAADLFLKDIQALSDELSMVKCTEEFR------QKYGDHI----- 307

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR ++ + R KL  t      LL      +sE+ + t
  gi|2609140   308 -----------EPYRAVVKELRSKLMTTLTYYDDLLTNRTPRVSENEIIT 346

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                      E+  EPL  CY+sL   G ++iA G LLD LR +  FG+ L +LDiRq
  gi|2609140   347 CDEQLWEPLYDCYQSLQASGMRIIANGLLLDCLRRIRCFGVTLSRLDIRQ 396
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                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+t+ +  it+ +++G Y +WsE  +q +L+ EL+ +RPLl+
  gi|2609140   397 ESTRHTEAIAEITRYIGLGDYAQWSESDKQAFLIRELSSRRPLLPLNWSP 446

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                        +++ld+ rv+AE P      Yiisma + sDvLAv LL +ECgv
  gi|2609140   447 SAPTQEILDTCRVIAEQPEGVISCYIISMAKTASDVLAVHLLLKECGVPY 496

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                     L+vvPLFE L DL A    +  LF i WY+  i+ Kq vm+GYsDs KD
  gi|2609140   497 HLPVVPLFETLDDLAASESVMTELFNIGWYRGIINNKQMVMIGYSDSAKD 546

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y AqE i+    k  + L+lFHGRGGt+GRGG P H A+L
  gi|2609140   547 AGMMAASWAQYCAQEAIVNLCHKLNIELTLFHGRGGTIGRGGAPAHAALL 596

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++  lRvt qGE+i f  G   +   sL  ++ A LE  + PP
  gi|2609140   597 SQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVGSLGLYASAILEANLLPPP 646

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR+Lm+e+       YR +v  E  Fv YFR+AtPE E  k+ +G
  gi|2609140   647 EPKAKWRELMNELSASSCKIYRDIVRGEKDFVPYFRSATPEQELSKLPLG 696

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR P GG+esLRAiPWiFaW q R  LP WLG GA  + Ai+K  +
  gi|2609140   697 SRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGASLRQAIEKGQR 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                    n+  ++Em ++WPFF   + +lEmvF K D  +   yD+ Lv   L+  G
  gi|2609140   747 NV--IEEMCETWPFFSTRIGMLEMVFSKTDTWLSEHYDQHLVDPSLWYLG 794

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    + LR++ +   + +L +     l+   P++   + LR+ Y   Ln +q
  gi|2609140   795 NALREQLKQDIQTVLSLSHENQLMSDLPWVAESIALRNVYTDPLNLLQVE 844

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L+R+R                              n  ++v   +E  L
  gi|2609140   845 LLRRLRT-----------------------------N-PDNVNADVEQAL 864

                    iLtmKGiAAGmqntG<-*
                    ++t+ G+AAGm ntG
  gi|2609140   865 MITITGVAAGMRNTG    879

gi|259906836|ref|YP_002647192.1|: domain 1 of 1, from 1 to 883: score 750.3, E = 1.4e-222
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  ++    vs           +l k L+D ++D  Ge++ +
  gi|2599068     1    -MNEQYSAMR-SNVS-----------MLGKLLgDTIKDALGENILDR 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls      +D+++ +EL + L  L   + + vA+a++  LnL n
  gi|2599068    35 VETIRKLSKSSRAGHDAHR-QELLSTLQNLSNDELLPVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +      i+         E+    E  +  t+++L  +   + +
  gi|2599068    84 VAEQYHT-----ISPNG------EGAKNPEL-LAKTFQRLKQQPALTEAA 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v eAL   s +LvltAHPt   RR L+ K   +  CL qL   D+   +
  gi|2599068   122 VHEALGSLSLELVLTAHPTEITRRTLIHKLVEVNSCLKQLDHNDLSDYEH 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L   +  A+ tDEiR+ +P P DE + G + +   +W+GvP+FL
  gi|2599068   172 AQIMRRLRQLVAQAWHTDEIRKYRPSPVDEAKWGFAVVENSLWEGVPQFL 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R     +        lP d   ++F+sWmGGDRDG nP vt ++tR v
  gi|2599068   222 RELNEQVEA-AFGYTLPVDFVPVQFTSWMGGDRDG-NPNVTADITRHVMQ 269

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
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                    L+R  A+ l++  +  L+ Elsm  C  E+R    El   +
  gi|2599068   270 LSRWKATDLFLRDIAVLISELSMSECTPEVR----ELCGNPEAL------ 309

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR i+ + R +L  t       L       + +    +
  gi|2599068   310 ----------EPYREIMKNLRSQLMSTQAYLAGRLKGERLARPADLLISN 349

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     E+   PL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRqE
  gi|2599068   350 -EQLWNPLYTCYQSLQACGMGIIANGQLLDTLRRVKCFGVPLVRIDIRQE 398

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+t+ +  it+ L++G + +WsE  +q +L+ EL  KRPL +
  gi|2599068   399 STRHTEAIAEITRYLGLGDFESWSEADKQAFLIRELNSKRPLTPRQWEPS 448

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     E k+vld+ rv AE P  s  aY+isma +PsDvL v LL +E g+  +
  gi|2599068   449 AETKEVLDTCRVAAEAPQGSIAAYVISMAKTPSDVLTVHLLLKEAGIGYA 498

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    ++v PLFE L DL+ A A + +L  iDWY+  i+GKq vm+GYsDs KDA
  gi|2599068   499 MPVAPLFETLDDLNNANAVMSQLLNIDWYRGLIQGKQMVMIGYSDSAKDA 548

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Ls
  gi|2599068   549 GVMAASWAQYQAQDALIKTCEKAGITLTLFHGRGGSIGRGGAPAHAALLS 598

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2599068   599 QPPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLSLYTGAILEANLLPPPE 648

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EW  +m+++  v    YR  v     Fv YFR+AtPE E  k+ +Gs
  gi|2599068   649 PKTEWIGIMDRLSTVSCQMYRGYVREHADFVPYFRSATPEQELAKLPLGS 698

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+P+GG+esLRAiPWiFaWtq R  LP WLG GAA + A+    +
  gi|2599068   699 RPAKRRPAGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQQAMADGHQD 748

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                      +L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lv   L+P Gk
  gi|2599068   749 --QLEAMCRDWPFFSTRLGMLEMVFSKADLWLAEYYDQRLVDKSLWPLGK 796

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LRd+ +   + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|2599068   797 QLRDRLESDIKAVLTIANDAHLMADQPWIAESIALRNVYTDPLNVLQAEL 846

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R             +E A  +           p  rv    E  L+
  gi|2599068   847 LHRSRQ------------QEAAGGE-----------PDARV----EQALM 869

                    LtmKGiAAGmqntG<-*
                    +t+ G+AAGm ntG
  gi|2599068   870 VTIAGVAAGMRNTG    883

gi|119944012|ref|YP_941692.1|: domain 1 of 1, from 6 to 878: score 750.2, E = 1.5e-222
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLH.GedLkEa
                            LR      vs           Ll + L      H Ge+  +
  gi|1199440     6    ---SNLRS----NVS-----------LLGQLLGKSIGGHlGEEFLDK 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls           +  L   Lt L   + + vA+a+ H LnLAn
  gi|1199440    35 IETIRQLSKSSRAGNQQDGVA-LIDMLTHLSDDELVPVARAFTHFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkl...nKs
                    +AE  +   R   +                   E +K L++k +++n s
  gi|1199440    84 IAEQFHGISRHCDSGVC--------------APEPIKDLISKFknsNLS 118

                    PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                     +E+ + +    +++vltAHPt   RR L+ K+  i  CL+ L   D+
  gi|1199440   119 QQEMQQSVNELKMEMVLTAHPTEITRRTLIHKHIAINDCLSYLEISDISD 168
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                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                     ++  L   L   i  A+ t +iR  +PtP DE + G + i   +W+ vP
  gi|1199440   169 KERDLLLNRLEQLITQAWHTNDIRQKRPTPVDEAKWGFATIEKSLWQAVP 218

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                    +F+R  +  L+  G+   lP ++  i F+sWmGGDRDG nP vt  vt +
  gi|1199440   219 QFIRDLESELQS-GLGLSLPLEASPITFTSWMGGDRDG-NPFVTAKVTQE 266

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                    v L +R +A  lY+  +  L  Elsm  C   LR       +    +
  gi|1199440   267 VLLSSRWVAVSLYLKDISQLTDELSMDNCDPALR-------SVVGDN--- 306

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                                EPYR iL   R  L  t       L    s+  E  +
  gi|1199440   307 -----------AAEPYRAILRKLRSELKETLASLSATLQNQRSD--EKDI 343

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                     t   +  EPL LCY+sL + G   iA G +LD+LR    FG+ L KLDi
  gi|1199440   344 ITTSKQLKEPLLLCYHSLKNMGMNSIANGLILDILRRLNCFGINLLKLDI 393

                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    Rq++eR+   l  +t+ L+iG Y  W Ee +q +Ll EL  KRPL++s
  gi|1199440   394 RQDAERHGNTLSELTRYLGIGDYNAWNEEDKQAFLLQELNNKRPLFPSQW 443

                    PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                        Ev++vld+ +v+A    ++ G Yiisma   sDvLAv L+ +E g
  gi|1199440   444 NPSAEVQEVLDTCKVVAQTDPEALGIYIISMARQASDVLAVQLILKEVGC 493

                    kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsG
                       ++v PLFE L DL+   A +++LF+iDWY+  i+G q+vm+GYsDs
  gi|1199440   494 PFRIPVAPLFETLDDLNNSAAVMKRLFAIDWYRGYINGIQHVMIGYSDSA 543

                    KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                    KDAG ++A W  Y  qE ++K   +  + LvlFHGRGGt+GRGG P   A
  gi|1199440   544 KDAGVIAANWAQYTSQEALVKLSAENDINLVLFHGRGGTIGRGGAPARQA 593

                    iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP
                    +LsqPP  ++G lRvt qGE+i f FG  ++  +sL  ++AA LE  + P
  gi|1199440   594 LLSQPPGSLKGGLRVTEQGEMIRFKFGLPKVAVQSLNQYAAAVLEANLLP 643

                    PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmn
                    P +Pk EWR++m++       EYR  v  EP Fv YFR+ tPE+E Gk+
  gi|1199440   644 PPAPKQEWRDVMQQFSDQSCQEYRHFVREEPDFVPYFRSVTPEVELGKLA 693

                    iGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                    +GsRP+KRkPsGGiesLRAiPWiFaW q R  LP WLG G   K  ++
  gi|1199440   694 LGSRPSKRKPSGGIESLRAIPWIFAWSQNRLMLPAWLGAGTSLKTLLNEG 743

                    iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP
                     K l  L+EmY+ WPFF   l++ EmvF K D  +   y++ Lv  eL+P
  gi|1199440   744 KKPL--LQEMYQHWPFFHTRLEMFEMVFLKADEELTKFYEERLVPKELWP 791

                    FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfq
                     G++LRd+   t++ +L+    + l+   P++K  + LR++Y+  Ln++q
  gi|1199440   792 LGQRLRDNLTLTRETVLETIPDHQLMQEQPWIKESISLRNPYVDPLNMLQ 841

                    AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                    A  L R R                  En           ++++ P ++
  gi|1199440   842 AELLYRSR-----------------EN-----------GDEICPVVDQ 861

                    tLiLtmKGiAAGmqntG<-*
                     L++t+ GiAAG+ ntG
  gi|1199440   862 ALMVTIAGIAAGLRNTG    878

gi|292486630|ref|YP_003529500.1|: domain 1 of 1, from 1 to 883: score 749.8, E = 2e-222
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  ++    vs           +l k L+D ++D  Ge++ +
  gi|2924866     1    -MNEQYSAMR-SNVS-----------MLGKLLgDTIKDALGENILDR 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
```

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                v     ls       D+++ + L + L  L   + + vA+a++  LnL n
gi|2924866    35 VETIRQLSKSSRAGNDAHR-QQLLSTLQNLSNDELLPVARAFSQFLNLTN 83

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                +AE  +      i+         E+    E  +  t+++L  +   + +
gi|2924866    84 VAEQYHT-----ISPNG------EGAKNPEL-LAKTFQRLKQQPGLTEAA 121

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                v eAL   s +LvltAHPt   RR L+ K   +  CL qL   D+   +
gi|2924866   122 VHEALGSLSLELVLTAHPTEITRRTLIHKLVEVNSCLKQLDHNDLSDYEH 171

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  +   L   +  A+ tDEiR+ +P P DE + G + +   +W+GvP+FL
gi|2924866   172 AQIMRRLRQLVAQAWHTDEIRKYRPSPIDEAKWGFAVVENSLWEGVPQFL 221

                RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                R     +        lP d   ++F+sWmGGDRDG nP vt ++tR v
gi|2924866   222 RELNEQVEA-AFGYTLPVDFVPVQFTSWMGGDRDG-NPNVTADITRHVLQ 269

                LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                L+R  A+ l++  +  L+ Elsm  C  E+R+    l   +
gi|2924866   270 LSRWKATDLFLRDIAVLISELSMSECTPEVRA----LCGNPEAL------ 309

                iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                          EPYR i+ + R +L  t       L       + +    +
gi|2924866   310 ----------EPYREIMKNLRSQLNGTQAYLAACLQGERVARPANLLISN 349

                vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                 E+   PL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRqE
gi|2924866   350 -EQLWAPLYTCYQSLQACGMGIIANGQLLDTLRRVKCFGVPLVRIDIRQE 398

                seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                s R+t+ +  it+ L++G + +WsE  +q +L+ EL  KRPL +
gi|2924866   399 STRHTEAIAEITRYLGLGDFESWSEADKQAFLIRELNSKRPLTPRQWEPS 448

                EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                 E ++vld+ rv AE P  s  aY+isma +PsDvLAv LL +E g+  +
gi|2924866   449 AETQEVLDTCRVAAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIGYA 498

                LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                ++v PLFE L DL+ A   + +L siDWY+  i+GKq vm+GYsDs KDA
gi|2924866   499 MPVAPLFETLDDLNNANEVMSQLLSIDWYRGLIQGKQMVMIGYSDSAKDA 548

                GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                G ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Ls
gi|2924866   549 GVMAASWAQYQAQDALIKTCEKAGITLTLFHGRGGSIGRGGAPAHAALLS 598

                qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                qPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
gi|2924866   599 QPPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLSLYTGAILEANLLPPPE 648

                PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                PkPEW  +m+++  v    YR  v     Fv YFR+AtPE E  k+ +Gs
gi|2924866   649 PKPEWISIMDRLSAVSCKMYRGYVREHADFVPYFRSATPEQELAKLPLGS 698

                RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                RPaKR+PsGG+esLRAiPWiFaWtq R  LP WLG GAA + A+    +
gi|2924866   699 RPAKRRPSGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQQAMADGQQD 748

                lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                  +L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lv   L+P Gk
gi|2924866   749 --QLEAMCRDWPFFSTRLGMLEMVFSKADLWLAEYYDQRLVDKSLWPLGK 796

                sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                +LRd+ +   + +L iA    l+   P++   + LR+ Y   Lnv+qA
gi|2924866   797 QLRDRLESDIKAVLTIANDAHLMADQPWIAESIALRNVYTDPLNVLQAEL 846

                LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                L R R                 +E             +++    +E  L+
gi|2924866   847 LHRSRQ----------------QEA-----------AGSEPDARVEQALM 869
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                  LtmKGiAAGmqntG<-*
                  +t+ G+AAGm ntG
  gi|2924866   870 VTIAGVAAGMRNTG    883

gi|114561377|ref|YP_748890.1|: domain 1 of 1, from 7 to 882: score 749.2, E = 3e-222
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      + A LR  v G                    + +q   G+   E v
  gi|1145613     7    DMYASLRSNV-GHLG-------------QILGETMQNHLGDAFLEKV 39

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   E   + A    + D    e + a Lt+L   + +  Aka+   LnLAn+
  gi|1145613    40 -EQIRILAKKSRQGDEASREQMLALLTALPDEELVPFAKAFNQFLNLANI 88

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AE  +   R   ++                 +E  l ++        ++v
  gi|1145613    89 AEQFHTISRNCDELVC-----------VPDPVEQLLGRMLDTD-LDKKDV 126

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     LKn  +DLvltAHPt   RR L+qK a +  CL+      +t  +++
  gi|1145613   127 IKSLKNLDIDLVLTAHPTEISRRTLIQKYAAVVDCLTEQENSQLTDRERQ 176

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                       L   i   + t EiR  +PtP DE R G+s i   +W+ +P FLR
  gi|1145613   177 QSTLRLRQLIAQIWHTNEIRNERPTPVDEARWGLSTIETSLWQAIPDFLR 226

                  Rv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    +D   +  G    lP dv  ++FssWmGGDRDG nP vt  vt +v
  gi|1145613   227 QLnDQVEQKTG--QQLPIDVSPVRFSSWMGGDRDG-NPFVTSLVTQEVLD 273

                  LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    R  Aa lY+  +  L+ Elsm   n EL +       t  ++
  gi|1145613   274 RNRHAAARLYLKDIVSLLGELSMEQANAELSA------LTDNSK------ 311

                  iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                            EPYR +L   R +L  t +     L     ++       +
  gi|1145613   312 ----------EPYRDVLRKLRCQLHGTIDYLNARLEGKKPDVDTSELIWH 351

                  vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    + LEPLEL YksL +CG k iA G LLD+LR    FG+ + +LDiRq+
  gi|1145613   352 KSDLLEPLELLYKSLTDCGMKLIANGLLLDILRRLACFGIHMLRLDIRQD 401

                  seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                  + R+ Dv+  +t+ L++G Y  W E+ +q +Ll EL  KRPL++     t
  gi|1145613   402 ATRHSDVIAELTRYLGMGDYNHWDENEKQAFLLRELTSKRPLIPTNWKPT 451

                  EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                  ++v++v+ + + +A  P+ + G+Y+isma  PsDvL v LL +E g  ++
  gi|1145613   452 DDVAEVVRTCNLVAQQPVNALGSYVISMASKPSDVLTVLLLLKEAGCTNP 501

                  LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                  +rvvPLFE LADLe A   +  L  iDWY+    G qevm+GYsDs KDA
  gi|1145613   502 MRVVPLFETLADLEGAADCMTSLLNIDWYRGYTKGMQEVMIGYSDSAKDA 551

                  GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                  G ++AAW  Y+AqE ++ v Kk  vKL+lFHGRGG +GRGGGP H AiLs
  gi|1145613   552 GVMAAAWAQYRAQEQLVAVCKKADVKLMLFHGRGGSIGRGGGPAHKAILS 601

                  qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                  qPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A LE  + PP
  gi|1145613   602 QPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVLEATLLPPPE 651

                  PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                  Pk  WR+ m+++A      YR +v  EP FvEYFR+AtPE+E Gk+ +Gs
  gi|1145613   652 PKKSWRDCMQRIAEESVLHYRGIVREEPDFVEYFRSATPEVELGKLPLGS 701

                  RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                  RPaKRk  GGiesLRAiPWiFaW q R  LP WLG G A + A d+
  gi|1145613   702 RPAKRKVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALQDAADRG--E 749

                  lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                  l  L+Em ++WPFF   + +lEmv+ K +P +A  y+  Lv  eL+  G+
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  gi|1145613   750 LELLREMEEQWPFFETRISMLEMVYTKAEPNLAKYYELCLVKPELHHLGE 799

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR++ +   + +L +    +l+   P+ +  ++LR++Yi  Ln +q
  gi|1145613   800 KLRQRLQLGIEAVLSLTQATELMSHTPWSRESVKLRNPYIDPLNFLQTEL 849

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R                 E   ++   v+L            L+
  gi|1145613   850 LARTR----------------REV--EPSADVQLA-----------LM 868

                    LtmKGiAAGmqntG<-*
                    Lt+ G+AAGm ntG
  gi|1145613   869 LTIAGVAAGMRNTG    882

gi|145633038|ref|ZP_01788770.1|: domain 1 of 1, from 2 to 879: score 749.1, E = 3.3e-222
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           q        +s           +l +FL++ + D  G d+ E
  gi|1456330     2    ---TQEYSTLRNNIS----------MLGRFLgETINDAQGTDILEL 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls +     D  + + L   L s+     i vA+a++  LnL n
  gi|1456330    35 IENIRKLSRNSRAGDDKAR-QALLDTLGSISNENIIPVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R     +                + E +K+L  +   s eE
  gi|1456330    84 IAEQYQTISREHSLAQS----------SSQSLSELFKRLKEQN-ASVEE 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v   +    ++LvltAHPt   RRsL+ K+  i  CL++L   D+t  ++
  gi|1456330   122 VHKTVEKLLIELVLTAHPTETTRRSLIHKHIEINKCLSKLEHNDLTEKER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      ++  L R i  A+ t EiR  +PtP DE + G + +   +W+ vP FL
  gi|1456330   172 NIIERLLLRLIAEAWHTNEIRTVRPTPFDEAKWGFAMLENSLWQAVPEFL 221

                    RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R  ++tA   +G    lP     ++ ssWmGGDRDG nP vt  +t+ v
  gi|1456330   222 RQLnETAREFLGYD--LPVGLKPVRISSWMGGDRDG-NPFVTAQITKKVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                      aR  Aa l+++ +  L  Elsm +C dE R            dk   +
  gi|1456330   269 YFARWKAADLFLQDISKLADELSMMKCSDEFR-----------DKYGEH 306

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR ++ + R +L  t       L      +sE+ +
  gi|1456330   307 L----------EPYRFVVKNLRNQLTATLAYFDDHLSNHTPRVSENEIIL 346

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  +  EPL  CY+sL +CG ++iA GsLLD+L  +s FG+ L ++DiRq
  gi|1456330   347 EDNQLWEPLYDCYQSLIQCGMRIIANGSLLDILHRISCFGVTLSQMDIRQ 396

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+tDv+  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|1456330   397 ESTRHTDVIAEITRYIGLGDYAQWTEDDKQAFLIRELSSRRPLIPQNWTP 446

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E +++ld+ +v+A         Y+isma + sDvLAv LL +E gv
  gi|1456330   447 SPETQEILDTCKVIAQQKQGVIACYVISMARSASDVLAVHLLLKEAGVPY 496

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                     ++vvPLFE L DL+AA   + +LF + WY+  i+ +q vm+GYsDs KD
  gi|1456330   497 HIPVVPLFETLEDLDAAEKVMTQLFNVGWYRGVINNRQMVMIGYSDSAKD 546

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+AqE ++    k G+ L+lFHGRGGt+GRGG P H A+L
  gi|1456330   547 AGMMAASWAQYRAQEALVNLTEKLGIELTLFHGRGGTIGRGGAPAHAALL 596

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++  lRvt qGE+i f  G   +   +   ++ A LE  + PP
  gi|1456330   597 SQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVETFDLYASAILEANLLPPP 646
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                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     PkPEWR +m+e+  +  + YR vv  +  Fv YFR+AtPE E  k+ +G
  gi|1456330   647 EPKPEWRTIMDELSTISCDIYRGVVRGDKDFVPYFRSATPEQELSKLPLG 696

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR P GG+esLRAiPWiFaW q R  LP WLG GA  +  i++
  gi|1456330   697 SRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGASIRQIIEQGKG 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     +  ++Em ++WPFF   + +lEmvF K D  +   yD+ Lv  eL+  G
  gi|1456330   747 DV--IHEMCENWPFFSTRIGMLEMVFSKSDTWLSQQYDQRLVKKELWYLG 794

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    ++LR + ++  + +L +    +l+   P++   + LR+ Y   Ln +q
  gi|1456330   795 ENLRKQLEDDIQTVLSLSHQSELMSDLPWIADSIALRNIYTDPLNLLQVE 844

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                  En             e+v P +E  L
  gi|1456330   845 LLHRFR------------------EN------------PEQVNPDVEQAL 864

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|1456330   865 MITITGIAAGMRNTG    879

gi|37528563|ref|NP_931908.1|: domain 1 of 1, from 1 to 878: score 748.9, E = 3.8e-222
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  ++    vs           +l k L+D +++  Ged+ +
  gi|3752856     1    -MNQQYSAMR-SNVS-----------MLGKLLgDTIKEALGEDILDK 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++++ + L + L  L   + + vA+a+   LnL n
  gi|3752856    35 VETIRKLSKSSRAGNEAHR-QQLLSTLQNLSNNELLPVARAFNQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +       +   hG+ a    A     +   + +L  k      +
  gi|3752856    84 VAEQYH-------SISPHGEAASNPVA-----LAKLFTRLKEKN-FNNGD 120

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                       A+   s++LvltAHPt  +RR L+ K   +  CL+qL   D+   ++
  gi|3752856   121 LKKAVNELSIELVLTAHPTEIARRTLIHKLVAVNTCLSQLDHDDLADYER 170

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L   +   + tDEiR+ +PtP DE + G + +   +W+GvP FL
  gi|3752856   171 NNIMRRLRQLVAQSWHTDEIRKIRPTPIDEAKWGFAMVENSLWEGVPAFL 220

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R     L    i   lP ++  ++F+sWmGGDRDG nP vt EvtR v L
  gi|3752856   221 REFNEQLEE-SIDYSLPVEAVPVRFTSWMGGDRDG-NPNVTAEVTRHVLL 268

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  Aa l++  +  L+ Elsm  C  E+R       + a  d +
  gi|3752856   269 LSRWKAADLFLKDIQVLVSELSMSECTPEVR-------KLAGGDEIL--- 308

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR i    R +L nt       L +G   ++      +
  gi|3752856   309 ----------EPYREIAKKLRTQLSNTLTYLEKQL-KGEQVLPPTDLLVD 347

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     E+   PL  CY+sL  CG  +iA G LLD+LR +  FGLsLv++D+RqE
  gi|3752856   348 NEQLWQPLYACYQSLKTCGMEIIANGQLLDILRRIRCFGLSLVRIDVRQE 397

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+t  +  +t+ Le+G Y +WsEe +q +Ll EL+ KRPL++
  gi|3752856   398 STRHTTAISELTQYLELGDYASWSEEEKQAFLLYELHSKRPLIPHNWQPS 447

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     E ++v  + +v+AE P D+  aY+isma aPsDvLAv LL +E g   t
  gi|3752856   448 AETQEVFATCKVIAESPQDAIAAYVISMAKAPSDVLAVHLLLKEAGCPFT 497

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    L+v PLFE L DL+ A   +++L  i WY+  i  Kq vm+GYsDs KDA
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  gi|3752856   498 LPVAPLFETLDDLNNAENIIQQLMNIQWYRELIHDKQMVMIGYSDSAKDA 547

                   GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                   G ++AAW  Y+Aq+ +i v  k G+ L+lFHGRGGt+GRGG P H A+Ls
  gi|3752856   548 GVMAAAWAQYRAQDALINVCEKEGITLTLFHGRGGTIGRGGAPAHAALLS 597

                   qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                   qPP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP
  gi|3752856   598 QPPGSLKGGLRVTEQGEMIRFKFGLPQVTISSLALYASAILEANLLPPPE 647

                   PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                   PkPEW ++m+ +  v    YR  v   P Fv YFR AtPE E  k+ +Gs
  gi|3752856   648 PKPEWHQVMDTLSDVSCKMYRDYVREQPDFVPYFRAATPEQELAKLPLGS 697

                   RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                   RPaKR+P+GG+esLRAiPWiFaWtq R  LP WLG GAA +  ++ D K
  gi|3752856   698 RPAKRHPAGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQQVVN-DGKQ 746

                   lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                      L Em ++WPFF   + +lEmvFAK D  +A  yD+ Lv  +L+P G+
  gi|3752856   747 -DVLAEMCRDWPFFTTRIGMLEMVFAKADLWLAEYYDHRLVDKNLWPLGQ 795

                   sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                   +LR +     + +L i     l+   P++   + LR+ Y   Lnv+q
  gi|3752856   796 KLRKQLSADIKTVLAISKDEHLMADLPWIAESIALRNVYTDPLNVLQVEL 845

                   LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                   L R R  +y                                 P +E  L+
  gi|3752856   846 LLRSRQQQYS------------------------------DPQVEQALM 864

                   LtmKGiAAGmqntG<-*
                   +t+ GiAAGm ntG
  gi|3752856   865 VTIAGIAAGMRNTG    878

gi|147809570|emb|CAN62388.1|: domain 1 of 1, from 16 to 1069: score 748.5, E = 4.8e-222
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      s D   RlL  G     +++++ +  +   F++ +     e  +
  gi|1478095    16    SFDDDCRLL--GSLL--NEVLQRE--VGSNFMEKV-----ERNRILA 51

                   qECYElsAeYEGKkDtkKLeE..LGakLtsLdPaDailvAkailHmLnLA
                   q    + A   G +Dt  L E++L + +  ++  +a+ +A+a++H LnL
  gi|1478095    52 QSACNMRAS--GIEDTAELLEkqLISEISQMNLEEALTLARAFSHYLNLM 99

                   nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    +AE     +R R  +           A      ++ + +L   +  sPe
  gi|1478095   100 GIAET---HHRLRKARNV---------AHMSKSCDDIFNQLLQGG-VSPE 136

                   EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                   E ++ +  q v++vltAHPtq  RR L  K+ Ri   L       +  eD
  gi|1478095   137 ELYNTVCKQEVEIVLTAHPTQINRRTLQYKHIRIAHLLDYNDRPNLGHED 186

                   KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                   ++ L E L REi   + tDE+RR +Pt  DE RaG+  +   +W+ vP +
  gi|1478095   187 REMLIEDLVREITSIWQTDELRRQKPTVVDEARAGLNIVEQSLWRAVPHY 236

                   LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   LRRv  ALK       lP     ikF sWmGGDRDG nP vt EvtRDv
  gi|1478095   237 LRRVSNALKK-HTGKSLPLTCTPIKFGSWMGGDRDG-NPNVTAEVTRDVS 284

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyr..........
                   LL+R mA  lYi  v+ L FElsm RC d L   A E+  +++++ ++++
  gi|1478095   285 LLSRWMAIDLYIREVDSLRFELSMNRCSDSLSRLAHEILEketssvdrne 334

                   .................................taardkvvKy.YiEF.
                   +++++ ++++ ++ ++ +++ +++ + + + ++ t  +d   Ky+ +EF+
  gi|1478095   335 srnqplnrsqlkpysqlgptlprqlpagadlpscTECKDGESKYpKLEFp 384

                   ..........WKqv...................................
                   +++  + +++ Kq+ ++     +   ++ + +  ++++++ ++++++ ++
  gi|1478095   385 gtdymplnrqVKQIlgkliflcgiclpsmdvkaasssdtsfqdsnkdfgk 434
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                    ..........................................PPtE
                    + ++++  +++++++++  ++++  ++ + ++++ ++  +++ +++P
  gi|1478095   435 tygngtvanssnshsgqllsqrklfsexqlgrssfqkllepslpqrPGIA 484

                    PYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkvEeFLEPLELC
                    PYR++LG+v+DKL  t  R   LL     e      y   +e LEPL LC
  gi|1478095   485 PYRIVLGNVKDKLMKTQRRLELLLEDLPCEHDPGDYYETADELLEPLLLC 534

                    YksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAi
                      s+  CG  ++ADG L Dl+R v tF + L+KLD+RqEs R+ + lDAi
  gi|1478095   535 HESMQSCGSGILADGRLADLIRRVATFRMVLMKLDLRQESARHAETLDAI 584

                    ttHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafr
                    t  L++G Y eW Ee++ ++L  ELkGKRPL+++ +    +vk+vld+fr
  gi|1478095   585 TSYLDMGIYSEWDEERKLDFLTRELKGKRPLVPPTIEVVADVKEVLDTFR 634

                    vLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq..........t
                    v AE+ +DsFGaY+isma   sDvLAvELLq++  +   ++ +++ +++t
  gi|1478095   635 VAAEIGSDSFGAYVISMASNASDVLAVELLQKDARLAVxgelgrpcsggT 684

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinri....dGKqevmvGYsDs
                    LrvvPLFE + DL+ A A + kL siDWY+ +i ++++G qevmvGYsDs
  gi|1478095   685 LRVVPLFETVKDLRGAGAVIRKLLSIDWYREHIiknhNGHQEVMVGYSDS 734

                    GKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHL
                    GKDAGR+ AAW LYkAqE+++    +yG+K++lFHGRGG +GRGGGPt L
  gi|1478095   735 GKDAGRFTAAWELYKAQEDVVAACNEYGIKVTLFHGRGGSIGRGGGPTYL 784

                    AiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmn
                    Ai sqPP  + G lR t qGE++   FG  +   r L  +t A L   m
  gi|1478095   785 AIQSQPPGSVMGTLRSTEQGEMVQAKFGLPHTAVRQLEIYTTAVLLATMR 834

                    PPvsPkPE.WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGk
                    PP+ P+ E+WR+Lmee+  +    YRs v+  P F  YF  AtP  E G
  gi|1478095   835 PPLPPREEkWRNLMEEISKISGQCYRSTVYENPEFLAYFHEATPQAELGF 884

                    mniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid
                    +niGsRP++Rk s Gi  LRAiPW+FaWtqtRF LP WLGvG   K   +
  gi|1478095   885 LNIGSRPTRRKSSTGIGHLRAIPWVFAWTQTRFVLPAWLGVGSGLKGVCE 934

                    KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL
                    K  K    L  mYkeWPFF  t+DL+Emv  K D  iA  yD++Lv+
  gi|1478095   935 KGHKE--DLIAMYKEWPFFQSTIDLIEMVLGKADITIAKHYDEVLVSPSR 982

                    kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnv
                    +  G +LR +   t +++L + GH  l      L+  +  R +++  +n+
  gi|1478095   983 QELGADLRRELLTTGKFVLVVTGHDKLSQNNRSLRRLIESRLPFLNPMNM 1032

                    fqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGL
                    +q   L+R+R                 d+n          n        L
  gi|1478095  1033 LQVEILRRLRR---------------DDDN----------N-------KL 1050

                    EDtLiLtmKGiAAGmqntG<-*
                     D L++t+ GiAAGm ntG
  gi|1478095  1051 RDALLITINGIAAGMRNTG    1069

gi|258637583|ref|ZP_05730332.1|: domain 1 of 1, from 1 to 883: score 748.4, E = 5.3e-222
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  ++    vs           +l k L+D ++D  Ge++ +
  gi|2586375     1    -MNEQYSAMR-SNVS-----------MLGKLLgDTIKDALGENILDK 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       Dt++  EL + L  L   + + vA+a++  LnL n
  gi|2586375    35 VETIRKLSKSSRAGNDTHR-KELLSTLQNLSNDELLPVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R           + E+    E  +  t+ +L  + +    +
  gi|2586375    84 VAEQYQTIAR----------SGEGANHPEL-LKSTFDRLKQQKDLNESD 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K   +  CL qL   D+t  +
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  gi|2586375   122 IRAAIESLSLELVLTAHPTEITRRTLIHKLVEVNSCLQQLDHSDITEYEY 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     +   L   +  A+ tDEiR+ +PtP DE + G + +   +W+GvP FL
  gi|2586375   172 NQVMRRLRQLVAQAWHTDEIRKYRPTPVDEAKWGFAVVENSLWEGVPAFL 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   R     +       RlP d   ++F+sWmGGDRDG nP vt  +tR
  gi|2586375   222 RELNEQVEET-FGMRLPVDFVPVQFTSWMGGDRDG-NPNVTASITRQAMQ 269

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   L R  Aa l++  v  L+ Elsm  C dE+R    El   +
  gi|2586375   270 LGRWKAADLFLRDVGVLISELSMSECSDEVR----ELCGDPEAL------ 309

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                             EPYRviL  +R +L  t       L       + +    +
  gi|2586375   310 ----------EPYRVILKRIRSQLMSTQAFLERRLKGERLPRPADLLVSN 349

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    ++   PL   Y+sL +CG  +iA G LLD LR v  FG+ Lv++D+RqE
  gi|2586375   350 -DQLWQPLFAIYQSLQQCGMGIIANGQLLDTLRRVKCFGVPLVRIDLRQE 398

                   seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                   s R+t+ +  +t+ L++G Y +WsE  +q +L+ EL  KRPLl+
  gi|2586375   399 STRHTEAIAEVTRYLGLGDYESWSEADKQAFLIRELNSKRPLLPRQWEPS 448

                   EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                   +  ++vld+ +v AE P  s  aY+isma  PsDvLAv LL +E g+  +
  gi|2586375   449 DNTREVLDTCKVAAEAPQGSIAAYVISMAKVPSDVLAVHLLLKEAGITYA 498

                   LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                   ++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDA
  gi|2586375   499 MPVAPLFETLDDLNNANDVMSQLLGIDWYRGFIQGKQMVMIGYSDSAKDA 548

                   GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                   G ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Ls
  gi|2586375   549 GVMAASWAQYQAQDALIKTCEKAGIALTLFHGRGGSIGRGGAPAHAALLS 598

                   qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                   qPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2586375   599 QPPGSLKGGLRVTEQGEMIRFKYGLPEVTIASLSLYTGAILEANLMPPPE 648

                   PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                   Pk EW ++m+ +       YR  v   P Fv YFR+AtPE E Gk+ +Gs
  gi|2586375   649 PKSEWCDIMDGLSAHSCAMYRGYVRENPDFVPYFRSATPEQELGKLPLGS 698

                   RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                   RPaKR+  GG+esLRAiPWiFaWtq R  LP WLG GAA + A+++  +
  gi|2586375   699 RPAKRRATGGVESLRAIPWIFAWTQNRLMLPAWLGAGAAIQKAMEQGHQD 748

                   lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                     +L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lv   L+P G+
  gi|2586375   749 --QLETMCRDWPFFSTRLGMLEMVFSKADLWLAEYYDQRLVDKSLWPLGQ 796

                   sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                   +LRd+     + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|2586375   797 QLRDQLDADIKAVLTIANDAHLMADQPWIAESIALRNVYTDPLNVLQAEL 846

                   LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                   L R R                A+E+           +++    +E  L+
  gi|2586375   847 LHRSR----------------AQEE-----------RGDEPDARVEQALM 869

                   LtmKGiAAGmqntG<-*
                   +t+ G+AAGm ntG
  gi|2586375   870 VTIAGVAAGMRNTG    883

gi|15602411|ref|NP_245483.1|: domain 1 of 1, from 2 to 879: score 747.9, E = 7.6e-222
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                          q        +s           +l +FL++ + D  G d+ E
  gi|1560241     2    ---IQQYSTMRNNIS----------MLGRFLgETISDAQGSDILEL 34
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                vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                +     ls +     D  + + L   L  +     i vA+a++  LnL n
gi|1560241    35 IENIRVLSRNSRHGDDQAR-NALLNTLATISNENIIPVARAFSQFLNLTN 83

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                +AE  +   R                   E  i   +K+L  +    P+E
gi|1560241    84 IAEQYQTISRHHHDHVA-----------SERSISALFKRLKAQQ--VPKE 120

                .vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                +v e ++   ++LvltAHPt   RRsL+ K+  i  CL++L   D+t  +
gi|1560241   121 nVMETVQKLLIELVLTAHPTEVTRRSLVHKHVEINKCLSKLEHTDLTDAE 170

                KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                +k ++  L   i  A+ t EiR  +PtP +E + G + i   +W+ vP F
gi|1560241   171 RKAIERRLLQLIAQAWHTNEIRTQRPTPFEEAKWGFAVIENSLWQAVPEF 220

                LRRvDt.ALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                LR   t+A+   G    lP +   i+FssWmGGDRDG nP vt EvtR v
gi|1560241   221 LRHLNTsAVEYFGF--HLPVELNPIRFSSWMGGDRDG-NPFVTAEVTRQV 267

                CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                  LaR  Aa l++  +  L  Els+ +C  E  ++         ++
gi|1560241   268 LRLARWKAADLFLTDIQALSDELSVVKCTPEFQAK-------YGSH---- 306

                yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                             EPYR ++ + R KL  t      LLA     ++Ee +
gi|1560241   307 -----------VEPYRTVVKALRSKLTATLAYYDDLLANRTPRVAEEDII 345

                tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                t+  +  EPL  CY+sL  CG ++iA G LLD LR +  FG+ L +LDiR
gi|1560241   346 TQDAQLWEPLYDCYQSLQACGMRIIANGLLLDCLRRIRCFGVTLSRLDIR 395

                qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                qEs R+ + +  it+ +++G Y +WsE  +q +L+ EL+ +RPLl+ +
gi|1560241   396 QESTRHAEAIAEITRYIGLGDYAQWSESDKQAFLIKELSSRRPLLPREWQ 445

                ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                     ++vld+ rv+AE P      Yiisma + sDvLAv LL +E gv
gi|1560241   446 PSAATQEVLDTCRVIAEQPEGVISCYIISMAKTASDVLAVHLLLKESGVP 495

                qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                  L+vvPLFE L DL+A    +  LF i WY+  i+ Kq vm+GYsDs K
gi|1560241   496 YHLPVVPLFETLDDLRASEQVMSELFNIGWYRGVINNKQMVMIGYSDSAK 545

                DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                DAG ++A W  Y AqE ++    k  + L+lFHGRGGt+GRGG P H A+
gi|1560241   546 DAGMMAASWAQYCAQEALVNLCDKCNIELTLFHGRGGTIGRGGAPAHAAL 595

                LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                LsqPP  ++  lRvt qGE+i f  G   +   sL  ++ A LE  + PP
gi|1560241   596 LSQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVESLGLYASAILEANLLPP 645

                vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                  Pk  WR +m+e+  +    YR vv  E  Fv YFR AtPE E  k+ +
gi|1560241   646 PEPKAQWRTVMDELSTISCQIYRDVVRGEKDFVPYFRAATPEQELSKLPL 695

                GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                GsRPaKR P GG+esLRAiPWiFaW q R  LP WLG GA  + Ai+K
gi|1560241   696 GSRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGASLRQAIEKGQ 745

                KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                K +  +++m k+WPFF   + +lEmvF K D  +   yD+ Lv   L+
gi|1560241   746 KTV--IEDMCKTWPFFSTRIGMLEMVFSKTDTWLSEHYDQHLVDPALWYL 793

                GksLRdkYvEtkdlLLkiAGHkDlLEGD.PYLKqrlRLRdsYittLnvfq
                G+sLR++ +   + +L +  H D L  D P++   + LR+ Y   Ln +q
gi|1560241   794 GESLREQLKQDIQTVLSLS-HEDQLMSDlPWIAESIALRNVYTDPLNLLQ 842

                AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                   L+R+R         P       d +          n      P +E
gi|1560241   843 VELLRRLR-------RNP-------DNP----------N------PDVEQ 862
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                  tLiLtmKGiAAGmqntG<-*
                   L++t+ G+AAGm ntG
  gi|1560241   863 ALMITITGVAAGMRNTG    879

gi|196155561|ref|YP_002125050.1|: domain 1 of 1, from 4 to 873: score 747.7, E = 8.5e-222
                  *->siDAqLRlLvP..GKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                       DA L+  v   GK     + i+    L   +LD +     e ++
  gi|1961555     4    HYDAELKDTVRylGKTL--GETIKNQ--LGQEWLDRI-----EKIRK 41

                  avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                           A Y G  D+   eEL      +  +D + v +a+   LnL
  gi|1961555    42 GGR------ASYQG--DATCSEELKETFKTMSDSDLLTVGRAFAQFLNLG 83

                  nLAEEvelAyRRRikkkkhGDFaDEasAttEsD..iEEtlKkLvlklnKs
                  n+AE                    E +A    D +i+  +K+L      +
  gi|1961555    84 NIAEQ------------------EYNAAMNVDasIDALFKHLDKAE-LT 113

                  PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                   + v +A+    +DLvltAHPt   RR L+ K+  +  CL  +    +
  gi|1961555   114 ADKVQDAVAKLNIDLVLTAHPTEVTRRTLIHKHKELADCLQAVHQASLSD 163

                  eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                   ++k ++  +   i  A+ t+EiR  +PtP DE R G s i   +W+ vP
  gi|1961555   164 VERKKIETRIADLIAQAWHTEEIRSVRPTPVDEARWGFSVIENSLWEAVP 213

                  KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                   F+R  D  L n      lP d+  ++FssWmGGDRDG nP vt  vt
  gi|1961555   214 DFMRELDGRL-NEDYDVSLPLDASPVQFSSWMGGDRDG-NPFVTSKVTEQ 261

                  vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                  v LLaR  Aa l+   ++ L  Elsm+ CndELR           d
  gi|1961555   262 VLLLARKRAAKLFALDLDRLQVELSMYDCNDELR-----------D--- 296

                  KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                         K    +EPYR +L     K   tR+     LA    + s
  gi|1961555   297 -------KVGDANEPYRALLRPLVNKFIATRDGIADYLAGKNPDTSN--W 337

                  ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                      +e +EPL LCY+sL +CG +v+A G LLD +R    FG+ L +LD+
  gi|1961555   338 IESDDELIEPLMLCYQSLIDCGMQVVANGLLLDTIRRARVFGIHLLRLDV 387

                  RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                  Rq+seR+ Dv   +t+ L++G Y +WsE  +q +Ll EL  KRPL+++
  gi|1961555   388 RQDSERHADVFSELTRYLGLGDYAQWSEADKQAFLLRELGSKRPLFPAQW 437

                  PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                     ++vk+vld+ +v+A      FG Yiisma  PsDv+Av LL  E gv
  gi|1961555   438 DASDDVKEVLDTCKVIAKHSKHGFGIYIISMASEPSDVMAVQLLLQESGV 487

                  kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsG
                    +++v PLFE L DL+  P  + kL siDWY+  + G+q vm+GYsDs
  gi|1961555   488 DWPMPVAPLFETLDDLNNSPDVMRKLLSIDWYRGYVKGRQFVMIGYSDSA 537

                  KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                  KDAG l+A W  Y+ qE ++ +A ++ v L+lFHGRGGt+GRGG P H A
  gi|1961555   538 KDAGALAAGWAQYQSQEALVAIAEEFDVSLTLFHGRGGTIGRGGLPAHAA 587

                  iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP
                  i sqPP  ++G  Rvt qGE i + FG  +L  rsL  ++ A +E  + P
  gi|1961555   588 IYSQPPGSLEGGFRVTEQGETIRYKFGMPKLAKRSLGIYASAIIEAMLFP 637

                  PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmn
                  P +Pk EWR+L+  mA    + YR+ v  +  Fv YFR+AtPE E Gk+
  gi|1961555   638 PPAPKEEWRELITTMAAQGRDNYRATVRHDEEFVPYFRVATPEQELGKLP 687

                  iGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                  +GsRPaKRkP GGiesLRAiPWiFaW qtR  LP WLGv  A      K
  gi|1961555   688 LGSRPAKRKPQGGIESLRAIPWIFAWAQTRLVLPSWLGVMRAIDSV--KT 735

                  iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP
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```
                     n + + Em+ eWPF+R  l +l+mvF K DP i   yD+ Lv  eLk
  gi|1961555   736 PENEKVVNEMFSEWPFYRSRLSMLDMVFHKADPRISEAYDERLVPKELKH 785

                    FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfq
                    FG+ LR + +E    LL i G  D++  DP  K  + +R  Y+  L  +q
  gi|1961555   786 FGEALRSELKESISSLLAITGDDDIMKNDPQGKESMEIRAGYLQPLHYLQ 835

                    AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                       L RiR               A ++          n        LE
  gi|1961555   836 IELLDRIRK---------------AGDD--------AQN------TSLER 856

                    tLiLtmKGiAAGmqntG<-*
                     +++t+ GiA Gm ntG
  gi|1961555   857 AMMVTIAGIAIGMRNTG    873

gi|120600645|ref|YP_965219.1|: domain 1 of 1, from 11 to 889: score 747.3, E = 1.1e-221
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        + A LR      vs           +l + L+D +    G++  E
  gi|1206006    11    DMYASLRS----NVS-----------MLGQILgDTMRTHLGDSFLEK 42

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     l+ +   + D    e +   Lt+L   + +  Aka+   LnLAn
  gi|1206006    43 VEQIRKLAKDSR-RGDQAAREQMLELLTALPDEELVPFAKAFNQFLNLAN 91

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    L E  +   R   ++                 +E  l ++
  gi|1206006    92 LSEQFHTISRNCDELVC-----------VPDPVEQLLGRMLNGR-IDQTK 129

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + + LK   +DLvltAHPt   RR L+qK a i  CL+      +   ++
  gi|1206006   130 MLDCLKTLDIDLVLTAHPTEISRRTLIQKYAAIVDCLTEQENDQLSDRER 179

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + +   L   i   + t EiRR +PtP DE R G+s i E +W+ vP FL
  gi|1206006   180 QQINLRLRQLIAQIWHTNEIRRERPTPVDEARWGLSTIEESLWHAVPDFL 229

                    RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R  +D   +  G    lP d+  ++FssWmGGDRDG nP vt  vt +v
  gi|1206006   230 RQLnDQVQQRTG--QQLPIDIAPVRFSSWMGGDRDG-NPFVTSKVTQEVL 276

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                       R  Aa l++  +  L+ Elsm   ndEL++       t
  gi|1206006   277 DRNRHAAARLFLKDIVLLVGELSMEEANDELKA------YTNNNC----- 315

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                              EPYR +L   R +L  t +     +     e+
  gi|1206006   316 -----------EPYRHVLRSLRQRLRDTIDYLNARIEGHNPEVDKSSLIW 354

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  +   PLE+ YksL +CG + iA G LLD+LR    FG+ + +LDiRq
  gi|1206006   355 QESDLKVPLEMLYKSLTDCGMRLIANGLLLDILRRLACFGIHMLRLDIRQ 404

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    ++ R+ Dvl  +t+ L++G +  W E  +q +Ll EL+ +RPL++s
  gi|1206006   405 DASRHSDVLAELTRYLGMGDFNHWDETEKQAFLLRELSNRRPLIPSNWQP 454

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      +v++vl++ r +A  P  + G+Y+isma  PsDvL v LL +E g  +
  gi|1206006   455 SADVAEVLNTCRLIAKHPAKALGSYVISMAGKPSDVLTVLLLLKETGCSH 504

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    ++rvvPLFE L DL+ A A +  L  iDWY+    G qevm+GYsDs KD
  gi|1206006   505 PMRVVPLFETLSDLNNAAACITDLLDIDWYRGYTKGMQEVMIGYSDSAKD 554

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++AAW  Y+AqE ++ v K+ GvKL+lFHGRGG +GRGGGP H AiL
  gi|1206006   555 AGVMAAAWAQYRAQEQLVAVCKQAGVKLTLFHGRGGSIGRGGGPAHKAIL 604

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A LE  + PP
  gi|1206006   605 SQPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVLEATLLPPP 654
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                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk EWR+ m+++A      YR +v  EP Fv YFR AtPE+E Gk+ +G
  gi|1206006   655 EPKQEWRNCMQRIAEESVGAYRGIVRDEPDFVAYFRAATPEVELGKLPLG 704

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+  GGiesLRAiPWiFaW q R  LP WLG G A + A ++
  gi|1206006   705 SRPAKRRVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALQAASERG-- 752

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     +  L++m +eWPFF   + +lEmv+AK +P +A  y+  Lv  +L+  G
  gi|1206006   753 EMGLLQDMEREWPFFSTRISMLEMVYAKAEPNLARYYETCLVPKDLHHLG 802

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    + LR++     + +L++     l+   P+ +  ++LR++Yi  Ln +q
  gi|1206006   803 ETLRQRLDLGIKVVLELTKSDSLMAHTPWNRESVKLRNPYIDPLNFLQTE 852

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R             KE  + +   a e v+L             L
  gi|1206006   853 LLARTR-------------KETTETP---ASEHVQLA------------L 874

                    iLtmKGiAAGmqntG<-*
                    +Lt+ G+AAGm ntG
  gi|1206006   875 MLTIAGVAAGMRNTG    889

gi|146294801|ref|YP_001185225.1|: domain 1 of 1, from 11 to 889: score 747.2, E = 1.2e-221
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        + A LR      vs           +l + L+D +    G++  E
  gi|1462948    11    DMYASLRS----NVS-----------MLGQILgDTMRTHLGDSFLEK 42

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     l+ +   + D    e +   Lt+L   + +  Aka+   LnLAn
  gi|1462948    43 VEQIRKLAKDSR-RGDQAAREQMLELLTALPDEELVPFAKAFNQFLNLAN 91

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    L E  +   R   ++                 +E  l ++
  gi|1462948    92 LSEQFHTISRNCDELVC----------VPDPVEQLLGRMLNGR-IDQTK 129

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + + LK   +DLvltAHPt   RR L+qK a i  CL+      +   ++
  gi|1462948   130 MLDCLKTLDIDLVLTAHPTEISRRTLIQKYAAIVDCLTEQENDQLSDRER 179

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + +   L   i   + t EiRR +PtP DE R G+s i E +W+ vP FL
  gi|1462948   180 QQINLRLRQLIAQIWHTNEIRRERPTPVDEARWGLSTIEESLWHAVPDFL 229

                    RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R  +D   +  G    lP d+  ++FssWmGGDRDG nP vt  vt +v
  gi|1462948   230 RQLnDQVQQRTG--QQLPIDIAPVRFSSWMGGDRDG-NPFVTAKVTQEVL 276

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                       R  Aa l++  +  L+ Elsm   ndEL++       t
  gi|1462948   277 DRNRHAAARLFLKDIVLLVGELSMEEANDELKA------YTNNNC----- 315

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR +L   R +L  t +     +     e+
  gi|1462948   316 -----------EPYRHVLRSLRQRLRDTIDYLNARIEGHNPEVDKSSLIW 354

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  +   PLE+ YksL +CG + iA G LLD+LR    FG+ + +LDiRq
  gi|1462948   355 QESDLKVPLEMLYKSLTDCGMRLIANGLLLDILRRLACFGIHMLRLDIRQ 404

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    ++ R+ Dvl  +t+ L++G +  W E  +q +Ll EL+ +RPL++s
  gi|1462948   405 DASRHSDVLAELTRYLGMGDFNHWDETEKQAFLLRELSNRRPLIPSNWQP 454

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      +v++vl++ r +A  P  + G+Y+isma  PsDvL v LL +E g  +
  gi|1462948   455 SADVAEVLNTCRLIAKHPAKALGSYVISMAGKPSDVLTVLLLLKETGCSH 504

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
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                    ++rvvPLFE L DL+ A A +  L  iDWY+    G qevm+GYsDs KD
  gi|1462948   505 PMRVVPLFETLSDLNNAAACITDLLDIDWYRGYTKGMQEVMIGYSDSAKD 554

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++AAW  Y+AqE ++ v K+ GvKL+lFHGRGG +GRGGGP H AiL
  gi|1462948   555 AGVMAAAWAQYRAQEQLVAVCKQAGVKLTLFHGRGGSIGRGGGPAHKAIL 604

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A LE  + PP
  gi|1462948   605 SQPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVLEATLLPPP 654

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk EWR+ m+++A      YR +v  EP Fv YFR AtPE+E Gk+ +G
  gi|1462948   655 EPKQEWRNCMQRIAEESVGAYRGIVRDEPDFVAYFRAATPEVELGKLPLG 704

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+  GGiesLRAiPWiFaW q R  LP WLG G A + A ++
  gi|1462948   705 SRPAKRRVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALQAASERG-- 752

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     +  L++m +eWPFF   + +lEmv+AK +P +A  y+  Lv  +L+  G
  gi|1462948   753 EMGLLQDMEREWPFFSTRISMLEMVYAKAEPNLARYYETCLVPKDLHHLG 802

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    + LR++     + +L++     l+   P+ +  ++LR++Yi  Ln +q
  gi|1462948   803 ETLRQRLDLGIKVVLELTKSDSLMAHTPWNRESVKLRNPYIDPLNFLQTE 852

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R            KE  + +   a e v+L           L
  gi|1462948   853 LLARTR-------------KETTETP---ASEHVQLA------------L 874

                    iLtmKGiAAGmqntG<-*
                    +Lt+ G+AAGm ntG
  gi|1462948   875 MLTIAGVAAGMRNTG    889

gi|188532292|ref|YP_001906089.1|: domain 1 of 1, from 1 to 883: score 747.1, E = 1.3e-221
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  ++    vs           +l k L+D ++D  Ge++ +
  gi|1885322     1    -MNEQYSAMR-SNVS-----------MLGKLLgDTIKDALGENILDR 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       D+++ +EL + L  L   + + vA+a++  LnL n
  gi|1885322    35 VETIRKLSKSSRAGNDAHR-QELLSTLQNLSNDELLPVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +      i+         E+    E  +  t+++L  + n + +
  gi|1885322    84 VAEQYHT-----ISPNG------EGAKNPEL-LLQTFQRLKQQPNLTEAA 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v eAL   s +LvltAHPt   RR L+ K   +  CL qL   D+   +
  gi|1885322   122 VCEALGSLSLELVLTAHPTEITRRTLIHKLVEVNSCLKQLDHNDLSDYEH 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L   +  A+ tDEiR+ +P P DE + G + +   +W+GvP+FL
  gi|1885322   172 AQIMRRLRQLVAQAWHTDEIRKYRPSPVDEAKWGFAVVENSLWEGVPQFL 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R     +        lP d   ++F+sWmGGDRDG nP vt ++tR v
  gi|1885322   222 RELNEQVEA-AFGYTLPVDFVPVQFTSWMGGDRDG-NPNVTADITRHVLQ 269

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L+R  A+ l++  +  L+ Elsm  C  E+R    El   +
  gi|1885322   270 LSRWKATDLFLRDIAVLISELSMSECTPEVR----ELCGNPEAL------ 309

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR i+ + R +L  t       L       + +    +
  gi|1885322   310 ----------EPYREIMKNLRSQLMSTQAYLAGRLKGERLTRPANLLIAN 349

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRqE
  gi|1885322   350 -EQLWEPLYTCYQSLQACGMGIIANGQLLDTLRRVKCFGVPLVRIDIRQE 398
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                    seRqtDvlDAitthLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s R+t+ +  it+ L++G Y +WsE  +q +L+ EL  KRPL +
  gi|1885322   399 STRHTEAIAEITRYLGLGDYESWSEADKQAFLIRELNSKRPLTPRQWEPS 448

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     + k+vld+ rv AE P  s  aY+isma +PsDvLAv LL +E g+  +
  gi|1885322   449 ADTKEVLDTCRVAAEAPKGSIAAYVISMAKTPSDVLAVHLLLKEAGIDYA 498

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    ++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDA
  gi|1885322   499 MPVAPLFETLDDLNNANGVMSQLLNIDWYRGLIQGKQMVMIGYSDSAKDA 548

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Ls
  gi|1885322   549 GVMAASWAQYQAQDALIKTCEKAGITLTLFHGRGGSIGRGGAPAHAALLS 598

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|1885322   599 QPPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLSLYTGAILEANLLPPPE 648

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EW  +me++  v    YR  v     Fv YFR+AtPE E  k+ +Gs
  gi|1885322   649 PKTEWIGIMERLSAVSCKMYRGYVREHAEFVPYFRSATPEQELAKLPLGS 698

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA +  ++   +
  gi|1885322   699 RPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQQVMEDGHQD 748

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                      +L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lv   L+P Gk
  gi|1885322   749 --QLEAMCRDWPFFSTRLGMLEMVFSKADLWLAEYYDQRLVDKSLWPLGK 796

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LRd+ +   + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|1885322   797 QLRDQLESDIKAVLTIANDAHLMADQPWIAESIALRNVYTDPLNVLQAEL 846

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R             +E A  +           p  rv    E  L+
  gi|1885322   847 LHRSRQ------------QEKAGGE-----------PDARV----EQALM 869

                    LtmKGiAAGmqntG<-*
                    +t+ G+AAGm ntG
  gi|1885322   870 VTIAGVAAGMRNTG    883

gi|261343020|ref|ZP_05970878.1|: domain 1 of 1, from 1 to 883: score 747.0, E = 1.4e-221
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L    vs           +l k L+D ++D  Ge++ +
  gi|2613430     1    -MNEQYSALR-SNVS-----------MLGKVLgDTIKDALGENILDR 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls       ++++ +EL + L  L   + + vA+a++  LnLAn
  gi|2613430    35 VETIRKLSKSSRAGNEAHR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  +      i+         Ea    E  i  tl+kL  + +   +
  gi|2613430    84 TAEQYH-----SISPNG------EAASNPEV-IARTLRKLKDQPDLNEDI 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  A+   s +LvltAHPt   RR L+ K   +  CL qL  KD+   ++
  gi|2613430   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNSCLKQLDNKDIADYER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|2613430   172 NQLMRRLRQLIAQSWHTDEIRKHRPSPVDEAKWGFAVVENSLWEGVPNYL 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G   RlP d   ++F+sWmGGDRDG nP vt E+tR v
  gi|2613430   222 RELNEQLeENLGY--RLPVDFVPVRFTSWMGGDRDG-NPNVTAEITRHVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
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                    LL+R  A+ l++  +  L+ Elsm     ELR+ A E     a++
  gi|2613430   269 LLSRWKATDLFLKDIQVLISELSMVEATPELRALAGE---EGASE----- 310

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                                PYR ++   R +L  t       L +G      e
  gi|2613430   311 ------------PYRYLMKKLRGQLMATQAWLEARL-KGQRLPKPEGLLS 347

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    + E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+Rq
  gi|2613430   348 QNEQLWEPLYACYQSLQACGMGIIANGELLDTLRRVKCFGVPLVRIDVRQ 397

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+t+ l  +t+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|2613430   398 ESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRSWEP 447

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      + ++vl++ + + + P  s  aY+isma +PsDvL v LL +E g+
  gi|2613430   448 SNDTREVLNTCKAIVDAPKGSVAAYVISMAKTPSDVLGVHLLLKEAGIDY 497

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    +L+v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|2613430   498 ALPVAPLFETLDDLNNANDVMTQLLNIDWYRGFIQGKQMVMIGYSDSAKD 547

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|2613430   548 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 597

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2613430   598 SQPPGSLKGGLRVTEQGEMIRFKYGLPEVTISSLSLYTSAILEANLLPPP 647

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  W ++m+e+  +  + YR  v     Fv YFR+AtPE E Gk+ +G
  gi|2613430   648 EPKASWCHIMDELSDISCDLYRGYVRENKDFVPYFRSATPEQELGKLPLG 697

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG GAA +  ++ D K
  gi|2613430   698 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQKVVE-DGK 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lv  eL+  G
  gi|2613430   747 Q-SELESMCRDWPFFSTRLGMLEMVFSKADLWLAEYYDQRLVKPELWALG 795

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    k+LR+  +   + +L iA    l+E  P++   + LR+ Y   Lnv+qA
  gi|2613430   796 KELRELLEGDIKVVLDIANDSHLMEDLPWIAESIQLRNVYTDPLNVLQAE 845

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R               A+E+            +++  P +E  L
  gi|2613430   846 LLHRSR---------------LAEEE-----------GKEPDPRVEQAL 868

                    iLtmKGiAAGmqntG<-*
                    ++t+ G+AAGm ntG
  gi|2613430   869 MVTIAGVAAGMRNTG    883

gi|126176310|ref|YP_001052459.1|: domain 1 of 1, from 11 to 889: score 746.7, E = 1.7e-221
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        + A LR      vs           +l + L+D +    G++  E
  gi|1261763    11    DMYASLRS----NVS-----------MLGQILgDTMRTHLGDSFLEK 42

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     l+ +   + D    e +   Lt+L   + +  Aka+   LnLAn
  gi|1261763    43 VEQIRKLAKDSR-RGDQAAREQMLELLTALPDEELVPFAKAFNQFLNLAN 91

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    L E  +   R   ++                +E  l ++
  gi|1261763    92 LSEQFHTISRNCDELVC----------VPDPVEQLLGRMLNGR-VDQTK 129

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + + LK   +DLvltAHPt   RR L+qK a i  CL+      +   ++
  gi|1261763   130 MLDCLKTLDIDLVLTAHPTEISRRTLIQKYAAIVDCLTEQENDQLSDRER 179
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                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + +   L   i   + t EiRR +PtP DE R G+s i E +W+ vP FL
  gi|1261763   180 QQISLRLRQLIAQIWHTNEIRRERPTPVDEARWGLSTIEESLWHAVPDFL 229

                    RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R  +D   +  G    lP d+  ++FssWmGGDRDG nP vt  vt +v
  gi|1261763   230 RQLnDQVQQRTG--QQLPIDIAPVRFSSWMGGDRDG-NPFVTAKVTQEVL 276

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                       R  Aa l++  +  L+ Elsm   ndEL++       t  +
  gi|1261763   277 DRNRHAAARLFLKDIVLLVGELSMEEANDELKA------YTNNSC----- 315

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                              EPYR +L  +R +L  t +     +     e+
  gi|1261763   316 -----------EPYRHVLRSIRQRLRDTIDYLNARIEGHNPEVDKSSLIW 354

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  +   PLE+ YksL +CG + iA G LLD+LR    FG+ + +LDiRq
  gi|1261763   355 QESDLKAPLEMLYKSLTDCGMRLIANGLLLDILRRLACFGIHMLRLDIRQ 404

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    ++ R+ Dvl  +t+ L++G +  W E  +q +Ll EL+ +RPL++s
  gi|1261763   405 DASRHSDVLAELTRYLGMGDFNHWDETEKQAFLLRELSNRRPLIPSNWQP 454

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      +v++vl++ r +A  P  + G+Y+isma  PsDvL v LL +E g  +
  gi|1261763   455 SADVAEVLNTCRLIAKHPAKALGSYVISMAGKPSDVLTVLLLLKETGCSH 504

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    ++rvvPLFE L DL+ A A +  L  iDWY+    G qevm+GYsDs KD
  gi|1261763   505 PMRVVPLFETLSDLNNAAACITDLLDIDWYRGYTKGMQEVMIGYSDSAKD 554

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++AAW  Y AqE ++ v K+ GvKL+lFHGRGG +GRGGGP H AiL
  gi|1261763   555 AGVMAAAWAQYHAQEQLVAVCKQAGVKLTLFHGRGGSIGRGGGPAHKAIL 604

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A LE  + PP
  gi|1261763   605 SQPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVLEATLLPPP 654

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR+ m+++A      YR +v  EP Fv YFR AtPE+E Gk+ +G
  gi|1261763   655 EPKQQWRDCMQRIAEESVGAYRGIVRDEPDFVAYFRAATPEVELGKLPLG 704

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+  GGiesLRAiPWiFaW q R  LP WLG G A + A ++
  gi|1261763   705 SRPAKRRVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALQAASERG-- 752

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     +  L++m +eWPFF   + +lEmv+AK +P +A  y+  Lv  +L+  G
  gi|1261763   753 EMGLLQDMEREWPFFSTRISMLEMVYAKAEPNLARYYETCLVPKDLHHLG 802

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    + LR++     + +L++     l+   P+ +  ++LR++Yi  Ln +q
  gi|1261763   803 ETLRQRLDLGIKVVLELTKSDSLMAHTPWNRESVKLRNPYIDPLNFLQTE 852

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R             KE  + +   a e v+L             L
  gi|1261763   853 LLARTR-------------KETTETP---ASEHVQLA------------L 874

                    iLtmKGiAAGmqntG<-*
                    +Lt+ G+AAGm ntG
  gi|1261763   875 MLTIAGVAAGMRNTG    889

gi|260772057|ref|ZP_05880974.1|: domain 1 of 1, from 1 to 877: score 746.0, E = 2.8e-221
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  +  +L    vs           +l + L+  +q   G+ +
  gi|2607720     1    -MNEKYAALK-SNVS----------MLGRLLgQTIQAADGDVILAK 34

                    vqECYEl..sAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
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                v     l++sA    + D +KL E    +  L+      vA+a+   LnL
gi|2607720    35 VETIRQLskSARAGNQADREKLIE---EIKHLNNDQLTPVARAFNQFLNL 81

                AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                 n+A+  +   R     +       Ea+A     +   + kL  k   s
gi|2607720    82 TNIADQYHTISRHSEDHLG------EANA-----LQSLFAKLADKK-ISQ 119

                eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                 +  +A++   ++LvltAHPt   RR ++    +i  CL+ L   D+
gi|2607720   120 FDAIQAVRDLNIELVLTAHPTEITRRTMINNLVKINQCLSNLELSDLSSK 169

                DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                +++  +  L   i   +  D iR+ +PtP DE + G + +   +W+ vP
gi|2607720   170 ERQKTERRLEQLIAQGWHSDVIRKQRPTPLDEAKWGFAVVENSLWQAVPE 219

                FLRRvDtALK.niGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                FLR     +K n+G  E lP d+  ++FssWmGGDRDG nP vt  vtR+
gi|2607720   220 FLRELNDNIKaNLG--EGLPIDARPVHFSSWMGGDRDG-NPFVTHSVTRE 266

                vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                v LL+R  Aa lY+  + +L+ Elsm +C d LR+ A E       +
gi|2607720   267 VLLLSRWKAADLYLADINELISELSMTKCTDALRALAGE------EE--- 307

                KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                             EPYR +L  vR  L  t +     L +G   ++  A
gi|2607720   308 ------------HEPYRAVLKGVRHLLQDTLDILDSKL-HG-QKLAVKAP 343

                ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                     +  +PL  CY+sL eCG  viADGsLLD LR v  FG+ Lv+LDi
gi|2607720   344 LRTESQLWDPLYACYQSLHECGMGVIADGSLLDALRRVKAFGVHLVRLDI 393

                RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                RqEs R+ + l  +t+ L+iG Y +WsE+ +  +L  EL+ KRPLl+ D
gi|2607720   394 RQESSRHAEALSELTRYLGIGDYNQWSEQDKLAFLTNELSSKRPLLPLDW 443

                PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                   E vk+vl++ +++A  P D+FGaY+isma + sDvLAv LL +E g
gi|2607720   444 QPSESVKEVLETCKIIAAQPQDAFGAYVISMAHTASDVLAVHLLLKESGC 493

                kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsG
                   + v PLFE L DL+ A   +++L +iD Y+  i+ +q vm+GYsDs
gi|2607720   494 PYRMSVCPLFETLDDLNNAESVIKQLLAIDLYRGFIQNQQMVMIGYSDSA 543

                KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                KDAG ++A W  Y+A E+++Kv  +  + L+lFHGRGG +GRGG P H A
gi|2607720   544 KDAGVMAAGWAQYRAMEDLVKVCEEESIDLTLFHGRGGSIGRGGAPAHAA 593

                iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP
                +LsqPP  ++  lRvt qGE+i f  G  ++   sL  ++ A LE  + P
gi|2607720   594 LLSQPPKSLKAGLRVTEQGEMIRFKLGLPEVAINSLHLYASAILEANLLP 643

                PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmn
                P  Pk EWR+Lme +  v  E YR++v  EP Fv YFR AtPElE Gk+
gi|2607720   644 PPEPKQEWRDLMEVLSQVSCEAYRAIVRGEPDFVPYFRQATPELELGKLP 693

                iGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                +GsRPaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ +dK
gi|2607720   694 LGSRPAKRNPQGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSVDKG 743

                iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP
                 + l  L+Em +eWPFF   l +lEmv+ K    +   yD+ Lv   L+P
gi|2607720   744 HQAL--LEEMCREWPFFSTRLGMLEMVYTKCNLDVSRYYDQRLVEPTLRP 791

                FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfq
                 G++LRd+ +   + +L +     l+  DP+    +RLR+ Y+  Ln++q
gi|2607720   792 LGDRLRDQLQKDIKAVLNVENNENLMQSDPWGHESIRLRNIYVEPLNMLQ 841

                AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                A  L R R                                + +  P LE+
gi|2607720   842 AELLYRTRQ------------------------------STEADPELEE 860
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                  tLiLtmKGiAAGmqntG<-*
                   L++t+ GiAAGm ntG
  gi|2607720   861 ALMVTIAGIAAGMRNTG    877

gi|167626000|ref|YP_001676294.1|: domain 1 of 1, from 3 to 878: score 745.9, E = 2.9e-221
                  *->siDAqLRlLvP..GKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                      + A LR  v + G++    + i+ D  L D FLD +     e+++
  gi|1676260     3    DMYASLRSNVGtlGQIL--GDTIRTD--LDDTFLDKI-----EQIRH 40

                  avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                           A    + D+    E+ + L sL   + +  Aka+   LnLA
  gi|1676260    41 L--------AKSSRQGDSAARKEMLTLLSSLSDDELVPFAKAFNQFLNLA 82

                  nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                  n+AE  +   R   ++                +E  l ++ l +n   e
  gi|1676260    83 NIAEQFHTISRNCDELVC-----------VPDPVEQLLGRM-LGGNIDQE 120

                  EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                   v   LK   +DLvltAHPt   RR L+qK + +   L+      +t ++
  gi|1676260   121 KVLACLKTLDIDLVLTAHPTEISRRTLIQKYSAVIDSLTAQENTQLTEQE 170

                  KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                  Kk     L   i   + t EiR  +PtP DE R G+  i   +W+ vP F
  gi|1676260   171 KKQHHLRLRQLIAQIWHTNEIRNERPTPVDEARWGLCTIEASLWQAVPDF 220

                  LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                  LR     +     n  lP d+  ++FssWmGGDRDG nP vt  vt +v
  gi|1676260   221 LRQLNQQVEE-RTNTQLPTDIAPVRFSSWMGGDRDG-NPFVTSAVTQEVL 268

                  LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     R  Aa lY+  v  L+ Elsm   n+ L      l  t  ++
  gi|1676260   269 DRNRHTAARLYLKDVVLLVNELSMEGANEAL------LAYTNNSN----- 307

                  YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                             EPYR +L   R KL nt +     L     ++    +
  gi|1676260   308 -----------EPYRDVLRTLRQKLRNTIDYLNGRLEGQHPDVDPSEIIW 346

                  kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                  +  +  +PL + Y+sLC+ G   iA G LLD+LR +  FG+ + +LD+Rq
  gi|1676260   347 HESDLKDPLMMLYQSLCDRGMSLIANGLLLDMLRRIACFGIHMLRLDVRQ 396

                  EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                  +++R+ Dv+  +t+ L++G Y  W E  +q +Ll EL+ KRPL+++
  gi|1676260   397 DADRHADVIAELTRYLGMGDYAHWDETEKQSFLLRELSSKRPLIPANWQA 446

                  tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                    Ev++v+ + r +A  P  + G+Y+isma  PsDvLAv LL +E g  +
  gi|1676260   447 SPEVEEVVKTCRLVATQPARAMGSYVISMASQPSDVLAVLLLLKETGCPH 496

                  tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                  ++rvvPLFE L DL+ A A +  LFsiDWY+    G qevm+GYsDs KD
  gi|1676260   497 PMRVVPLFETLDDLNNASACMSALFSIDWYRGYTKGIQEVMIGYSDSAKD 546

                  AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                  AG ++AAW  Y AqE ++ + ++  +KL+lFHGRGGt+GRGGGP H AiL
  gi|1676260   547 AGVMAAAWAQYTAQEKLVAISQEANIKLTLFHGRGGTIGRGGGPAHEAIL 596

                  sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                  sqPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A +E  + PP
  gi|1676260   597 SQPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVMEATLLPPP 646

                  sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                   PkPEWR+ m+++A      YR++v  EP Fv YFR AtPE+E Gk+ +G
  gi|1676260   647 EPKPEWRQCMQQLAEESVLAYRAIVREEPDFVSYFRAATPEIELGKLPLG 696

                  sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                  sRPaKR+  GGiesLRAiPWiFaW q R  LP WLG G A K A ++
  gi|1676260   697 SRPAKRRVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALKAASERG-- 744

                  nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                   l  L+Em k WPFF+  + +lEmv+AK +P +   y+  Lv  eL+  G
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  gi|1676260   745 DLPLLQEMEKHWPFFKTRISMLEMVYAKAEPNLSKFYETSLVPKELHHLG 794

                   ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    +LR++     + +L++     l+   P+ +  + LR++Yi  Ln +qA
  gi|1676260   795 VQLRERLAIGIEAVLELTQAESLMAHTPWNRESVELRNPYIDPLNFLQAE 844

                   tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    L R R              E    n       v+L             L
  gi|1676260   845 LLARTR------------REEQSSKN-------VELA------------L 863

                   iLtmKGiAAGmqntG<-*
                   +Lt+ G+AAGm ntG
  gi|1676260   864 MLTIAGVAAGMRNTG    878

gi|145630943|ref|ZP_01786719.1|: domain 1 of 1, from 2 to 879: score 745.0, E = 5.7e-221
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                          q        +s           +l +FL++ + D  Ged+ E
  gi|1456309     2    ---TQEYSTLRNNIS-----------MLGRFLgETINDAQGEDILEL 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +     ls +     D  + +EL   L s+     i vA+a++  LnL n
  gi|1456309    35 IENIRKLSRNSRAGDDKAR-QELLDTLGSISNENIIPVARAFSQFLNLTN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +   R     +                + E +K+L  +   s eE
  gi|1456309    84 IAEQYQTISREHSLAQS-----------SSQSLSELFKRLKEQN-ASVEE 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   v   +    ++LvltAHPt   RRsL+ K+  i  CL++L   D+t  ++
  gi|1456309   122 VHKTVEKLLIELVLTAHPTETTRRSLIHKHIEINKCLSKLEHHDLTEKER 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     ++  L R i  A+ t EiR  +PtP DE + G + +   +W+ vP FL
  gi|1456309   172 NIIERLLLRLIAEAWHTNEIRTVRPTPFDEAKWGFAMLENSLWQAVPEFL 221

                   RRvDtALKniGinERlPYdvPL....ikFssWmGGDRDGknPRvtPEvtR
                   R       n    E l Yd P++ ++++ ssWmGGDRDG nP vt  +t+
  gi|1456309   222 RQL-----NETTREFLGYDLPVglkpVRISSWMGGDRDG-NPFVTAQITK 265

                   DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                    v   aR  Aa l+++ +  L  Elsm +C dE Rv            k
  gi|1456309   266 KVLYFARWKAADLFLQDISKLADELSMMKCSDEFRV------------KY 303

                   vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                     +           EPYR ++ + R +L  t       L      +sE
  gi|1456309   304 GNHL----------EPYRFVVKNLRNQLTATLAYFDDHLSNRTPRVSESE 343

                   vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                   +  +  +  EPL  CY+sL +CG ++iA GsLLD+L  +s FG+ L ++D
  gi|1456309   344 IILEDNQLWEPLYDCYQSLIQCGMRIIANGSLLDILHRISCFGVTLSQMD 393

                   iRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
                   iRqEs R+tD +  it  +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|1456309   394 IRQESTRHTDAIAEITHYIGLGDYAQWTEDDKQAFLIRELSSRRPLIPQN 443

                   LPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECg
                        E +++ld+ +v+A         Y+isma   sDvLAv LL +E g
  gi|1456309   444 WTPSPETQEILDTCKVIAQQKQGVIACYVISMARNASDVLAVHLLLKEAG 493

                   vkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDs
                   v   ++vvPLFE L DL+AA   + +LF + WY+  i+ +q vm+GYsDs
  gi|1456309   494 VSYHIPVVPLFETLEDLDAAEKVMTQLFNVGWYRGVINNRQMVMIGYSDS 543

                   GKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHL
                    KDAG ++A W  Y+AqE ++    k G+ L+lFHGRGGt+GRGG P H
  gi|1456309   544 AKDAGMMAASWAQYRAQEALVNLTEKLGIELTLFHGRGGTIGRGGAPAHA 593

                   AiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmn
                   A+LsqPP  ++  lRvt qGE+i f  G   +   +   ++ A LE  +
  gi|1456309   594 ALLSQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVETFDLYASAILEANLL 643
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                    PPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkm
                    PP  PkPEWR++m+e+  +  + YR vv  +  Fv YFR+AtPE E  k+
  gi|1456309   644 PPPEPKPEWRNIMDELSTISCDIYRGVVRGDKDFVPYFRSATPEQELSKL 693

                    niGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidK
                     +GsRPaKR P GG+esLRAiPWiFaW q R  LP WLG  AA +  i++
  gi|1456309   694 PLGSRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGASAAIRQIIEQ 743

                    DiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk
                        +  ++ m ++WPFF   + +lEmvF K D  +   yD+ Lv  eL+
  gi|1456309   744 GKGDI--IHKMCENWPFFSTRIGMLEMVFSKSDTWLSQQYDQRLVKKELW 791

                    PFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvf
                      G++LR + ++  + +L +    +l+   P++   + LR+ Y   Ln +
  gi|1456309   792 YLGENLRKQLEDDIQTVLSLSHQSELMSDLPWIADSIALRNIYTDPLNLL 841

                    qAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLE
                    q   L R R                  En             e+v P +E
  gi|1456309   842 QVELLHRFR------------------EN------------PEQVNPDVE 861

                    DtLiLtmKGiAAGmqntG<-*
                      L++t+ GiAAGm ntG
  gi|1456309   862 QALMITITGIAAGMRNTG    879

gi|157960054|ref|YP_001500088.1|: domain 1 of 1, from 3 to 878: score 745.0, E = 5.7e-221
                    *->siDAqLRlLvP..GKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                        + A LR  v + G++    + i+ D  L D FL+ +     e+++
  gi|1579600     3    DMYASLRSNVGtlGQIL--GDTIRTD--LDDTFLEKI-----EQIRH 40

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                             A    + D    eE+ + L sL   + +  Aka+   LnLA
  gi|1579600    41 L--------AKSSRQGDDASREEMLTLLSSLSDDELVPFAKAFNQFLNLA 82

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE  +   R   ++                  +E  l ++        e
  gi|1579600    83 NIAEQFHTISRNCDELVC-----------VPDPVEQLLGRMLGGK-IDQE 120

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                     v   LK   +DLvltAHPt   RR L+qK + +   L+ L    +t ++
  gi|1579600   121 KVLACLKTLDIDLVLTAHPTEISRRTLIQKYSAVIDSLTALENTQLTEQE 170

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    Kk     L   i   + t EiR  +PtP DE R G+s i   +W+ +P F
  gi|1579600   171 KKQHHLRLRQLIAQIWHTNEIRNERPTPVDEARWGLSTIEASLWQAIPDF 220

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    LR     +     n  lP d+  ++FssWmGGDRDG nP vt  vt +v
  gi|1579600   221 LRQLNQQVEE-RTNTQLPIDIAPVRFSSWMGGDRDG-NPFVTSTVTQEVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                       R  Aa lY+  v  L+ Elsm   n+EL      l     ++
  gi|1579600   269 DRNRHTAARLYLKDVVLLVNELSMEGANEEL------LAYCNNSN----- 307

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR +L d R KL  t +     L     ++    +
  gi|1579600   308 -----------EPYRDVLRDLRKKLRATIDYLNEKLEGHQPDVNPKDIIW 346

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  +  +PL + YksLC+ G   iA G LLD+LR +  FG+ + +LD+Rq
  gi|1579600   347 HESDLKDPLMMLYKSLCDQGMSLIANGLLLDMLRRIACFGIHMLRLDVRQ 396

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    +++R+ Dv+  +t+ L++G Y  W E  +q +Ll EL+ KRPL+++
  gi|1579600   397 DAQRHADVIAELTRYLGMGDYAHWDESEKQSFLLRELSSKRPLIPANWQA 446

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      Ev++v+ + r +A  P  + G+Y+isma  PsDvLAv LL +E g  +
  gi|1579600   447 SAEVEEVVKTCRLVASQPARAMGSYVISMASQPSDVLAVLLLLKETGCPH 496

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    ++rvvPLFE L DL+ A   +  LF+iDWY+    G qevm+GYsDs KD
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  gi|1579600   497 PIRVVPLFETLDDLNNASNCMSALFAIDWYRGYTKGIQEVMIGYSDSAKD 546

                   AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                   AG ++AAW  Y AqE ++ + ++  +KL+lFHGRGGt+GRGGGP H AiL
  gi|1579600   547 AGVMAAAWAQYTAQEKLVAISQEANIKLTLFHGRGGTIGRGGGPAHQAIL 596

                   sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                   sqPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A +E  + PP
  gi|1579600   597 SQPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVMEATLLPPP 646

                   sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                    PkPEWR+ m+++A      YR++v  EP Fv YFR AtPE+E Gk+ +G
  gi|1579600   647 EPKPEWRQCMQQLADESVVAYRAIVREEPDFVSYFRAATPEIELGKLPLG 696

                   sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                   sRPaKR+  GGiesLRAiPWiFaW q R  LP WLG G A K A ++
  gi|1579600   697 SRPAKRRVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALKAASERG-- 744

                   nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                    l  L+Em k WPFF+  + +lEmv+AK +P +   y+  Lv  eL+  G
  gi|1579600   745 DLALLQEMEKHWPFFKTRISMLEMVYAKAEPNLSKFYETSLVPSELHHLG 794

                   ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    +LR++     + +L++     l+   P+ +  + LR++Yi  Ln +qA
  gi|1579600   795 VQLRERLATGVEAVLELTQAESLMAHTPWNRESVELRNPYIDPLNFLQAE 844

                   tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    L R R              E    n       v+L             L
  gi|1579600   845 LLARTR------------REEQSSQN-------VELA------------L 863

                   iLtmKGiAAGmqntG<-*
                   +Lt+ G+AAGm ntG
  gi|1579600   864 MLTIAGVAAGMRNTG    878

gi|148828375|ref|YP_001293128.1|: domain 1 of 1, from 2 to 879: score 744.9, E = 6.1e-221
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                          q        +s           +l +FL++ + D  Ged+ E
  gi|1488283     2    ---TQEYSTLRNNIS-----------MLGRFLgETINDAQGEDILEL 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +     ls +     D  + + L   L s+     i vA+a++  LnL n
  gi|1488283    35 IENIRKLSRNSRAGDDKAR-QALLDTLGSISNENIIPVARAFSQFLNLTN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +   R     +               + E +K+L  +   s eE
  gi|1488283    84 IAEQYQTISREHSLAQS-----------SSQSLSELFKRLKEQN-ASVEE 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   v   +    ++LvltAHPt   RRsL+ K+  i  CL++L   D+t  ++
  gi|1488283   122 VHKTVEKLLIELVLTAHPTETTRRSLIHKHIEINKCLSKLEHHDLTEKER 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     ++  L R i  A+ t EiR  +PtP DE + G + +   +W+ vP FL
  gi|1488283   172 NIIERLLLRLIAEAWHTNEIRTVRPTPFDEAKWGFAMLENSLWQAVPEFL 221

                   RRvDtALKniGinERlPYdvPL....ikFssWmGGDRDGknPRvtPEvtR
                   R       n    E l Yd P++ ++++ ssWmGGDRDG nP vt  +t+
  gi|1488283   222 RQL-----NETTREFLGYDLPVglkpVRISSWMGGDRDG-NPFVTAQITK 265

                   DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                    v   aR  Aa l+++ +  L  Elsm +C dE R            dk
  gi|1488283   266 KVLYFARWKAADLFLQDISKLADELSMMKCSDEFR------------DKY 303

                   vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                     +           EPYR ++ + R +L  t       L      +sE
  gi|1488283   304 GEHL----------EPYRFVVKNLRNQLTATLAYFDDHLSNRTPRVSESE 343

                   vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                   +  +  +  EPL  CY+sL +CG ++iA GsLLD+L  +s FG+ L ++D
  gi|1488283   344 IILEDNQLWEPLYDCYQSLIQCGMRIIANGSLLDILHRISCFGVTLSQMD 393
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                    iRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
                    iRqEs R+tD +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|1488283   394 IRQESTRHTDAIAEITRYIGLGDYSQWMEDDKQAFLIRELSSRRPLIPQN 443

                    LPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECg
                         E k++ld+ +v+A         Y+isma + sDvLAv LL +E g
  gi|1488283   444 WTPSPETKEILDTCKVIAQQKQGVIACYVISMARSASDVLAVHLLLKESG 493

                    vkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDs
                    v   ++vvPLFE L DL+AA   + +LF + WY+  i+ +q vm+GYsDs
  gi|1488283   494 VPYHIPVVPLFETLEDLDAAEKVMTQLFNVGWYRGVINNRQMVMIGYSDS 543

                    GKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHL
                     KDAG ++A W  Y+AqE ++    k G+ L+lFHGRGGt+GRGG P H
  gi|1488283   544 AKDAGMMAASWAQYRAQEALVNLTEKLGIELTLFHGRGGTIGRGGAPAHA 593

                    AiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmn
                    A+LsqPP  ++  lRvt qGE+i f  G   +   +   ++ A LE  +
  gi|1488283   594 ALLSQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVETFDLYASAILEANLL 643

                    PPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkm
                    PP  PkPEWR +m+e+  +  + YR vv  +  Fv YFR+AtPE E  k+
  gi|1488283   644 PPPEPKPEWRTIMDELSTISCDIYRGVVRGDKDFVPYFRSATPEQELSKL 693

                    niGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidK
                     +GsRPaKR P GG+esLRAiPWiFaW q R  LP WLG GAA +  i++
  gi|1488283   694 PLGSRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGAAIRQIIEQ 743

                    DiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk
                        +  ++ m ++WPFF   + +lEmvF K D  +   yD+ Lv  eL+
  gi|1488283   744 GKGDI--IHKMCENWPFFSTRIGMLEMVFSKSDTWLSQQYDQRLVKKELW 791

                    PFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvf
                      G++LR + ++  + +L +     l+   P++   + LR+ Y   Ln +
  gi|1488283   792 YLGENLRKQLEDDIQTVLSLSHQSKLMSDLPWIADSIALRNIYTDPLNLL 841

                    qAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLE
                    q   L R R                   En             e+v P +E
  gi|1488283   842 QVELLHRFR------------------EN------------PEQVNPDVE 861

                    DtLiLtmKGiAAGmqntG<-*
                      L++t+ GiAAGm ntG
  gi|1488283   862 QALMITITGIAAGMRNTG    879

gi|229846259|ref|ZP_04466371.1|: domain 1 of 1, from 2 to 879: score 744.6, E = 7.4e-221
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           q        +s           +l +FL++ + D  Ged+ E
  gi|2298462     2    ---TQEYSTLRNNIS-----------MLGRFLgETINDAQGEDILEL 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls +     D  + + L   L s+     i vA+a++  LnL n
  gi|2298462    35 IENIRKLSRNSRAGDDKAR-QALLDTLGSISNENIIPVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R     +                + E +K+L  +   s eE
  gi|2298462    84 IAEQYQTISREHSLAQS-----------SSQSLSELFKRLKEQN-ASVEE 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v   +    ++LvltAHPt   RRsL+ K+  i  CL++L   D+t  ++
  gi|2298462   122 VHKTVEKLLIELVLTAHPTETTRRSLIHKHIEINKCLSKLEHHDLTEKER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      ++  L R i  A+ t EiR  +PtP DE + G + +   +W+ vP FL
  gi|2298462   172 NIIERLLLRLIAEAWHTNEIRTVRPTPFDEAKWGFAMLENSLWQAVPEFL 221

                    RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R  ++tA   +G    lP     ++ ssWmGGDRDG nP vt  +t+ v
  gi|2298462   222 RQLnETAREFLGYD--LPVGLKPVRISSWMGGDRDG-NPFVTAQITKKVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                      aR  Aa l+++ +  L  Elsm +C dE R +  E       +
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  gi|2298462   269 YFARWKAADLFLQDISKLADELSMMKCSDEFRDKYGE-------Q----- 306

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                              EPYR ++ + R +L  t       L      +sE  +
  gi|2298462   307 ----------LEPYRFVVKNLRNQLAATLAYFDDHLSNRTPRVSESEIIL 346

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  +  EPL  CY+sL +CG ++iA GsLLD+L  +s FG+ L ++DiRq
  gi|2298462   347 EDNQLWEPLYDCYQSLIQCGMRIIANGSLLDILHRISCFGVTLSQMDIRQ 396

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+tD +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|2298462   397 ESTRHTDAIAEITRYIGLGDYSQWMEDDKQAFLIRELSSRRPLIPQNWTP 446

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E k++ld+ +v+A         Y+isma + sDvLAv LL +E gv
  gi|2298462   447 SPETKEILDTCKVIAQQKQGVIACYVISMARSASDVLAVHLLLKESGVPY 496

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                     ++vvPLFE L DL+AA   + +L+ + WY+  i+ +q vm+GYsDs KD
  gi|2298462   497 HIPVVPLFETLEDLDAAEKVMTQLYNVGWYRGVINNRQMVMIGYSDSAKD 546

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+AqE ++    k G+ L+lFHGRGGt+GRGG P H A+L
  gi|2298462   547 AGMMAASWAQYRAQEALVNLTEKLGIELTLFHGRGGTIGRGGAPAHAALL 596

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++  lRvt qGE+i f  G   +   +   ++ A LE  + PP
  gi|2298462   597 SQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVETFDLYASAILEANLLPPP 646

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     PkPEWR++m+e+  +  + YR vv  +  Fv YFR+AtPE E  k+ +G
  gi|2298462   647 EPKPEWRNIMDELSTISCDIYRGVVRGDKDFVPYFRSATPEQELSKLPLG 696

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR P GG+esLRAiPWiFaW q R  LP WLG GAA +  i++
  gi|2298462   697 SRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGAAIRQIIEQGKG 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     +  ++ m ++WPFF   + +lEmvF K D  +   yD+ Lv  eL+  G
  gi|2298462   747 DI--IHKMCENWPFFSTRIGMLEMVFSKSDTWLSQQYDQRLVKKELWYLG 794

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    ++LR + ++  + +L +    +l+   P++   + LR+ Y   Ln +q
  gi|2298462   795 ENLRKQLEDDIQTVLSLSHQSELMSDLPWIADSIALRNIYTDPLNLLQVE 844

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                 En             e+v P +E  L
  gi|2298462   845 LLHRFR------------------EN------------PEQVNPDVEQAL 864

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|2298462   865 MITITGIAAGMRNTG    879

gi|113972037|ref|YP_735830.1|: domain 1 of 1, from 11 to 889: score 744.6, E = 7.4e-221
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        + A LR      vs           +l + L+D +    G++  E
  gi|1139720    11    DMYASLRS----NVS-----------MLGQILgDTMRTHLGDSFLEK 42

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     l+ +   + D    e +   Lt+L   + +  Aka+   LnLAn
  gi|1139720    43 VEQIRKLAKDSR-RGDEAAREQMLELLTALPDEELVPFAKAFNQFLNLAN 91

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    L E  +   R   ++                +E  l ++
  gi|1139720    92 LSEQFHTISRNCDELVC-----------VPDPVEQLLGRMLNGR-IDQTK 129

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + + LK   +DLvltAHPt   RR L+qK a i  CLa      +   ++
  gi|1139720   130 MLDCLKTLDIDLVLTAHPTEISRRTLIQKYAAIVDCLAEQENNQLSDRER 179
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                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + +   L   i   + t EiRR +PtP DE R G+s i E +W+ vP FL
  gi|1139720   180 RQINLRLRQLIAQIWHTNEIRRERPTPVDEARWGLSTIEESLWHAVPDFL 229

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R     ++       lP d+  ++FssWmGGDRDG nP vt  vt +v
  gi|1139720   230 RQLNDQVQD-RTGQQLPIDIAPVRFSSWMGGDRDG-NPFVTAKVTQEVLD 277

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                      R  Aa l++  +  L+ Elsm   n+EL +       t  +
  gi|1139720   278 RNRHAAARLFLKDIVLLVGELSMEEANSELMA------YTNNSC------ 315

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR +L   R KL  t +     +     e+       +
  gi|1139720   316 ----------EPYRFVLRSLRQKLRDTIDYLNARIEGHNPEVDKSTLIWQ 355

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      +   PLE+ YksLC+CG + iA G LLD+LR    FG+ + +LDiRq+
  gi|1139720   356 ESDLKAPLEMLYKSLCDCGMRLIANGLLLDILRRLACFGIHMLRLDIRQD 405

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    + R+ Dvl  +t+ L++G +  W E  +q +Ll EL+ +RPL++s
  gi|1139720   406 AGRHCDVLAELTRYLGMGDFNHWDETEKQAFLLRELSNRRPLIPSNWQPS 455

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     +v++vl++ r +A  P  + G+Y+isma  PsDvL v LL +E g  ++
  gi|1139720   456 ADVAEVLNTCRLIAKHPAKALGSYVISMASKPSDVLTVLLLLKETGCTHP 505

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    +rvvPLFE L DL+ A   +  L  iDWY+    G qevm+GYsDs KDA
  gi|1139720   506 MRVVPLFETLSDLNNAAECITALLDIDWYRGYTKGMQEVMIGYSDSAKDA 555

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++AAW  Y+AqE ++ v K+ GvKL+lFHGRGG +GRGGGP H AiLs
  gi|1139720   556 GVMAAAWAQYRAQEQLVAVCKQAGVKLTLFHGRGGSIGRGGGPAHKAILS 605

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qP   ++G +Rvt qGE+i f FG  +L  +sL  +t A LE  + PP
  gi|1139720   606 QPLGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVLEATLLPPPE 655

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EWR+ me++A      YR +v  EP Fv YFR AtPE+E Gk+ +Gs
  gi|1139720   656 PKQEWRNCMERIAEESVSAYRGIVREEPDFVPYFRAATPEVELGKLPLGS 705

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+  GGiesLRAiPWiFaW q R  LP WLG G A + A ++
  gi|1139720   706 RPAKRRVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALQAACQRG--E 753

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    +  L++m +eWPFF   + +lEmv+AK +P +A  y+  Lv  +L+  G+
  gi|1139720   754 MGLLQDMEREWPFFSTRISMLEMVYAKAEPNLARYYETCLVPPNLHHLGE 803

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                     LR++     + +L++     l+   P+ +  ++LR++Yi  Ln +q
  gi|1139720   804 TLRQRLDLGIKVVLELTKSDTLMAHTPWNRESVKLRNPYIDPLNFLQTEL 853

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R             KE  + +   a e v+L            L+
  gi|1139720   854 LARTR-------------KETTEAP---ASEHVQLA------------LM 875

                    LtmKGiAAGmqntG<-*
                    Lt+ G+AAGm ntG
  gi|1139720   876 LTIAGVAAGMRNTG    889

gi|238754721|ref|ZP_04616073.1|: domain 1 of 1, from 1 to 878: score 744.4, E = 8.5e-221
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +  q  ++    vs          +L     + +++  Ge + + v
  gi|2387547     1    -MNEQYSAMR-SNVS----------MLGTLLGETIKEALGEHILDRV 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       ++++ +EL + L  L   + + vA+a++  LnL n
```

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gi|2387547    36 ETIRKLSKSSRAGNEAHR-QELLSTLQNLSNDELLPVARAFSQFLNLTNT 84

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                 AE  +       +   hG+ a   +A     +   + +L  k   s +++
gi|2387547    85 AEQYH-------SISPHGEAASNPEA-----LAQLFNRLKDKN-LSNKDM 121

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
gi|2387547   122 CKAVDELSIELVLTAHPTEITRRTLIHKLVEVNSCLSQLDHNDLADYERN 171

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                  +   L   +   + tDEiR+ +P P DE + G + +   +W+GvP FLR
gi|2387547   172 KIMRRLRQLVAQSWHTDEIRKLRPSPIDEAKWGFAVVENSLWEGVPAFLR 221

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                      L n  +  RlP ++  i+F+sWmGGDRDG nP vt EvtR v LL
gi|2387547   222 EFNEQLEN-SLDYRLPVEAVPIRFTSWMGGDRDG-NPNVTAEVTRHVLLL 269

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRA..EElyrtaardkvvKy
                 +R  A+ l++  +  L+ Elsm  C  ELR  A++EE+
gi|2387547   270 SRWKATDLFLRDIQVLVSELSMSECTPELRKLAggEEVL----------- 308

                 YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                            EPYR ++  +R +L nt       L +G   ++ +
gi|2387547   309 -----------EPYRELMKRIRSQLINTQVYLEGRL-KGERVLPPDDLLV 346

                 kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   ++  EPL   Y+sL  CG  +iA G LLD LR v  FG+ Lv++D+Rq
gi|2387547   347 SNDQLWEPLYASYQSLKACGMEIIANGQLLDTLRRVRCFGVPLVRIDVRQ 396

                 EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                 Es R+tD +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
gi|2387547   397 ESTRHTDAIAELTRYLGLGDYENWSESDKQAFLIRELNSKRPLVPLKWQP 446

                 tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                   E ++vl++ rv+AE P  s  aY+isma  PsDvLAv LL +E g
gi|2387547   447 SAETEEVLETCRVIAEAPEGSIAAYVISMAKVPSDVLAVHLLLKEAGCPF 496

                 tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                 tL+v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
gi|2387547   497 TLPVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 546

                 AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                 AG ++A W  Y+Aq+ +iK   k Gv L+lFHGRGG +GRGG P H A+L
gi|2387547   547 AGVMAASWAQYRAQDALIKTCEKAGVALTLFHGRGGSIGRGGAPAHAALL 596

                 sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                 sqPP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP
gi|2387547   597 SQPPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLALYAGAILEANLLPPP 646

                 sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                  Pk EW ++m+ +     + YR  v   P Fv YFR AtPElE Gk+ +G
gi|2387547   647 EPKKEWIEVMDLLSEASCDMYRGYVRENPDFVPYFRAATPELELGKLPLG 696

                 sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                 sRPaKR+  GG+esLRAiPWiFaWtq R  LP WLG GA  + Ai  D
gi|2387547   697 SRPAKRRANGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQKAI--DAG 744

                 nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                   q L  m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P G
gi|2387547   745 KQQELATMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVDKKLWPLG 794

                 ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                 k+LRd+     +l+L i     l+   P++   + LR+ Y   Lnv+qA
gi|2387547   795 KQLRDQLAADIKLVLAISNDDHLMADLPWIAESIALRNVYTDPLNVLQAE 844

                 tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                  L R R             +E+ d                     +E  L
gi|2387547   845 LLHRSRQ------------QEHPDAR------------------VEQAL 863

                 iLtmKGiAAGmqntG<-*
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                  ++t+ G+AAGm ntG
  gi|2387547   864 MVTIAGVAAGMRNTG    878

gi|68249774|ref|YP_248886.1|: domain 1 of 1, from 2 to 879: score 743.5, E = 1.6e-220
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                         q        +s           +l +FL++ + D  Ged+ E
  gi|6824977     2    ---TQEYSTLRNNIS-----------MLGRFLgETINDAQGEDILEL 34

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  +     ls +     D  + + L   L s+     i vA+a++  LnL n
  gi|6824977    35 IENIRKLSRNSRAGDDKAR-QALLDTLGSISNENIIPVARAFSQFLNLTN 83

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  +AE  +   R     +                + E +K+L  +   s eE
  gi|6824977    84 IAEQYQTISREHSLAQS-----------SSQSLSELFKRLKEQN-ASVEE 121

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  v   +    ++LvltAHPt   RRsL+ K+  i  CL++L   D+t  ++
  gi|6824977   122 VHKTVEKLLIELVLTAHPTETTRRSLIHKHIEINKCLSKLEHHDLTEKER 171

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    ++  L R i  A+ t EiR  +PtP DE + G + +   +W+ vP FL
  gi|6824977   172 NIIERLLLRLIAEAWHTNEIRTVRPTPFDEAKWGFAMLENSLWQAVPEFL 221

                  RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                  R  ++tA   +G    lP     ++ ssWmGGDRDG nP vt  +t+ v
  gi|6824977   222 RQLnETAREFLGYD--LPVGLKPVRISSWMGGDRDG-NPFVTAQITKKVL 268

                  LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    aR  Aa l+++ +  L  Elsm +C dE R            dk   +
  gi|6824977   269 YFARWKAADLFLQDISKLADELSMMKCSDEFR-----------DKYGEH 306

                  YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                            EPYR ++ + R +L  t       L      +sE  +
  gi|6824977   307 L----------EPYRFVVKNLRNQLTATLAYFDDHLSNRTPRVSESEIIL 346

                  kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                  +  +  EPL  CY+sL +CG ++iA GsLLD+L  +s FG+ L ++DiRq
  gi|6824977   347 EDNQLWEPLYDCYQSLIQCGMRIIANGSLLDILHRISCFGVTLSQMDIRQ 396

                  EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                  Es R+tD +  i + +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|6824977   397 ESTRHTDAIAEIMRYIGLGDYSQWMEDDKQAFLIRELSSRRPLIPQNWTP 446

                  tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                    E k++ld+ +v+A         Y+isma + sDvLAv LL +E gv
  gi|6824977   447 SPETKEILDTCKVIAQQKQGVIACYVISMARSASDVLAVHLLLKEAGVPY 496

                  tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                   ++vvPLFE L DL+AA   + +LF + WY+  i+ +q vm+GYsDs KD
  gi|6824977   497 HIPVVPLFETLEDLDAAEKVMTQLFNVGWYRGVINNRQMVMIGYSDSAKD 546

                  AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                  AG ++A W  Y+AqE ++    k G+ L+lFHGRGGt+GRGG P H A+L
  gi|6824977   547 AGMMAASWAQYRAQEALVNLTEKLGIELTLFHGRGGTIGRGGAPAHAALL 596

                  sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                  sqPP  ++  lRvt qGE+i f  G   +   +   ++ A LE  + PP
  gi|6824977   597 SQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVETFDLYASAILEANLLPPP 646

                  sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                   PkPEWR +m+e+  +  + YR vv  +  Fv YFR+AtPE E  k+ +G
  gi|6824977   647 EPKPEWRTIMDELSTISCDIYRGVVRGDKDFVPYFRSATPEQELSKLPLG 696

                  sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                  sRPaKR P GG+esLRAiPWiFaW q R  LP WLG GAA +  i++
  gi|6824977   697 SRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGAAIRQVIEQGKG 746

                  nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                   +  ++ m ++WPFF   + +lEmvF K D  +   yD+ Lv  eL+  G
  gi|6824977   747 DI--IHKMCENWPFFSTRIGMLEMVFSKSDTWLSQQYDQRLVKKELWYLG 794
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                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    ++LR + ++  + +L +    +l+   P++   + LR+ Y   Ln +q
  gi|6824977   795 ENLRKQLEDDIQTVLSLSHQSELMSDLPWIADSIALRNIYTDPLNLLQVE 844

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                 En            e+v P +E  L
  gi|6824977   845 LLHRFR-----------------EN-----------PEQVNPDVEQAL 864

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|6824977   865 MITITGIAAGMRNTG    879

gi|145627780|ref|ZP_01783581.1|: domain 1 of 1, from 2 to 879: score 743.4, E = 1.7e-220
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           q        +s           +l +FL++ + D  Ged+ E
  gi|1456277     2    ---TQEYSTLRNNIS-----------MLGRFLgETINDAQGEDILEL 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls +     D  + + L   L s+     i vA+a++  LnL n
  gi|1456277    35 IENIRKLSRNSRAGDDKAR-QALLDTLGSISNENIIPVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R     +                + E +K+L  +   s eE
  gi|1456277    84 IAEQYQTISREHSLAQS-----------SSQSLSELFKRLKEQN-ASVEE 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v   +    ++LvltAHPt   RRsL+ K+  i  CL++L   D+t  ++
  gi|1456277   122 VHKTVEKLLIELVLTAHPTETTRRSLIHKHIEINKCLSKLEHHDLTEKER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      ++  L R i  A+ t EiR  +PtP DE + G + +   +W+ vP FL
  gi|1456277   172 NIIERLLLRLIAEAWHTNEIRTVRPTPFDEAKWGFAMLENSLWQAVPEFL 221

                    RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R  ++tA   +G    +      ++ ssWmGGDRDG nP vt  +t+ v
  gi|1456277   222 RQLnETAREFLGYDLSVGLKP--VRISSWMGGDRDG-NPFVTAQITKKVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                      aR  Aa l+++ +  L+ Elsm +C dE R++  E
  gi|1456277   269 YFARWKAADLFLQDISKLVDELSMMKCSDEFRAKYGEHL----------- 307

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR ++ + R +L  t       L      +sE  +
  gi|1456277   308 -----------EPYRFVVKNLRNQLTATLAYFDDHLSNRTPRVSESEIIL 346

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  +  EPL  CY+sL +CG ++iA GsLL +L  +s FG+ L ++DiRq
  gi|1456277   347 EDNQLWEPLYDCYQSLIQCGMRIIANGSLLNILHRISCFGVTLSQMDIRQ 396

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+tD +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|1456277   397 ESTRHTDAIAEITRYIGLGDYSQWMEDDKQAFLIRELSSRRPLIPQNWTP 446

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E k++ld+ +v+A         Y+isma + sDvLAv LL +E gv
  gi|1456277   447 SPETKEILDTCKVIAQQKQGVIACYVISMARSASDVLAVHLLLKEAGVPY 496

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                     ++vvPLFE L DL+AA   + +LF + WY+  i+ +q vm+GYsDs KD
  gi|1456277   497 HIPVVPLFETLEDLDAAEKVMTQLFNVGWYRGVINNRQMVMIGYSDSAKD 546

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+AqE ++    k G+ L+lFHGRGGt+GRGG P H A+L
  gi|1456277   547 AGMMAASWAQYRAQEALVNLTEKLGIELTLFHGRGGTIGRGGAPAHAALL 596

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++  lRvt qGE+i f  G   +   +   ++ A LE  + PP
  gi|1456277   597 SQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVETFDLYASAILEANLLPPP 646

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
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                     PkPEWR +m+e+  +  + YR vv  +  Fv YFR+AtPE E  k+ +G
  gi|1456277   647 EPKPEWRTIMDELSTISCDIYRGVVRGDKDFVPYFRSATPEQELSKLPLG 696

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR P GG+esLRAiPWiFaW q R  LP WLG GAA +  i++
  gi|1456277   697 SRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGAAIRQVIEQGKG 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     +  ++ m ++WPFF   + +lEmvF K D  +   yD+ Lv  eL+  G
  gi|1456277   747 DI--IHKMCENWPFFSTRIGMLEMVFSKSDTWLSQQYDQRLVKKELWYLG 794

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    ++LR + ++  + +L +    +l+   P++   + LR+ Y   Ln +q
  gi|1456277   795 ENLRKQLEDDIQTVLSLSHQSELMSDLPWIADSIALRNIYTDPLNLLQVE 844

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                  En             e+v P +E  L
  gi|1456277   845 LLHRFR------------------EN------------PEQVNPDVEQAL 864

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|1456277   865 MITITGIAAGMRNTG    879

gi|114045747|ref|YP_736297.1|: domain 1 of 1, from 11 to 889: score 743.2, E = 1.9e-220
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        + A LR      vs           +l + L+D +    G++  E
  gi|1140457    11    DMYASLRS----NVS-----------MLGQILgDTMRTHLGDSFLEK 42

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     l+ +   + D    e +   Lt+L   + +  Aka+   LnLAn
  gi|1140457    43 VEQIRKLAKDSR-RGDEAAREQMLELLTALPDEELVPFAKAFNQFLNLAN 91

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    L E  +   R   ++                +E  l ++
  gi|1140457    92 LSEQFHTISRNCDELVC-----------VPDPVEQLLGRMLNGR-IDQTK 129

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvteDK
                    + + LK   +DLvltAHPt   RR L+qK a i  CLa      +   ++
  gi|1140457   130 MLDCLKTLDIDLVLTAHPTEISRRTLIQKYAAIVDCLAEQENNQLSDRER 179

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + +   L   i   + t EiRR +PtP DE R G+s i E +W+ vP FL
  gi|1140457   180 RQINLRLRQLIAQIWHTNEIRRERPTPVDEARWGLSTIEESLWHAVPDFL 229

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R     ++       lP d+  ++FssWmGGDRDG nP vt  vt +v
  gi|1140457   230 RQLNDQVQD-RTGQQLPIDIAPVRFSSWMGGDRDG-NPFVTAKVTQEVLD 277

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                      R  Aa l++  +  L+ Elsm   n+EL +       t  +
  gi|1140457   278 RNRHAAARLFLKDIVLLVGELSMEEANSELMA------FTNNSC------ 315

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR +L   R KL  t +     +     e+       +
  gi|1140457   316 ----------EPYRFVLRSLRQKLRDTIDYLNARIEGHNPEVDKSTLIWQ 355

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      +   PLE+ YksLC+CG + iA G LLD+LR    FG+ + +LDiRq+
  gi|1140457   356 ESDLKAPLEMLYKSLCDCGMRLIANGLLLDILRRLACFGIHMLRLDIRQD 405

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    + R+ Dvl  +t+ L++G +  W E  +q +Ll EL+ +RPL++s
  gi|1140457   406 AGRHCDVLAELTRYLGMGDFNHWDETEKQAFLLRELSNRRPLIPSNWQPS 455

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                     +v++vl++ r +A  P  + G+Y+isma  PsDvL v LL +E g  ++
  gi|1140457   456 ADVAEVLNTCRLIAKHPAKALGSYVISMASKPSDVLTVLLLLKETGCTHP 505

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    +rvvPLFE L DL+ A   +  L  iDWY+    G qevm+GYsDs KDA
  gi|1140457   506 MRVVPLFETLSDLNNAAECITALLDIDWYRGYTKGMQEVMIGYSDSAKDA 555
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                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    G ++AAW  Y+AqE ++ v ++ GvKL+lFHGRGG +GRGGGP H AiLs
  gi|1140457   556 GVMAAAWAQYRAQEQLVAVCQQAGVKLTLFHGRGGSIGRGGGPAHKAILS 605

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A LE  + PP
  gi|1140457   606 QPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVLEATLLPPPE 655

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    Pk EWR+ +e++A      YR +v  EP Fv YFR AtPE+E Gk+ +Gs
  gi|1140457   656 PKQEWRNCVERIAEESVSAYRGIVREEPDFVPYFRAATPEVELGKLPLGS 705

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RPaKR+  GGiesLRAiPWiFaW q R  LP WLG G A + A ++
  gi|1140457   706 RPAKRRVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALQAACQRG--E 753

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    +  L++m +eWPFF   + +lEmv+AK +P +A  y+  Lv  +L+  G+
  gi|1140457   754 IGLLQDMEREWPFFSTRISMLEMVYAKAEPNLARYYETCLVPPNLHHLGE 803

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                     LR++     + +L++     l+   P+ +  ++LR++Yi  Ln +q
  gi|1140457   804 TLRQRLDLGIKVVLELTKSDTLMAHTPWNRESVKLRNPYIDPLNFLQTEL 853

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    L R R             KE  + +   a e v+L             L+
  gi|1140457   854 LARTR-------------KETTEAP---ASEHVQLA------------LM 875

                    LtmKGiAAGmqntG<-*
                    Lt+ G+AAGm ntG
  gi|1140457   876 LTIAGVAAGMRNTG    889

gi|229844816|ref|ZP_04464954.1|: domain 1 of 1, from 2 to 879: score 740.3, E = 1.5e-219
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           q  +     +            +l +FL++ + D  G d+ E
  gi|2298448     2    ---TQEYATLRNNIN-----------MLGRFLgETINDAQGADILEL 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls +     D  + + L   L s+     i vA+a++  LnL n
  gi|2298448    35 IENIRKLSRNSRAGDDKAR-QALLDTLGSISNENIIPVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R     +               + E +K+L  +   s eE
  gi|2298448    84 IAEQYQTISREHSLAQS-----------SSQSLSELFKRLKEQN-ASVEE 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v   +    ++LvltAHPt   RRsL+ K+  i  CL++L   D+t  ++
  gi|2298448   122 VHKTVEKLLIELVLTAHPTETTRRSLIHKHIEINKCLSKLEHNDLTEKER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      ++  L R i  A+ t EiR  +PtP DE + G + +   +W+ vP FL
  gi|2298448   172 NIIERLLLRLIAEAWHTNEIRTVRPTPFDEAKWGFAMLENSLWQAVPEFL 221

                    RRvDtALKniGinERlPYdvPL....ikFssWmGGDRDGknPRvtPEvtR
                    R       n    E l Yd P++ ++++ ssWmGGDRDG nP vt  +t+
  gi|2298448   222 RQL-----NETAREFLSYDLPVglkpVRISSWMGGDRDG-NPFVTAQITK 265

                    DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                     v   aR  Aanl+++ +  L  Elsm +C dE Rv            k
  gi|2298448   266 KVLYFARWKAANLFLQDINKLADELSMMKCSDEFRV------------KY 303

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                      +           EPYR ++ + R +L  t       L      +sE
  gi|2298448   304 GNHL----------EPYRFVVKNLRNQLTATLAYFDDHLSNRTPRVSESE 343

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                    +  +  +  EPL  CY+sL +CG ++iA GsLLD+L  +s FG+ L ++D
  gi|2298448   344 IILEDNQLWEPLYDCYQSLIQCGMRIIANGSLLDILHRISCFGVTLSQMD 393

                    iRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
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                    iRqEs R+tD +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|2298448   394 IRQESTRHTDAIAEITRYIGLGDYAQWTEDDKQAFLIRELSSRRPLIPQN 443

                    LPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECg
                         E +++ld+ +v+A         Y+isma   sDvLAv LL +E
  gi|2298448   444 WTPSPETQEILDTCKVIAQQKQGVIACYVISMARNASDVLAVHLLLKEAS 493

                    vkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDs
                    v   ++vvPLFE L DL+AA   + +LF + WY+  i+ +q vm+GYsDs
  gi|2298448   494 VPYHIPVVPLFETLEDLDAAEKVMTQLFNVGWYRGVINNRQMVMIGYSDS 543

                    GKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHL
                     KDAG ++A W  Y+AqE ++    k G+ L+lFHGRGGt+GRGG P H
  gi|2298448   544 AKDAGMMAASWAQYRAQEALVNLTEKLGIELTLFHGRGGTIGRGGAPAHA 593

                    AiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmn
                    A+LsqPP  ++  lRvt qGE+i f  G   +   +   ++ A LE  +
  gi|2298448   594 ALLSQPPRSLKNGLRVTEQGEMIRFKLGLPTVAVETFDLYASAILEANLL 643

                    PPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkm
                    PP  PkPEWR++m+e+  +  + YR vv  +  Fv YFR+AtPE E  k+
  gi|2298448   644 PPPEPKPEWRNIMDELSTISCDIYRGVVRGDKDFVPYFRSATPEQELSKL 693

                    niGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidK
                     +GsRPaKR P GG+esLRAiPWiFaW q R  LP WLG GA  +  i++
  gi|2298448   694 PLGSRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGASIRQIIEQ 743

                    DiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk
                        +  ++ m ++WPFF   + +lEmvF K D  +   yD+ Lv  eL+
  gi|2298448   744 GKGDI--IHKMCENWPFFSTRIGMLEMVFSKSDTWLSQQYDQRLVKKELW 791

                    PFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvf
                      G++LR + ++  + +L +    +l+   P++   + LR+ Y   Ln +
  gi|2298448   792 YLGENLRKQLEDDIQTVLSLSHQSELMSDLPWIADSIALRNIYTDPLNLL 841

                    qAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLE
                    q   L R R                  En             e+v P +E
  gi|2298448   842 QVELLHRFR------------------EN------------PEQVNPDVE 861

                    DtLiLtmKGiAAGmqntG<-*
                      L++t+ GiAAGm ntG
  gi|2298448   862 QALMITITGIAAGMRNTG    879

gi|238764489|ref|ZP_04625437.1|: domain 1 of 1, from 1 to 865: score 740.1, E = 1.7e-219
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                  GK                  D +++  Ge + + v
  gi|2387644     1    ---------MLGKLL----------------GDTIKEALGEHILDRV 22

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       ++++ +EL + L  L   + + vA+a++  LnL n
  gi|2387644    23 ETIRKLSKSSRAGNEASR-QELLTTLQNLSNDELLPVARAFSQFLNLTNT 71

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +       +   hG+ a   +A     +   + +L  k   s +++
  gi|2387644    72 AEQYH-------SISPHGEAASNPEA-----LAQLFTRLKDKK-LSEQDM 108

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
  gi|2387644   109 RSAVDELSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHNDLADYERN 158

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +   L   +   + tDEiR+ +P P DE + G + +   +W+GvP FLR
  gi|2387644   159 KIMRRLRQLVAQSWHTDEIRKIRPSPVDEAKWGFAVVENSLWEGVPAFLR 208

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         L+n  +  RlP ++  i+F+sWmGGDRDG nP vt E+tR v LL
  gi|2387644   209 EFNEQLQN-SLDYRLPVEAVPIRFTSWMGGDRDG-NPNVTAEITRHVLLL 256

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    +R  A+ l++  +  L+ Elsm  C  ELR    El
  gi|2387644   257 SRWKATDLFLRDIQVLVSELSMSECTPELR----ELAGGEEVL------- 295
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                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             EPYR ++  vR +L nt       L +G   ++
  gi|2387644   296 ---------EPYRELMKRVRTQLTNTQAYLEDRL-KGERVLPPTDLLVSN 335

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    ++  +PL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+RqEs
  gi|2387644   336 DQLWDPLYACYQSLKACGMEIIANGQLLDTLRRVRCFGVPLVRIDVRQES 385

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     R+tD +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
  gi|2387644   386 TRHTDAIAELTRYLGLGDYESWSEADKQAFLIRELNSKRPLVPLKWEPSA 435

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    + ++vl++ rv+AE P  s  aY+isma  PsDvLAv LL +E g   tL
  gi|2387644   436 DTQEVLETCRVIAEAPQGSIAAYVISMAKVPSDVLAVHLLLKEAGCPFTL 485

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDAG
  gi|2387644   486 PVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKDAG 535

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Lsq
  gi|2387644   536 VMAASWAQYRAQDALIKTCEKAGISLTLFHGRGGSIGRGGAPAHAALLSQ 585

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP  P
  gi|2387644   586 PPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLALYASAVLEANLLPPPEP 635

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    k EW ++m+ +     E YR  v   P Fv YFR AtPElE Gk+ +GsR
  gi|2387644   636 KKEWNEVMDILSDASCEMYRGYVRENPEFVPYFRAATPELELGKLPLGSR 685

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+P GG+esLRAiPWiFaWtq R  LP WLG GA  + Aid   +
  gi|2387644   686 PAKRRPNGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQKAIDAGKRE- 734

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L  m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P G++
  gi|2387644   735 -ELATMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVDKSLWPLGQQ 783

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRd+ +   + +L iA    l+   P++   + LR+ Y   Lnv+qA  L
  gi|2387644   784 LRDQLEADIKVVLAIANDDHLMADLPWIAESIALRNVYTDPLNVLQAELL 833

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     R R             +E+ d                    +E  L++
  gi|2387644   834 HRSRQ------------QEHPDAR-------------------VEQALMV 852

                    tmKGiAAGmqntG<-*
                    t+ G+AAGm ntG
  gi|2387644   853 TIAGVAAGMRNTG    865

gi|212634871|ref|YP_002311396.1|: domain 1 of 1, from 3 to 878: score 739.9, E = 2e-219
                    *->siDAqLRlLvP..GKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                        + A LR  v + G++    + i+ D  L D FLD +  +
  gi|2126348     3    DMYASLRSNVGtlGQIL--GDTIRTD--LDDTFLDKIEQIR------ 39

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                           ls       D+ + eE+ + L +L   + +  Aka+   LnLA
  gi|2126348    40 ------HLSKSSRQGNDAAR-EEMLTLLSALSDDELVPFAKAFNQFLNLA 82

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE  +   R   ++                 +E  l ++ l +n   e
  gi|2126348    83 NIAEQFHTISRNCDELVC-----------VPDPVEQLLGRM-LGGNIDQE 120

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                     + e LK   +DLvltAHPt   RR L+qK + +   L+ L    +t ++
  gi|2126348   121 KMLECLKSLDIDLVLTAHPTEISRRTLIQKYSAVVDSLTALENPQLTEQE 170

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
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                    Kk     L   i   + t EiR  +PtP DE R G+s i   +W+ +P F
  gi|2126348   171 KKQHHLRLRQLIAQIWHTNEIRNERPTPVDEARWGLSTIEVSLWQAIPDF 220

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    LR     +     n  lP d+  ++FssWmGGDRDG nP vt  vt +v
  gi|2126348   221 LRQLNQQVEE-RTNTQLPIDIAPVRFSSWMGGDRDG-NPFVTSVVTQEVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                       R  Aa lY+  v  L+ +lsm   ndEL      l  t  ++
  gi|2126348   269 DRNRHSAARLYLKDVVLLVNDLSMETANDEL------LAYTNNSN----- 307

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR +L d R KL nt +     L     e+    +
  gi|2126348   308 -----------EPYRDVLRDLRGKLRNTIDYLNARLEGHKPEVDLADIIW 346

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  +  EPL + Y+sL +CG   iA G LLD+LR +  FG+ + +LDiRq
  gi|2126348   347 DERDLKEPLMMLYRSLSDCGMSLIANGLLLDMLRRIACFGIHMLRLDIRQ 396

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    +++R+ Dv+  +t+ L++G Y  W E  +q +Ll EL  KRPL++s
  gi|2126348   397 DAQRHADVIAELTRYLGMGDYAHWGEAEKQSFLLRELTSKRPLIPSNWQG 446

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     +Ev++vl + r +A  P  + G+Y+isma  PsDvL v LL +E g  +
  gi|2126348   447 SDEVAEVLRTCRLVATQPARAMGSYVISMASQPSDVLTVLLLLKETGCPH 496

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    ++rvvPLFE L DL+ A   +  LFsiDWY+    G qevm+GYsDs KD
  gi|2126348   497 PMRVVPLFETLDDLNNASQCMSSLFSIDWYRGYTKGIQEVMIGYSDSAKD 546

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++AAW  Y AqE ++ v ++  +KL+lFHGRGGt+GRGGGP H AiL
  gi|2126348   547 AGVMAAAWAQYSAQEKLVAVSQDADIKLTLFHGRGGTIGRGGGPAHEAIL 596

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A +E  + PP
  gi|2126348   597 SQPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVMEATLLPPP 646

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     PkPEWR+ me +A      YR++v  E  Fv YFR AtPE+E Gk+ +G
  gi|2126348   647 EPKPEWRRCMELLADESVLAYRAIVREEADFVSYFRAATPEVELGKLPLG 696

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+  GGiesLRAiPWiFaW q R  LP WLG G A + A  +
  gi|2126348   697 SRPAKRRIDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALQAASLRG-- 744

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     l  L+Em +eWPFF+  + +lEmv+AK +P +A  y+  Lv  eL+  G
  gi|2126348   745 ELPLLQEMEQEWPFFKTRISMLEMVYAKAEPNLAKYYETSLVPKELHHLG 794

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                     +LR++     d +L++     l+   P+ +  + LR++Yi  Ln +qA
  gi|2126348   795 VQLRERLAIGVDAVLELTQAESLMSHTPWNRESVELRNPYIDPLNFLQAE 844

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                   E+  +    v+L           L
  gi|2126348   845 LLARTR-----------------REE--ETSKNVELA-----------L 863

                    iLtmKGiAAGmqntG<-*
                    +Lt+ G+AAGm ntG
  gi|2126348   864 MLTIAGVAAGMRNTG    878

gi|16273525|ref|NP_439778.1|: domain 1 of 1, from 2 to 879: score 739.8, E = 2.1e-219
                    *->siDAqLRLLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           q        +s           +l +FL++ + D  Ged+ E
  gi|1627352     2    ---TQEYSTLRNNIS-----------MLGRFLgETINDAQGEDILEL 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls +     D  + + L   L s+     i vA+a++  LnL n
  gi|1627352    35 IENIRKLSRNSRAGDDKAR-QALLDTLGSISNENIIPVARAFSQFLNLTN 83
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                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                +AE  +   R     +                + E +K+L  +   s eE
gi|1627352    84 IAEQYQTISREHSLAQS-----------SSQSLSELFKRLKEQN-ASVEE 121

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                v   +    ++LvltAHPt   RRsL+ K+  i  CL++L   D+t  ++
gi|1627352   122 VHKTVEKLLIELVLTAHPTETTRRSLIHKHIEINKCLSKLEHHDLTEKER 171

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  ++  L R i  A+ t EiR  +PtP DE + G + +   +W+ vP FL
gi|1627352   172 NIIERLLLRLIAEAWHTNEIRTVRPTPFDEAKWGFAMLENSLWQAVPEFL 221

                RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                R  ++tA   +G    +      ++ ssWmGGDRDG nP vt  +t+ v
gi|1627352   222 RQLnETAREFLGYDLSVGLKP--VRISSWMGGDRDG-NPFVTAQITKKVL 268

                LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                  aR  Aa l+++ +  L  Elsm +C dE R            dk   +
gi|1627352   269 YFARWKAADLFLQDISKLADELSMMKCSDEFR-----------DKYGEH 306

                YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                           EPYR ++ + R +L  t       L      +sE  +
gi|1627352   307 L----------EPYRFVVKNLRNQLTATLAYFDDHLSNRTPRVSESEIIL 346

                kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                +  +  EPL  CY+sL +CG ++iA GsLL +L  +s FG+ L ++DiRq
gi|1627352   347 EDNQLWEPLYDCYQSLIQCGMRIIANGSLLNILHRISCFGVTLSQMDIRQ 396

                EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                Es R+tD +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
gi|1627352   397 ESTRHTDAIAEITRYIGLGDYSQWMEDDKQAFLIRELSSRRPLIPQNWTP 446

                tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                  E k++ld+ +v+A         Y+isma + sDvLAv LL +E gv
gi|1627352   447 SPETKEILDTCKVIAQQKQGVIACYVISMARSASDVLAVHLLLKESGVPY 496

                tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                 ++vvPLFE L DL+AA   + +LF + WY+  i+ +q vm+GYsDs KD
gi|1627352   497 HIPVVPLFETLEDLDAAEKVMTQLFNVGWYRGVINNRQMVMIGYSDSAKD 546

                AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                AG ++A W  Y+AqE ++    k G+ L+lFHGRGGt+GRGG P H A+L
gi|1627352   547 AGMMAASWAQYRAQEALVNLTEKLGIELTLFHGRGGTIGRGGAPAHAALL 596

                sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                sqPP  ++  lRvt qGE+i f  G   +   +   ++ A LE  + PP
gi|1627352   597 SQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVETFDLYASAILEANLLPPP 646

                sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                 PkPEWR +m+e+  +  + YR vv  +  Fv YFR+AtPE E  k+ +G
gi|1627352   647 EPKPEWRTIMDELSTISCDIYRGVVRGDKDFVPYFRSATPEQELSKLPLG 696

                sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                sRPaKR P GG+esLRAiPWiFaW q R  LP WLG GAA +  i++
gi|1627352   697 SRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGAAIRQVIEQGKG 746

                nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                 +  ++ m ++WPFF   + +lEmvF K D  +   yD+ Lv  eL+  G
gi|1627352   747 DI--IHKMCENWPFFSTRIGMLEMVFSKSDTWLSQQYDQRLVKKELWYLG 794

                ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                ++LR + ++  + +L +    +l+   P++   + LR+ Y   Ln +q
gi|1627352   795 ENLRKQLEDDIQTVLSLSHQSELMSDLPWIADSIALRNIYTDPLNLLQVE 844

                tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                 L R R                  En             e+v P +E  L
gi|1627352   845 LLHRFR-----------------EN------------PEQVNPDVEQAL 864

                iLtmKGiAAGmqntG<-*
                ++t+ GiAAGm ntG
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  gi|1627352   865 MITITGIAAGMRNTG    879

gi|163751629|ref|ZP_02158849.1|: domain 1 of 1, from 3 to 877: score 739.7, E = 2.2e-219
                  *->siDAqLRlLvP..GKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                      + A LR  v + G++  d    + D   lDk   i q
  gi|1637516     3    DMYASLRSNVGtlGQILGDTIRTNLDDTFLDKIEQIRQ--------- 40

                  avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                           A    + D    +E+   L +L   + +  Aka+   LnLA
  gi|1637516    41 --------LAKSSRQGDETSRDEMLKLLAALPDNELVPFAKAFNQFLNLA 82

                  nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                  n+AE  +   R   ++               D  E l   vl  n   e
  gi|1637516    83 NIAEQFHTISRNCDELVC------------VPDPVEQLLGRVLSSNIDQE 120

                  EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                   + + L+n  +DLvltAHPt   RR L+qK + +   La L    +   +
  gi|1637516   121 KMLDCLQNLDIDLVLTAHPTEISRRTLIQKYSSVIDSLAALENPQLSQRE 170

                  KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                  Kk     L   i   + t EiR  +PtP DE + G+s i   +W+ +P F
  gi|1637516   171 KKQQHLRLRQLIAQIWHTNEIRHERPTPVDEAKWGLSTIEVSLWQAIPDF 220

                  LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                  LR     +        lP d+  ++FssWmGGDRDG nP vt  vt +v
  gi|1637516   221 LRQLNEQVEE-RTGKQLPIDIAPVRFSSWMGGDRDG-NPFVTAVVTQEVL 268

                  LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     R  Aa lY+  +  L+ +lsm   ndEL +       t  ++
  gi|1637516   269 DRNRHTAARLYLKDIILLVNDLSMESANDELSA------LTNNSH----- 307

                  YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                            EPYR +L + R KL nt +     L     e+    +
  gi|1637516   308 -----------EPYRDVLHELRLKLRNTIDYLNERLEGHKPEVDHSSIIW 346

                  kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                  +  +  EPL + Y+sL e G   iA G LLD+LR +  FG+ + +LDiRq
  gi|1637516   347 HESDLKEPLMMLYRSLSEKGMSLIANGLLLDMLRRIACFGIHMLRLDIRQ 396

                  EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                  ++eR+ Dv+  +t+ L++G +  W E+ +q +Ll EL  KRPL++
  gi|1637516   397 DAERHSDVIAELTRYLGMGDFNHWDENEKQAFLLRELTSKRPLIPTNWQP 446

                  tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                    +v++v+ + r +A  P  + G+Y+isma  PsDvL v LL +E g  +
  gi|1637516   447 SADVAEVISTCRLIASQPARALGSYVISMASKPSDVLTVLLLLKETGCPH 496

                  tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                  ++rvvPLFE L DL+ A   +  LF+iDWY+    G qe+m+GYsDs KD
  gi|1637516   497 PMRVVPLFETLDDLNNAATCMSALFAIDWYRGYTKGHQEIMIGYSDSAKD 546

                  AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                  AG ++AAW  Y AqE ++ + ++  vKL+lFHGRGGt+GRGGGP H AiL
  gi|1637516   547 AGVMAAAWAQYHAQEQLVEISRQADVKLTLFHGRGGTIGRGGGPAHEAIL 596

                  sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                  sqPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A +E  + PP
  gi|1637516   597 SQPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVMEATLLPPP 646

                  sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                   PkPEWR  m+++A      YR++v  EP Fv YFR AtPE+E Gk+ +G
  gi|1637516   647 EPKPEWRACMQQLAEESVKSYRAIVREEPDFVAYFRAATPEVELGKLPLG 696

                  sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                  sRPaKRk  GGiesLRAiPWiFaW q R  LP WLG G A + Aid+
  gi|1637516   697 SRPAKRKVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALQAAIDRG-- 744

                  nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                   +  L+Em +eWPFF+  + +lEmv+ K +P +A  y+  Lv E+L+  G
  gi|1637516   745 DMPLLQEMEQEWPFFKTRISMLEMVYSKAEPNLAKYYETCLVPENLHHLG 794
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                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    + LR++     + +L++     l+   P+ K  + LR++Yi  Ln +qA
  gi|1637516   795 EALRERLATGIKAVLELTQSDTLMSHTPWNKESITLRNPYIDPLNFMQAE 844

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R             K  A  n       v+L             L
  gi|1637516   845 LLARTR-------------KKDASAN-------VELA------------L 862

                    iLtmKGiAAGmqntG<-*
                    +Lt+ G+AAGm ntG
  gi|1637516   863 MLTIAGVAAGMRNTG    877

gi|145639250|ref|ZP_01794856.1|: domain 1 of 1, from 2 to 879: score 739.4, E = 2.7e-219
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           q        +s           +l +FL++ + D  Ged+ E
  gi|1456392     2    ---TQEYSTLRNNIS-----------MLGRFLgETINDAQGEDILEL 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls +     D  + + L   L s+     i vA+a++  LnL n
  gi|1456392    35 IENIRKLSRNSRAGDDKAR-QALLDTLGSISNENIIPVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R     +                + E +K+L  +   s eE
  gi|1456392    84 IAEQYQTISREHSLAQS-----------SSQSLSELFKRLKEQN-ASVEE 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v   +    ++LvltAHPt   RRsL+ K+  i  CL++L   D+t  ++
  gi|1456392   122 VHKTVEKLLIELVLTAHPTETTRRSLIHKHIEINKCLSKLEHHDLTEKER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      ++  L R i  A+ t EiR  +PtP DE + G + +   +W+ vP FL
  gi|1456392   172 NIIERLLLRLIAEAWHTNEIRTVRPTPFDEAKWGFAMLENSLWQAVPEFL 221

                    RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R  ++tA   +G    +      ++ ssWmGGDRDG nP vt  +t+ v
  gi|1456392   222 RQLnETAREFLGYDLSVGLKP--VRISSWMGGDRDG-NPFVTAQITKKVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                      aR  Aa l+++ +  L  Elsm +C dE R            dk   +
  gi|1456392   269 YFARWKAADLFLQDISKLADELSMMKCSDEFR------------DKYGEH 306

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR ++ + R +L  t       L      +sE  +
  gi|1456392   307 L----------EPYRFVVKNLRNQLTATLAYFDDHLSNRTPRVSESEIIL 346

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  +  EPL  CY+sL +CG ++iA GsLL +L  +s FG+ L ++DiRq
  gi|1456392   347 EDNQLWEPLYDCYQSLIQCGMRIIANGSLLNILHRISCFGVTLSQMDIRQ 396

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+tD +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|1456392   397 ESTRHTDAIAEITRYIGLGDYSQWMEDDKQAFLIRELSSRRPLIPQNWTP 446

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E k++ld+ +v+A         Y+isma + sDvLAv LL +E gv
  gi|1456392   447 SPETKEILDTCKVIAQQKQGVIACYVISMARSASDVLAVHLLLKESGVPY 496

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                     ++vvPLFE L DL+AA   + +LF + WY+  i+ +q vm+GYsDs KD
  gi|1456392   497 HIPVVPLFETLEDLDAAEKVMTQLFNVGWYRGVINNRQMVMIGYSDSAKD 546

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+AqE ++    k G+ L+lFHGRGGt+GRGG P H A+L
  gi|1456392   547 AGMMAASWAQYRAQEALVNLTEKLGIELTLFHGRGGTIGRGGAPAHAALL 596

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++  lRvt qGE+i f  G   +   +   ++ A LE  + PP
  gi|1456392   597 SQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVETFDLYASAILEANLLPPP 646

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     PkPEWR +m+e+  +  + YR vv  +  Fv YFR+AtPE E  k+ +G
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  gi|1456392   647 EPKPEWRTIMDELSTISCDIYRGVVRGDKDFVPYFRSATPEQELSKLPLG 696

                   sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                   sRPaKR P GG+esLRAiPWiFaW q R  LP WLG GAA +  i++
  gi|1456392   697 SRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGAAIRQIIEQGKG 746

                   nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                    +  ++ m ++WPFF   + +lEmvF K D  +   yD+ Lv  eL+  G
  gi|1456392   747 DI--IHKMCENWPFFSTRIGMLEMVFSKSDTWLSQQYDQRLVKKELWYLG 794

                   ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                   ++LR + ++  + +L +    +l+   P++   + LR+ Y   Ln +q
  gi|1456392   795 ENLRKQLEDDIQTVLSLSHQSELMSDLPWIADSIALRNIYTDPLNLLQVE 844

                   tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    L R R                  En             e+v P +E  L
  gi|1456392   845 LLHRFR-----------------EN-----------PEQVNPDVEQAL 864

                   iLtmKGiAAGmqntG<-*
                   ++t+ GiAAGm ntG
  gi|1456392   865 MITITGIAAGMRNTG    879

gi|170717721|ref|YP_001784792.1|: domain 1 of 1, from 1 to 879: score 739.4, E = 2.7e-219
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                               P K s     ++    +l +FL++ + D  G d+ +
  gi|1707177     1    ---------MPQKYS----TLKNNINMLGHFLgETISDAQGSDILDL 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +     ls +     D k  e L   L  +     i vA+a++  LnL n
  gi|1707177    35 IENIRVLSRDSRS-GDEKAREKLLDTLSTISNENIIPVARAFSQFLNLTN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +   R+ i +      +D +       +E  + +L  +    P+E
  gi|1707177    84 IAEQYQTISRKHIDQVA----SDRS-------LEALFERLKAQN--VPAE 120

                   .vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                   +v   +    ++LvltAHPt   RRsLL K   i  CL+ L   D+t  +
  gi|1707177   121 kVISTVEKLLIELVLTAHPTEVTRRSLLHKYVEINRCLSRLEHDDLTQSE 170

                   KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                      L   L   i  A+ t EiR  +PtP DE + G++ i   +Wk vP F
  gi|1707177   171 STKLKRRLMQLIALAWHTNEIRTQRPTPVDEAKWGIAVIENSLWKAVPDF 220

                   LRRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    R     L+Kn G+   +  +   +kFssW+GGDRDG nP vt E tR v
  gi|1707177   221 CRQLNLHLeKNFGVQHSV--NLAPVKFSSWIGGDRDG-NPFVTAETTRQV 267

                   CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                    ++ R  Aa l++  +  L  Els+  C +E R++          d
  gi|1707177   268 LIMNRWKAAELFLADIQVLSEELSVVHCTEEFRAK--------YGD---- 305

                   yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                              EPYRv++ + R KL  t      +L    s i  + +
  gi|1707177   306 ----------HLEPYRVVVKNLRAKLVKTVAYYGEILENKPSTINTNDIL 345

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                   t+  +  EPL  CY+sL +CG ++iA G LLD LR +  FGLsL  LDiR
  gi|1707177   346 TDDQQLWEPLYDCYQSLHQCGMRIIANGILLDCLRRIRCFGLSLSHLDIR 395

                   qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                   qEs R+t  l  it+ +++G Y +W E+ +q +L+ EL+ +RPLl+
  gi|1707177   396 QESLRHTKALSEITRYIGLGDYSQWMEDDKQAFLIRELSSRRPLLPRNWT 445

                   ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                      E +++l++ rv+A  P      Yiisma + sDvLAv LL +E gv
  gi|1707177   446 PSPETQEILETCRVIAQQPEGVISCYIISMARTASDVLAVHLLLKEAGVT 495

                   qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                     L+vvPLFE L DL+A    + +LF + WY+  i+ Kq vm+GYsDs K
  gi|1707177   496 YYLPVVPLFETLDDLNASKEVMTQLFNVGWYRGVINNKQMVMIGYSDSAK 545
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                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG ++A W  Y+AqE ++    k Gv L+lFHGRGGt+GRGG P H A+
  gi|1707177   546 DAGMMAASWAQYRAQEQLVNLCEKMGVELTLFHGRGGTIGRGGAPAHAAL 595

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPP  ++  lRvt qGE+i f  G   +   s   ++ A LE  + PP
  gi|1707177   596 LSQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVNSFDLYASAILEANLLPP 645

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      Pk  WR +m+e+       YRsvv  +  Fv YFR+AtPE E  k+ +
  gi|1707177   646 PEPKESWRAIMNELSDSSCNIYRSVVRGDKDFVPYFRSATPEQELSKLPL 695

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRP+KR P GG+esLRAiPWiFaW q R  LP WLG  A  +  i+K
  gi|1707177   696 GSRPSKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGASASIRQSIEKGN 745

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    K    ++Em k+WPFF   + +lEmvF K D  +   yD  Lv  eL+
  gi|1707177   746 KE--TIEEMCKNWPFFSTRIGMLEMVFSKTDTWLSEHYDLNLVKKELWYL 793

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G+sLR++ +   + +L +    +l+   P++   + LR+ Y   Ln +q
  gi|1707177   794 GQSLREQLQADIKTILSLSHEDELMSDLPWIAESIALRNIYTDPLNLLQV 843

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L+R+R             E  + +          n      P +E
  gi|1707177   844 ELLRRLR--------------ENPENP----------N------PDVEQA 863

                    LiLtmKGiAAGmqntG<-*
                    L++t+ GiAAGm ntG
  gi|1707177   864 LMITITGIAAGMRNTG    879

gi|238786115|ref|ZP_04630071.1|: domain 1 of 1, from 1 to 865: score 739.2, E = 3e-219
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                              GK     + i+ +AL             Ge + + v
  gi|2387861     1    ---------MLGKLL--GETIK-EAL-------------GEHILDRV 22

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       ++++ +EL + L  L   + + vA+a++  LnL n
  gi|2387861    23 ETIRKLSKSSRAGNEASR-QELLTTLQNLSNDELLPVARAFSQFLNLTNT 71

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +       +   hG+ a   +A     +   + +L  k   s +++
  gi|2387861    72 AEQYH-------SISPHGEAASNPEA-----LAQLFTRLKDKK-LSEKDM 108

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
  gi|2387861   109 RSAVDELSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHNDLADYERN 158

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +   L   +   + tDEiR+ +P P DE + G + +   +W+GvP FLR
  gi|2387861   159 KIMRRLRQLVAQSWHTDEIRKIRPSPVDEAKWGFAVVENSLWEGVPAFLR 208

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         L+n  +  RlP ++  i+F+sWmGGDRDG nP vt E+tR v LL
  gi|2387861   209 EFNEQLQN-SLDYRLPVEAVPIRFTSWMGGDRDG-NPNVTAEITRHVLLL 256

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    +R  A+ l++  +  L+ Elsm  C  ELR         a  d
  gi|2387861   257 SRWKATDLFLRDIQVLVSELSMSECTPELR-------ELAGGD------- 292

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                         vP  EPYR ++  vR +L nt       L +G   ++
  gi|2387861   293 ----EVP--EPYRELMKRVRTQLTNTQAYLEKRL-KGERVLPPTDLLVSN 335

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    ++  +PL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+RqEs
  gi|2387861   336 DQLWDPLYACYQSLKACGMEIIANGQLLDTLRRVRCFGVPLVRIDVRQES 385

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     R+tD +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
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  gi|2387861   386 TRHTDAIAELTRYLGLGDYESWSEADKQAFLIRELNSKRPLVPLKWEPSA 435

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    + ++vl++ rv+AE P  s  aY+isma  PsDvLAv LL +E g   tL
  gi|2387861   436 DTQEVLETCRVIAEAPEGSIAAYVISMAKVPSDVLAVHLLLKEAGCPFTL 485

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDAG
  gi|2387861   486 PVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKDAG 535

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Lsq
  gi|2387861   536 VMAASWAQYRAQDSLIKTCEKAGISLTLFHGRGGSIGRGGAPAHAALLSQ 585

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP  P
  gi|2387861   586 PPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLALYAGAILEANLLPPPEP 635

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    k EW ++m+ +     + YR  v   P Fv YFR+AtPElE Gk+ +GsR
  gi|2387861   636 KSEWIEVMDILSNASCDMYRGYVRENPEFVPYFRSATPELELGKLPLGSR 685

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+P GG+esLRAiPWiFaWtq R  LP WLG GA  + Aid   +
  gi|2387861   686 PAKRRPNGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQKAIDAGKRD- 734

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L  m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P G++
  gi|2387861   735 -ALATMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVDKSLWPLGQQ 783

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRd+ +   + +L iA    l+   P++   + LR+ Y   Lnv+qA  L
  gi|2387861   784 LRDQLEADIKVVLAIANDDHLMADLPWIAESIALRNVYTDPLNVLQAELL 833

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     R R             +E+ d                     +E  L++
  gi|2387861   834 HRSRQ------------QEHPDAR-------------------VEQALMV 852

                    tmKGiAAGmqntG<-*
                    t+ G+AAGm ntG
  gi|2387861   853 TIAGVAAGMRNTG    865

gi|260582158|ref|ZP_05849952.1|: domain 1 of 1, from 2 to 879: score 738.9, E = 3.8e-219
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           q        +s           +l +FL++ + D  Ged+ E
  gi|2605821     2    ---TQEYSTLRNNIS-----------MLGRFLgETINDAQGEDILEL 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls +     D  + + L   L s+     i vA+a++  LnL n
  gi|2605821    35 IENIRKLSRNSRAGDDKAR-QALLDTLGSISNENIIPVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R     +               + E +K+L  +   s eE
  gi|2605821    84 IAEQYQTISREHSLAQS-----------SSQSLSELFKRLKEQN-ASLEE 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v   +    ++LvltAHPt   RRsL+ K+  i  CL++L   D+t  ++
  gi|2605821   122 VHKTVEKLLIELVLTAHPTETTRRSLIHKHIEINKCLSKLEHHDLTEKER 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      ++  L R i  A+ t EiR  +PtP DE + G + +   +W+ vP FL
  gi|2605821   172 NIIERLLLRLIAEAWHTNEIRTVRPTPFDEAKWGFAMLENSLWQAVPEFL 221

                    RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R  ++tA   +G    +      ++ ssWmGGDRDG nP vt  +t+ v
  gi|2605821   222 RQLnETAREFLGYDLSVGLKP--VRISSWMGGDRDG-NPFVTAQITKKVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                      aR  Aa l+++ +  L  Elsm +C dE R            dk   +
  gi|2605821   269 YFARWKAADLFLQDISKLADELSMMKCSDEFR------------DKYGEH 306
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                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR ++ + R +L  t       L      +sE  +
  gi|2605821   307 L----------EPYRFVVKNLRNQLTATLAYFDDHLSNRTPRVSESEIIL 346

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  +  EPL  CY+sL +CG ++iA GsLL +L  +s FG+ L ++DiRq
  gi|2605821   347 EDNQLWEPLYDCYQSLIQCGMRIIANGSLLNILHRISCFGVTLSQMDIRQ 396

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+tD +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|2605821   397 ESTRHTDAIAEITRYIGLGDYSQWMEDDKQAFLIRELSSRRPLIPQNWTP 446

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E k++ld+ +v+A         Y+isma + sDvLAv LL +E gv
  gi|2605821   447 SPETKEILDTCKVIAQQKQGVIACYVISMARSASDVLAVHLLLKESGVPY 496

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                     ++vvPLFE L DL+AA   + +LF + WY+  i+ +q vm+GYsDs KD
  gi|2605821   497 HIPVVPLFETLEDLDAAEKVMTQLFNVGWYRGVINNRQMVMIGYSDSAKD 546

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+AqE ++    k G+ L+lFHGRGGt+GRGG P H A+L
  gi|2605821   547 AGMMAASWAQYRAQEALVNLTEKLGIELTLFHGRGGTIGRGGAPAHAALL 596

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++  lRvt qGE+i f  G   +   +   ++ A LE  + PP
  gi|2605821   597 SQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVETFDLYASAILEANLLPPP 646

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     PkPEWR +m+e+  +  + YR vv  +  Fv YFR+AtPE E  k+ +G
  gi|2605821   647 EPKPEWRTIMDELSTISCDIYRGVVRGDKDFVPYFRSATPEQELSKLPLG 696

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR P GG+esLRAiPWiFaW q R  LP WLG GAA +  i++
  gi|2605821   697 SRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGAAIRQIIEQGKG 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     +  ++ m ++WPFF   + +lEmvF K D  +   yD+ Lv  eL+  G
  gi|2605821   747 DI--IHKMCENWPFFSTRIGMLEMVFSKSDTWLSQQYDQRLVKKELWYLG 794

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    ++LR + ++  + +L +    +l+   P++   + LR+ Y   Ln +q
  gi|2605821   795 ENLRKQLEDDIQTVLSLSHQSELMSDLPWIADSIALRNIYTDPLNLLQVE 844

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                  En             e+v P +E  L
  gi|2605821   845 LLHRFR------------------EN------------PEQVNPDVEQAL 864

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|2605821   865 MITITGIAAGMRNTG    879

gi|113461137|ref|YP_719205.1|: domain 1 of 1, from 1 to 879: score 738.8, E = 4.2e-219
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                P K s     ++    +l +FL++ + D  G d+ +
  gi|1134611     1    ---------MPQKYS----TLKNNINMLGHFLgETISDAQGSDILDL 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls +     D k  e L   L  +     i vA+a++  LnL n
  gi|1134611    35 IENIRVLSRDSRS-GDEKAREKLLDTLSTISNENIIPVARAFSQFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R+ i +      +D +       +E  + +L  +    P+E
  gi|1134611    84 IAEQYQTISRKHIDQVA----SDRS-------LEALFERLKAQN--VPAE 120

                    .vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    +v   +    ++LvltAHPt   RRsLL K   i  CL+ L   D+t  +
  gi|1134611   121 kVISTVEKLLIELVLTAHPTEVTRRSLLHKYVEINRCLSRLEHDDLTQSE 170

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                       L   L   i  A+ t EiR  +PtP DE + G++ i   +Wk vP F
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  gi|1134611   171 STKLKRRLMQLIALAWHTNEIRTQRPTPVDEAKWGIAVIENSLWKAVPDF 220

                    LRRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     R     L+Kn G+   +  +   +kFssW+GGDRDG nP vt E tR v
  gi|1134611   221 CRQLNLHLeKNFGVQHSV--NLAPVKFSSWIGGDRDG-NPFVTAETTRQV 267

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                     ++ R  Aa l++  +  L  Els+  C +E R++          d
  gi|1134611   268 LIMNRWKAAELFLADIQVLSEELSVVHCTEEFRAK--------YGD---- 305

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                                EPYRv++ + R KL  t      +L    s i  + +
  gi|1134611   306 ----------HLEPYRVVVKNLRAKLVKTVAYYGEILENKPSTINTNDIL 345

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                    t+  +  EPL  CY+sL +CG ++iA G LLD LR +  FGLsL  LDiR
  gi|1134611   346 TDDQQLWEPLYDCYQSLHQCGMRIIANGILLDCLRRIRCFGLSLSHLDIR 395

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+t  l  it+ +++G Y +W E+ +q +L+ EL+ +RPLl+
  gi|1134611   396 QESLRHTKALSEITRYIGLGDYSQWMEDDKQAFLIRELSSRRPLLPRNWT 445

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                       E +++l++ rv+A  P      Yiisma + sDvLAv LL +E gv
  gi|1134611   446 PSLETQEILETCRVIAQQPEGVISCYIISMARTASDVLAVHLLLKEAGVT 495

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                      L+vvPLFE L DL+A    + +LF + WY+  i+ Kq vm+GYsDs K
  gi|1134611   496 YYLPVVPLFETLDDLNASKEVMTQLFNVGWYRGVINNKQMVMIGYSDSAK 545

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG ++A W  Y+AqE ++    k Gv L+lFHGRGGt+GRGG P H A+
  gi|1134611   546 DAGMMAASWAQYRAQEQLVNLCEKMGVELTLFHGRGGTIGRGGAPAHAAL 595

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPP  ++  lRvt qGE+i f  G   +   s   ++ A LE  + PP
  gi|1134611   596 LSQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVNSFDLYASAILEANLLPP 645

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      Pk  WR +m+e+       YRsvv  +  Fv YFR+AtPE E  k+ +
  gi|1134611   646 PEPKESWRAIMNELSDSSCNIYRSVVRGDKDFVPYFRSATPEQELSKLPL 695

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRP+KR P GG+esLRAiPWiFaW q R  LP WLG  A  +  i+K
  gi|1134611   696 GSRPSKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGASASIRQSIEKGN 745

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    K    ++Em k+WPFF   + +lEmvF K D  +   yD  Lv  eL+
  gi|1134611   746 KE--TIEEMCKNWPFFSTRIGMLEMVFSKTDTWLSEHYDLNLVKKELWYL 793

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G+sLR++ +   + +L +    +l+   P++   + LR+ Y   Ln +q
  gi|1134611   794 GQSLREQLQADIKTILSLSHEDELMSDLPWIAESIALRNIYTDPLNLLQV 843

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L+R+R              E  + +          n      P +E
  gi|1134611   844 ELLRRLR--------------ENPENP----------N------PDVEQA 863

                    LiLtmKGiAAGmqntG<-*
                    L++t+ GiAAGm ntG
  gi|1134611   864 LMITITGIAAGMRNTG    879

gi|238798303|ref|ZP_04641787.1|: domain 1 of 1, from 1 to 865: score 738.7, E = 4.6e-219
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                  GK                  D +++  Ge + + v
  gi|2387983     1    ---------MLGKLL----------------GDTIKEALGEHILDRV 22

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       ++++ +EL + L  L   + + vA+a++  LnL n
  gi|2387983    23 ETIRKLSKSSRAGNEASR-QELLTTLQNLSNDELLPVARAFSQFLNLTNT 71
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                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AE  +       +   hG+ a   +A     +   + +L  k   s +++
gi|2387983    72 AEQYH-------SISPHGEAASNPEA-----LAQLFTRLKDKK-LSEQDM 108

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                  A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
gi|2387983   109 RSAVDELSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHNDLADYERN 158

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                 +   L   +   + tDEiR+ +P P DE + G + +   +W+GvP FLR
gi|2387983   159 KIMRRLRQLVAQSWHTDEIRKIRPSPVDEAKWGFAVVENSLWEGVPAFLR 208

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     L+n  +  RlP ++  i+F+sWmGGDRDG nP vt E+tR v LL
gi|2387983   209 EFNEQLQN-SLDYRLPVEAVPIRFTSWMGGDRDG-NPNVTAEITRHVLLL 256

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                +R  A+ l++  +  L+ Elsm  C  ELR         a  d
gi|2387983   257 SRWKATDLFLRDIQVLVSELSMSECTPELR-------ELAGGD------- 292

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                     +P  EPYR ++  vR +L nt       L +G   ++
gi|2387983   293 ----EIP--EPYRELMKRVRTQLTNTQVYLEKRL-KGERVLPPTDLLVSN 335

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                ++  +PL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+RqEs
gi|2387983   336 DQLWDPLYACYQSLKACGMEIIANGQLLDTLRRVRCFGVPLVRIDVRQES 385

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                 R+tD +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
gi|2387983   386 TRHTDAIAELTRYLGLGDYESWSEADKQAFLIRELNSKRPLVPLKWEPSA 435

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                + ++vl++ rv+AE P  s  aY+isma  PsDvLAv LL +E g   tL
gi|2387983   436 DTQEVLETCRVIAEAPEGSIAAYVISMAKVPSDVLAVHLLLKEAGCPFTL 485

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                +v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDAG
gi|2387983   486 PVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKDAG 535

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Lsq
gi|2387983   536 VMAASWAQYRAQDSLIKTCEKAGITLTLFHGRGGSIGRGGAPAHAALLSQ 585

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP  P
gi|2387983   586 PPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLALYAGAILEANLLPPPEP 635

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                k EW ++m+ +     + YR  v   P Fv YFR+AtPElE Gk+ +GsR
gi|2387983   636 KKEWVEVMDILSNASCDMYRGYVRENPEFVPYFRSATPELELGKLPLGSR 685

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                PaKR+P GG+esLRAiPWiFaWtq R  LP WLG GA  + Aid   + +
gi|2387983   686 PAKRRPNGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQKAIDAGKRDV 735

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  L  m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P G++
gi|2387983   736 --LATMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVDKSLWPLGQQ 783

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LRd+     + +L iA    l+   P++   + LR+ Y   Lnv+qA  L
gi|2387983   784 LRDQLAADINVVLAIANDDHLMADLPWIAESIALRNVYTDPLNVLQAELL 833

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                 R R             +E+ d                    +E  L++
gi|2387983   834 HRSRQ------------QEHPDAR-------------------VEQALMV 852

                tmKGiAAGmqntG<-*
                t+ G+AAGm ntG
gi|2387983   853 TIAGVAAGMRNTG    865
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gi|238760149|ref|ZP_04621297.1|: domain 1 of 1, from 1 to 865: score 738.6, E = 4.6e-219
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          L  L    +         +AL             Ge + E v
  gi|2387601     1    ----MLGTLLGDTIK--------EAL-------------GEHILEKV 22

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       ++++ +EL + L  L   + + vA+a++  LnL n
  gi|2387601    23 ETIRKLSKSSRAGNEASR-QELLTTLQNLSNDELLPVARAFSQFLNLTNT 71

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  +       +   hG+ a   +A     +   + +L  k   s +++
  gi|2387601    72 AEQYH-------SISPHGEAASNPEA-----LAQLFTRLKDKK-LSEQDM 108

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
  gi|2387601   109 RSAVDELSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHNDLADYERN 158

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +   L   +   + tDEiR+ +P P DE + G + +   +W+GvP FLR
  gi|2387601   159 KIMRRLRQLVAQSWHTDEIRKIRPSPVDEAKWGFAVVENSLWEGVPAFLR 208

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         L+n  +  RlP ++  i+F+sWmGGDRDG nP vt E+tR v LL
  gi|2387601   209 EFNEQLQN-SLDYRLPVEAVPIRFTSWMGGDRDG-NPNVTAEITRHVLLL 256

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    +R  A+ l++  +  L+ Elsm  C  ELR         a  d vv
  gi|2387601   257 SRWKATDLFLRDIQVLVSELSMSECTPELR-------ELAGGDEVV---- 295

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             EPYR ++ ++R +L nt       L +G   ++
  gi|2387601   296 ---------EPYRELMKQMRTQLTNTQTYLEGRL-KGERVLPPTDLLVSN 335

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    ++   PL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+RqEs
  gi|2387601   336 DQLWNPLYACYQSLKACGMEIIANGQLLDTLRRVRCFGVPLVRIDVRQES 385

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     R+tD +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
  gi|2387601   386 TRHTDAIAELTRYLGLGDYESWSEADKQAFLIRELNSKRPLVPLKWEPSA 435

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    + ++vl++ rv+AE P  s  aY+isma  PsDvLAv LL +E g   tL
  gi|2387601   436 DTQEVLETCRVIAEAPQGSIAAYVISMAKVPSDVLAVHLLLKEAGCPFTL 485

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDAG
  gi|2387601   486 PVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKDAG 535

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Lsq
  gi|2387601   536 VMAASWAQYRAQDALIKTCEKAGISLTLFHGRGGSIGRGGAPAHAALLSQ 585

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP  P
  gi|2387601   586 PPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLALYAGAILEANLLPPPEP 635

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    k EW ++m+ +     E YR  v   P Fv YFR AtPElE Gk+ +GsR
  gi|2387601   636 KKEWVEVMDILSDASCEMYRGYVRENPQFVPYFRAATPELELGKLPLGSR 685

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+P GG+esLRAiPWiFaWtq R  LP WLG GA  + Aid   K
  gi|2387601   686 PAKRRPNGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQKAIDAGKKD- 734

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L  m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P G++
  gi|2387601   735 -ALATMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVDKSLWPLGQQ 783

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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                    LRd+     + +L iA    l+   P++   + LR+ Y   Lnv+qA  L
  gi|2387601   784 LRDQLAADIKVVLAIANDDHLMADLPWIAESIALRNVYTDPLNVLQAELL 833

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     R R             +E+ d                     +E  L++
  gi|2387601   834 HRSRQ------------QEHPDAR------------------VEQALMV 852

                    tmKGiAAGmqntG<-*
                    t+ G+AAGm ntG
  gi|2387601   853 TIAGVAAGMRNTG    865

gi|293329260|dbj|BAJ03991.1|: domain 1 of 1, from 3 to 877: score 737.3, E = 1.2e-218
                    *->siDAqLRlLvP..GKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                        + A LR  v + G++    + i+    L D FLD +     e+++
  gi|2933292     3    DMYASLRSNVGtlGQIL--GETIRTN--LDDAFLDKI-----EQIRQ 40

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                             A    + D    eE+   L +L   + +  Aka+   LnLA
  gi|2933292    41 L--------AKSSRQGDEASREEMLKLLAALPDNELVPFAKAFNQFLNLA 82

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE  +   R   ++               D  E l   vl  n   e
  gi|2933292    83 NIAEQFHTISRNCDELVC------------VPDPVEQLLGRVLSSNIDQE 120

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    ++ + L+n  +DLvltAHPt   RR L+qK + +   La L    +t  +
  gi|2933292   121 DMLDCLQNLDIDLVLTAHPTEISRRTLIQKYSSVIDSLAALENPQLTERE 170

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    Kk     L   i   + t EiR  +PtP DE R G+s i   +W+ +P F
  gi|2933292   171 KKQQHLRLRQLIAQIWHTNEIRHERPTPVDEARWGLSTIEVSLWQAIPDF 220

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    LR     +        lP d+  ++FssWmGGDRDG nP vt  vt +v
  gi|2933292   221 LRQLNEQVEE-RTGKQLPIDISPVRFSSWMGGDRDG-NPFVTALVTQEVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                       R  Aa lY+  +  L+ +lsm   ndEL        +   +d
  gi|2933292   269 DRNRHTAARLYLKDIVLLVNDLSMEDANDEL--------SSLTKD----- 305

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                                EPYR +L + R KL nt +     L      +    +
  gi|2933292   306 ---------SHEPYRYVLRELRVKLRNTIDYLNDRLEGHNPKVDNSTIIW 346

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  +  EPL + Y+sL + G   iA G LLD+LR +  FG+ + +LDiRq
  gi|2933292   347 HEKDLKEPLMMLYRSLSDKGMSLIANGLLLDMLRRIACFGIHMLRLDIRQ 396

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    ++eR+ Dv+  +t+ L++G +  W E  +q +Ll EL  KRPL++
  gi|2933292   397 DAERHSDVIAELTRYLGMGDFNHWDESEKQTFLLKELTSKRPLIPTNWQP 446

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     + v++v+ + r +A  P  + G+Y+isma  PsDvL v LL +E g  +
  gi|2933292   447 SDNVAEVISTCRLIATQPARALGSYVISMASKPSDVLTVLLLLKETGCPH 496

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    ++rvvPLFE L DL+ A   +  LF+iDWY+    G qe+m+GYsDs KD
  gi|2933292   497 PMRVVPLFETLDDLNNAATCMSALFAIDWYRGYTKGHQEIMIGYSDSAKD 546

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++AAW  Y AqE ++ + ++  vKL+lFHGRGGt+GRGGGP H AiL
  gi|2933292   547 AGVMAAAWAQYHAQEQLVEISRQADVKLTLFHGRGGTIGRGGGPAHEAIL 596

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A +E  + PP
  gi|2933292   597 SQPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVMEATLLPPP 646

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     PkPEWR  ++++A      YRs+v  E  Fv YFR AtPE+E Gk+ +G
  gi|2933292   647 EPKPEWRACIQRLAEESVKAYRSIVREEADFVAYFRAATPEVELGKLPLG 696
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                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKRk  GGiesLRAiPWiFaW q R  LP WLG G A +  id+
  gi|2933292   697 SRPAKRKVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALQASIDRG-- 744

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     +  L+Em +eWPFF+  + +lEmv+ K +P +A  y+  Lv E+L+  G
  gi|2933292   745 DMSLLQEMEQEWPFFKTRISMLEMVYSKAEPNLAKYYETCLVPENLHHLG 794

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    + LR++     + +L++     l+   P+ K  + LR++Yi  Ln +qA
  gi|2933292   795 EALRERLATGIKAVLELTQSDTLMSHTPWNKESITLRNPYIDPLNFMQAE 844

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R             KE A  n       v+L             L
  gi|2933292   845 LLARTR-------------KEDASAN-------VELA------------L 862

                    iLtmKGiAAGmqntG<-*
                    +Lt+ G+AAGm ntG
  gi|2933292   863 MLTIAGVAAGMRNTG    877

gi|127511134|ref|YP_001092331.1|: domain 1 of 1, from 3 to 878: score 737.2, E = 1.2e-218
                    *->siDAqLRlLvP..GKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                        + A LR  v + G++  d    + D   lDk   i q  H
  gi|1275111     3    DMYASLRSNVGtlGQILGDTIRTHMDEPFLDK---IEQIRH------ 40

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                           l+       Dt + e + + L +L   + +  Aka+   LnLA
  gi|1275111    41 -------LAKSSRQGNDTAR-EQMLTLLAALPDEELVPFAKAFNQFLNLA 82

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE  +   R   ++                ++  l ++        +
  gi|1275111    83 NIAEQFHTISRNCDELVC-----------VPDPVDQLLGRMLNGR-IDQD 120

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                     + e L+   +DLvltAHPt   RR L+qK + +  CLa +    +t  +
  gi|1275111   121 KMLECLQTLDIDLVLTAHPTEISRRTLIQKYSAVVDCLATMENPQLTERE 170

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    Kk     L   i   + t EiR  +PtP DE R G+s i   +W+ +P F
  gi|1275111   171 KKQNHLRLRQLIAQIWHTNEIRHERPTPVDEARWGLSTIEASLWQAIPDF 220

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    LR     +        lP d+  i+FssWmGGDRDG nP vt  vt +v
  gi|1275111   221 LRQLNEQVEE-RTGKQLPSDIAPIRFSSWMGGDRDG-NPFVTAKVTQEVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                       R  Aa lY+  v  L+ Elsm   n+EL      l  t  ++
  gi|1275111   269 DRNRHTAARLYLKDVVLLVNELSMEEANEEL------LALTDNSH----- 307

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                              EPYRv+L + R KL  t +     L     e+  +
  gi|1275111   308 -----------EPYRVVLRELRQKLRDTIDYLNARLEGHSPEVDLDSLIW 346

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    + ++   PL L Y+sL e G   iA G LLD+LR    FG+ + +LDiRq
  gi|1275111   347 HEDDLKQPLTLLYRSLTESGMSLIANGLLLDMLRRLACFGIHMLRLDIRQ 396

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    +++R+ Dv+  +t+ L++G +  W E  +q +Ll EL+GKRPL++
  gi|1275111   397 DAQRHSDVIAELTRYLGLGDFDHWDEHEKQAFLLRELSGKRPLIPHNWEP 446

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      Ev++v+ ++r +A     + G+Y+isma  PsDvL v LL +E g ++
  gi|1275111   447 SAEVAEVISTVRLIASQSPKALGSYVISMASQPSDVLTVLLLLKEAGCQH 496

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    ++rvvPLFE L DL+ A   +  LF+iDWY+    G qevm+GYsDs KD
  gi|1275111   497 PMRVVPLFETLEDLNNAASCISALFAIDWYRGYCKGSQEVMIGYSDSAKD 546

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
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                    AG ++AAW  Y AqE ++Kv  +  +KL+lFHGRGGt+GRGGGP H AiL
  gi|1275111   547 AGVMAAAWAQYSAQEKLVKVCNQADIKLTLFHGRGGTIGRGGGPAHKAIL 596

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++G +Rvt qGE+i f FG  +L  +sL  +t A +E  + PP
  gi|1275111   597 SQPPGSVDGRIRVTEQGEMIRFKFGLPKLAVQSLALYTSAVMEATLLPPP 646

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     PkPEWR+ me++A      YR++v  EP Fv YFR AtPE+E Gk+ +G
  gi|1275111   647 EPKPEWREAMERLASDSVTAYRAIVREEPDFVAYFRAATPEVELGKLPLG 696

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR+  GGiesLRAiPWiFaW q R  LP WLG G A + A d+
  gi|1275111   697 SRPAKRRVDGGIESLRAIPWIFAWSQNRLMLPAWLGAGEALQQAADRG-- 744

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     l  L+Em ++WPFF   + +lEmv+AK +P +A  y+  Lv  eL+  G
  gi|1275111   745 ELTLLREMEQQWPFFETRISMLEMVYAKAEPNLAKYYETCLVPQELHHLG 794

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    + LR +     + +L++     l+   P+ +  + LR++Yi  Ln +qA
  gi|1275111   795 EALRSRMATGIKVVLELTQSDALMSHTPWNRESVELRNPYIDPLNFLQAE 844

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R             KE A             n        +E  L
  gi|1275111   845 LLARTR-------------KEQAGSS----------N--------VELAL 863

                    iLtmKGiAAGmqntG<-*
                    +Lt+ G+AAGm ntG
  gi|1275111   864 MLTIAGVAAGMRNTG    878

gi|126207823|ref|YP_001053048.1|: domain 1 of 1, from 2 to 879: score 737.1, E = 1.4e-218
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           q       +           +L D   + + +  G+++ E +
  gi|1262078     2    ---NQPYSAMRNNIH----------MLGDFLGETIREAQGNEILELI 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls +     D k  e L  kL  +     + vA+a++  LnL n+
  gi|1262078    36 ESIRVLSRDSRA-GDEKAREQLLDKLANISTENVLPVARAFSQFLNLTNI 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE.
                    AE  +   R        G  +  a           + +L  ++  +P E+
  gi|1262078    85 AEQYQTISRHHQDESL-GNRSLSA----------LFARLKAQG--TPVEt 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v   +   s++LvltAHPt   RRsL+ K+  i  CL qL   D+t  ++
  gi|1262078   122 VIKTVEKLSIELVLTAHPTEVTRRSLVHKHVEINKCLGQLEHDDLTEAEQ 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L   L   i  A+ t EiR a+PtP DE + Gm+ i   +Wk vP F
  gi|1262078   172 TKLKRRLMQLIALAWHTNEIRAARPTPVDEAKWGMAIIENSLWKAVPDFC 221

                    RRvDtALKniGinERlPYdvPL..ikFssWmGGDRDGknPRvtPEvtRDv
                    R     L        + Y+v L++++FssWmGGDRDG nP vt E+t  v
  gi|1262078   222 RELNFQLEK---HFDVQYEVALspVRFSSWMGGDRDG-NPFVTAEITQKV 267

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      + R  Aa l+++ v DL+ Els+  C  E R            +k
  gi|1262078   268 LRMNRWKAAELFLNDVSDLVEELSIVQCTPEFR-----------EKYGD 305

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                    +           EPYRv++   R KL  t      L+      +    +
  gi|1262078   306 HI----------EPYRVVVKGLRSKLQKTLTYFGELIEAKPTTVDPSEII 345

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                    t   +  EPL  CY+sL  CG ++iA GsLLD LR +  FGL L +LDiR
  gi|1262078   346 TCDNDLWEPLYDCYQSLHACGMRIIANGSLLDCLRRIRCFGLGLSRLDIR 395

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+   +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|1262078   396 QESSRHETAIAEITRYIGLGDYAQWTEDDKQAFLVRELSSRRPLVPTNWT 445
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                  ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                     E +++ld+ +v+A  P  +  aY+isma   sDvLAv LL +E g
  gi|1262078   446 PSPETQEILDTCKVVAQQPEGTISAYVISMAREASDVLAVHLLLKEAGCN 495

                  qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                   tL+v PLFE L DL+     +  LF i WY+  i+  q vm+GYsDs K
  gi|1262078   496 YTLPVAPLFETLDDLDHSEKVMTDLFNIGWYRGVINNYQMVMIGYSDSAK 545

                  DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                  DAG l+A W  Y+AqE ++  A ky + LvlFHGRGGtvGRGG P H A+
  gi|1262078   546 DAGMLAASWAQYRAQEALVNLAEKYHIELVLFHGRGGTVGRGGAPAHAAL 595

                  LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                  LsqPP  ++  lRvt qGE+i f  G   +   +L  ++ A LE  + PP
  gi|1262078   596 LSQPPRSLKSGLRVTEQGEMIRFKLGLPAVAVETLNLYASAILEANLLPP 645

                  vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                    Pk  WR++m++ A +  E YR vv  EP Fv YFR+AtPE E Gk+ +
  gi|1262078   646 PEPKQKWRDIMDKGAAISCEIYRGVVRGEPDFVPYFRSATPEQELGKLPL 695

                  GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                  GsRP+KR P GG+esLRAiPWiFaW q R  LP WLG GAA +  i++
  gi|1262078   696 GSRPSKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGAALRQMIEQGE 745

                  KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                       LkEm +eWPFF   + +lEmvF K D  +A  yD+ Lva eL+
  gi|1262078   746 ES--TLKEMCNEWPFFSTRIGMLEMVFSKADLWLAEHYDQRLVAKELHRL 793

                  GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                  Gk LR++     + +L +A    l+   P++   + LR+ Y   Ln +q
  gi|1262078   794 GKTLRAQLSADIQTVLTLAHDGQLMADLPWIAESIALRNVYTDPLNLLQV 843

                  YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                    L+R+R                                 +e   P LE
  gi|1262078   844 ELLQRLRS------------------------------QGEVRDPQLEQA 863

                  LiLtmKGiAAGmqntG<-*
                  L++t+ GiAAGm ntG
  gi|1262078   864 LMITITGIAAGMRNTG    879

gi|146283084|ref|YP_001173237.1|: domain 1 of 1, from 4 to 879: score 733.7, E = 1.4e-217
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      iDA LR      v           LL +     +   HG++  + +
  gi|1462830     4    IIDARLR----DNVH----------LLGELLGNTIRAQHGDQFFDKI 36

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   E     A    K  ++  + L   L sLd ++ + + +a+   LnLAn+
  gi|1462830    37 -ERIRKGAKAARKGSAEGAQLLAETLDSLDESELLPMTRAFNQFLNLANI 85

                  AEEvelAyRRRikk...kkhGDFaD..EasAttEsDiEEtlKkLvlklnK
                  AE  +   RR    + +   G FaD  E       D  E + + v++l
  gi|1462830    86 AEQYHQVRRRAAGEpapFEIGVFADliERLKAAGHD-NEFIARQVSRL-- 132

                  sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt
                              ++LvltAHPt   RR L+qK   i   La     D+
  gi|1462830   133 ------------EIELVLTAHPTEVSRRTLIQKYDAIAQQLAARDHTDLS 170

                  veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGv
                    ++  ++  L R i   + t+EiRR +PtP +E + G + i   +Wk v
  gi|1462830   171 DAERASIELSLQRLIAEVWHTEEIRRNRPTPVEEAKWGFAAIENSLWKAV 220

                  PKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                  P  LR  D  L  +     lP ++  i+F+sWmGGDRDG nP vt  v R
  gi|1462830   221 PNVLRQTDATLHRL-TGLHLPLEAAPIRFASWMGGDRDG-NPNVTAMVSR 268

                  DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                  +v L aR +Aa lY+  +E L+  lsm    dEL      l +   +
  gi|1462830   269 EVLLTARWVAADLYLREIEGLITALSMREASDEL------LRQSGDSA-- 310

                  vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
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                                EPYRv+L   R +L  tRE aR  + +G    +E
  gi|1462830   311 --------------EPYRVLLKPLRQRLRATREWARAAIEHGQPAPAE-- 344

                   vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                   v  +  e   PLELCY+sL  CG  viADG+LLD LR    FGL Lv+LD
  gi|1462830   345 VLQDCAELRRPLELCYRSLHACGMGVIADGALLDCLRRLAVFGLFLVRLD 394

                   iRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
                   iRq++ R+   l  it  L++G Y +W E+KR +WL  EL  +RPLl++
  gi|1462830   395 IRQDAARHAAALAEITDYLGLGDYQQWDEQKRLDWLQHELANRRPLLPAH 444

                   LPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECg
                        + ++vl +  v+AE P  s G+Y+isma a sDvLAv LL +E g
  gi|1462830   445 YHPSADTAEVLATCAVIAEAPAASLGSYVISMAHAASDVLAVQLLLKEAG 494

                   vkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDs
                   +++++rvvPLFE L DL+ A  ++++L s+  Y+ r+ G qevm+GYsDs
  gi|1462830   495 LQRPMRVVPLFETLDDLNNAAPTIDRLLSLPGYRQRLHGPQEVMIGYSDS 544

                   GKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHL
                    KDAG  +AAW  Y+AqE ++ v +++Gv L lFHGRGGtvGRGGGP H
  gi|1462830   545 AKDAGTTAAAWAQYRAQEQLVEVCREHGVELLLFHGRGGTVGRGGGPAHA 594

                   AiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmn
                   AiLsqPP  + G  R t qGE+i f FG  ++  + L  + AA LE  +
  gi|1462830   595 AILSQPPGSVAGRFRTTEQGEMIRFKFGLPDIAEQNLNLYLAAVLEATLL 644

                   PPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkm
                   PP  P P WR+ m+++A      YR vv   P Fv+YFR AtPElE G++
  gi|1462830   645 PPPPPEPGWRETMDRLAAEGVAAYRGVVREHPLFVDYFRQATPELELGRL 694

                   niGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidK
                    +GsRPaKR+  GG+esLRAiPWiFaWtqtR  LP WLG   A   A+++
  gi|1462830   695 PLGSRPAKRR-EGGVESLRAIPWIFAWTQTRLMLPAWLGWEQALHGALQR 743

                   DiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk
                         +L Em   WPFF   +D+lEmv AK D  iA  yD+ Lv  eL
  gi|1462830   744 GEGE--RLAEMRARWPFFSTRIDMLEMVLAKADADIARRYDERLVQPELL 791

                   PFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvf
                     G +LRd+     + +L + G  DlL+  P  +    LR+ Y+  L  +
  gi|1462830   792 SLGSDLRDRLSQVIEAVLSLTGQSDLLDHSPKTQEAFSLRNTYLDPLHLM 841

                   qAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLE
                   q   L R R        + +     A+ +                   LE
  gi|1462830   842 QIELLARSRQ------RQGP-----AESP-------------------LE 861

                   DtLiLtmKGiAAGmqntG<-*
                     L++ + GiAAG+ ntG
  gi|1462830   862 QALLVSVAGIAAGLRNTG    879

gi|190149613|ref|YP_001968138.1|: domain 1 of 1, from 2 to 879: score 733.3, E = 1.8e-217
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          q        +           +L D   + + +  G+++ E +
  gi|1901496     2    ---NQPYSAMRNNIH----------MLGDFLGETIREAQGNEILELI 35

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        ls +     D k  e L  kL  +     + vA+a++  LnL n+
  gi|1901496    36 ESIRVLSRDSRA-GDEKAREQLLDKLANISTENVLPVARAFSQFLNLTNI 84

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE.
                   AE  +   R        G  +  a           + +L  ++  +P E+
  gi|1901496    85 AEQYQTISRHHQDESL-GNRSLSA----------LFARLKAQG--TPVEt 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   v   +    ++LvltAHPt   RRsL+ K+  i  CL qL   D+t  ++
  gi|1901496   122 VIKTVEKLLIELVLTAHPTEVTRRSLVHKHVEINKCLGQLEHDDLTEAEQ 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     L   L   i  A+ t EiR a+PtP DE + Gm+ i   +Wk vP F
  gi|1901496   172 TKLKRRLMQLIALAWHTNEIRAARPTPVDEAKWGMAIIENSLWKAVPDFC 221
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                    RRvDtALKniGinERlPYdvPL..ikFssWmGGDRDGknPRvtPEvtRDv
                    R     L        + Y+v L++++FssWmGGDRDG nP vt E+t  v
  gi|1901496   222 RELNFQLEK---HFDVQYEVALspVRFSSWMGGDRDG-NPFVTAEITQKV 267

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      + R  Aa l+++ v DL+ Els+  C  E R            +k
  gi|1901496   268 LRMNRWKAAELFLNDVSDLVEELSIVQCTPEFR------------EKYGD 305

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                    +           EPYRv++   R KL  t      L+      +    +
  gi|1901496   306 HI----------EPYRVVVKGLRSKLQKTLTYFGELIEAKPTTVDPSEII 345

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                    t   +  EPL  CY+sL  CG ++iA GsLLD LR +  FGL L +LDiR
  gi|1901496   346 TCDNDLWEPLYDCYQSLHACGMRIIANGSLLDCLRRIRCFGLGLSRLDIR 395

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+   +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|1901496   396 QESSRHETAIAEITRYIGLGDYAQWTEDDKQAFLVRELSSRRPLVPTNWT 445

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                       E +++ld+ +v+A  P  +  aY+isma   sDvLAv LL +E g
  gi|1901496   446 PSPETQEILDTCKVVAQQPEGTISAYVISMAREASDVLAVHLLLKEAGCN 495

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                     tL+v PLFE L DL+     +  LF i WY+  i+  q vm+GYsDs K
  gi|1901496   496 YTLPVAPLFETLDDLDHSEKVMTDLFNIGWYRGVINNYQMVMIGYSDSAK 545

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG l+A W  Y+AqE ++  A ky + LvlFHGRGGtvGRGG P H A+
  gi|1901496   546 DAGMLAASWAQYRAQEALVNLAEKYHIELVLFHGRGGTVGRGGAPAHAAL 595

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPP  ++  lRvt qGE+i f  G   +   +L  ++ A LE  + PP
  gi|1901496   596 LSQPPRSLKSGLRVTEQGEMIRFKLGLPAVAVETLNLYASAILEANLLPP 645

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      Pk  WR++m++ A +  E YR vv  EP Fv YFR+AtPE E Gk+ +
  gi|1901496   646 PEPKQKWRDIMDKGAAISCEIYRGVVRGEPDFVPYFRSATPEQELGKLPL 695

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRP+KR P GG+esLRAiPWiFaW q R  LP WLG GAA +  i++
  gi|1901496   696 GSRPSKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGAALRQMIEQGE 745

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                         LkEm +eWPFF   + +lEmvF K D  +A  yD+ Lva eL+
  gi|1901496   746 ES--TLKEMCNEWPFFSTRIGMLEMVFSKADLWLAEHYDQRLVAKELHRL 793

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    Gk LR++     + +L +A    l+   P++   + LR+ Y   Ln +q
  gi|1901496   794 GKTLRAQLSADIQTVLTLAHDGQLMADLPWIAESIALRNVYTDPLNLLQV 843

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L+R+R                                  +e   P LE
  gi|1901496   844 ELLQRLRS------------------------------QGEVRDPQLEQA 863

                    LiLtmKGiAAGmqntG<-*
                    L++t+ GiAAGm ntG
  gi|1901496   864 LMITITGIAAGMRNTG    879

gi|223998678|ref|XP_002289012.1|: domain 1 of 1, from 1 to 883: score 732.3, E = 3.8e-217
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            +  L    +s                      HG d+ E v
  gi|2239986     1    -----MGTLLGDAIS--------------------THHGRDVLEKV 21

                    qECYElsAe..YEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                         ++ e++  G   +++L+ +   + +L  ++ ++v +a+ H L +A
  gi|2239986    22 EALRTMAKEsrRSGDSSSERLQSMVDFVSGLSATELVVVSRAFAHFLGVA 71

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
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                n AE    A+ R  ++k   D   E s        E +K L + +  +Pe
gi|2239986    72 NAAE----AHQRCRRLKL--DLEREVSG-------EDVKGLLVEGAPTPE 108

                EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL..aqLsAKDvtv
                EvF  L  q+v++vltAHPtq  RR LL K++R+   L++a       t+
gi|2239986   109 EVFKSLTSQTVEIVLTAHPTQVNRRTLLEKHGRVQKILndADGLRESGTP 158

                eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                  +k LD+AL REi   + tDE+ R +PtPq E   G   +   +W+  P
gi|2239986   159 YQRKLLDDALRREIASIWQTDEVSRVKPTPQSEAERGTLVVETVLWEALP 208

                KFLRRvDtALK.niGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                 FLR+ D  +K  +G    lP  +   kF+sWmGGDRDG nP vtP+vtR
gi|2239986   209 SFLRKLDATMKwGLGEKYGLPLTASPFKFASWMGGDRDG-NPNVTPDVTR 257

                DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                +vCL  R+ Aa l    v +Lm           +    E ++r   r
gi|2239986   258 EVCLTNRIKAAQLLEGDVRELM----------GVGTESEAMQRVRERS-- 295

                vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                              PYR  L  v  KL nt   a   L +     + +
gi|2239986   296 ----------GDSRAPYRAYLNPVATKLANTATWAQQELRKSTTSFAPDE 335

                vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                vy + +e ++ L    +sLC+ G  v+A G L D++R+ s FGL Lv LD
gi|2239986   336 VYLHKDELMDELLTVHQSLCDSGNTVVANGRLADIIRKLSSFGLTLVPLD 385

                iRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLl...
                iRqEs+R+ + l  it+ L++GsY +W E  R  W+   L+ K PL++++
gi|2239986   386 IRQESDRHEEALNCITKYLGLGSYSQWDEGTRVSWITKQLQSKQPLIrdg 435

                .....gsDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAv
                  +++g +   t    D l++f+++ ++  +s GaY+is +t+ sD+LAv
gi|2239986   436 awnqpGNEQFFTPTSIDTLETFKMISDMHEESLGAYVISQCTSVSDILAV 485

                ELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG.Kq
                 LLq + gv +tLrvvPLFE L DL+ A A++e+LFsi  Y+  ++G+Kq
gi|2239986   486 LLLQLDAGVNKTLRVVPLFETLDDLNGAAATMEHLFSIPAYVGSLEGrKQ 535

                evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                e+mvGYsDs KDAGRl+A W  Y  q  +  vAKk+ v +v FHG+GGtv
gi|2239986   536 EIMVGYSDSAKDAGRLAASWAQYETQVTLSEVAKKHSVDVVYFHGKGGTV 585

                GRGGGP.tHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                GRGG P+t  AiLs  P tinG  Rvt qGE+i + FG  +   r+L  +
gi|2239986   586 GRGGNPnTFEAILSHAPGTINGQFRVTEQGEMINQNFGFSDRAERTLDIY 635

                tAAtL.EHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                tAA L E   + P+ P  EW+++m+++  +  + YR +v  + RFv YFR
gi|2239986   636 TAALLaEQNTDRPL-PTKEWKDMMDKLSQISCDAYRKIVRGDERFVPYFR 684

                lAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG
                 AtPElE   +niGsRPaKRk sGG+esLRAiPWiFaWtqtR  LP WLG
gi|2239986   685 AATPELELSNLNIGSRPAKRKASGGVESLRAIPWIFAWTQTRLNLPTWLG 734

                vGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaL
                vG A    +   +   q L+ mYkeW  FR t+DL+Em   K D  iA
gi|2239986   735 VGEAINEVLS--SPDEQTLRTMYKEWGSFRTTIDLVEMTLSKSDSSIARH 782

                yDkLLvaE.eLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                y+++Lv ++     G ++R+    t+  ++ + GHk l E D  L+  +
gi|2239986   783 YENVLVRDpAAVALGGEIRNIHDATERAVMDLTGHKTLSEHDILLQRLMA 832

                LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                +R++Y+  Lnv+qA tLKR+R+           s    +E+
gi|2239986   833 VRNPYVDCLNVLQAETLKRLRE-----------SEGSSEEE--------- 862

                LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                          L D L+ t+ G+A Gm ntG
gi|2239986   863 ---------VLKDALLTTITGVANGMGNTG    883
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gi|32033610|ref|ZP_00133921.1|: domain 1 of 1, from 1 to 872: score 732.1, E = 4.2e-217
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                  +           +L D   + + +  G+++ E +
  gi|3203361     1    ---------MRNNIH----------MLGDFLGETIREAQGNEILELI 28

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       ls +     D k  e L  kL  +     + vA+a++  LnL n+
  gi|3203361    29 ESIRVLSRDSRA-GDEKAREQLLDKLANISTENVLPVARAFSQFLNLTNI 77

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE.
                  AE  +   R        G  +  a           + +L  ++  +P E+
  gi|3203361    78 AEQYQTISRHHQDESL-GNRSLSA----------LFARLKAQG--TPVEt 114

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  v   +   s++LvltAHPt   RRsL+ K+  i  CL qL   D+t  ++
  gi|3203361   115 VIKTVEKLSIELVLTAHPTEVTRRSLVHKHVEINKCLGQLEHDDLTEAEQ 164

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    L   L   i  A+ t EiR a+PtP DE + Gm+ i   +Wk vP F
  gi|3203361   165 TKLKRRLMQLIALAWHTNEIRAARPTPVDEAKWGMAIIENSLWKAVPDFC 214

                  RRvDtALKniGinERlPYdvPL..ikFssWmGGDRDGknPRvtPEvtRDv
                  R     L        + Y+v L++++FssWmGGDRDG nP vt E+t  v
  gi|3203361   215 RELNFQLEK---HFDVQYEVALspVRFSSWMGGDRDG-NPFVTAEITQKV 260

                  CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                    + R  Aa l+++ v DL+ Els+  C  E R            +k
  gi|3203361   261 LRMNRWKAAELFLNDVSDLVEELSIVQCTPEFR-----------EKYGD 298

                  yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                  +           EPYRv++   R KL  t      L+      +    +
  gi|3203361   299 HI----------EPYRVVVKGLRSKLQKTLTYFGELIEAKPTTVDPSEII 338

                  tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                  t   +  EPL  CY+sL  CG ++iA GsLLD LR +  FGL L +LDiR
  gi|3203361   339 TCDNDLWEPLYDCYQSLHACGMRIIANGSLLDCLRRIRCFGLGLSRLDIR 388

                  qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                  qEs R+   +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|3203361   389 QESSRHETAIAEITRYIGLGDYAQWTEDDKQAFLVRELSSRRPLVPTNWT 438

                  ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                     E +++ld+ +v+A  P  +  aY+isma   sDvLAv LL +E g
  gi|3203361   439 PSPETQEILDTCKVVAQQPEGTISAYVISMAREASDVLAVHLLLKEAGCN 488

                  qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                   tL+v PLFE L DL+     +  LF i WY+  i+  q vm+GYsDs K
  gi|3203361   489 YTLPVAPLFETLDDLDHSEKVMTDLFNIGWYRGVINNYQMVMIGYSDSAK 538

                  DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                  DAG l+A W  Y+AqE ++  A ky + LvlFHGRGGtvGRGG P H A+
  gi|3203361   539 DAGMLAASWAQYRAQEALVNLAEKYHIELVLFHGRGGTVGRGGAPAHAAL 588

                  LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                  LsqPP  ++  lRvt qGE+i f  G   +   +L  ++ A LE  + PP
  gi|3203361   589 LSQPPRSLKSGLRVTEQGEMIRFKLGLPAVAVETLNLYASAILEANLLPP 638

                  vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                    Pk  WR++m++ A +  E YR vv  EP Fv YFR+AtPE E Gk+ +
  gi|3203361   639 PEPKQKWRDIMDKGAAISCEIYRGVVRGEPDFVPYFRSATPEQELGKLPL 688

                  GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                  GsRP+KR P GG+esLRAiPWiFaW q R  LP WLG GAA +  i++
  gi|3203361   689 GSRPSKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGAALRQMIEQGE 738

                  KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                       LkEm +eWPFF   + +lEmvF K D  +A  yD+ Lva eL+
  gi|3203361   739 ES--TLKEMCNEWPFFSTRIGMLEMVFSKADLWLAEHYDQRLVAKELHRL 786

                  GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                  Gk LR++     + +L +A    l+   P++   + LR+ Y   Ln +q
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  gi|3203361   787 GKTLRAQLSADIQTVLTLAHDGQLMADLPWIAESIALRNVYTDPLNLLQV 836

                   YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                     L+R+R                                  +e   P LE
  gi|3203361   837 ELLQRLRS-----------------------------QGEVRDPQLEQA 856

                   LiLtmKGiAAGmqntG<-*
                   L++t+ GiAAGm ntG
  gi|3203361   857 LMITITGIAAGMRNTG    872

gi|148826161|ref|YP_001290914.1|: domain 1 of 1, from 2 to 879: score 731.8, E = 5.2e-217
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                          q        +s           +l +FL++ + D  Ged+ E
  gi|1488261     2    ---TQEYSTLRNNIS-----------MLGRFLgETINDAQGEDILEL 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +     ls +     D  + + L   L s+     i vA+a++  LnL n
  gi|1488261    35 IENIRKLSRNSRAGDDKAR-QALLDTLGSISNENIIPVARAFSQFLNLTN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +   R     +                + E +K+L  +   s eE
  gi|1488261    84 IAEQYQTISREHSLAQS-----------SSQSLSELFKRLKEQN-ASVEE 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   v   +    ++LvltAHPt   RRsL+ K+  i  CL++L   D+t  ++
  gi|1488261   122 VHKTVEKLLIELVLTAHPTETTRRSLIHKHIEINKCLSKLEHHDLTEKER 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     ++  L R i  A+ t EiR  +PtP DE + G + +   +W+ vP FL
  gi|1488261   172 NIIERLLLRLIAEAWHTNEIRTVRPTPFDEAKWGFAMLENSLWQAVPEFL 221

                   RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   R  ++tA   +G    lP     ++ ssWmGGDRDG nP vt  +t+ v
  gi|1488261   222 RQLnETAREFLGYD--LPVGLKPVRISSWMGGDRDG-NPFVTAQITKKVL 268

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     aR  Aa l+++ +  L  Elsm +C dE R            dk   +
  gi|1488261   269 YFARWKAADLFLQDISKLADELSMMKCSDEFR-----------DKYGEH 306

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                              EPYR ++ + R +L  t       L      +sE  +
  gi|1488261   307 L----------EPYRFVVKNLRNQLTATLAYFDDHLSNRTPRVSESEIIL 346

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   +  +  EPL  CY+sL + G ++iA GsLL +L  +s FG+ L ++DiRq
  gi|1488261   347 EDNQLWEPLYDCYQSLIQYGMRIIANGSLLNILHRISCFGVTLSQMDIRQ 396

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   Es R+tD +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|1488261   397 ESTRHTDAIAEITRYIGLGDYAQWTEDDKQAFLIRELSSRRPLIPQNWTP 446

                   tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     E +++ld+ +v+A         Y+isma   sDvLAv LL +E gv
  gi|1488261   447 SPETQEILDTCKVIAQQKQGVIACYVISMARNASDVLAVHLLLKEAGVPY 496

                   tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    ++vvPLFE L DL+AA   + +LF + WY+  i+ +q vm+GYsDs KD
  gi|1488261   497 HIPVVPLFETLEDLDAAEKVMTQLFNVGWYRGVINNRQMVMIGYSDSAKD 546

                   AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                   AG ++A W  Y+AqE ++    k G+ L+lFHGRGGt+GRGG P H A+L
  gi|1488261   547 AGMMAASWAQYRAQEALVNLTEKLGIELTLFHGRGGTIGRGGAPAHAALL 596

                   sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                   sqPP  ++  lRvt qGE+i f  G   +   +   ++ A LE  + PP
  gi|1488261   597 SQPPRSLKNGLRVTEQGEMIRFKLGLPTVAVETFDLYASAILEANLLPPP 646

                   sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                    PkPEWR++m+e+  +  + YR vv  +  Fv YFR+AtPE E  k+ +G
  gi|1488261   647 EPKPEWRNIMDELSTISCDIYRGVVRGDKDFVPYFRSATPEQELSKLPLG 696
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                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR P GG+esLRAiPWiFaW q R  LP WLG GA  +  i++
  gi|1488261   697 SRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGASIRQIIEQGKG 746

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     +  ++ m ++WPFF   + +lEmvF K D  +   yD+ Lv  eL+  G
  gi|1488261   747 DI--IHKMCENWPFFSTRIGMLEMVFSKSDTWLSQQYDQRLVKKELWYLG 794

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    ++LR + ++  + +L +    +l+   P++   + LR+ Y   Ln +q
  gi|1488261   795 ENLRKQLEDDIQTVLSLSHQSELMSDLPWIADSIALRNIYTDPLNLLQVE 844

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                  En            e+v P +E  L
  gi|1488261   845 LLHRFR------------------EN------------PEQVNPDVEQAL 864

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|1488261   865 MITITGIAAGMRNTG    879

gi|92113764|ref|YP_573692.1|: domain 1 of 1, from 8 to 883: score 730.3, E = 1.5e-216
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s+   +R+L  G      + i  D  L D F+D +  + G
  gi|9211376     8    SLRDNVRIL--GDSL--GRTIADD--LGDGFVDKIETIRGL------ 42

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                           A    + D++   EL   L +L   D + v +a+   Ln  n+
  gi|9211376    43 -------AKRGRQDDSESRRELIEYLRALPEKDLLPVTRAFNQFLNFSNI 85

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE    A  RR++  k           t  D+ E l ++   +  +P
  gi|9211376    86 AEQHYRARFRRVEDYK---------PGTQPDLGELLERIRGAG-HAPRKL 125

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     e L    v+LvltAHPt  +RR L+ K   i  CL+ +       e
  gi|9211376   126 VETLAAMRVELVLTAHPTEVIRRTLIRKYDAIDECLTTMEGATEREEIAA 175

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                         L   i  A+ tDEiR  +PtP DE + G + i   +W+ vP F R
  gi|9211376   176 RARGRLEELISQAWHTDEIRHERPTPVDEAKWGFAVIENSLWQAVPDFHR 225

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                      D  L      ERlP d+  ++F+sWmGGDRDG nP vt  vt +v LL
  gi|9211376   226 ELDDLLLA-SAGERLPLDAAPLRFASWMGGDRDG-NPNVTARVTEEVLLL 273

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                     R mAa lY   +  L  ElsmW+ n  LR+   E+ + +
  gi|9211376   274 GRWMAADLYARDLLRLKSELSMWKANGALRA---EVGSDP---------- 310

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             EPYR +L     ++  tR+ a+  L  G    s  A+
  gi|9211376   311 ---------EPYRALLKRLLARVEATRDWAKARL-DGRPFDSNVAIIETR 350

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    ++   PL  CY+sLC+ G   iA G+LLD LR v  FG+sL KLDiRqE+
  gi|9211376   351 DQLYAPLLSCYRSLCDVGLDTIANGALLDTLRRVAVFGVSLTKLDIRQEA 400

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     R+  v D +   L++G YR+W E +Rq++Ll EL+  RPL++
  gi|9211376   401 GRHAQVFDELSDCLGLGHYRDWDEAQRQDFLLEELESPRPLIPRRWDCSA 450

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E ++v+d+frv+A    ++ G Y+isma  PsDvLAv LL +E g    L
  gi|9211376   451 ETREVIDTFRVIAREHREALGTYVISMAGQPSDVLAVALLMKEVGGDLQL 500

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    ++ PLFE L DL+ A   +e+L s+  Y+      qevm+GYsDs KDAG
  gi|9211376   501 PIAPLFETLDDLNRAGDVIERLLSLPGYRRMAGDGQEVMIGYSDSAKDAG 550

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     l+AAW  Y+AqE ++ + +++ v L+lFHGRGGtvGRGGGP H AiLsq
```

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  gi|9211376   551 QLAAAWAQYRAQEQLVGICRQHDVALTLFHGRGGTVGRGGGPAHAAILSQ 600

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP  +nGslRvt qGE+i f FG  ++  rs+  ++ A LE  + PP  P
  gi|9211376   601 PPGSVNGSLRVTEQGEMIRFKFGQPDIALRSMEIYACAVLEATLLPPPDP 650

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    P WR+ m+++  +A   Y  vv  +P Fv YFR+ tPE   G++ +GsR
  gi|9211376   651 EPVWREEMDRLSDIAHRAYVGVVREDPDFVPYFRSVTPESALGRLPLGSR 700

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKR+  GG+esLRAiPWiFaWtqtR  LP WLG G AF   +d
  gi|9211376   701 PAKRRQEGGVESLRAIPWIFAWTQTRLMLPAWLGSGEAFATRLDEPGGR- 749

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaE.eLkPFGk
                    +L++m   WPFF   lD+lEm  AK DP iAa y++ Lv E+ L+  Gk
  gi|9211376   750 ERLRDMRARWPFFGTYLDMLEMLLAKADPDIAAYYERRLVDEpALQALGK 799

                   sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                   sLR++    +  LL i     lLE  P ++q + +R++Yi  L  +qA
  gi|9211376   800 SLRERLSRLETVLLDILDQDTLLEHTPLIRQAIEVRNPYIDPLHGLQAEL 849

                   LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                   L+R RD               Ad                 ++P L   L+
  gi|9211376   850 LQRNRD---------------ADGA---------------ISPELSRALM 869

                   LtmKGiAAGmqntG<-*
                   +tm GiAAG+ ntG
  gi|9211376   870 VTMAGIAAGLRNTG    883

gi|165975797|ref|YP_001651390.1|: domain 1 of 1, from 2 to 879: score 730.1, E = 1.7e-216
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          q        +           +L D   + + +  G+++ E +
  gi|1659757     2    ---NQPYSAMRNNIH----------MLGDFLGETIREAQGNEILELI 35

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        ls +     D k  e L  kL  +     + vA+a++  LnL n+
  gi|1659757    36 ESIRVLSRDSRA-GDEKAREQLLDKLANISTENVLPVARAFSQFLNLTNI 84

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE.
                   AE  +   R        G  +  a           + +L  +   +P E+
  gi|1659757    85 AEQYQTISRHHQDESL-GNRSLSA----------LFARLKAQS--TPVEt 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   v   +    ++LvltAHPt   RRsL+ K+  i  CL qL   D+t  ++
  gi|1659757   122 VIKTVEKLLIELVLTAHPTEVTRRSLVHKHVEINKCLGQLEHDDLTEAEQ 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     L   L   i  A+ t EiR a+PtP DE + Gm+ i   +Wk vP F
  gi|1659757   172 TKLKRRLMQLIALAWHTNEIRAARPTPVDEAKWGMAIIENSLWKAVPDFC 221

                   RRvDtALKniGinERlPYdvPL..ikFssWmGGDRDGknPRvtPEvtRDv
                   R     L        + Y+v L++++FssWmGGDRDG nP vt E+t  v
  gi|1659757   222 RELNFQLEK---HFDVQYEVALspVRFSSWMGGDRDG-NPFVTAEITQKV 267

                   CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                     + R  Aa l+++ v DL  Els+  C  E R            +k
  gi|1659757   268 LRMNRWKAAELFLNDVSDLAEELSIVQCTPEFR------------EKYGD 305

                   yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                   +           EPYRv++   R KL  t      L+      +    +
  gi|1659757   306 HI----------EPYRVVVKGLRSKLQKTLTYFGELIEAKPTTVDPSEII 345

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                   t   +  EPL  CY+sL  CG ++iA GsLLD LR +  FGL L +LDiR
  gi|1659757   346 TCDNDLWEPLYDCYQSLHACGMRIIANGSLLDCLRRIRCFGLGLSRLDIR 395

                   qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                   qEs R+   +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|1659757   396 QESTRHETAIAEITRYIGLGDYAQWTEDDKQAFLVRELSSRRPLVPTNWT 445
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                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                       E +++ld+ +v+A  P  +  aY+isma   sDvLAv LL +E g
  gi|1659757   446 PSPETQEILDTCKVVAQQPEGTISAYVISMAREASDVLAVHLLLKEAGCN 495

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                     tL+v PLFE L DL+     +  LF i WY+  i+  q vm+GYsDs K
  gi|1659757   496 YTLPVAPLFETLDDLDHSEKVMTDLFNIGWYRGVINNYQMVMIGYSDSAK 545

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG l+A W  Y+AqE ++  A ky + LvlFHGRGGtvGRGG P H A+
  gi|1659757   546 DAGMLAASWAQYRAQEALVNLAEKYHIELVLFHGRGGTVGRGGAPAHAAL 595

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPP  ++  lRvt qGE+i f  G   +   +L  ++ A LE  + PP
  gi|1659757   596 LSQPPRSLKSGLRVTEQGEMIRFKLGLPAVAVETLNLYASAILEANLLPP 645

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      Pk  WR++m++ A +  E YR vv  EP Fv YFR+AtPE E Gk+ +
  gi|1659757   646 PEPKQKWRDIMDKGAAISCEIYRGVVRGEPDFVPYFRSATPEQELGKLPL 695

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRP+KR P GG+esLRAiPWiFaW q R  LP WLG GAA +  i++
  gi|1659757   696 GSRPSKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGAALRQMIEQGE 745

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                         LkEm +eWPFF   + +lEmvF K D  +A  yD+ Lva eL+
  gi|1659757   746 ES--TLKEMCNEWPFFSTRIGMLEMVFSKADLWLAEHYDQRLVAKELHRL 793

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    Gk LR++     + +L +A    l+   P++   + LR+ Y   Ln +q
  gi|1659757   794 GKTLRAQLSADIQTVLTLAHDGQLMADLPWIAESIALRNVYTDPLNLLQV 843

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L+R+R                                 +e   P LE
  gi|1659757   844 ELLQRLRS-----------------------------QGEVRDPQLEQA 863

                    LiLtmKGiAAGmqntG<-*
                    L++t+ GiAAGm ntG
  gi|1659757   864 LMITITGIAAGMRNTG    879

gi|53732877|ref|ZP_00155206.2|: domain 1 of 1, from 1 to 866: score 728.6, E = 4.9e-216
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                                +l +FL++ + D  Ged+ E
  gi|5373287     1    -------------------------MLGRFLgETINDAQGEDILEL 21

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls +     D  + + L   L s+     i vA+a++  LnL n
  gi|5373287    22 IENIRKLSRNSRAGDDKAR-QALLDTLGSISNENIIPVARAFSQFLNLTN 70

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R     +                + E +K+L  +   s eE
  gi|5373287    71 IAEQYQTISREHSLAQS-----------SSQSLSELFKRLKEQN-ASVEE 108

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v   +    ++LvltAHPt   RRsL+ K+  i  CL++L   D+t  ++
  gi|5373287   109 VHKTVEKLLIELVLTAHPTETTRRSLIHKHIEINKCLSKLEHHDLTEKER 158

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      ++  L R i  A+ t EiR  +PtP DE + G + +   +W+ vP FL
  gi|5373287   159 NIIERLLLRLIAEAWHTNEIRTVRPTPFDEAKWGFAMLENSLWQAVPEFL 208

                    RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R  ++tA   +G    lP     ++ ssWmGGDRDG nP vt  +t+ v
  gi|5373287   209 RQLnETAREFLGYD--LPVGLKPVRISSWMGGDRDG-NPFVTAQITKKVL 255

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                      aR  Aa l+++ +  L  Elsm +C dE R            dk   +
  gi|5373287   256 YFARWKAADLFLQDISKLADELSMMKCSDEFR-----------DKYGEH 293

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR ++ + R +L  t       L      +sE  +
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  gi|5373287   294 L----------EPYRFVVKNLRNQLTATLAYFDDHLSNRTPRVSESEIIL 333

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   +  +  EPL  CY+sL +CG ++iA GsLL +L  +s FG+ L ++DiRq
  gi|5373287   334 EDNQLWEPLYDCYQSLIQCGMRIIANGSLLNILHRISCFGVTLSQMDIRQ 383

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   Es R+tD +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|5373287   384 ESTRHTDAIAEITRYIGLGDYSQWMEDDKQAFLIRELSSRRPLIPQNWTP 433

                   tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     E k++ld+ +v+A         Y+isma + sDvLAv LL +E gv
  gi|5373287   434 SPETKEILDTCKVIAQQKQGVIACYVISMARSASDVLAVHLLLKESGVPY 483

                   tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    ++vvPLFE L DL+AA   + +LF + WY+  i+ +q vm+GYsDs KD
  gi|5373287   484 HIPVVPLFETLEDLDAAEKVMTQLFNVGWYRGVINNRQMVMIGYSDSAKD 533

                   AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                   AG ++A W  Y+AqE ++    k G+ L+lFHGRGGt+GRGG P H A+L
  gi|5373287   534 AGMMAASWAQYRAQEALVNLTEKLGIELTLFHGRGGTIGRGGAPAHAALL 583

                   sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                   sqPP  ++  lRvt qGE+i f  G   +   +   ++ A LE  + PP
  gi|5373287   584 SQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVETFDLYASAILEANLLPPP 633

                   sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                    PkPEWR +m+e+  +  + YR vv  +  Fv YFR+AtPE E  k+ +G
  gi|5373287   634 EPKPEWRTIMDELSTISCDIYRGVVRGDKDFVPYFRSATPEQELSKLPLG 683

                   sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                   sRPaKR P GG+esLRAiPWiFaW q R  LP WLG GAA +  i++
  gi|5373287   684 SRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGAAIRQVIEQGKG 733

                   nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                    +  ++ m ++WPFF   + +lEmvF K D  +   yD+ Lv  eL+  G
  gi|5373287   734 DI--IHKMCENWPFFSTRIGMLEMVFSKSDTWLSQQYDQRLVKKELWYLG 781

                   ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                   ++LR + ++  + +L +    +l+   P++   + LR+ Y   Ln +q
  gi|5373287   782 ENLRKQLEDDIQTVLSLSHQSELMSDLPWIADSIALRNIYTDPLNLLQVE 831

                   tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    L R R                              n  e+v P +E  L
  gi|5373287   832 LLHRFRK----------------------------N-PEQVNPDVEQAL 851

                   iLtmKGiAAGmqntG<-*
                   ++t+ GiAAGm ntG
  gi|5373287   852 MITITGIAAGMRNTG    866

gi|283896778|emb|CAX65690.1|: domain 1 of 1, from 1 to 502: score 728.1, E = 6.9e-216
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838967     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838967     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838967     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838967     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838967     - ---------------------------------------------- -
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                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838967     - ------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838967     - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838967     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838967     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDvlDAittHL+iGsY eWsEeKRq+WLl+EL+GKRPL+gsDLP+tE
  gi|2838967     1 --HTDVLDAITTHLGIGSYAEWSEEKRQDWLLSELRGKRPLFGSDLPQTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl++f+vLAELP D+FGaYiismat+PsDvLAvELLqREC+vkq+L
  gi|2838967    49 EVADVLGTFHVLAELPADCFGAYIISMATSPSDVLAVELLQRECHVKQPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLeAAPAav++LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|2838967    99 RVVPLFEKLADLEAAPAAVARLFSIDWYMNRINGKQEVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWq+YkAqEE+iKvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838967   149 RLSAAWQMYKAQEELIKVAKHYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE sFGEE+LCFr+LqR+tAAtLEHGm+PP+sP
  gi|2838967   199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRYTAATLEHGMHPPISP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+emAvvAt EYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|2838967   249 KPEWRALMDEMAVVATKEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+n+
  gi|2838967   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIMQKDIRNI 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAa+yDkLLva++L+ FG+
  gi|2838967   349 HTLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAAVYDKLLVADDLQSFGEM 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR +Y+Etk+lLL++AGHkD+LEGDPYLKqrlRLR+sYittLnv+qAYtL
  gi|2838967   399 LRKNYEETKELLLQVAGHKDVLEGDPYLKQRLRLRESYITTLNVCQAYTL 448

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDP+++v ++P lsKE+AdE   +++eLv+Ln  +++aPGLEDtLiL
  gi|2838967   449 KRIRDPNFQVSPQPALSKEFADEK--QPAELVQLNTESEYAPGLEDTLIL 496

                  tmKGiAAGmqntG<-*
                  tmKGiA
  gi|2838967   497 TMKGIA-------    502

gi|219870613|ref|YP_002474988.1|: domain 1 of 1, from 1 to 879: score 728.0, E = 7.1e-216
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                              +s+  + ++    +l  FL++ + D  G+++ +
  gi|2198706     1    -------------MSQIYESMRSNIHMLGDFLgETIRDAQGNEILDL 34

                  vqECYEls.AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                  +     ls+A   G  D k  e L   L  +   D i vA+a++  LnL
  gi|2198706    35 IENIRILSrASRSG--DEKSREQLLDILANISNEDVIPVARAFSQFLNLT 82

                  nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                  n+AE     y    +  k         A  E  +   + +L  +    P+
```

```
  gi|2198706    83 NIAEQ----YHTISRHNK-------DAALGERSMGALFTRLKAQN--VPA 119

                   E.vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                   E+v   +    +DLvltAHPt   RRsL+ K+  i  CL+ L   D+t
  gi|2198706   120 EkVIATVEKLLIDLVLTAHPTEVTRRSLVHKHVEINRCLSRLEHDDLTDA 169

                   DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                   +   L   L   i  A+ t EiR  +PtP DE + Gm+ i   +Wk vP
  gi|2198706   170 ETTKLKRRLMQLIALAWHTNEIRTQRPTPVDEAKWGMAVIENSLWKAVPE 219

                   FLRRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                   F R     L+Kn G+    P     ++FssWmGGDRDG nP vt E tR
  gi|2198706   220 FCRQLNFHLeKNFGVQH--PVGLAPVRFSSWMGGDRDG-NPFVTAETTRK 266

                   vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                   v  + R  Aa l+++ +  L  Els+    d  R++          d
  gi|2198706   267 VLRMNRYKAAELFLEDIKSLADELSVIHATDAFRAK--------YGD--- 305

                   KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                                EPYRv++ d R KL  t      LL      is + +
  gi|2198706   306 -----------HLEPYRVVVKDLRAKLIKTLAYYDELLQDKPLTISRDEI 344

                   ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    t+ E+  EPL  CY+sL +CG ++iA G LLD LR +  FGL L +LDi
  gi|2198706   345 LTDDEQLWEPLYDCYQSLHQCGMRIIANGGLLDCLRRIRCFGLGLSRLDI 394

                   RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                   RqEs R+   +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|2198706   395 RQESTRHEMAIAEITRYIGLGDYSQWTEDDKQAFLVRELSSRRPLVPTNW 444

                   PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                       E k++ld+ +v+AE P     aY+isma   sDvLAv LL +E g
  gi|2198706   445 TPSPETKEILDTCKVVAEQPEGVISAYVISMAREASDVLAVHLLLKEAGC 494

                   kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsG
                   k t++v PLFE L DL+     +  LF i WY+  i+ Kq vm+GYsDs
  gi|2198706   495 KTTIPVSPLFETLDDLDHCEKVMTDLFNIGWYRGVINNKQMVMIGYSDSA 544

                   KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                   KDAG l+A W  Y+AqE ++    ky v L+lFHGRGGt+GRGG P H A
  gi|2198706   545 KDAGMLAASWAQYRAQEALVNLSEKYNVELTLFHGRGGTIGRGGAPAHAA 594

                   iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP
                   +LsqPP  ++  lRvt qGE+i f  G   +   sL  ++ A LE  + P
  gi|2198706   595 LLSQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVSSLDLYASAILEANLCP 644

                   PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmn
                   P  Pk EWR++m++   +  + YR +v  EP Fv YFR AtPE E  k+
  gi|2198706   645 PPEPKQEWRDIMDKGSEISCDIYRGIVRGEPDFVPYFRAATPEQELSKLP 694

                   iGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                   +GsRPaKR P GG+esLRAiPWiFaW q R  LP WLG G A +  i++
  gi|2198706   695 LGSRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGQALQQLIEQG 744

                   iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP
                      l  LkEm  eWPFF   + +lEmvF K D  +A  yD+ Lv   L+
  gi|2198706   745 NEVL--LKEMCTEWPFFSTRIGMLEMVFSKADLWLAEHYDQRLVPQHLHR 792

                   FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfq
                    G+ LR++     + +L +A    l+   P++   + LR+ Y   Ln +q
  gi|2198706   793 LGNTLRNQLAADINTVLSLAHEGQLMADLPWVAESIALRNVYTDPLNLLQ 842

                   AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                      L R+R                +E              e+  P LE
  gi|2198706   843 VELLHRLR-----------------AEG-------------ENPNPALEQ 862

                   tLiLtmKGiAAGmqntG<-*
                    L++t+ GiAAGm ntG
  gi|2198706   863 ALMITITGIAAGMRNTG    879

gi|238794908|ref|ZP_04638507.1|: domain 1 of 1, from 1 to 865: score 727.4, E = 1.1e-215
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                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          L  L    +         +AL             Ge + E v
gi|2387949     1    ----MLGTLLGDTIK--------EAL-------------GEHILEKV 22

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       ls       ++++ +EL + L  L   + + vA+a++  LnL n
gi|2387949    23 ETIRKLSKSSRAGNEASR-QELLTTLQNLSNDELLPVARAFSQFLNLTNT 71

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AE  +       +   hG+ a   +A     +   + +L  k   s +++
gi|2387949    72 AEQYH-------SISPHGEAASNPEA-----LAQLFTRLKDKK-LSEKDM 108

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
gi|2387949   109 RSAVDELSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHNDLADYERN 158

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   +   L   +   + tDEiR+ +P P DE + G + +   +W+GvP FLR
gi|2387949   159 KIMRRLRQLVAQSWHTDEIRKIRPSPVDEAKWGFAVVENSLWEGVPAFLR 208

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                       L+n  +  RlP ++  i+F+sWmGGDRDG nP vt E+tR v LL
gi|2387949   209 EFNEQLQN-SLDYRLPVEAVPIRFTSWMGGDRDG-NPNVTAEITRHVLLL 256

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                  +R  A+ l++  +  L+ Elsm  C  ELR    El
gi|2387949   257 SRWKATDLFLRDIQVLVSELSMSECTPELR----ELAGGEEVV------- 295

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                           EPYR ++  vR +L nt       L +G   ++
gi|2387949   296 ---------EPYRELMKRVRTQLTNTQAYLEGRL-KGERVLPPTDLLVSN 335

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                  ++  +PL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+RqEs
gi|2387949   336 DQLWDPLYACYQSLKACGMEIIANGQLLDTLRRVRCFGVPLVRIDVRQES 385

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   R+t  +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
gi|2387949   386 TRHTNAIAELTRYLGLGDYESWSEADKQAFLVRELNSKRPLVPLKWEPSA 435

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  + ++vl++ rv+AE P  s  aY+isma  PsDvLAv LL +E g   tL
gi|2387949   436 DTQEVLETCRVIAEAPQGSIAAYVISMAKVPSDVLAVHLLLKEAGCPFTL 485

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDAG
gi|2387949   486 PVAPLFETLDDLNNADEVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKDAG 535

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Lsq
gi|2387949   536 VMAASWAQYRAQDALIKTCEKAGISLTLFHGRGGSIGRGGAPAHAALLSQ 585

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP  P
gi|2387949   586 PPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLALYAGAILEANLLPPPEP 635

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  k EW ++m+ +     + YR  v   P Fv YFR AtPElE Gk+ +GsR
gi|2387949   636 KEEWIEVMDLLSDASCDMYRGYVRENPEFVPYFRAATPELELGKLPLGSR 685

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKR+  GG+esLRAiPWiFaWtq R  LP WLG GA  + Aid   K
gi|2387949   686 PAKRRADGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQKAIDAGKKE- 734

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L  m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P G++
gi|2387949   735 -ALATMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVDKSLWPLGQQ 783

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LRd+     + +L iA    l+   P++   + LR+ Y   Lnv+qA  L
gi|2387949   784 LRDQLAADIKVVLAIANDDHLMADLPWIAESIALRNVYTDPLNVLQAELL 833
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                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   R R              E+ d                     +E  L++
  gi|2387949   834 HRSRQ------------HEHPDAR------------------VEQALMV 852

                  tmKGiAAGmqntG<-*
                  t+ G+AAGm ntG
  gi|2387949   853 TIAGVAAGMRNTG    865

gi|262363644|gb|ACY60365.1|: domain 1 of 1, from 2 to 852: score 727.3, E = 1.2e-215
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                                        Ge + + v
  gi|2623636     2    ---------------------------------------GEHILDRV 9

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       ls       ++++ +EL + L  L   + + vA+a++  LnL n
  gi|2623636    10 ETIRKLSKSSRAGNEASR-QELLTTLQNLSNDELLPVARAFSQFLNLTNT 58

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AE  +       +   hG+ a   +A     +   + +L  k   s +++
  gi|2623636    59 AEQYH-------SISPHGEAASNPEA-----LAQLFTRLKDKK-LSDQDM 95

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
  gi|2623636    96 RSAVDDLSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHNDLADYERN 145

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   +   L   +   + tDEiR+ +P P DE + G + +   +W+GvP FLR
  gi|2623636   146 KIMRRLRQLVAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWEGVPAFLR 195

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                       L n  +  RlP ++  i+F+sWmGGDRDG nP vt E+tR v LL
  gi|2623636   196 EFNEQLEN-SLDYRLPVEAVPIRFTSWMGGDRDG-NPNVTAEITRHVLLL 243

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                  +R  A+ l++  +  L+ Elsm  C  ELR    El
  gi|2623636   244 SRWKATDLFLRDIQVLVSELSMSECTPELR----ELAGGEEVL------- 282

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                           EPYR ++ +vR +L nt       L +G   ++
  gi|2623636   283 ---------EPYRQLMKNVRTQLTNTQAYLEARL-KGERVLPPHDLLVSN 322

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                  ++  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+RqEs
  gi|2623636   323 DQLWEPLYACYQSLKACGMEIIANGQLLDTLRRVRCFGVPLVRIDVRQES 372

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   R+tD +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
  gi|2623636   373 TRHTDAIAELTRYLGLGDYESWSESDKQAFLVRELNSKRPLVPLKWEPSA 422

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E ++vl++ rv+AE P  s  aY+isma  PsDvLAv LL +E g   tL
  gi|2623636   423 ETQEVLETCRVIAEAPQGSIAAYVISMAKVPSDVLAVHLLLKEAGCPFTL 472

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDAG
  gi|2623636   473 PVAPLFETLDDLNNADDVMTQLLGIDWYRGLIQGKQMVMIGYSDSAKDAG 522

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Lsq
  gi|2623636   523 VMAASWAQYRAQDALIKTCEKAGITLTLFHGRGGSIGRGGAPAHAALLSQ 572

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP  P
  gi|2623636   573 PPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLALYAGAILEANLLPPPEP 622

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  k EW ++m+ +     + YRs v   P Fv YFR AtPElE Gk+ +GsR
  gi|2623636   623 KKEWIEVMDLLSDASCDMYRSYVRENPEFVRYFRAATPELELGKLPLGSR 672

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
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                    PaKR+P GG+esLRAiPWiFaWtq R  LP WLG GA  + Aid   + +
  gi|2623636   673 PAKRRPDGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQRAIDAGKQDV 722

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L  m ++WPFF   + +lEmvFAK D  +A  yD+ Lv   L+P G++
  gi|2623636   723 --LATMCRDWPFFSTRIGMLEMVFAKADLWLAEYYDQRLVDKSLWPLGQQ 770

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRd+     + +L iA    l+   P++   + LR+ Y   Lnv+qA  L
  gi|2623636   771 LRDQLAADIKVVLAIANDDHLMADLPWIAESIALRNVYTDPLNVLQAELL 820

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     R R             +E+ d                    +E  L++
  gi|2623636   821 HRSRQ------------QEHPDAC-------------------VEQALMV 839

                    tmKGiAAGmqntG<-*
                    t+ G+AAGm ntG
  gi|2623636   840 TIAGVAAGMRNTG    852

gi|110833541|ref|YP_692400.1|: domain 1 of 1, from 1 to 888: score 726.7, E = 1.8e-215
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +D  + +     v           LL D   + L    G+++ E v
  gi|1108335     1    -MDHNVNAPLRDDVR----------LLGDLLGECLRQQAGDSIYETV 36

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          s        ++ L  L   L  Ld a  + vA+a++  LnL n+
  gi|1108335    37 EKIRQASVATRTEGGAS-LASLRDLLSPLDDATLLEVARAFSQFLNLSNI 85

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE     +R R ++++       ++A t+  + E l++L      + e +
  gi|1108335    86 AEQ---HHRERLHRQH---QRYPGDAGTDQGLQEVLQRLADND-IAKEQI 128

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L   sv+LvltAHPt   RR L+ K   +   L+ L   D   ++++
  gi|1108335   129 SGTLEQLSVELVLTAHPTEVTRRTLIRKYDQMADLLSELDRPDFNEDERE 178

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                       E L R i AA+ tDEiRR +PtP DE + G + i   +W+ vP  LR
  gi|1108335   179 LRRERLRRVILAAWCTDEIRREKPTPVDEAKWGFATIEQSLWQAVPDVLR 228

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                      +  L   G+    P d   +k +sWmGGDRDG nP vt  vtR+v LL
  gi|1108335   229 QLEAQLADRGLPAP-PSDWAPVKLASWMGGDRDG-NPNVTAPVTREVLLL 276

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aR mAa lY+  vE L+ +lsm    +EL          aa
  gi|1108335   277 ARWMAADLYLRDVENLLADLSMKSASEEL---------LAATG------- 310

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                          P  EPYRv+L +vR +L  tR R       G+  ++E   y +
  gi|1108335   311 ------PTHEPYRVLLREVRSRLRLTR-RQMEAQVEGLP-VPEGQAYLRR 352

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    Ee + PL L  +sL   G   iADG L   LR    FG+ L +LDiRqEs
  gi|1108335   353 EELMAPLQLLDRSLRAVGLSDIADGDLKNTLRRLNCFGITLLRLDIRQES 402

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL....
                     R+ DvlDAit+ L++G Y +W E  Rq +L+ EL+ +RPL+ +  ++++
  gi|1108335   403 TRHSDVLDAITRYLQLGRYSDWDEAARQAFLVDELQARRPLIDAAFrdse 452

                    PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                      t Ev++vl + +v+AE  ++  GaY+ismat+PsDv+Av LLq+  gv
  gi|1108335   453 HCTAEVAEVLATCEVIAEQGSEGLGAYVISMATTPSDVMAVMLLQKIAGV 502

                    kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsG
                    ++++rvvPLFE L DL+ A  ++  L ++ +Y+ r+   qe+m+GYsDs
  gi|1108335   503 REPMRVVPLFETLDDLDGAEQTMSALLALPFYRERVAAGQEIMIGYSDSA 552

                    KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                    KDAG l AAW  Y+AqE +     + G+ L+lFHGRGG + RGG Pt +A
  gi|1108335   553 KDAGFLGAAWAQYRAQEKLTALFADNGIPLTLFHGRGGSISRGGSPTRMA 602
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                    iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP
                    +LsqPP  + G +Rvt qGEvi f +G   +    L  + AAtLE  + P
  gi|1108335   603 LLSQPPGSVAGRIRVTEQGEVIRFKYGRPSVAVFNLEQYVAATLEATLLP 652

                    PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmn
                    P + +PEWR+ m+ +       YR vv  EP  v Y R  tPE+E  ++
  gi|1108335   653 PQAARPEWRQQMQALTDTSVAGYRGVVRDEPELVRYLRTVTPETELSRLA 702

                    iGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                    +GsRPa+Rk   Gi sLRAiPW+FaWtq R  LP WLG GAA   A + D
  gi|1108335   703 LGSRPARRKSDQGISSLRAIPWVFAWTQIRLMLPAWLGTGAALEDA-QND 751

                    iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEe..L
                         +++Em  eWPFF   +D+lEmv AK D  +Aa y++ L  ++++L
  gi|1108335   752 AAQHAMVREMASEWPFFQGVVDMLEMVLAKSDLRVAAWYEERLAGDDpgL 801

                    kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnv
                       G+ LR++   t   L  + G  DlL+  P ++  +R+Rd+Y   L
  gi|1108335   802 MRLGEVLRERLTATVSALSALTGREDLLDNNPVMRWSIRVRDPYTDPLHL 851

                    fqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGL
                    +qA  + R+R  +              dE                    L
  gi|1108335   852 LQAELMARLRQQD-------------GDET-------------------L 869

                    EDtLiLtmKGiAAGmqntG<-*
                    E  L++t+ GiAAG+ ntG
  gi|1108335   870 ESALMVTIAGIAAGLRNTG    888

gi|167855566|ref|ZP_02478327.1|: domain 1 of 1, from 1 to 879: score 726.6, E = 2e-215
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                  +s+  + ++    +l  FL++ + D  G+++ +
  gi|1678555     1    -------------MSQIYESMRSNIHMLGDFLgETIRDAQGNEILDL 34

                    vqECYEls.AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    +     ls+A   G  D k  e L   L  +   D i vA+a++  LnL
  gi|1678555    35 IENIRILSrASRSG--DEKSREQLLDILANISNEDVIPVARAFSQFLNLT 82

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE     y    +  k         A  E  +   + +L  +    P+
  gi|1678555    83 NIAEQ----YHTISRHNK-------DAALGERSMGALFTRLKAQN--VPA 119

                    E.vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    E+v   +    +DLvltAHPt   RRsL+ K+  i  CL  L   D+t
  gi|1678555   120 EkVIATVEKLLIDLVLTAHPTEVTRRSLVHKHVEINRCLNRLEHNDLTDA 169

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    +   L   L   i  A+ t EiR  +PtP DE + Gm+ i   +Wk vP
  gi|1678555   170 ETTKLKRRLMQLIALAWHTNEIRTQRPTPVDEAKWGMAVIENSLWKAVPE 219

                    FLRRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                    F R     L+Kn G+    P     ++FssWmGGDRDG nP vt E tR
  gi|1678555   220 FCRQLNFHLeKNFGV--QYPVGLAPVRFSSWMGGDRDG-NPFVTAETTRK 266

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                    v  + R  Aa l+++ +  L  Els+    d  R++          d
  gi|1678555   267 VLRMNRYKAAELFLEDIKSLADELSVIHATDTFRAK--------YGD--- 305

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                                 EPYRv++ d R KL  t      LL      is + +
  gi|1678555   306 -----------HLEPYRVVVKDLRAKLIKTLAYYDELLQDKPLTISRDEI 344

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                     t+ E+  EPL  CY+sL +CG ++iA G LLD LR +  FGL L +LDi
  gi|1678555   345 LTDDEQLWEPLYDCYQSLHQCGMRIIANGGLLDCLRRIRCFGLGLSRLDI 394

                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    RqEs R+   +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|1678555   395 RQESTRHEMAIAEITRYIGLGDYSQWTEDDKQAFLVRELSSRRPLVPTNW 444

                    PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv
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                       E k++ld+ +v+AE P     aY+isma   sDvLAv LL +E g
  gi|1678555   445 TPSPETKEILDTCKVVAEQPEGVISAYVISMAREASDVLAVHLLLKEAGC 494

                   kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsG
                   k t++v PLFE L DL+     +  LF i WY+  i+ Kq vm+GYsDs
  gi|1678555   495 KTTIPVSPLFETLDDLDHCEKVMTDLFNIGWYRGVINNKQMVMIGYSDSA 544

                   KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                   KDAG l+A W  Y+AqE ++    ky v L+lFHGRGGt+GRGG P H A
  gi|1678555   545 KDAGMLAASWAQYRAQEALVNLSEKYNVELTLFHGRGGTIGRGGAPAHAA 594

                   iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP
                   +LsqPP  ++  lRvt qGE+i f  G   +   sL  ++ A LE  + P
  gi|1678555   595 LLSQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVSSLDLYASAILEANLCP 644

                   PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmn
                   P  Pk EWR++m++   +  + YR +v  EP Fv YFR AtPE E  k+
  gi|1678555   645 PPEPKQEWRDVMDKGSEISCDIYRGIVRGEPDFVPYFRAATPEQELSKLP 694

                   iGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                   +GsRPaKR P GG+esLRAiPWiFaW q R  LP WLG G A +  i++
  gi|1678555   695 LGSRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGQALQQLIEQG 744

                   iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP
                      l  LkEm  eWPFF   + +lEmvF K D  +A  yD+ Lv   L+
  gi|1678555   745 NEAL--LKEMCTEWPFFSTRIGMLEMVFSKADLWLAEHYDQRLVPQYLHR 792

                   FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfq
                    G+ LR++     + +L +A    l+   P++   + LR+ Y   Ln +q
  gi|1678555   793 LGNTLRNQLAADINSVLSLAHEGQLMADLPWVAESIALRNVYTDPLNLLQ 842

                   AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                      L R+R                +E              e+  P LE
  gi|1678555   843 VELLHRLR-----------------AEG-------------ENPNPALEQ 862

                   tLiLtmKGiAAGmqntG<-*
                    L++t+ GiAAGm ntG
  gi|1678555   863 ALMITITGIAAGMRNTG    879

gi|46133363|ref|ZP_00157068.2|: domain 1 of 1, from 1 to 866: score 726.5, E = 2e-215
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                              +l +FL++ + D  Ged+ E
  gi|4613336     1    --------------------------MLGRFLgETINDAQGEDILEL 21

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +     ls +     D  + + L   L s+     i vA+a++  LnL n
  gi|4613336    22 IENIRKLSRNSRAGDDKAR-QALLDTLGSISNENIIPVARAFSQFLNLTN 70

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +   R     +                + E +K+L  +   s eE
  gi|4613336    71 IAEQYQTISREHSLAQS-----------SSQSLSELFKRLKEQN-ASVEE 108

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   v   +    ++LvltAHPt   RRsL+ K+  i  CL++L   D+t  ++
  gi|4613336   109 VHKTVEKLLIELVLTAHPTETTRRSLIHKHIEINKCLSKLEHHDLTEKER 158

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     ++  L R i  A+ t EiR  +PtP DE + G + +   +W+ vP FL
  gi|4613336   159 NIIERLLLRLIAEAWHTNEIRTVRPTPFDEAKWGFAMLENSLWQAVPEFL 208

                   RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   R  ++tA   +G    +      ++ ssWmGGDRDG nP vt  +t+ v
  gi|4613336   209 RQLnETAREFLGYDLSVGLKP--VRISSWMGGDRDG-NPFVTAQITKKVL 255

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     aR  Aa l+++ +  L  Elsm +C dE R            dk   +
  gi|4613336   256 YFARWKAADLFLQDISKLADELSMMKCSDEFR------------DKYGEH 293

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                             EPYR ++ + R +L  t       L      +sE  +
  gi|4613336   294 L----------EPYRFVVKNLRNQLTATLAYFDDHLSNRTPRVSESEIIL 333
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                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  +  EPL  CY+sL +CG ++iA GsLL +L  +s FG+ L ++DiRq
  gi|4613336   334 EDNQLWEPLYDCYQSLIQCGMRIIANGSLLNILHRISCFGVTLSQMDIRQ 383

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+tD +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|4613336   384 ESTRHTDAIAEITRYIGLGDYSQWMEDDKQAFLIRELSSRRPLIPQNWTP 433

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E k++ld+ +v+A         Y+isma + sDvLAv LL +E gv
  gi|4613336   434 SPETKEILDTCKVIAQQKQGVIACYVISMARSASDVLAVHLLLKESGVPY 483

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                     ++vvPLFE L DL+AA   + +LF + WY+  i+ +q vm+GYsDs KD
  gi|4613336   484 HIPVVPLFETLEDLDAAEKVMTQLFNVGWYRGVINNRQMVMIGYSDSAKD 533

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG ++A W  Y+AqE ++    k G+ L+lFHGRGGt+GRGG P H A+L
  gi|4613336   534 AGMMAASWAQYRAQEALVNLTEKLGIELTLFHGRGGTIGRGGAPAHAALL 583

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++  lRvt qGE+i f  G   +   +   ++ A LE  + PP
  gi|4613336   584 SQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVETFDLYASAILEANLLPPP 633

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     PkPEWR +m+e+  +  + YR vv  +  Fv YFR+AtPE E  k+ +G
  gi|4613336   634 EPKPEWRTIMDELSTISCDIYRGVVRGDKDFVPYFRSATPEQELSKLPLG 683

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR P GG+esLRAiPWiFaW q R  LP WLG GAA +  i++
  gi|4613336   684 SRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGAAIRQIIEQGKG 733

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     +  ++ m ++WPFF   + +lEmvF K D  +   yD+ Lv  eL+  G
  gi|4613336   734 DI--IHKMCENWPFFSTRIGMLEMVFSKSDTWLSQQYDQRLVKKELWYLG 781

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    ++LR + ++  + +L +    +l+   P++   + LR+ Y   Ln +q
  gi|4613336   782 ENLRKQLEDDIQTVLSLSHQSELMSDLPWIADSIALRNIYTDPLNLLQVE 831

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                  En             e+v P +E  L
  gi|4613336   832 LLHRFR------------------EN------------PEQVNPDVEQAL 851

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|4613336   852 MITITGIAAGMRNTG    866

gi|125524127|gb|EAY72241.1|: domain 1 of 1, from 16 to 1009: score 726.5, E = 2.1e-215
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       + +   RlL  G    d  L e    L  +F+ +L     e +
  gi|1255241    16    AFEDDCRLL--GSLLHDVLLRE----LGPRFIHLL-----ERITILA 51

                    qECYElsAeYEGKkDtkKLeE..LGakLtsLdPaDailvAkailHmLnLA
                    q    +     G +Dt  + E++LGa L ++   D++ +A+a++H LnL
  gi|1255241    52 QSAVNMRSA--GVEDTAVVVEkqLGAELAAMSLEDSLCLARAFSHHLNLM 99

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                     +A+  +     R++k +   FaD +        ++t+ kL+  +  sPe
  gi|1255241   100 TIADTYH-----RVRKAR--NFADLSKSC-----DDTFAKLIQSG-VSPE 136

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    E ++ +  q                 LL  n R           D+  eD
  gi|1255241   137 ELYDTVCKQH----------------LLEFNERA----------DLSLED 160

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    K+ L E L REi A + tDE+RR +PtP DE RaG+  +   +Wk +P +
  gi|1255241   161 KEILIEDLVREITAIWQTDELRRHKPTPVDEARAGLHIVEQSLWKAIPHY 210

                    LRRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
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                    LRRv  AL+Kn G    lP     ikF sWmGGDRDG nP vt  vtRDv
  gi|1255241   211 LRRVSNALkKNTG--KPLPLTCTPIKFGSWMGGDRDG-NPNVTAKVTRDV 257

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEly.........
                     +L+  mA  lYi  ++ L FEls+ RC + L   A ++  +++ +++++
  gi|1255241   258 SILSQWMAIDLYIRELDTLSFELSINRCSEKLANLANDILlkesasedqk 307

                    ..................................................
                    +++ ++++++++ + +++   + + +++ + ++ ++ ++++++ + ++ +
  gi|1255241   308 tntwnqtgpqnnlklqhslalpaqlpsgadlpsctecndgesqirmsklp 357

                    ............................rtaardkvvKyYiE.......
                    ++++++   + ++++++++ +++++++ +rt+   ++ K + E++ ++++
  gi|1255241   358 gnpkhklalnitekredsplpspshrpmgRTPSGGQLRKMFTEsqigrss 407

                    FWKqvPP.......tEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                    F K + P+ +++++  PYRv+LGdv++KL nt  R   LL     +
  gi|1255241   408 FRKLLEPsiserpgSTPYRVVLGDVKEKLMNTQRRLELLLEDLPCDRDTS 457

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y   ++ LEPL LCY+sL  CG  v+ADG L Dl+R v tFG+ L+KL
  gi|1255241   458 EYYDTSDKLLEPLLLCYQSLQSCGSSVLADGRLADLIRRVATFGMVLMKL 507

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    D+RqEs R+t+ lDAit  L++G Y eW E+K+ ++L  ELkGKRPL+++
  gi|1255241   508 DVRQESGRHTETLDAITSYLDLGVYSEWDEQKKLDFLTRELKGKRPLVPP 557

                    DLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqREC
                     +  t +v++vld+frv AEL +D+ GaY+isma   sDvLAvELLq++
  gi|1255241   558 YIQVTADVQEVLDTFRVAAELGSDALGAYVISMASNASDVLAVELLQKDA 607

                    gvkq..........tLrvvPLFEkLADLeAAPAavekLFsiDWYinri.
                     +  +++ +++ +++tLrvvPLFE + DL+ A  a+ kL siDWY+ +i
  gi|1255241   608 RLTVsgdlgrpcpggTLRVVPLFETVNDLREAGPAIRKLLSIDWYRDHIi 657

                    ...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                    ++++G qevmvGYsDsGKDAGR+ AAW LYkAqE+++     +G+K++lF
  gi|1255241   658 knhNGHQEVMVGYSDSGKDAGRFTAAWELYKAQEDVVAACNAFGIKVTLF 707

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGG +GRGGGPt LAi sqPP  + G lR t qGE++   FG  +
  gi|1255241   708 HGRGGSIGRGGGPTYLAIQSQPPGSVMGTLRSTEQGEMVQAKFGLPQTSV 757

                    rsLqRFtAAtLEHGmnPPvsPkPE.WRkLmeemAvvAtEEYRsvvvKEPR
                    r L  +t A L   + PP  P+ ++WR +mee+  v    YRs v+  P
  gi|1255241   758 RQLEIYTTAVLLATLRPPQPPRDDkWRGVMEEISRVSCAQYRSTVYENPE 807

                    FvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFH
                    F+ YF  AtP  E G +niGsRPaKR+   Gi  LRAiPW+FaWtqtR
  gi|1255241   808 FIKYFQEATPQAELGYLNIGSRPAKRRTTPGISNLRAIPWVFAWTQTRLV 857

                    LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                    LP WLGvG   + A dK       L+ mY+eWPFF  t+DL+Emv AK D
  gi|1255241   858 LPAWLGVGRGLQDACDKGHT--HELRAMYEEWPFFQSTVDLIEMVVAKAD 905

                    PGiAaLyDkLLvaEe.LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                      +A  yD++Lv + + +  G +LR++   t++ +L + GHk l
  gi|1255241   906 APMAKHYDDVLVHDAgRRALGAELRQELARTENCVLAVSGHKKLSANNRS 955

                    LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                    L++ +  R  Y+  +n++q   L+R+R                 d+n
  gi|1255241   956 LRKLIDSRLTYLNPMNMLQVEVLRRLRQ---------------DDDN--- 987

                    adeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                         kL           D L++t+ GiAAGm ntG
  gi|1255241   988 ----RKLR----------DALLITINGIAAGMRNTG    1009

gi|254481871|ref|ZP_05095114.1|: domain 1 of 1, from 15 to 879: score 724.7, E = 7e-215
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s    L  +    v+         A   D FL ++     e ++
  gi|2544818    15    SNVSDLGRILGDTVA---------AAEGDEFLALI-----ERVRGLS 47
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                +   E sAe           EL  +L +Ld    + vA+a+   LnLAn+
gi|2544818    48 KGAREGSAE--------DRAELLDQLRALDNDQLVPVARAFAQFLNLANI 89

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                A+  +l  R    ++                +   l  L   +  s +E+
gi|2544818    90 ADQQHLVSRAMDPLLS-----------ASRNLNNSLGELREEG-VSVAEI 127

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                 +A+    ++LvltAHPt   RR L+ K++ i  CL +L    +t  +
gi|2544818   128 EQAIAELKIELVLTAHPTEITRRTLIHKHSEIGACLGKLELGGLTSREES 177

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                 L   L   +   +  D+ RR +PtP DE + G + + E +W+ vP FLR
gi|2544818   178 QLQSRLREVVAQIWYGDDFRRERPTPVDEAKWGFAVVEESLWRAVPEFLR 227

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                R D AL     n  lP ++  + F sWmGGDRDG nP vt EvtR+v LL
gi|2544818   228 RLDDALAQ-HCNSHLPLEAAPVNFVSWMGGDRDG-NPNVTAEVTREVMLL 275

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                +R  Aa lY+  +  L+ Elsm RCn  LR  A         d
gi|2544818   276 SRWQAADLYLGDINQLLEELSMTRCNAALRSLA--------GD------- 310

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                         EPYR iL ++R  L nt       L   + e + eA   +
gi|2544818   311 -------AHEPYRAILREIRKLLRNTIASIEQQL---VGEPAGEAEVLQS 350

                EeFL.EPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                E+ L  PL  CY+sL eCG  +iA GsLLD+LR +  FG+ Lv+ DiRq+
gi|2544818   351 EQQLwQPLLACYQSLTECGMEIIAGGSLLDVLRRIRCFGVHLVRHDIRQD 400

                seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                s R+t+ +  it+ L++G Y +W Ee R+ +Ll EL  +RPL++
gi|2544818   401 SARHTEAMSEITRCLGLGDYADWDEETRRAFLLRELGNRRPLIPRHWQPS 450

                EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                 Ev++vld+  v AE P  + GaY+isma   sDvLAv LL  E gv  t
gi|2544818   451 AEVQEVLDTCAVAAEQPPGALGAYVISMARQASDVLAVHLLLQEAGVSDT 500

                LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                ++v PLFE L DL  A   v  L    WY+ +i G+  vm+GYsDs KDA
gi|2544818   501 VPVAPLFETLDDLSRAKDVVSDLLQNHWYRGQIAGQLMVMIGYSDSAKDA 550

                GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                G l+A W  Y+AqE +  v   + v L+lFHGRGGt+GRGG P   A+Ls
gi|2544818   551 GVLAASWAQYRAQEQLLEVCSGHNVELTLFHGRGGTIGRGGAPAREALLS 600

                qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                qPP  ++  lRvt qGE+i    G   L  ++L  +t A     +  P +
gi|2544818   601 QPPGSLKNGLRVTEQGEMIRTKLGWTSLAVKTLALYTVAICRANLRTPPA 650

                PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                Pk  WR++m+e+A      YR +v  EP Fv YFR AtPE E  k+ +Gs
gi|2544818   651 PKDSWREVMDELAENSCRAYREIVREEPEFVPYFRHATPEQELAKLPLGS 700

                RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                RPa+Rk +GGiesLRAiPWiFaW q R  LP WLG GAA   A+ +D
gi|2544818   701 RPARRKGGGGIESLRAIPWIFAWSQNRLMLPAWLGAGAAL--AMAQDNGR 748

                lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                 q + Em ++WPFF   + +lEmv+AK D G+ a yD+ Lv  +L   G+
gi|2544818   749 EQLMTEMAEKWPFFATRMSMLEMVYAKADLGLSAYYDETLVPAQLTFIGE 798

                sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                +LR++       +L i GH++lL   P+    +RLR+ Y   Ln +qA
gi|2544818   799 QLRAQLTADIATVLGINGHRELLSDQPWTAESIRLRNIYTDPLNFLQAEL 848

                LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                LKR R+                E+                P  E  ++
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  gi|2544818   849 LKRNRE----------------MEE-----------------PDAERAIM 865

                   LtmKGiAAGmqntG<-*
                   +t+ GiAAGm ntG
  gi|2544818   866 VTIAGIAAGMRNTG    879

gi|283896806|emb|CAX65704.1|: domain 1 of 1, from 1 to 503: score 720.9, E = 9.7e-214
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838968     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838968     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838968     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838968     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838968     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838968     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838968     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838968     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838968     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDvlD ittHL+iGsY eWsEeKRq+WLl+EL+GKRPL+gsDLP tE
  gi|2838968     1 --HTDVLDSITTHLGIGSYAEWSEEKRQDWLLSELRGKRPLFGSDLPLTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E +Dvl+af+vLAELP D+FGaYiismataPsDvLAvELLqREC+vkq+L
  gi|2838968    49 ETADVLGAFHVLAELPADCFGAYIISMATAPSDVLAVELLQRECHVKQPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAav++LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|2838968    99 RVVPLFEKLADLEAAPAAVARLFSIDWYMNRINGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWq+YkAqEE+iKvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838968   149 RLSAAWQMYKAQEELIKVAKHYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE sFGEE+LCFr+LqR+tAAtLEHGm+PP+sP
  gi|2838968   199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRYTAATLEHGMHPPISP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emA+vAt EYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|2838968   249 KPEWRALMDEMAIVATKEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+n+
  gi|2838968   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIMQKDIRNI 348
```

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                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAa+yDkLLva++L+ FG++
  gi|2838968   349 HTLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAAVYDKLLVADDLQSFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Etk+lLL++AGHkD+LEGDPYLKqrlRLR+sYittLnv+qAYtL
  gi|2838968   399 LRKNYEETKELLLQVAGHKDVLEGDPYLKQRLRLRESYITTLNVCQAYTL 448

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPs++v ++P lsKE+ dE  ++a++Lv+Lnp +++aPGLEDtLiL
  gi|2838968   449 KRIRDPSFEVSPQPALSKEFVDES-QPAAQLVQLNPESEYAPGLEDTLIL 497

                    tmKGiAAGmqntG<-*
                    tmKGiA
  gi|2838968   498 TMKGIA-------    503

gi|283896784|emb|CAX65693.1|: domain 1 of 1, from 1 to 503: score 720.7, E = 1.2e-213
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838967     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838967     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838967     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838967     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838967     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838967     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838967     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838967     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838967     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDvlDAitt L+iGsYReW+Ee+RqEWLl+EL GKRPL+g+DLPktE
  gi|2838967     1 --HTDVLDAITTYLGIGSYREWPEERRQEWLLSELNGKRPLFGPDLPKTE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvld+f+v+AELP D FGaYiismat+PsDvLAvELLqREC+vk +L
  gi|2838967    49 EVADVLDTFHVIAELPADNFGAYIISMATSPSDVLAVELLQRECHVKTPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAa+++LFsiDWY+ ri GKqevm+GYsDsGKDAG
  gi|2838967    99 RVVPLFEKLADLEAAPAALARLFSIDWYRHRIHGKQEVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838967   149 RLSAAWQLYKAQEELIKVAKDFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP +P
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  gi|2838967   199 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPNAP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L++emAvvAtEEYRs+v+KEPRFvEYFRlAtPE+EYG+mniGsR
  gi|2838967   249 KPEWRALLDEMAVVATEEYRSIVFKEPRFVEYFRLATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|2838967   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLQKDIRNL 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+E+L+P G++
  gi|2838967   349 HMLQEMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEDLQPLGEK 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Et++lLL++AGH+DlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|2838967   399 LRANYEETQKLLLQVAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 448

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y+v lrPhlsK+  d   k+a+eLvkLnp++++aPGLEDtL L
  gi|2838967   449 KRIRDPDYHVALRPHLSKDIMDSS-KPAAELVKLNPASEYAPGLEDTLTL 497

                   tmKGiAAGmqntG<-*
                   tmKGiA
  gi|2838967   498 TMKGIA-------    503

gi|283896814|emb|CAX65708.1|: domain 1 of 1, from 1 to 502: score 719.1, E = 3.5e-213
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838968     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838968     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838968     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838968     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838968     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838968     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838968     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838968     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838968     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDvlD ittHL+iGsY eWsEeKRq+WLl+EL+GKRPL+gsDLP tE
  gi|2838968     1 --HTDVLDSITTHLGIGSYAEWSEEKRQDWLLSELRGKRPLFGSDLPLTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E +Dvl+af+vLAELP D+FGaYiismataPsDvLAvELLqREC+vk++L
  gi|2838968    49 ETADVLGAFHVLAELPADCFGAYIISMATAPSDVLAVELLQRECHVKHPL 98
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                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAav++LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|2838968     99 RVVPLFEKLADLEAAPAAVARLFSIDWYMNRINGKQEVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWq+YkAqEE+iKvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838968    149 RLSAAWQMYKAQEELIKVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti GslRvtvqGEviE sFGEE+LCFr+LqR+tAAtLEHGm+PP+sP
  gi|2838968    199 PPDTIRGSLRVTVQGEVIEHSFGEEHLCFRTLQRYTAATLEHGMHPPISP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emA+vAt EYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|2838968    249 KPEWRALMDEMAIVATKEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+n+
  gi|2838968    299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHLMQKDIRNI 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAa+yDkLLvaE+L+ FG++
  gi|2838968    349 HTLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAAVYDKLLVAEDLQSFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Etk+lLL++AGHkD+LEGDPYLKqrlRLR++YittLnv+qAYtL
  gi|2838968    399 LRKNYEETKELLLQVAGHKDVLEGDPYLKQRLRLREPYITTLNVCQAYTL 448

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP ++v ++P lsKE+ dE   +++eLv+Lnp +++aPGLEDtLiL
  gi|2838968    449 KRIRDPGFQVSPQPALSKEFTDES--QPAELVQLNPESEYAPGLEDTLIL 496

                    tmKGiAAGmqntG<-*
                    tmKGiA
  gi|2838968    497 TMKGIA-------    502

gi|293336483|ref|NP_001170654.1|: domain 1 of 1, from 1 to 506: score 716.8, E = 1.7e-212
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2933364      -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2933364      - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2933364      - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2933364      - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2933364      - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2933364      - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2933364      - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2933364      - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
```

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  gi|2933364     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                         +DAit+ L+iGsYR+W+EeKRqEWLl+EL GKRPL+g+DLPk +
  gi|2933364     1 ------MDAITEYLGIGSYRKWPEEKRQEWLLSELNGKRPLFGPDLPKSD 44

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dvld+f+vLAELP+DsFGaY+ismataPsDvLAvELLqREC+vk++L
  gi|2933364    45 EIADVLDTFHVLAELPSDSFGAYVISMATAPSDVLAVELLQRECHVKKPL 94

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLe APAa+++LFs++WY+nri GKqevm+GYsDsGKDAG
  gi|2933364    95 RVVPLFEKLADLESAPAALARLFSVEWYRNRISGKQEVMIGYSDSGKDAG 144

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   R+sAAWqLYkAqEE+i vAK yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2933364   145 RFSAAWQLYKAQEELINVAKLYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 194

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP+ti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2933364   195 PPETIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 244

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emA+vAt EYRs+v+ EPRFvEYFRlAtPE+EYG+mniGsR
  gi|2933364   245 KPEWRALMDEMAIVATKEYRSIVFEEPRFVEYFRLATPEMEYGRMNIGSR 294

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPs GiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh +dKDi+nl
  gi|2933364   295 PSKRKPSAGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLDKDIRNL 344

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q L+EmY++WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+  G +
  gi|2933364   345 QTLQEMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWALGAR 394

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Etk+lLL++AGHkDlLEGDPYLKqrlR+RdsY t Lnv+qAYtL
  gi|2933364   395 LRANYEETKQLLLQVAGHKDLLEGDPYLKQRLRIRDSYTTALNVCQAYTL 444

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP ++v +rPhlsK+  d   k+a eLvkLn t+++aPGLEDtLiL
  gi|2933364   445 KRIRDPGFQVKPRPHLSKDIMDMG-KPASELVKLNTTSEYAPGLEDTLIL 493

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|2933364   494 TMKGIAAGMQNTG    506

gi|254784775|ref|YP_003072203.1|: domain 1 of 1, from 3 to 878: score 716.0, E = 2.9e-212
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                  K    e L e   +L D   + L +  G+ L   v
  gi|2547847     3    ------------KLP--ETLRENVRMLGDLLGENLLEHQGPKLFRKV 35

                   qECYEls...AeYEGKkDtkK..LeELGakLtsLdPaDailvAkailHmL
                    E    s++ A  +   D++K+ +e L   L  ++ aD + +A+a+   L
  gi|2547847    36 EEIRAFSkqlAKSDRSSDAHKeaVESLLESLSQVEDADILPIARAFNQFL 85

                   nLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnK
                   nLAn+A+             +h  ++ E  A  E  ++E l  L
  gi|2547847    86 NLANIAD-------------QHYFYSSE--AREEDALDEILENLADAK-- 118

                   sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt
                     ++ +  +    ++LvltAHPt   RR L+ K   +   L+ L   D+
  gi|2547847   119 GKDDLYKLVNELNIELVLTAHPTEVTRRTLIRKYEQVAKALSDLRRNDLL 168

                   veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGv
                     +   + E L R i   + t EiR ++Pt  DE + G + i   +W+ v
  gi|2547847   169 DYEVAQIKESLQRYIEEIWHTNEIRTTRPTAVDEAKWGFAVIENSLWHAV 218

                   PKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                   P F+R  D   +   +   lP  +   +F sWmGGDRDG nP vt  vt
  gi|2547847   219 PDFIRHLDSVCRR-RLGKPLPLGITPFRFYSWMGGDRDG-NPNVTHKVTE 266
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                    DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                     v L+ R  Aa lYi  + ++  +lsm     EL     El
  gi|2547847   267 QVLLMGRWRAADLYIKDINEVAGDLSMHAASHELL----ELVGEDSAT-- 310

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                                  PYR +L   R +L  t   a   +   +   + +
  gi|2547847   311 ---------------PYRDLLHGLRNRLQATLNWAEARMNDPMLPEPANI 345

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                    ++ +  e L PL LCY sL e G   iA GsL Dl+R +  FG+ Lv LD
  gi|2547847   346 IHSR-NELLQPLMLCYESLHELGLSQIANGSLTDLIRRIHAFGINLVPLD 394

                    iRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
                    iRq+ +R+ + lD +t  Le+GsYR+W EeKRq +Ll  L+ KRPLl+ +
  gi|2547847   395 IRQDGDRHVELLDELTIYLELGSYRSWDEEKRQAFLLEQLESKRPLLPEE 444

                    LPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECg
                     P  E+ ++v+++ rv+A  P ++   Y+isma  PsDvLAv LL +ECg
  gi|2547847   445 WPVSEDSREVINTCRVIAAQPRETLAHYVISMAQQPSDVLAVALLLKECG 494

                    vkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDs
                    v+  +++ PLFE L DL+ AP  ++ L+ + WY   idG+q vm+GYsDs
  gi|2547847   495 VRWKMPIDPLFETLDDLDRAPRVMNALWQMHWYQRYIDGQQTVMIGYSDS 544

                    GKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHL
                     KDAG+++A W  YkAqE ++  A ++ vKL lFHGRGGtvGRGGGP
  gi|2547847   545 AKDAGKFAATWAQYKAQEKLVSLADQHDVKLNLFHGRGGTVGRGGGPVEK 594

                    AiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmn
                    A+ sqPP  ++  +Rvt qGE+i + FG   + F sL  +  AtL
  gi|2547847   595 AMASQPPGSVKARIRVTEQGEMIRYKFGMPRVAFASLSNYVLATLRATET 644

                    PPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkm
                    P   PkPEWR+Lme+mA      YR vv     Fv YFR+ tPE E  k+
  gi|2547847   645 PAPNPKPEWRELMENMAQASLTAYRGVVRGHESFVPYFRSLTPEQELSKL 694

                    niGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidK
                     +GsRP KRk sGG+esLRAiPW+FaWtq R  LP WLG   A  + ++
  gi|2547847   695 ALGSRPPKRKASGGVESLRAIPWVFAWTQVRLNLPGWLGTRQALEYGLQN 744

                    DiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk
                    +      Lk+m ++WPFF   +DLlEmv  K D  i a y++ Lv  +L+
  gi|2547847   745 EQ---DTLKDMQQNWPFFNSFIDLLEMVLGKADTSICAHYEEQLVDKDLR 791

                    PFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvf
                    P G++LR + +    l+  +    +lLE  P L+q + +R +Y+  Ln +
  gi|2547847   792 PLGEQLRGDLEALAGLINTMKEQPELLENTPLLQQSINIRKPYMDPLNYL 841

                    qAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLE
                    qA  LKR                   E             + +++P LE
  gi|2547847   842 QAELLKR--------------------ER-----------KAGEISPDLE 860

                    DtLiLtmKGiAAGmqntG<-*
                      L +tm GiAAGm ntG
  gi|2547847   861 RALKVTMTGIAAGMRNTG    878

gi|255566797|ref|XP_002524382.1|: domain 1 of 1, from 1 to 986: score 714.5, E = 8.5e-212
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                          + D   Di  ++   + + +
  gi|2555667     1    -------------------------MTDTTDDIAEEI---SFQSFD 18

                    qEC....YElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLn
                     +C + +Y    e   K   kKL               +  A+++ H+
  gi|2555667    19 DDCcpfrYFRTREEREKGKEKKL---------------VRKARSMTHL-- 51

                    LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                                   +k                  ++ + +L   +  s
  gi|2555667    52 ----------------SKSC----------------DDIFNQLLQSG-IS 68

                    PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                     eE ++ +  q v++vltAHPtq  RR L  K+ Ri   L      D+t
```

```
gi|2555667    69 AEELYDTVCKQEVEIVLTAHPTQINRRTLQYKHIRIAHLLDYNDRPDLTH 118

                 eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                 eD++ L E L REi   + tDE+RR +PtP DE RaG+  +   +Wk  P
gi|2555667   119 EDREMLIEDLVREITSIWQTDELRRHKPTPVDEARAGLNIVEQSLWKALP 168

                 KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                  +LRRv tALK       lP     i+F sWmGGDRDG nP vt  vtRD
gi|2555667   169 HYLRRVSTALKK-HTGKPLPLTCMPIRFGSWMGGDRDG-NPNVTAKVTRD 216

                 vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEl..........
                 v LL+R mA  lYi  v+ L FElsm  C d L   A ++  ++++++++
gi|2555667   217 VSLLSRWMAVDLYIREVDSLRFELSMVQCSDRLLKVANDIlieetssedh 266

                 ...yrtaardkvvKy.................................
                 +++   +a+   +K+++++ +++ +++ + +  ++ ++++++ ++ + ++
gi|2555667   267 hesWNQPASRSQTKFprkslptqlppradlpactecndgesqypklelpg 316

                 ..YiEFWK.......................................
                 ++Y+ F +++  +++ +++++++ +++ ++++++++  +++++++ + ++
gi|2555667   317 tdYMPFNRqealgssysesssqdinhglpkttgngsvanssgsprasfss 366

                 ............................qvPPtEPYRviLGdvRDKLYn
                  +   +++   +++ ++++ ++  +++ +q P   PYR++LG+v+DKL
gi|2555667   367 aqlvaqrklfaeskigrssfqkllepslpQRPGIAPYRIVLGNVKDKLMR 416

                 tRERaRHLLAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADG
                 tR R   LL     e      y   ++ L+PL LCY sL  CG  v+ADG
gi|2555667   417 TRRRLELLLEDLPCEYDQWDYYETTDQLLDPLLLCYESLQSCGAGVLADG 466

                 sLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEe
                  L Dl+R v tFG+ L+KLD+RqEs R+ D lDAit+ Le+G Y eW Ee
gi|2555667   467 RLADLIRRVATFGMVLMKLDLRQESGRHADTLDAITKYLEMGTYSEWDEE 516

                 KRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGaYii
                 K+ E+L  ELkGKRPL+++ +    +vk+vldafrv AEL +Ds GaY+i
gi|2555667   517 KKLEFLTRELKGKRPLVPPTIEVAPDVKEVLDAFRVAAELGSDSLGAYVI 566

                 smataPsDvLAvELLqRECgvkq...........tLrvvPLFEkLADLeA
                 sma   sDvLAvELLq++  +  +++ +++ +++tLrvvPLFE + DL+
gi|2555667   567 SMASNASDVLAVELLQKDARLAVsgelgrpcpggTLRVVPLFETVKDLRG 616

                 APAavekLFsiDWYinri....dGKqevmvGYsDsGKDAGRlsAAWqLYk
                 A   + kL siDWY+ +i ++++G qevmvGYsDsGKDAGR+ AAW LYk
gi|2555667   617 AGSVIRKLLSIDWYREHIiknhNGHQEVMVGYSDSGKDAGRFTAAWELYK 666

                 AqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslR
                 AqE+++    ++G+K++lFHGRGG +GRGGGPt LAi sqPP  + G lR
gi|2555667   667 AQEDVVAACNDFGIKVTLFHGRGGSIGRGGGPTYLAIQSQPPGSVMGTLR 716

                 vtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE.WRkLme
                  t qGE++   FG  +   r L  +t A L   + PP  P+ E+WR++me
gi|2555667   717 STEQGEMVQAKFGLPHTAIRQLEIYTTAVLLATLRPPHPPREEkWRNVME 766

                 emAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGG
                 e+  +    YRs v+  P F  YF  AtP  E G +niGsRP++Rk s G
gi|2555667   767 EISKISCQNYRSTVYENPEFLAYFHEATPQAELGFLNIGSRPTRRKSSTG 816

                 iesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYke
                 i  LRAiPW+FaWtqtRF LP WLGvGA  K A +K       Lk mYke
gi|2555667   817 IGHLRAIPWVFAWTQTRFVLPAWLGVGAGLKGACEKGFTE--DLKAMYKE 864

                 WPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtk
                 WPFF  t+DL+Emv  K D  iA  yD++Lv+E  +  G +LR +   t+
gi|2555667   865 WPFFQSTIDLIEMVLGKADIPIAKHYDEVLVSESRRELGAELRSELLTTE 914

                 dlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsyk
                 +++L + GH  l      L+  +  R +Y+  +n++q   LKR+R
gi|2555667   915 KYVLVVSGHEKLSQNNRSLRRLIESRLPYLNPMNMLQVEVLKRLRR---- 960

                 vtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGm
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                              d+n          n        L D L++t+ GiAAGm
  gi|2555667   961 -----------DDDN----------N-------KLRDALLITINGIAAGM 982

                   qntG<-*
                    ntG
  gi|2555667   983 RNTG    986

gi|213616153|ref|ZP_03371979.1|: domain 1 of 1, from 2 to 840: score 714.1, E = 1.2e-211
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                    s
  gi|2136161     2    --------------S------------------------------- 2

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          A  E  +     +EL + L  L   + + vA+a++  LnLAn
  gi|2136161     3 ------RAGNEANR-----QELLTTLQNLSNDELLPVARAFSQFLNLANT 41

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AE  +      i+ k       Ea    E  i  tl+kL  + +   + +
  gi|2136161    42 AEQYH-----SISPKG------EAASNPEV-IAHTLRKLKNQPDLNDATI 79

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     A+   s +LvltAHPt   RR L+ K + i nCL qL   D+   +++
  gi|2136161    80 KKAVESLSLELVLTAHPTEITRRTLIHKMGEINNCLKQLDNTDIADYERH 129

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    +   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +LR
  gi|2136161   130 QVMRRLRQLIAQSWHTDEIRKQRPSPVDEAKWGFAVVENSLWQGVPNYLR 179

                   RvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                        L+ n+G   +lP d   ++F+sWmGGDRDG nP vt E+tR v L
  gi|2136161   180 ELNEQLeENLGY--KLPVDFVPVRFTSWMGGDRDG-NPNVTAEITRHVLL 226

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   L+R  A+ l++  +  L+ Elsm     EL +   E     a++
  gi|2136161   227 LSRWKATDLFLKDIHVLVSELSMVDATPELLALVGE---EGASE------ 267

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vyt
                              PYR ++   R +L  t       L      ++  A+  t
  gi|2136161   268 -----------PYRYLMKKLRARLMATQSWLEARLKG--EKLPKPAgLLT 304

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   + E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiRq
  gi|2136161   305 QNEQLWEPLYACYQSLQACGMGIIANGELLDTLRRVKCFGVPLVRIDIRQ 354

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   Es R+t+ l  it+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|2136161   355 ESTRHTEALGEITRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWEP 404

                   tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     + ++vl++ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|2136161   405 SNDTREVLETCKVIAEAPKGSIAAYVISMAKTPSDVLAVHLLLKEAGIGF 454

                   tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                   +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KD
  gi|2136161   455 AMPVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKD 504

                   AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                   AG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+L
  gi|2136161   505 AGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALL 554

                   sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                   sqPP  ++G lRvt qGE+i f +G  ++   sL  +t A LE  + PP
  gi|2136161   555 SQPPGSLKGGLRVTEQGEMIRFKYGLPEVTVSSLSLYTSAILEANLLPPP 604

                   sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                    Pk  WR++m+e+ v+  E YR  v     Fv YFR+AtPE E Gk+ +G
  gi|2136161   605 EPKDSWRHIMDELSVISCETYRGYVRENKDFVPYFRSATPEQELGKLPLG 654

                   sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                   sRPaKR+P GG+esLRAiPWiFaWtq R  LP WLG G A +  ++ D K
  gi|2136161   655 SRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVE-DGK 703
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                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                        L+ m ++WPFF   l +lEmvF K D  +A  yD+ Lva  L+P G
  gi|2136161   704 Q-SELEAMCRDWPFFSTRLGMLEMVFSKADLWLADYYDQRLVAKTLWPLG 752

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    k+LRd  +E  + +L iA    l+   P++   + LR+ Y   Lnv+qA
  gi|2136161   753 KELRDLLEEDIKVVLAIANDSHLMADLPWIAESIQLRNVYTDPLNVLQAE 802

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L R R                 +E+ k +d            P +E  L
  gi|2136161   803 LLYRSR---------------LTEEQGKSPD------------PRVEQAL 825

                    iLtmKGiAAGmqntG<-*
                    ++t+ G+AAGm ntG
  gi|2136161   826 MVTIAGVAAGMRNTG    840

gi|254360733|ref|ZP_04976881.1|: domain 1 of 1, from 1 to 879: score 712.6, E = 3.2e-211
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                    + s     i+    +l  FL++ + D  G+ + E
  gi|2543607     1    ---------MNQQYS----TIQHNIHMLGEFLgETIRDAQGNYILEL 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls +     D    e L  kL  +   D + vA+a++H LnL n
  gi|2543607    35 IESIRVLSRNSRA-GDENAREQLLDKLANISNDDVLPVARAFSHFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R  i           +s   +s     + +L ++     e
  gi|2543607    84 IAEQHQTVSRHHIDESL-------GSRSLDS----LFLRLKSQN-IPVEK 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v   +    +DLvltAHPt   RRsL  K+  i  CL  L   D+t  +
  gi|2543607   122 VIKTVESLMIDLVLTAHPTEVTRRSLGHKHVEINKCLNLLEHDDLTEAES 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L   i  A+ t EiR  +PtP DE + Gm+ i   +Wk vP F
  gi|2543607   172 YKIKRRLMQLIALAWHTNEIRTQRPTPVDEAKGGMAVIENSLWKAVPEFC 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+K  G+    P +   ++FssWmGGDRDG nP vt E tR v
  gi|2543607   222 RQLNFYLeKHFGV--QYPVNLAPVRFSSWMGGDRDG-NPFVTAETTRRVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     + R  A+ l+++ +  L  Els+  C             t+a     Ky
  gi|2543607   269 RMNRWKATELFLQDIKNLAEELSITQC-------------TPAFR--AKY 303

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYRv+L   R KL nt      LL   is i E  + t
  gi|2543607   304 GNHL-------EPYRVLLKVLRQKLINTEIYYAELLEGKISTIDESDILT 346

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                       +  EPL  CY sL  CG ++iA G+LLD LR +  FGL L +LDiRq
  gi|2543607   347 SDQQLWEPLFDCYESLQACGMRIIANGALLDCLRRINCFGLGLSRLDIRQ 396

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+   +  it+ +++G Y  W E+ +q +L+ EL+ +RPL++
  gi|2543607   397 ESTRHEMAIAEITRYIGLGDYAHWTEDDKQAFLVRELSSRRPLIPTNWTP 446

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E k+vld+ +++AE P     aY+isma   sDvL v LL +E g k
  gi|2543607   447 SPETKEVLDTCKIVAEQPEGVISAYVISMAREASDVLSVHLLLKEAGCKF 496

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    t++v PLFE L DL+     +  LF i WY+  i+  q +m+GYsDs KD
  gi|2543607   497 TIPVAPLFETLGDLDHSEKVMTDLFNIGWYRGVINNYQMIMIGYSDSAKD 546

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG l+A W  Y+AqE ++    ky + L+lFHGRGGt+GRGG P H A+L
  gi|2543607   547 AGMLAAGWAQYRAQEALVNLCEKYNIELTLFHGRGGTIGRGGAPAHAALL 596

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
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                    sqPP  ++  lRvt qGE+i f  G   +   sL  ++ A LE  + PP
  gi|2543607   597 SQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVESLELYASAILEANIFPPP 646

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR+++ +   +    YR +v  E  Fv YFR+AtPE E  ++ +G
  gi|2543607   647 EPKQQWRDVLAKASDISCQIYRDMVRGELDFVPYFRSATPEQELSRLPLG 696

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR P GG+esLRAiPWiFaW q R  LP WLG G A +  i  D
  gi|2543607   697 SRPAKRNPKGGVESLRAIPWIFAWMQNRLMLPAWLGAGQALQQLI--DEG 744

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                    n   LkEm +eWPFF   + +lEmvF K D  +A  yD+ Lv   L+  G
  gi|2543607   745 NETLLKEMCNEWPFFSTRIGMLEMVFSKADIWLAEYYDQRLVEPKLHRLG 794

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    + LR + +   + +L +A    l+   P++   + LR+ Y   Ln +q
  gi|2543607   795 NMLRTQLQADLKTVLALAHDGQLMADLPWIAESIALRNIYTDPLNLLQVE 844

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L RiR                  +           +e+  P LE  L
  gi|2543607   845 LLDRIR-----------------KQ-----------GENADPVLEQAL 864

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|2543607   865 MITITGIAAGMRNTG    879

gi|261496916|ref|ZP_05993284.1|: domain 1 of 1, from 1 to 879: score 711.6, E = 6.2e-211
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                  + s     i+    +l  FL++ + D  G+ + E
  gi|2614969     1    ---------MNQQYS----TIQHNIHMLGEFLgETIRDAQGNYILEL 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls +     D    e L  kL  +   D + vA+a++H LnL n
  gi|2614969    35 IESIRVLSRNSRA-GDENAREQLLDKLANISNDDVLPVARAFSHFLNLTN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R  i           +s   +s     + +L ++     e
  gi|2614969    84 IAEQHQTVSRHHIDESL-------GSRSLDS----LFLRLKSQN-IPVEK 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v   +    +DLvltAHPt   RRsL  K+  i  CL  L   D+t  +
  gi|2614969   122 VIKTVESLMIDLVLTAHPTEVTRRSLGHKHVEINKCLNLLEHDDLTEAES 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L   i  A+ t EiR  +PtP DE + Gm+ i   +Wk vP F
  gi|2614969   172 YKIKRRLMQLIALAWHTNEIRTQRPTPVDEAKGGMAVIENSLWKAVPEFC 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+K  G+    P +   ++FssWmGGDRDG nP vt E tR v
  gi|2614969   222 RQLNFYLeKHFGV--QYPVNLAPVRFSSWMGGDRDG-NPFVTAETTRRVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     + R  A+ l+++ +  L  Els+  C             t+a     Ky
  gi|2614969   269 RMNRWKATELFLQDIKNLAEELSITQC-------------TPAFR--AKY 303

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                              EPYRv+L   R KL nt      LL   is i E  + t
  gi|2614969   304 GNHL-------EPYRVLLKVLRQKLINTEIYYAELLEGKISTIDESDILT 346

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                       +  EPL  CY sL  CG ++iA G+LLD LR +  FGL L +LDiRq
  gi|2614969   347 SDQQLWEPLFDCYESLQACGMRIIANGALLDCLRRINCFGLGLSRLDIRQ 396

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es R+   +  it+ +++G Y  W E+ +q +L+ EL+ +RPL++
  gi|2614969   397 ESTRHEMAIAEITRYIGLGDYAHWTEDDKQAFLVRELSSRRPLIPTNWTP 446

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      E k+vld+ +++AE P     aY+isma   sDvL v LL +E g k
  gi|2614969   447 SPETKEVLDTCKIVAEQPEGVISAYVISMAREASDVLSVHLLLKEAGCKF 496
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                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    t++v PLFE L DL+     +  LF i WY+  i+  q +m+GYsDs KD
  gi|2614969   497 TIPVAPLFETLGDLDHSEKVMTDLFNIGWYRGVINNYQMIMIGYSDSAKD 546

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG l+A W  Y+AqE ++    ky + L+lFHGRGGt+GRGG P H A+L
  gi|2614969   547 AGMLAAGWAQYRAQEALVNLCEKYNIELTLFHGRGGTIGRGGAPAHAALL 596

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++  lRvt qGE+i f  G   +   sL  ++ A LE  + PP
  gi|2614969   597 SQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVESLELYASAILEANIFPPP 646

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR+++ +   +    YR +v  E  Fv YFR+AtPE E  ++ +G
  gi|2614969   647 EPKQQWRDVLAKASDISYQIYRDMVCGELDFVPYFRSATPEQELSRLPLG 696

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR P GG++sLRAiPWiFaW q R  LP WLG G A +  i  D
  gi|2614969   697 SRPAKRNPKGGVDSLRAIPWIFAWMQNRLMLPAWLGAGQALQQLI--DEG 744

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                    n   LkEm +eWPFF   + +lEmvF K D  +A  yD+ Lv   L+  G
  gi|2614969   745 NETLLKEMCNEWPFFSTRIGMLEMVFSKADIWLAEYYDQRLVEPKLHRLG 794

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    + LR + +   + +L +A    l+   P++   + LR+ Y   Ln +q
  gi|2614969   795 NMLRTQLQADLKTVLALAHDGQLMADLPWIAESIALRNIYTDPLNLLQVE 844

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L RiR                  +            +e+  P LE  L
  gi|2614969   845 LLDRIR-----------------KQ------------GENADPVLEQAL 864

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|2614969   865 MITITGIAAGMRNTG    879

gi|94500599|ref|ZP_01307129.1|: domain 1 of 1, from 1 to 877: score 710.9, E = 1e-210
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiL.qDLHGedLkEa
                            +  L       d+ L e   LL     D+++qDL G++  +
  gi|9450059     1    -----MNTL-------DDALKENVRLLGNLLGDVIeQDL-GPNFIDK 34

                    vqECYEls..AeYEGKkDtkKLe.ELGakLtsLdPaDailvAkailHmLn
                    +     l+++A     +D +  ++EL   L  L   + i + +a+   Ln
  gi|9450059    35 IVTIRTLAktARANSTQDDEHFGdELIQYLNNLPDDEVIPITRAFNQFLN 84

                    LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                    LAn+AE  +   RRR +  +               ++E l  L      s
  gi|9450059    85 LANIAEQYHDVVRRRRQDEH----------DMLHNLDEVLDELKQSN--S 122

                    PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                      +   A+    + LvltAHPt   RR L+qK   + n L qL  +   v
  gi|9450059   123 STDLTHAIEQMDIQLVLTAHPTEVTRRTLIQKYEHVFNSLNQLDTQPYEV 172

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                    e  + L   L   i   + tDEiR  +PtP DE + G + i   +W+ +P
  gi|9450059   173 ERHQILNR-LKQIITQIWYTDEIRHQRPTPEDEAKWGFAVIEGSLWQAIP 221

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                     F R  D  L    + + l  d+  i+  sWmGGDRDG nP vt  vt
  gi|9450059   222 NFYRQLDELLLSKDL-DPLSLDIAPIRIHSWMGGDRDG-NPNVTAKVTQN 269

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                    v  L R mAa lY+  +  L  Elsm  C + LR +          d
  gi|9450059   270 VVWLGRWMAADLYLRDIHTLGSELSMQQCSESLRKKV--------GD--- 308

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                                +EPYR +L + R++L  tR  a+  L         + +
  gi|9450059   309 -----------ANEPYRALLHELREQLKQTRAYAKMRLEG--KKATRQGI 345

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
```

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                    +    +    L  CY sL eC    +A G LLD LR v  FG+ L  LD+
  gi|9450059   346 FSA-NDLFSTLKHCYDSLIECNMPLVANGTLLDTLRRVKAFGMTLCPLDV 394

                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    RqEs R+  v   +t+ LeiG Y +W E+++q +L+aEL+ KRPLl++
  gi|9450059   395 RQESGRHAQVFSELTEYLEIGDYAQWTEDQKQAFLIAELENKRPLLPPHW 444

                    PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                        Ev++vld+ rv+A     +F  Y+ismat+PsDvLAv L+ + Cg
  gi|9450059   445 QPSAEVQEVLDTARVIAQEDDACFSNYVISMATSPSDVLAVALILKMCGQ 494

                    kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsG
                    + ++++ PLFE L DL+ A  ++++L siDWY+    GKq vm+GYsDs
  gi|9450059   495 QSPMPIAPLFETLSDLDGAAQTINRLLSIDWYRAYNGGKQMVMIGYSDSA 544

                    KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                    KDAG l+A W  Y+AqEE++Kv  ++   L+lFHGRGGtvGRGGGP   A
  gi|9450059   545 KDAGQLAASWAQYRAQEELVKVCDEHSTELMLFHGRGGTVGRGGGPSLGA 594

                    iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP
                    iLsqPP  + G +Rvt qGE+i f FG  +L  rsLq ++ A L    +P
  gi|9450059   595 ILSQPPGSVRGRIRVTEQGEMIRFKFGHPELAVRSLQLYASAVLKASYQP 644

                    PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmn
                    P++P   WR++m+++       YR +v     Fv YFR  tPE E Gk+
  gi|9450059   645 PLAPSDHWREIMNQISDESVKSYRQIVRENQEFVPYFRAITPEQELGKLA 694

                    iGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                    +GsRPaKRk sGG+esLRAiPWiFaW q R  LP WLG   A  h +  D
  gi|9450059   695 LGSRPAKRKASGGVESLRAIPWIFAWMQIRLMLPAWLGSDEALDHYMRSD 744

                    iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP
                    +   + L+ m keWPFF    D+lEmv  K D  iA  y++ L   e +
  gi|9450059   745 SGK-KELQKMAKEWPFFSTLTDMLEMVLSKTDSNIAHYYERRLTNKEQQG 793

                    FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfq
                     G+ LR++ +     + +i    +lLE  P +   + +R++Y   L  +q
  gi|9450059   794 LGRILRQRLQVAITNICQIKQVDELLENAPIIAESMGVRNPYTDPLHFLQ 843

                    AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                    A  LKR R              E   En                  ++
  gi|9450059   844 AELLKRTR--------------EQETEN-------------------IDH 860

                    tLiLtmKGiAAGmqntG<-*
                     L +tm GiAAGm ntG
  gi|9450059   861 ALKVTMAGIAAGMRNTG    877

gi|240949435|ref|ZP_04753776.1|: domain 1 of 1, from 1 to 879: score 710.8, E = 1.1e-210
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                 + s    L +   +L D   + +++  G+++ E +
  gi|2409494     1    ---------MNQQHS---ALRQNIHMLGDFLGETIKETQGNEILELI 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D++  e L  kL  +     + vA+a++  LnL n+
  gi|2409494    36 ESIRILSKKSRA-GDAQAREQLLNKLANISTENVLPVARAFSQFLNLTNI 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE.
                    AE  +   R        G  +  a           + +L  +   +P E+
  gi|2409494    85 AEQYQTISRHDYDETL-GNRSLGA----------LFARLKAQN--TPVEt 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v + +    ++LvltAHPt   RRsL+ K+  i  CL +L   D+t+ +
  gi|2409494   122 VIQTINKLLIELVLTAHPTEVTRRSLVHKHVEINKCLEKLEHDDLTPPET 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L   i  A+ t EiR a+PtP DE + G++ i   +Wk vP F
  gi|2409494   172 YRIQRRLMQLIALAWHTNEIRVARPTPIDEAKWGIAIIENSLWKAVPDFC 221

                    RRvDtAL.KniGinERlPYdvPL..ikFssWmGGDRDGknPRvtPEvtRD
                    R +   L+K  G+     Y+v L +++ ssWmGGDRDG nP vt EvtR
  gi|2409494   222 REINFQLeKHFGVQ----YNVELapVRLSSWMGGDRDG-NPFVTAEVTRK 266
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                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                    v  + R  Aa l++  + DL  Els+  C  E R++          d
  gi|2409494   267 VLWMNRWKAADLFLKDISDLAEELSITQCTPEYRAK--------YGD--- 305

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                                EPYR ++   R KL  t      LL      i    +
  gi|2409494   306 -----------HVEPYRTVVKGLRSKLQKTLAYFGELLEGKQITIEQSEI 344

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                      +  e  EPL   YksL  CG ++iA G LLD LR +  FGLsL +LDi
  gi|2409494   345 ISNDNELWEPLFDSYKSLHACGMRIIANGGLLDCLRRIRCFGLSLSRLDI 394

                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    RqEs R+   +  it+ +++G Y  W E+ +q +L+ EL+ +RPL++
  gi|2409494   395 RQESTRHEMAIAEITRYIGLGDYSHWTEDDKQAFLVRELSSRRPLIPTNW 444

                    PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                        E +++ld+ +v+AE P     aY+isma   sDvLAv LL +E g
  gi|2409494   445 TPSAETQEILDTCKVIAEQPEGVISAYVISMAREASDVLAVHLLLKEAGC 494

                    kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsG
                    k t++v PLFE L DL+     +  LF i WY+  i+  q vm+GYsDs
  gi|2409494   495 KYTIPVAPLFETLDDLDHSEKVMTDLFNIGWYRGVINNYQMVMIGYSDSA 544

                    KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                    KDAG l+A W  Y+ qE ++  A ky + LvlFHGRGGtvGRGG P H A
  gi|2409494   545 KDAGMLAASWAQYRSQEALVNLAEKYNIELVLFHGRGGTVGRGGAPAHAA 594

                    iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP
                    +LsqPP  ++  lRvt qGE+i f  G   +   +   ++ A LE  + P
  gi|2409494   595 LLSQPPRSLKSGLRVTEQGEMIRFKLGLPAVAVDTFNLYASAILEANLLP 644

                    PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmn
                    P  Pk  WR++m++ A +  E YR vv  EP Fv YFR AtPE E  k+
  gi|2409494   645 PPEPKQSWRDVMDKGAEISCEIYRGVVRGEPDFVPYFRAATPEQELAKLP 694

                    iGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                    +GsRPaKR P GG+esLRAiPWiFaW q R  LP WLG GAA +  i++
  gi|2409494   695 LGSRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGAALRQLIEQG 744

                    iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP
                    +     LkEm keWPFF   + +lEmvF K D  +A  yD+ Lva eL+
  gi|2409494   745 SEA--TLKEMSKEWPFFSTRVGMLEMVFSKADLNLAEYYDQRLVAPELHR 792

                    FGksLRdkYvEtkdlLLkiAGHkDlLEGD.PYLKqrlRLRdsYittLnvf
                     Gk LR +  E  + +L +  H   L GD P++   + LR+ Y   Ln +
  gi|2409494   793 LGKALRKQLSEDINTILALS-HDGQLMGDlPWIADSIALRNVYTDPLNLL 841

                    qAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLE
                    q   L R+R                                  +e   P LE
  gi|2409494   842 QVELLARLR-----------------------------AQGETPDPQLE 861

                    DtLiLtmKGiAAGmqntG<-*
                      L++t+ GiAAGm ntG
  gi|2409494   862 QALMITIAGIAAGMRNTG    879

gi|283896780|emb|CAX65691.1|: domain 1 of 1, from 1 to 503: score 710.3, E = 1.6e-210
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838967     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838967     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838967     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|2838967     - ------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838967     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838967     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838967     - ------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838967     - ------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838967     - ------------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDvlDAitt L+iGsYReWsEe+RqEWLl+EL GKRPL+g+DLPktE
  gi|2838967     1 --HTDVLDAITTYLGIGSYREWSEERRQEWLLSELNGKRPLFGADLPKTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvld+f+v+AELP DsFGaYiismat+PsDvLAvELLqREC+vk +L
  gi|2838967    49 EVADVLDTFHVIAELPADSFGAYIISMATSPSDVLAVELLQRECHVKTPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAa+++LFsiDWY+ ri+GKqevm+GYsDsGKDAG
  gi|2838967    99 RVVPLFEKLADLEAAPAALARLFSIDWYRQRINGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAA q+YkAqE++iKvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838967   149 RLSAARQMYKAQEDLIKVAKDYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP +P
  gi|2838967   199 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPNAP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L++emAvvAt EYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|2838967   249 KPEWRALLDEMAVVATKEYRSIVFQEPRFVEYFRLATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+nl
  gi|2838967   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHALQKDIRNL 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY++WPFFRvt+DL+EmvFAKG P iAaLyD LLv+EeL+P G++
  gi|2838967   349 HMLQEMYNQWPFFRVTIDLVEMVFAKGNPDIAALYDSLLVSEELRPLGER 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Et++lLL++AGH+DlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|2838967   399 LRANYEETQKLLLQVAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 448

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y+v lrPhlsKE  d   k+a+eLvkLnp++++aPGLEDtLiL
  gi|2838967   449 KRIRDPDYHVALRPHLSKEIMDSS-KPAAELVKLNPGSEYAPGLEDTLIL 497

                   tmKGiAAGmqntG<-*
                   tmKGiA
  gi|2838967   498 TMKGIA-------    503

gi|257465177|ref|ZP_05629548.1|: domain 1 of 1, from 1 to 879: score 710.2, E = 1.6e-210
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                + s    L +   +L D   + +++  G+++ E +
  gi|2574651     1    ---------MNQQHS---ALRQNIHMLGDFLGETIKETQGNEILELI 35
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     ls       D +  e L  kL  +     + vA+a++  LnL n+
gi|2574651    36 ESIRILSKKSRA-GDIQAREQLLNKLANISTENVLPVARAFSQFLNLTNI 84

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE.
                AE  +   R        G  +  a           + +L  +   +P E+
gi|2574651    85 AEQYQTISRHDYDETL-GNRSLGA----------LFARLKAQN--TPVEt 121

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                v + +    ++LvltAHPt   RRsL+ K+  i  CL +L   D+t+ +
gi|2574651   122 VIQTVNKLLIELVLTAHPTEVTRRSLVHKHVEINKCLEKLEHDDLTPPET 171

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  +   L   i  A+ t EiR a+PtP DE + G++ i   +Wk vP F
gi|2574651   172 YRIQRRLMQLIALAWHTNEIRVARPTPIDEAKWGIAIIENSLWKAVPDFC 221

                RRvDtAL.KniGinERlPYdvPL..ikFssWmGGDRDGknPRvtPEvtRD
                R +   L+K  G+     Y+v L +++ ssWmGGDRDG nP vt EvtR
gi|2574651   222 REINFQLeKHFGVQ----YNVELapVRLSSWMGGDRDG-NPFVTAEVTRK 266

                vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                v  + R  Aa l++  + DL  Els+  C  E R+
gi|2574651   267 VLWMNRWKAADLFLKDISDLAEELSITQCTPEYRA--------------- 301

                KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                Ky +         EPYR ++   R KL  t      LL      i    +
gi|2574651   302 KYGVHV-------EPYRTVVKGLRSKLQKTLAYFGELLEGKQITIEPSEI 344

                ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                  +  e  EPL   YksL  CG ++iA G LLD LR +  FGLsL +LDi
gi|2574651   345 ISNDNELWEPLFDSYKSLHACGMRIIANGGLLDCLRRIRCFGLSLSRLDI 394

                RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                RqEs R+   +  it+ +++G Y  W E+ +q +L+ EL+ +RPL++
gi|2574651   395 RQESTRHEMAIAEITRYIGLGDYSHWTEDDKQAFLVRELSSRRPLIPTNW 444

                PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                    E +++ld+ +v+AE P     aY+isma   sDvLAv LL +E g
gi|2574651   445 TPSAETQEILDTCKVIAEQPEGVISAYVISMAREASDVLAVHLLLKEAGC 494

                kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsG
                k t++v PLFE L DL+     +  LF i WY+  i+  q vm+GYsDs
gi|2574651   495 KYTIPVAPLFETLDDLDHSEKVMTDLFNIGWYRGVINNYQMVMIGYSDSA 544

                KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                KDAG l+A W  Y+ qE ++  A ky + LvlFHGRGGtvGRGG P H A
gi|2574651   545 KDAGMLAASWAQYRSQEALVNLAEKYNIELVLFHGRGGTVGRGGAPAHAA 594

                iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP
                +LsqPP  ++  lRvt qGE+i f  G   +   +   ++ A LE  + P
gi|2574651   595 LLSQPPRSLKSGLRVTEQGEMIRFKLGLPAVAVDTFNLYASAILEANLLP 644

                PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmn
                P  Pk  WR++m++ A +  E YR vv  EP Fv YFR AtPE E  k+
gi|2574651   645 PPEPKQSWRDVMDKGAEISCEIYRGVVRGEPDFVPYFRAATPEQELAKLP 694

                iGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                +GsRPaKR P GG+esLRAiPWiFaW q R  LP WLG GAA +  i++
gi|2574651   695 LGSRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGAALRQLIEQG 744

                iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP
                  n   LkEm keWPFF   + +lEmvF K D  +A  yD+ Lva eL+
gi|2574651   745 --NEATLKEMSKEWPFFSTRVGMLEMVFSKADLNLAEYYDQRLVAPELHR 792

                FGksLRdkYvEtkdlLLkiAGHkDlLEGD.PYLKqrlRLRdsYittLnvf
                 Gk LR +  E  + +L +  H   L GD P++   + LR+ Y   Ln +
gi|2574651   793 LGKALRKQLSEDINTILALS-HDGQLMGDlPWIADSIALRNVYTDPLNLL 841

                qAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLE
                q   L R+R               A+ +          np     P LE
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  gi|2574651   842 QVELLARLR----------------AQGE----------NP----DPQLE 861

                   DtLiLtmKGiAAGmqntG<-*
                     L++t+ GiAAGm ntG
  gi|2574651   862 QALMITIAGIAAGMRNTG    879

gi|283896790|emb|CAX65696.1|: domain 1 of 1, from 1 to 502: score 710.2, E = 1.6e-210
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838967     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838967     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838967     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838967     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838967     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838967     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838967     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838967     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838967     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDvlD ittHL+iGsY eWsEeKRq+WLl+EL+GKRPL+gsDLP tE
  gi|2838967     1 --HTDVLDSITTHLGIGSYAEWSEEKRQDWLLSELRGKRPLFGSDLPLTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E +Dvl++f+vLAELP D+FGaYiismataPsDvLAvELLqREC+vkq+L
  gi|2838967    49 ETADVLGTFHVLAELPADCFGAYIISMATAPSDVLAVELLQRECHVKQPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAav++LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|2838967    99 RVVPLFEKLADLEAAPAAVARLFSIDWYMNRINGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWq+YkAqEE+iKvAK+yGvKL++ HGRGGtvGRGGGPtHLAiLsq
  gi|2838967   149 RLSAAWQMYKAQEELIKVAKHYGVKLTMLHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE sFGEE+LCFr+LqR+tAAtLEHGm+PP++P
  gi|2838967   199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRYTAATLEHGMHPPIAP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emA+vAt EYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|2838967   249 KPEWRALMDEMAIVATKEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+n+
  gi|2838967   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIMQKDIRNI 348
```

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                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAa+yDkLLv+++L+ FG++
  gi|2838967   349 HTLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAAVYDKLLVSDDLQFFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Etk+lLL++AGHkD+LEGDPYLKqrlRLR+sYittLnv+qAYtL
  gi|2838967   399 LRKNYEETKELLLQVAGHKDVLEGDPYLKQRLRLRESYITTLNVCQAYTL 448

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPs+kv ++P lsKE+ dE   ++++Lv+Lnp +++aPGLEDtLiL
  gi|2838967   449 KRIRDPSFKVSPQPALSKEFTDES--QPAQLVELNPESEYAPGLEDTLIL 496

                    tmKGiAAGmqntG<-*
                     mKGiA
  gi|2838967   497 AMKGIA-------    502

gi|283896810|emb|CAX65706.1|: domain 1 of 1, from 1 to 503: score 710.1, E = 1.7e-210
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838968     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838968     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838968     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838968     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838968     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838968     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838968     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838968     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838968     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDv+DAit+ L++ sYReW EeKRqEWLl+EL GKRPL+g+DLP  +
  gi|2838968     1 --HTDVMDAITEYLGLESYREWTEEKRQEWLLSELNGKRPLFGPDLPTSD 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dv+d+f+vLAELP+DsFGaY+ismataPsDvLAvELLqREC+vk++L
  gi|2838968    49 EIADVIDTFHVLAELPSDSFGAYVISMATAPSDVLAVELLQRECHVKKPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAa+++LFs+DWY+nri+GKqevm+GYsDsGKDAG
  gi|2838968    99 RVVPLFEKLADLEAAPAALAQLFSVDWYRNRINGKQEVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    R+sAAWqLYkAqEE+iKvAK yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838968   149 RFSAAWQLYKAQEELIKVAKLYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP+t++GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
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  gi|2838968   199 PPETVHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emA+vAt EYRs+v+ EPRFvEYFRlAtPElEYG+mniGsR
  gi|2838968   249 KPEWRALMDEMAIVATKEYRSIVFEEPRFVEYFRLATPELEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|2838968   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLKKDIRNL 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+PFG++
  gi|2838968   349 QILQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWPFGER 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Etk+lLL++AGHkDlLEGDPYLKqrl +RdsY t Lnv+qAYtL
  gi|2838968   399 LRANYEETKQLLLQVAGHKDLLEGDPYLKQRLQIRDSYFTALNVCQAYTL 448

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP ++v +rPhlsK+  d   k+a+eLvkLn t+++aPGLEDtLiL
  gi|2838968   449 KRIRDPGFQVKPRPHLSKDIMDSG-KPAAELVKLNTTSEYAPGLEDTLIL 497

                   tmKGiAAGmqntG<-*
                   tmKGiA
  gi|2838968   498 TMKGIA-------    503

gi|261492498|ref|ZP_05989052.1|: domain 1 of 1, from 1 to 879: score 710.1, E = 1.8e-210
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                + s     i+    +l  FL++ + D  G+ + E
  gi|2614924     1    ---------MNQQYS----TIQHNIHMLGEFLgETIRDAQGNYILEL 34

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +     ls +     D    e L  kL  +   D + vA+a++H LnL n
  gi|2614924    35 IESIRVLSRNSRA-GDENAREQLLDKLANISNDDVLPVARAFSHFLNLTN 83

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE  +   R  i           +s   +s     + +L ++     e
  gi|2614924    84 IAEQHQTVSRHHIDESL-------GSRSLDS----LFLRLKSQN-IPVEK 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   v   +    +DLvltAHPt   RRsL  K+  i  CL  L   D+t  +
  gi|2614924   122 VIKTVESLMIDLVLTAHPTEVTRRSLGHKHVEINKCLNLLEHDDLTEAES 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     +   L   i  A+ t EiR  +PtP DE + Gm+ i   +Wk vP F
  gi|2614924   172 YKIKRRLMQLIALAWHTNEIRTQRPTPVDEAKGGMAVIENSLWKAVPEFC 221

                   RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   R     L+K  G+    P +   ++FssWmGGDRDG nP vt E tR v
  gi|2614924   222 RQLNFYLeKHFGV--QYPVNLAPVRFSSWMGGDRDG-NPFVTAETTRRVL 268

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    + R  A+ l+++ +  L  Els+  C             t+a     Ky
  gi|2614924   269 RMNRWKATELFLQDIKNLAEELSITQC-------------TPAFR--AKY 303

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                                EPYRv+L   R KL nt      LL   is i E  + t
  gi|2614924   304 GNHL-------EPYRVLLKVLRQKLINTEIYYAELLEGKISTIDESDILT 346

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                      +  EPL  CY sL  CG ++iA G+LLD LR +  FGL L +LDiRq
  gi|2614924   347 SDQQLWEPLFDCYESLQACGMRIIANGALLDCLRRINCFGLGLSRLDIRQ 396

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   Es R+   +  it+ +++G Y  W E+ +q +L+ EL+ +RPL++
  gi|2614924   397 ESTRHEMAIAEITRYIGLGDYAHWTEDDKQAFLVRELSSRRPLIPTNWTP 446

                   tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                     E k+vld+ +++AE P     aY+isma   sDvL v LL +E g k
  gi|2614924   447 SPETKEVLDTCKIVAEQPEGVISAYVISMAREASDVLSVHLLLKEAGCKF 496
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                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                    t++v PLFE L DL+     +  LF i WY+  i+  q +m+GYsDs KD
  gi|2614924   497 TIPVAPLFETLGDLDHSEKVMTDLFNIGWYRGVINNYQMIMIGYSDSAKD 546

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    AG l+A W  Y+AqE ++    ky + L+lFHGRGGt+GRGG P H A+L
  gi|2614924   547 AGMLAAGWAQYRAQEALVNLCEKYNIELTLFHGRGGTIGRGGAPAHAALL 596

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++  lRvt qGE+i f  G   +   sL  ++ A LE  + PP
  gi|2614924   597 SQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVESLEFYASAILEANIFPPP 646

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                     Pk  WR+++ +   +    YR +v  E  Fv YFR+AtPE E  ++ +G
  gi|2614924   647 EPKQQWRDVLAKASDISYQIYRDMVRGELDFVPYFRSATPEQELSRLPLG 696

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRPaKR P GG++sLRAiPWiFaW q R  LP WLG G A +  i  D
  gi|2614924   697 SRPAKRNPKGGVDSLRAIPWIFAWMQNRLMLPAWLGAGQALQQLI--DEG 744

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                    n   LkEm +eWPFF   + +lEmvF K D  +A  yD+ Lv   L+  G
  gi|2614924   745 NETLLKEMCNEWPFFSTRIGMLEMVFSKADIWLAEYYDQRLVEPKLHRLG 794

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    + LR + +   + +L +A    l+   P++   + LR+ Y   Ln +q
  gi|2614924   795 NMLRTQLQADLKTVLALAHDGQLMADLPWIAESIALRNIYTDPLNLLQVE 844

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L RiR                  +            +e+  P LE  L
  gi|2614924   845 LLDRIR-----------------KQ------------GENADPVLEQAL 864

                    iLtmKGiAAGmqntG<-*
                    ++t+ GiAAGm ntG
  gi|2614924   865 MITITGIAAGMRNTG    879

gi|283896818|emb|CAX65710.1|: domain 1 of 1, from 1 to 503: score 709.6, E = 2.5e-210
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838968     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838968     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838968     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838968     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838968     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838968     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838968     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838968     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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  gi|2838968     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDvlDAitt L+iGsYReW+Ee+RqEWLl+EL GKRPL+g+DLPktE
  gi|2838968     1 --HTDVLDAITTYLGIGSYREWPEERRQEWLLSELNGKRPLFGADLPKTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvld+f+v+ ELP D FGaYiismataPsDvLAvELLqREC+vk +L
  gi|2838968    49 EVADVLDTFNVISELPADNFGAYIISMATAPSDVLAVELLQRECHVKTPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLe APAa+++LFsiDWY+ ri+GKqevm+GYsDsGKDAG
  gi|2838968    99 RVVPLFEKLADLEGAPAALARLFSIDWYRQRINGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838968   149 RLSAAWQLYKAQEELIKVAKDFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+G lRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP++P
  gi|2838968   199 PPDTIHGHLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPIAP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L++emAvvAt EYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|2838968   249 KPEWRALLDEMAVVATKEYRSIVFQEPRFVEYFRLATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|2838968   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLQKDIRNL 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY++WPFFRvt+DL+EmvFAKG P iAaLyDkLLv+ eL+P G++
  gi|2838968   349 HMLQEMYNQWPFFRVTIDLVEMVFAKGNPDIAALYDKLLVSQELQPLGEK 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++YvEt++lLL++AGHkD+LEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|2838968   399 LRANYVETQKLLLQVAGHKDILEGDPYLKQRLRLRDAYITTLNVCQAYTL 448

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y+v lrPhlsKE  d   k+a+eLvkLnp++++aPGLEDtLiL
  gi|2838968   449 KRIRDPDYHVALRPHLSKEIMDSS-KPAAELVKLNPASEYAPGLEDTLIL 497

                   tmKGiAAGmqntG<-*
                   tmKGiA
  gi|2838968   498 TMKGIA-------    503

gi|283896796|emb|CAX65699.1|: domain 1 of 1, from 1 to 503: score 709.6, E = 2.6e-210
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838967     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838967     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838967     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838967     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838967     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838967     - ------------------------------------------------ -
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                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838967     - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838967     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838967     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDvlDAitt L+iGsYReWsEe+RqEWLl+EL GKRPL+g+DLPk E
  gi|2838967     1 --HTDVLDAITTYLGIGSYREWSEERRQEWLLSELNGKRPLFGADLPKNE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvld+f+v+AELP D FGaYiismataPsDvLAvELLqREC+vk +L
  gi|2838967    49 EVADVLDTFHVIAELPADNFGAYIISMATAPSDVLAVELLQRECHVKTPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLeAAPAa+++LFsiDWY+ ri+GKqevm+GYsDsGKDAG
  gi|2838967    99 RVVPLFEKLADLEAAPAALARLFSIDWYRQRINGKQEVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWq+YkAqE++iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838967   149 RLSAAWQMYKAQEDLIKVAKDFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP +P
  gi|2838967   199 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPNAP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++emAvvAt EYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|2838967   249 KPEWRALLDEMAVVATKEYRSIVFQEPRFVEYFRLATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+nl
  gi|2838967   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHALQKDIRNL 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+EmY++WPFFRvt+DL+EmvFAKG P iAaLyDkLLv+EeL+P G++
  gi|2838967   349 HMLQEMYNQWPFFRVTIDLIEMVFAKGNPDIAALYDKLLVSEELRPLGDK 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y+Et++lLL++AGH+DlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|2838967   399 LRANYEETQKLLLQVAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 448

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDP+y+v lrPhlsKE  d   k+a+eLvkLnp++++aPGLEDtLiL
  gi|2838967   449 KRIRDPDYHVALRPHLSKEIMDSS-KPAAELVKLNPASEYAPGLEDTLIL 497

                  tmKGiAAGmqntG<-*
                  tmKGiA
  gi|2838967   498 TMKGIA-------    503

gi|283896768|emb|CAX65685.1|: domain 1 of 1, from 1 to 503: score 708.8, E = 4.4e-210
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838967     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838967     - ------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838967     - ------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|2838967     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838967     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838967     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838967     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838967     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838967     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDvlDAit  L+iGsYReWsEe+RqEWLl+EL GKRPL+g+DLP t+
  gi|2838967     1 --HTDVLDAITSYLGIGSYREWSEERRQEWLLSELNGKRPLFGPDLPTTD 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dvld+frv+AELP D FGaYiismataPsDvLAvELLqREC+vk +L
  gi|2838967    49 EIADVLDTFRVIAELPADNFGAYIISMATAPSDVLAVELLQRECHVKTPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLe APAa+++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|2838967    99 RVVPLFEKLADLEGAPAALARLFSVDWYRERINGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838967   149 RLSAAWQLYKAQEELIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2838967   199 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L++emAvvAt EYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|2838967   249 KPEWRALLDEMAVVATKEYRSIVFQEPRFVEYFRLATPEMEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++KDi+nl
  gi|2838967   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHVLEKDIRNL 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+ eL+P G++
  gi|2838967   349 HTLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSAELWPLGEK 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Etk lLL++AGH+DlLEGD YLKqrlRLRd+Yitt+nv+q Yt+
  gi|2838967   399 LRANYEETKRLLLQVAGHRDLLEGDLYLKQRLRLRDAYITTMNVCQTYTM 448

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y+vtlrPhlsKE  d n k+a+eLvkLnpt+++aPGLEDtLiL
  gi|2838967   449 KRIRDPDYHVTLRPHLSKEIMDWN-KPAAELVKLNPTSEYAPGLEDTLIL 497

                   tmKGiAAGmqntG<-*
                   tmKGiA
  gi|2838967   498 TMKGIA-------    503

gi|254514836|ref|ZP_05126897.1|: domain 1 of 1, from 2 to 885: score 708.3, E = 6.4e-210
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      s D      + G+      L     LL     + +   HGed    v
  gi|2545148     2    SNDPSASKGASGQEY--RSLRSNVSLLGSILGETMAQSHGEDFLASV 46
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     ls       D++  e L + L +L+     lvA+a+   LnLAn+
gi|2545148    47 ERVRLLSKSGSMGDDAS-WEHLESLLGGLETEQLGLVARAFAQFLNLANI 95

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AE           + +  D    as t    +   l  L   +    + +
gi|2545148    96 AE-------QHHGLSREMDAVNSASRT----LTRALDLLGEEG-LDQQAI 133

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                 + +   s++LvltAHPt   RRsL+ K   i  CL  L    +t  ++
gi|2545148   134 ANSVSDLSIELVLTAHPTEITRRSLIHKYEEIQRCLGRLESPGLTNYERS 183

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                 +D  L   i   + t E R ++P P DE R G + +   +W+ vP FLR
gi|2545148   184 RMDRRLRELIAQLWHTHEFRESRPSPVDEARWGYAVVENSLWQAVPDFLR 233

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                R D AL       RlP d+  ++FssWmGGDRDG nP vt EvtR+v LL
gi|2545148   234 RLDDALLA-ATGQRLPLDAAPVQFSSWMGGDRDG-NPFVTAEVTREVLLL 281

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                 R  Aa lY+  v+ L+ Elsm  Cn  LR+RA +
gi|2545148   282 GRWQAAALYLKTVDQLVQELSMIECNGALRARAGDTR------------- 318

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                         EPYR +L + R +L          LL    ++  Ee    +v
gi|2545148   319 ---------EPYRRVLKELRSRLRKWLSALESLLEGRPAN--EEDLIRDV 357

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                E   EPL LCY+sLC+CG   iA+G LLDlLRq   FG+ Lv+LDiRq s
gi|2545148   358 EVLSEPLMLCYQSLCDCGMTRIAEGTLLDLLRQLRCFGINLVRLDIRQHS 407

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                eR+   l  it+ L++G Y +W Ee R+ W+  EL  +RPL++     tE
gi|2545148   408 ERHSAALTEITEFLGLGRYLDWDEETRRAWIQQELVSRRPLIPQHWTPTE 457

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                E ++vld   v+ E P  +   Yiisma   sDvLAv LL +  g  ++L
gi|2545148   458 ETQEVLDCCSVVVEQPPGALACYIISMARQASDVLAVRLLLKAAGGGESL 507

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                ++ PLFE L DL+ AP  +  L +++    ++  +q vm+GYsDs KDAG
gi|2545148   508 PIAPLFETLDDLDRAPSVITDLLAVEAALDHLPEQQMVMIGYSDSAKDAG 557

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 l+AAW  Y+AqE +  v  + Gv+L lFHGRGGt+GRGG P H A+Lsq
gi|2545148   558 ILAAAWAQYRAQEALLEVCARAGVRLQLFHGRGGTIGRGGAPAHDALLSQ 607

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PP  ++  lRvt qGE+i    G   L  ++L  +t A LE     P  P
gi|2545148   608 PPGSLECGLRVTEQGEMIRTKLGMTGLAVKTLALYTSAVLEARTAHPPTP 657

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                k +WR+ m+++A    + YR+vv  +PRF  YFR AtPE E G + + sR
gi|2545148   658 KADWRQTMDRLAAKSCDAYRAVVRDDPRFLSYFRQATPEGELGALPLASR 707

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+ Rk  GGiesLRAiPWiF+Wtq R  LP WLG GAA   A + D
gi|2545148   708 PTSRKKDGGIESLRAIPWIFSWTQNRLMLPSWLGAGAAL--ARELDEHGD 755

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                q +  m+++WPFF   + +lEmv+ K D  + a yD  Lv  eL   G++
gi|2545148   756 QVIAQMFRQWPFFATRMSMLEMVYSKTDSRLSAHYDSKLVDPELLSIGEQ 805

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LRd+     + +Lk+ G   lLE   + +  l LR+ Y   Lnv+qA  L
gi|2545148   806 LRDQLDNDVKTVLKVLGQDSLLEHLHWTRESLELRNIYTGPLNVLQAELL 855

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                 R+R               Ad++  + + ++ +
gi|2545148   856 SRLR-------------RNADDD-TRQAIMISIA--------------- 875
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                  tmKGiAAGmqntG<-*
                     G+AAGm ntG
  gi|2545148   876 ---GVAAGMRNTG    885

gi|283896770|emb|CAX65686.1|: domain 1 of 1, from 1 to 503: score 706.5, E = 2.1e-209
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838967     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838967     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838967     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838967     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838967     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838967     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838967     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838967     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838967     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDvlDAitt L+iGsYReWsEe+RqEWLl+EL GKRPL+g+DLPktE
  gi|2838967     1 --HTDVLDAITTYLGIGSYREWSEERRQEWLLSELNGKRPLFGPDLPKTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvld+f+v+ ELP D FGaY+ismataPsDvLAvELLqREC+vk +L
  gi|2838967    49 EVADVLDTFHVISELPADNFGAYVISMATAPSDVLAVELLQRECHVKTPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLeAAPAa+++LFsiDWY+ r++GKqevm+GYsDsGKDAG
  gi|2838967    99 RVVPLFEKLADLEAAPAALARLFSIDWYRQRMNGKQEVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838967   149 RLSAAWQLYKAQEELIKVAKDFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+G lRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP +P
  gi|2838967   199 PPDTIHGHLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPNAP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++emAvvAtEEYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|2838967   249 KPEWRALLDEMAVVATEEYRSIVFQEPRFVEYFRLATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|2838967   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLQKDIRNL 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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                    +L+EmY++WPFFRvt+DL+EmvFAKG P iAaLyDkLLv+EeL+P G++
  gi|2838967   349 NMLQEMYNQWPFFRVTIDLIEMVFAKGNPDIAALYDKLLVSEELQPLGEK 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++YvEt++lLL++AGH+D+LEGDPYLKqrlRLRd+Yit Lnv+qAYtL
  gi|2838967   399 LRANYVETQKLLLQVAGHRDILEGDPYLKQRLRLRDAYITALNVCQAYTL 448

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+v lrPhlsKE  d   k+a+eLvkLnp++++aPGLEDtLiL
  gi|2838967   449 KRIRDPDYHVALRPHLSKEIMDSS-KPAAELVKLNPASEYAPGLEDTLIL 497

                    tmKGiAAGmqntG<-*
                    tmKGiA
  gi|2838967   498 TMKGIA-------    503

gi|283896776|emb|CAX65689.1|: domain 1 of 1, from 1 to 503: score 706.4, E = 2.3e-209
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838967     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838967     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838967     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838967     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838967     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838967     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838967     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838967     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838967     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDvlDAitt L+iGsYReWsEe+RqEWLl+EL GKRPL+g+DLPktE
  gi|2838967     1 --HTDVLDAITTYLGIGSYREWSEERRQEWLLSELNGKRPLFGADLPKTE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvld+f+v+AELP D FGaY+ismataPsDvLAvELLqREC+vk +L
  gi|2838967    49 EVADVLDTFHVIAELPADNFGAYVISMATAPSDVLAVELLQRECHVKTPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLe APAa+++LFsiDWY+ ri+GKqevm+GYsDsGKDAG
  gi|2838967    99 RVVPLFEKLADLESAPAALARLFSIDWYRQRINGKQEVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWq+YkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838967   149 RLSAAWQMYKAQEELIKVAKDFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEHGm+PP +P
  gi|2838967   199 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHGMHPPSAP 248
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                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emAvvAt EYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|2838967   249 KPEWRALLDEMAVVATKEYRSIVFREPRFVEYFRLATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|2838967   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLQKDIRNL 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY++WPFFRvt+DL+EmvFAKG P iAaLyDkLLv+EeL+P G++
  gi|2838967   349 HMLQEMYNQWPFFRVTIDLIEMVFAKGNPDIAALYDKLLVSEELQPLGER 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Et++lLL++AGH+DlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|2838967   399 LRANYEETQKLLLQVAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 448

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+v lrPhlsKE  d   k+a+eLvkLnp++++aPGLEDtLiL
  gi|2838967   449 KRIRDPDYHVALRPHLSKEIMDSS-KPAAELVKLNPASEYAPGLEDTLIL 497

                    tmKGiAAGmqntG<-*
                    tmKGiA
  gi|2838967   498 TMKGIA-------    503

gi|283896804|emb|CAX65703.1|: domain 1 of 1, from 1 to 503: score 706.0, E = 3.1e-209
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838968     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838968     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838968     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838968     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838968     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838968     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838968     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838968     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838968     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDvlDAitt L+iGsYR+WsEe+RqEWLl+EL GKRPL+g+DLP t+
  gi|2838968     1 --HTDVLDAITTYLGIGSYRKWSEERRQEWLLSELNGKRPLFGPDLPTTD 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+frv+AELP D FGaYiismataPsDvLAvELLqREC+vk +L
  gi|2838968    49 EIADVLDTFRVIAELPADDFGAYIISMATAPSDVLAVELLQRECQVKTPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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                    rvvPLFEkLADL  APAa+++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|2838968     99 RVVPLFEKLADLXGAPAALARLFSVDWYRERINGKQEVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838968    149 RLSAAWQLYKAQEELIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2838968    199 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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  gi|2838968    249 KPEWRALLDEMAVVTTKEYRSIVFQEPRFVEYFRLATPEMEYGRMNIGSR 298

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                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|2838968    299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHILEKDIRNL 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+ eL+P G++
  gi|2838968    349 HMLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSSELWPLGEK 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++YvEtk lLL++AGHkDlLEGD YLKqrlRLRd+Yit Lnv+qAYt+
  gi|2838968    399 LRANYVETKRLLLQVAGHKDLLEGDLYLKQRLRLRDAYITPLNVCQAYTM 448

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                    KRiRDP+y+vtlrPhlsKE  d n k+a+eLvkLnpt+++aPGLEDtLiL
  gi|2838968    449 KRIRDPDYHVTLRPHLSKEIMDWN-KPAAELVKLNPTSEYAPGLEDTLIL 497

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                    tmKGiA
  gi|2838968    498 TMKGIA-------    503

gi|283896772|emb|CAX65687.1|: domain 1 of 1, from 1 to 503: score 705.5, E = 4.4e-209
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838967     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838967     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838967     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838967     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838967     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838967     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838967     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838967     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838967     - ---------------------------------------------- -
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                    eRqtDvlDAitthLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|2838967     1 --HTDVLDAITNYLGIGSYREWSEERRQEWLLSELNGKRPLFGPDLPTTD 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+frv+AELP D FGaYiismataPsDvLAvELLqREC+vk +L
  gi|2838967    49 EIADVLDTFRVIAELPADNFGAYIISMATAPSDVLAVELLQRECHVKTPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLe APAa+++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|2838967    99 RVVPLFEKLADLEGAPAALARLFSVDWYRERINGKQEVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838967   149 RLSAAWQLYKAQEELIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2838967   199 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emAvvAt EYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|2838967   249 KPEWRALLDEMAVVATKEYRSIVFQEPRFVEYFRLATPEMEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFK+ ++KDi+nl
  gi|2838967   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKYVLEKDIRNL 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+ eL+P G++
  gi|2838967   349 HMLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSAELWPLGEK 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Etk lLL++AGHkDlLEGD YLKqrlRLRd+Yi t+nv+qAYt+
  gi|2838967   399 LRANYEETKRLLLQVAGHKDLLEGDLYLKQRLRLRDAYIITMNVCQAYTM 448

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+ tlrPhlsKE  d n k+a+eLvkLnpt+++aPGLEDtLiL
  gi|2838967   449 KRIRDPDYHATLRPHLSKEIMDWN-KPAAELVKLNPTSEYAPGLEDTLIL 497

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                    tmKGi
  gi|2838967   498 TMKGIV-------    503

gi|283896782|emb|CAX65692.1|: domain 1 of 1, from 1 to 503: score 705.1, E = 5.6e-209
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838967     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838967     - ------------------------------------------------ -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838967     - ------------------------------------------------ -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838967     - ------------------------------------------------ -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838967     - ------------------------------------------------ -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838967     - ------------------------------------------------ -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|2838967     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838967     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838967     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDv+DAit  L+iGsYR+W+EeKRqEWLl+EL GKRPL+g+DLP+ E
  gi|2838967     1 --HTDVMDAITNYLGIGSYRDWPEEKRQEWLLSELNGKRPLFGPDLPRSE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E+++vld+f+vLAELP DsFGaY+ismat+PsDvLAvELLqREC+vk++L
  gi|2838967    49 EIAEVLDTFHVLAELPADSFGAYVISMATSPSDVLAVELLQRECHVKKPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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  gi|2838967    99 RVVPLFEKLADLEAAPAALARLFSVEWYRNRINGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   R+sAAWqLYkAqE++iKvAK +GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838967   149 RFSAAWQLYKAQEDLIKVAKSHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP+ti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2838967   199 PPETIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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  gi|2838967   249 KPEWRALMDEMALVATKEYRSIVFEEPRFVEYFRLATPEMEYGRMNIGSR 298

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                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+ AAFKh + KDi+nl
  gi|2838967   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFRAAFKHVLGKDIRNL 348

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                   q L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+PFG++
  gi|2838967   349 QTLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWPFGER 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Etk lLL++AGHkDlLEGDPYLKqrlR+RdsYit Lnv+qAYtL
  gi|2838967   399 LRANYEETKHLLLQVAGHKDLLEGDPYLKQRLRIRDSYITALNVCQAYTL 448

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                   KRiRDP ++v  rPhlsK+  d   k+a++LvkLn t+++aPGLEDtLiL
  gi|2838967   449 KRIRDPGFQVNTRPHLSKDIMDSG-KPAADLVKLNTTSEYAPGLEDTLIL 497

                   tmKGiAAGmqntG<-*
                   tmKGiA
  gi|2838967   498 TMKGIA-------    503

gi|283896792|emb|CAX65697.1|: domain 1 of 1, from 1 to 503: score 704.7, E = 7.7e-209
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  gi|2838967     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838967     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838967     - ------------------------------------------------ -
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                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838967     - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838967     - ------------------------------------------------ -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838967     - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838967     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838967     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDvlDAitt L+iGsYReWsEe+RqEWLl+EL GKRPL+g+DLPktE
  gi|2838967     1 --HTDVLDAITTYLGIGSYREWSEERRQEWLLSELNGKRPLFGADLPKTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvld+f+v+AELP D FGaYiismataPsDvLAvELLqREC+vk +L
  gi|2838967    49 EVADVLDTFHVIAELPADNFGAYIISMATAPSDVLAVELLQRECHVKTPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLe APAa+++LFsiDWY+ ri+G qevm+GYsDsGKDAG
  gi|2838967    99 RVVPLFEKLADLEDAPAALARLFSIDWYRQRINGEQEVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
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  gi|2838967   149 RLSAAWQMYKAQEDLIKVAKDYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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  gi|2838967   199 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPNAP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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  gi|2838967   249 KPEWRALLDEMAVVATKEYRSIVFQEPRFVEYFRLATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
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  gi|2838967   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLQKDIRNL 348

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  gi|2838967   349 HVLQEMYNQWPFFRVTIDLVEMVFAKGNPDIAALYDNLLVSEELRPLGEK 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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  gi|2838967   399 LRANYEETQKLLLQVAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 448

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDP+y+v lrPhlsKE  d n k+a+eLvkLnp++++aPGLEDtLiL
  gi|2838967   449 KRIRDPDYHVALRPHLSKEIMDQN-KPAAELVKLNPGSEYAPGLEDTLIL 497

                  tmKGiAAGmqntG<-*
                  tmKGiA
  gi|2838967   498 TMKGIA-------    503

gi|283896808|emb|CAX65705.1|: domain 1 of 1, from 1 to 503: score 704.5, E = 8.5e-209
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  gi|2838968     -    ------------------------------------------- -

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gi|2838968     - ------------------------------------------------- -

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|2838968     - ------------------------------------------------- -

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|2838968     - ------------------------------------------------- -

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gi|2838968     - ------------------------------------------------- -

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gi|2838968     - ------------------------------------------------- -

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|2838968     - ------------------------------------------------- -

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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gi|2838968     1 --HTDVLDAITTYLGIGSYREWSEECRQEWLLSELNGKRPLFGPDLPTTD 48

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gi|2838968    49 EIADVLDTFRVIAELPADNFGAYIISMATAPSDVLAVELLQRECHVKVPL 98

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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gi|2838968    99 RVVPLFEKLADLEGAPAALARLFSVDWYKERINGKQEVMIGYSDSGKDAG 148

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|2838968   149 RLSAAWQLYKAQEELINVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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gi|2838968   199 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPISP 248

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gi|2838968   249 KPEWRALLDEMAVVATKEYRSIVFQEPRFVEYFRLATPEMEYGRMNIGSR 298

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gi|2838968   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKYILEKDIRNL 348

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                  +L+EmYkeWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+ eL+P G++
gi|2838968   349 HMLQEMYKEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSAELWPLGEK 398

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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gi|2838968   399 LRSNYEETKRLLLQVAGHKDLLEGDLYLKQRLRLRDAYITTLNVCQAYTM 448

                 KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                 KRiRDP y+vtlrPhlsKE  d n k a+eLvkLnpt+++aPGLEDtLiL
gi|2838968   449 KRIRDPGYHVTLRPHLSKEIMDWN-KAAAELVKLNPTSEYAPGLEDTLIL 497
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                  tmKGiA
  gi|2838968   498 TMKGIA-------    503

gi|283896786|emb|CAX65694.1|: domain 1 of 1, from 1 to 503: score 704.5, E = 8.5e-209
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  gi|2838967     -    ---------------------------------------------- -

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  gi|2838967     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838967     - ---------------------------------------------- -

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  gi|2838967     - ---------------------------------------------- -

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  gi|2838967     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838967     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838967     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838967     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838967     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDvlDAitt L+iGsYReWsEe+RqEWLl+EL GKRPL+g+DLP t+
  gi|2838967     1 --HTDVLDAITTYLGIGSYREWSEERRQEWLLSELNGKRPLFGPDLPTTD 48

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  gi|2838967    49 EIADVLDTFRVIAELPADNFGAYIISMATAPSDVLAVELLQRECQVKTPL 98

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                  rvvPLFEkLADLe APAa+++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|2838967    99 RVVPLFEKLADLEGAPAALARLFSVDWYRERINGKQEVMIGYSDSGKDAG 148

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                  RlsAAWqLYkAqEE+iKvAK +GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838967   149 RLSAAWQLYKAQEELIKVAKLFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

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                  PP ti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2838967   199 PPGTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++emAvvAt EYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|2838967   249 KPEWRALLDEMAVVATKEYRSIVFQEPRFVEYFRLATPEMEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+ l
  gi|2838967   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHILEKDIRKL 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+ eL+P G++
```

```
  gi|2838967   349 HMLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSSELWPLGEK 398

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                 LR++Y++tk lLL++AGHkDlLEGD YLKqrlRLRd+YittLnv+qAYt+
  gi|2838967   399 LRANYEDTKRLLLQVAGHKDLLEGDLYLKQRLRLRDAYITTLNVCQAYTM 448

                 KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                 KRiRDP+y+vtlrPhlsKE  d n k+a+eLvkLnpt+++aPGLEDtLiL
  gi|2838967   449 KRIRDPDYHVTLRPHLSKEIMDWN-KPAAELVKLNPTSEYAPGLEDTLIL 497

                 tmKGiAAGmqntG<-*
                 tmKGiA
  gi|2838967   498 TMKGIA-------    503

gi|88857492|ref|ZP_01132135.1|: domain 1 of 1, from 1 to 873: score 704.5, E = 8.7e-209
                 *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                              +s+   L     LL       ++   G+ +   v
  gi|8885749     1    -------------MSNYSALKSNVNLLGQLLGQTIKAAQGDAILAKV 34

                 qECYEls.AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                      ls+A   G  D +   EL   L  L  a+ + vA+a+   LnLAn
  gi|8885749    35 EQIRALSkASRSG--DGQSRHELIDLLHQLTDAELLPVARAFNQFLNLAN 82

                 LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                 +AE  +   R      +     D  +    s             n s +
  gi|8885749    83 VAEQFHTISRQNEANNH--PLLDSLNTIAAS-------------NVSADA 117

                 vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                 v +A+ n  vDLvltAHPt   RR L+ K+  +  CL  L    + + ++
  gi|8885749   118 VQQAIVNLKVDLVLTAHPTEITRRTLVNKHRELNDCLVALELDSLLPSEQ 167

                 kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   L   +   i  A+ t EiR  +PtP DE + G + i   +W+ vP FL
  gi|8885749   168 AILLNRIEQLICQAWHTNEIRQQRPTPVDEAKWGFAVIENSLWQAVPDFL 217

                 RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                 R   t L        lP d   i F+sWmGGDRDG nP vt  vt++v
  gi|8885749   218 REF-TDLVDHKFKFSLPLDYNPIVFTSWMGGDRDG-NPFVTAKVTKEVLD 265

                 LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                 L R mA nlY+  ++ L  Elsm  C +EL     El  t   +
  gi|8885749   266 LGRWMAINLYLRDIDKLSAELSMNQCDSEL----GEL--TGHAH------ 303

                 iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA..vy
                           EPYR ++ + RD+L   RE   HL A+ i   s +A+++
  gi|8885749   304 ----------EPYRFVISQLRDQL---RETEHHLTAK-IKGHSSDAkdII 339

                 tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                 t +++   PLE CY+sL      viADG LLD+LR +  FGL L KLDiR
  gi|8885749   340 TSIDQLKQPLEACYRSLHHSKMGVIADGLLLDVLRRIHCFGLYLTKLDIR 389

                 qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                 q+s+R+  v   +t  L iG Y  WsE+++q +Ll+EL+ KRPL++
  gi|8885749   390 QDSDRHSQVFAELTDYLAIGDYNAWSEQQKQTFLLTELQSKRPLIPRNWQ 439

                 ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                    +v++v+d+ +v+AE   + FG Yiisma   sDvLAv LL +E g
  gi|8885749   440 PSSDVQEVIDTCKVIAETSQERFGIYIISMARKASDVLAVHLLLKEAGCP 489

                 qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                   L+v PLFE L DL+A PA +e LF   WY+n++  +q vm+GYsDs K
  gi|8885749   490 YVLPVAPLFETLDDLNAGPAVIETLFNEPWYKNHVKNQQYVMIGYSDSAK 539

                 DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                 DAG ++A W  Y A + +++   +  + L+lFHGRGGtvGRGG P   A+
  gi|8885749   540 DAGMMAAGWAQYEAMDKLVQFSEQQDIELILFHGRGGTVGRGGAPAAQAL 589

                 LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                  sqPP  ++  lRvt qGE+i f FG  ++  +sL  ++ A LE  + PP
  gi|8885749   590 RSQPPGSLKSGLRVTEQGEMIRFTFGLPQVAQQSLSLYAGAVLENNLLPP 639
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                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                      P+  W ++m  +  v  E YR++v     Fv YFR AtPE E  ++ +
  gi|8885749   640 PEPQAKWQEVMAVISAVSCEHYRAIVREHQDFVPYFRAATPEQELAQLPL 689

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKRk  GG+esLRAiPWiFaW q R  LP WLG  A    A ++
  gi|8885749   690 GSRPAKRKANGGVESLRAIPWIFAWSQNRLMLPAWLGAAAGLVAAEKQFG 739

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                      +  L  m k+WPFFR  +++lEmvF K D  +   yD+ Lv  eL+P
  gi|8885749   740 PDV--LAQMNKQWPFFRTRIEMLEMVFCKADTWLSEHYDHHLVPKELQPL 787

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G+ LR +     +l+        lL   P+++q + LR++Y   Lnv+q
  gi|8885749   788 GETLRSELTAAVELVRGYCQNGVLLAAQPWVQQSIELRNPYTDPLNVLQV 837

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L+R R             +E  +E         ++n
  gi|8885749   838 ELLRRAR-------------RESLAEG-------CEVN----------QA 857

                    LiLtmKGiAAGmqntG<-*
                    L++tm GiAAGm ntG
  gi|8885749   858 LMITMAGIAAGMRNTG    873

gi|283896800|emb|CAX65701.1|: domain 1 of 1, from 1 to 503: score 701.9, E = 5.3e-208
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838968     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838968     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838968     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838968     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838968     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838968     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838968     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838968     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838968     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDv+DAit  L++GsYReW+EeKRqEWLl+EL GKRPL+g+DLPkt
  gi|2838968     1 --HTDVMDAITNYLGVGSYREWPEEKRQEWLLSELNGKRPLFGPDLPKTN 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E+++vld+f+vLAELP+DsFGaY+ismataPsDvLAvELLqREC+vk++L
  gi|2838968    49 EIAEVLDTFHVLAELPSDSFGAYVISMATAPSDVLAVELLQRECHVKKPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAa+++LFs++WY+nri+GKqevm+GYsDsGKDAG
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  gi|2838968    99 RVVPLFEKLADLEAAPAALARLFSVEWYRNRINGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   R+sA WqLYkAqE++iK AK +GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838968   149 RFSAGWQLYKAQEDLIKAAKAFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP+ti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2838968   199 PPETIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emAvvAtEEYRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|2838968   249 KPEWRALMDEMAVVATEEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|2838968   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLQKDIRNL 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q L+ mY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+++L+ FG++
  gi|2838968   349 QTLQQMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSDDLWSFGER 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Etk+lLL++AGHkDlLEGDPYL+qrlR+RdsYit Lnv+qAYtL
  gi|2838968   399 LRANYEETKQLLLQVAGHKDLLEGDPYLRQRLRIRDSYITALNVCQAYTL 448

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPs++  + Phl KE  +   k a+eLvkLn t+++aPGLEDtLiL
  gi|2838968   449 KRIRDPSFHSKPGPHLPKEIMESG-KSAAELVKLNTTSEYAPGLEDTLIL 497

                   tmKGiAAGmqntG<-*
                   tmKGiA
  gi|2838968   498 TMKGIA-------    503

gi|283896774|emb|CAX65688.1|: domain 1 of 1, from 1 to 503: score 698.0, E = 8e-207
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838967     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838967     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838967     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838967     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838967     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838967     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838967     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838967     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838967     - ---------------------------------------------- -
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                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDvlDAitt L+iGsYReWsE++RqEWLl+E  GKRPL+g+DLP t+
  gi|2838967     1 --HTDVLDAITTYLGIGSYREWSEDRRQEWLLSERNGKRPLFGPDLPTTD 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvld+frv+AELP D FGaYiismataPsDvLAvELLqREC+vk +L
  gi|2838967    49 EIADVLDTFRVIAELPADNFGAYIISMATAPSDVLAVELLQRECHVKTPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLe APAa+++LFs++WY+ ri+GKqevm+GYsDsGKDAG
  gi|2838967    99 RVVPLFEKLADLECAPAALARLFSVEWYRERINGKQEVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838967   149 RLSAAWQLYKAQEELINVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHG++PP+sP
  gi|2838967   199 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGIHPPISP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emAvvAt EYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|2838967   249 KPEWRALLDEMAVVATKEYRSIVFQEPRFVEYFRLATPEMEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi n+
  gi|2838967   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLEKDITNV 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+ eL+ FG++
  gi|2838967   349 HMLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSSELWSFGEK 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Etk lLL++A HkDlLEGD YLKqrlRLRd+YittLnv+qAYt+
  gi|2838967   399 LRTNYEETKRLLLQVARHKDLLEGDLYLKQRLRLRDAYITTLNVCQAYTM 448

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+vtlrPhlsKE  d n k+a+eLvkLnpt+++aPGLEDtLiL
  gi|2838967   449 KRIRDPDYHVTLRPHLSKEIMDWN-KPAAELVKLNPTSEYAPGLEDTLIL 497

                    tmKGiAAGmqntG<-*
                    tmKGiA
  gi|2838967   498 TMKGIA-------    503

gi|283896788|emb|CAX65695.1|: domain 1 of 1, from 1 to 503: score 697.8, E = 8.9e-207
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838967     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838967     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838967     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838967     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838967     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838967     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|2838967     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838967     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838967     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDv+DAit+ L+iGsYReW EeKRqEWLl+EL GKRPL+g+DLPk +
  gi|2838967     1 --HTDVMDAITEYLGIGSYREWTEEKRQEWLLSELNGKRPLFGPDLPKSD 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dvl++f+vLAELP+DsFGaY+ismataPsDvLAvELLqREC+vk++L
  gi|2838967    49 EIADVLETFHVLAELPSDSFGAYVISMATAPSDVLAVELLQRECHVKKPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAa+++LFs++WY+nri GKqevm+GYsDsGKDAG
  gi|2838967    99 RVVPLFEKLADLEAAPAALARLFSVEWYRNRISGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   R+sAAWqLYkAqEE+iKvAK yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838967   149 RFSAAWQLYKAQEELIKVAKLYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP+ti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAA LEHGm+PP+sP
  gi|2838967   199 PPETIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAASLEHGMHPPISP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emA+vAt EYRs+v+ E RFvEYFRlAtPE+EYG+mniGsR
  gi|2838967   249 KPEWRALMDEMAIVATKEYRSIVFEEQRFVEYFRLATPEMEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh +dKD  nl
  gi|2838967   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLDKDKWNL 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q L+EmY++WPFFRvt+DL+EmvFAKGDPGiAaLyD+LLv+E+L+ FG++
  gi|2838967   349 QTLQEMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDNLLVSEDLWSFGER 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR +Y+Etk+lLL++AGHkDlLEGDPYLKqrlR+RdsYit Lnv+qAYtL
  gi|2838967   399 LRTNYEETKQLLLQVAGHKDLLEGDPYLKQRLRIRDSYITALNVCQAYTL 448

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP + v +rPhlsK+  d   k+a+eLvkLn t+++aPGLEDtLiL
  gi|2838967   449 KRIRDPGFLVNPRPHLSKDIMDSG-KPAAELVKLNTTSEYAPGLEDTLIL 497

                   tmKGiAAGmqntG<-*
                   tmKGiA
  gi|2838967   498 TMKGIA-------    503

gi|90023020|ref|YP_528847.1|: domain 1 of 1, from 2 to 873: score 697.5, E = 1.1e-206
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                              GK    e+L e   +L D   + L +  G+ L   v
  gi|9002302     2    -----------GKLP--ERLRENVRILGDLLGETLLEHEGPALFRKV 35

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    E   l A    K  ++    L   L  L+  D + + +a+   LnLAn+
  gi|9002302    36 EEIRAL-AKSLNKGTASDASQLVDLLSQLEDKDILPIVRAFNQFLNLANI 84

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   A+            +    +   a+A     ++  l kL +      +
  gi|9002302    85 AD------------LE---YFSSADAQDNDGLDTLLTKLSSDV--GKDQL 117

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   ++ +    +DLvltAHPt   RR L+ K  +i   L+ L   D+   +
  gi|9002302   118 YDLMSTLRIDLVLTAHPTEVTRRTLIRKYEKIARTLSDLTRGDLLTYESN 167
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                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     L   LHR +   + t EiR  +Pt  DE + G + i   +W+ vP F+R
  gi|9002302   168 KLQGRLHRLVEEVWNTNEIRDERPTAVDEAKWGFAVIENSLWHAVPDFIR 217

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                      D  L    +   lP d    kF sWmGGDRDG nP vt  vt +v +L
  gi|9002302   218 HFDR-LSRRRLGQALPLDLQPFKFYSWMGGDRDG-NPNVTHKVTEEVIML 265

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                     R  Aa lY++ + +L  +lsm    dEL +    l   a
  gi|9002302   266 GRWKAADLYLQDLYELGGDLSMHEASDELLA---NLPNGASPT------- 305

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                              PYR  L + R +L  t + +   LA      +E+A++ +
  gi|9002302   306 ----------PYRERLHALRKRLEVTLDWTERTLAGENLPEPENAIHHR- 344

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    ++ L PL     sL e G   iA G + D LR ++ FG+sL  LDiRq+s
  gi|9002302   345 DDLLKPLLDIHSSLIESGFEHIANGPISDTLRRIYAFGISLAPLDIRQDS 394

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+  vlD +t  Le+GsYReW EeKRq +Ll  L  KRPLl++  P  +
  gi|9002302   395 DRHVQVLDELTNYLEMGSYREWDEEKRQAFLLEQLNSKRPLLPANWPVSD 444

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    + ++vl + + +A  P ++   Y+isma   sDvL v LL +E gv   +
  gi|9002302   445 DSAEVLATCKAIARQPQETLSHYVISMARQASDVLSVALLLKESGVTWDM 494

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    ++vPLFE L DLe     ++ L+ + WY    +G q vm+GYsDs KDAG
  gi|9002302   495 PIVPLFETLSDLENGASVMNTLWQMHWYQRYTQGHQTVMIGYSDSAKDAG 544

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    ++sA W  Yk qE ++  A +y + LvlFHGRGGtvGRGGGP   A+ sq
  gi|9002302   545 KFSATWAQYKCQEKLVDLANQYEINLVLFHGRGGTVGRGGGPVEKAMASQ 594

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  + G +Rvt qGE+i + FG   + FrsL  ++ At+   + P  +P
  gi|9002302   595 PPGSVAGRIRVTEQGEMIRYKFGLPRVAFRSLSNYACATIKATVTPNPAP 644

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    k  WR L+e+m     E YRs+v     Fv YFR+ tPE E  k+ +GsR
  gi|9002302   645 KEQWRALIEDMSDASLEGYRSIVRGHKHFVPYFRSLTPEQELNKLALGSR 694

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRk  GG+esLRAiPW+FaWtq R  LP WLG   A +hA++
  gi|9002302   695 PAKRKATGGVESLRAIPWVFAWTQVRLNLPGWLGAHQALQHALKEQP--- 741

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+Em  eWPFF   +DLlEmv  K D  i + y++ Lv Ee +  G+
  gi|9002302   742 DLLQEMLTEWPFFSSFIDLLEMVLGKADSAICGHYERQLVDEEYRDLGEF 791

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR + v   +l+ +i     lLE DP L+q + +R +Yi  Ln +qA  L
  gi|9002302   792 LRGDLVALAQLIKEIKNQPALLEDDPMLQQSINVRKPYIDPLNYLQAELL 841

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KR                   E             + +++P LE  L +
  gi|9002302   842 KR--------------------ER-----------SAGEISPELEQALKV 860

                    tmKGiAAGmqntG<-*
                    tm Gi AGm ntG
  gi|9002302   861 TMAGISAGMRNTG    873

gi|167041901|gb|ABZ06640.1|: domain 1 of 1, from 4 to 906: score 697.2, E = 1.4e-206
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                           + + L+  K s   k+++    Ll k L  ++++  G  L
  gi|1670419     4    --KTKYKNLAILKLS---KIVH----LLGKILGlVIKEQEGTYLFNK 41

                    vqECYElsAeYEGKk........DtkKLeELGakLtsLdPaDailvAkai
                    +     ls    GKk++++ + ++tkK   L + +  L   +++++ +++
```

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gi|1670419    42 IEKIRLLSKTSRGKKnkkkirlnETKKFRQLKSNIRKLSYQESLVISRSF 91

                 lHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDi.EEtlKkLv
                 +  Ln  n+AE     ++  +   +       a+ t E  i +E + +L+
gi|1670419    92 SQFLNFSNIAESLYSVHKIHNLDVR------KAQGTNELVIlDEAVDRLI 135

                 lklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL....
                      s +  F+ +K   ++LvltAHPt   RR L+ K + + n L++
gi|1670419   136 KNKSISKNKFFQTVKKLKIELVLTAHPTEVKRRTLIHKFTHVNNILesfv 185

                 .aqLsAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGms
                 +  ++ K     + k L+E LH Ei   ++tDEi+R++PtP DE + G++
gi|1670419   186 nLRIFTKKNVDREVKLLEESLHEEITSIWKTDEIKRSRPTPIDEAKWGLA 235

                 YiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGk
                  i + +W+  PK     D A++n  +  RlP +   i F sWmGGDRDG
gi|1670419   236 IIEDSLWNALPKICSYFDQAIQNY-VGKRLPINFSPITFGSWMGGDRDG- 283

                 nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEE
                 n  vt  +t +v LL+R mAanlY   +  L+  ls+  C   L
gi|1670419   284 NSSVTSKITEEVVLLSRWMAANLYEKELTKLIRNLSIHECSKTLQ----- 328

                 lyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaR.HLL
                   +   +                 EPYRv L  +RDK+ nt      HL
gi|1670419   329 -DKVGNSS---------------EPYRVFLRPIRDKMKNTQKLIElHLN 361

                 AtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqv
                  + +  + E      + e + PL + Y sLC+     iA Gs+LDlLR
gi|1670419   362 NKKV--LNESYLVRSINEVIQPLNIVYNSLCDVKCESIANGSVLDLLRRA 409

                 stFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaE
                 + FGL L KLDiRqE++R+   l  i   L++G Y eWsEeK+  +L
gi|1670419   410 YSFGLNLAKLDIRQEANRHGKLLKNICLRLGLGNYQEWSEEKKISFLSKH 459

                 LkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDv
                  k KR L++  +    E k+v  +f+++A LP ++ GaYiisma   sD+
gi|1670419   460 FKSKRSLIPKNIVLDKEDKEVWSTFQMIAKLPQECLGAYIISMASDVSDI 509

                 LAvELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                 LAv  Lq+E g+k  LrvvPLFE L DL+ A   ++ L+ i WY  +
gi|1670419   510 LAVMFLQKESGIKTYLRVVPLFETLSDLQNAHQVIKSLYNISWYLKKFKR 559

                 KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                  qevm+GYsDs KDAG+l+A W  Y AqE +  v  ++ vKL+lFHGRGG
gi|1670419   560 HQEVMIGYSDSSKDAGKLAASWAQYNAQENLQSVSNDHRVKLTLFHGRGG 609

                 tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                  vGRGGGP   A+LsqPP t+nG  Rvt qGE+i + +  E L  ++L
gi|1670419   610 SVGRGGGPIYSALLSQPPGTVNGRTRVTEQGEIIQQKYSTESLAEHTLGT 659

                 FtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                 + A  LE  +nPP  Pk  WR+Lm++m   A   YRs  +    F  Y+R
gi|1670419   660 YIASVLEATLNPPAQPKKSWRELMDDMSKAASTAYRS-HIHNSNFLRYYR 708

                 lAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG
                   tP     ++ iGsRP+KRk s  ie LRAiPW+FaWtq RF LP WLG
gi|1670419   709 TITPQKILDQLSIGSRPTKRKKSDEIENLRAIPWVFAWTQIRFILPAWLG 758

                 vGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaL
                        A  K  +n   Lk+m ++WPFF   +D+l+mv  K D  +
gi|1670419   759 TLEGLELA--KKGQNKVILKDMLNKWPFFYAMMDMLDMVLTKTDLRVIQF 806

                 yDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRL
                 y++ L   eL+  G++LR +      ++ k    k +LE     +  +R+
gi|1670419   807 YEECLGDHELQNIGDKLRKQLLSLI-YINKTLIPKYILEQRKSYRESIRI 855

                 RdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkL
                 R+ Y  tLn +qA  +K+++  + +           Ad           L
gi|1670419   856 RNTYAETLNLLQADIMKKLKITNLR----------NADRK--------LL 887

                 nptervaPGLEDtLiLtmKGiAAGmqntG<-*
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                            D +++t+ Gi A m+ntG
  gi|1670419   888 M----------DAMMVTIAGISAAMKNTG    906

gi|283896812|emb|CAX65707.1|: domain 1 of 1, from 1 to 503: score 696.1, E = 3e-206
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838968     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838968     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838968     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838968     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838968     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838968     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838968     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838968     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838968     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDvlDAitt L+iGsYReWsEe RqEWLl+EL GKRPL+g+DLP t+
  gi|2838968     1 --HTDVLDAITTYLGIGSYREWSEEGRQEWLLSELNGKRPLFGPDLPTTD 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    +++Dvld+frv+AELP D F aYiismataPsDvLAvELLqREC+vk +L
  gi|2838968    49 DIADVLDTFRVIAELPADNFEAYIISMATAPSDVLAVELLQRECHVKTPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLe APAa+++LFs+DWY+ ri+GKqe+m+GYsDsGKDAG
  gi|2838968    99 RVVPLFEKLADLEGAPAALARLFSVDWYRERINGKQEIMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838968   149 RLSAAWQLYKAQEELIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDt++GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2838968   199 PPDTVHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emAvvAtEEYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|2838968   249 KPEWRALLDEMAVVATEEYRSIVFQEPRFVEYFRLATPEMEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFK   dKDi+nl
  gi|2838968   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKSIPDKDIRNL 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+ eL+P G++
  gi|2838968   349 HMLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSSELWPLGEK 398
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                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Etk lLL++AGHkDlLEGD YLKqrlRLRd+Yitt+nv+qAYt+
  gi|2838968   399 LRENYEETKRLLLQVAGHKDLLEGDLYLKQRLRLRDAYITTMNVCQAYTM 448

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+vtlrPh sKE  d n k+a+eLvkLnpt+++aPGLEDtLiL
  gi|2838968   449 KRIRDPDYHVTLRPHQSKEIMDWN-KPAAELVKLNPTSEYAPGLEDTLIL 497

                    tmKGiAAGmqntG<-*
                    t+KGiA
  gi|2838968   498 TIKGIA-------    503

gi|283896822|emb|CAX65712.1|: domain 1 of 1, from 1 to 503: score 695.4, E = 4.7e-206
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838968     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838968     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838968     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838968     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838968     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838968     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838968     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838968     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838968     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDvlDAitt L+iGsYReWsEe+RqEWLl+EL GKRPL+gsDLPktE
  gi|2838968     1 --HTDVLDAITTYLGIGSYREWSEERRQEWLLSELNGKRPLFGSDLPKTE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvld+f+v+ EL  D FGaYiismataPsDvLAvELLqREC+vk +L
  gi|2838968    49 EVADVLDTFHVISELSADNFGAYIISMATAPSDVLAVELLQRECHVKTPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLe APAa+++LFsiDWY+ ri+GKqevm+GYsDsGKDAG
  gi|2838968    99 RVVPLFEKLADLESAPAALARLFSIDWYRQRINGKQEVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838968   149 RLSAAWQLYKAQEELIKVAKDFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+  lRvtvqGEviE+sFGEE+LCFr+LqR tAAtLEHGm+PP +P
  gi|2838968   199 PPDTIHEHLRVTVQGEVIEQSFGEEHLCFRTLQRLTAATLEHGMHPPSAP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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                    kPEWR L++emAvvAt EYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|2838968   249 KPEWRALLDEMAVVATKEYRSMVFQEPRFVEYFRLATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|2838968   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLQKDIRNL 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY++WPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+ eL+P G++
  gi|2838968   349 HMLQEMYNQWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSQELQPLGEK 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++YvEt++lLL++AGHkD+LEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|2838968   399 LRANYVETQKLLLQVAGHKDILEGDPYLKQRLRLRDAYITTLNVCQAYTL 448

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+v lrPhlsKE  d   k+a+eLvkLnp++++aPGLEDtLiL
  gi|2838968   449 KRIRDPDYHVALRPHLSKEIMDSS-KPAAELVKLNPASEYAPGLEDTLIL 497

                    tmKGiAAGmqntG<-*
                    tmKGiA
  gi|2838968   498 TMKGIA-------    503

gi|119468657|ref|ZP_01611709.1|: domain 1 of 1, from 1 to 881: score 695.2, E = 5.3e-206
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L  G v            Ll + L+  ++D  G+ + +
  gi|1194686     1    -MSEQYAALR-GNVG-----------LLGQLLgQTIKDAQGQAILDK 34

                    vqECYEls.AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    v E   ls+    G +D +K   L  +L +L   + + vA+++ H LnLA
  gi|1194686    35 VEEIRALSkSSRSGNEDDRK--ALIEVLHALSDEELLPVARSFNHFLNLA 82

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlk...lnK
                    n+AE  +   R     +               +  tlK L  k ++++
  gi|1194686    83 NVAEQFHTVSRFNDAGLG-----------QQNPLTQTLKTLAAKaqeGQL 121

                    sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt
                      +   + L    + LvltAHPt   RR ++ K+  +  CLa L  KD
  gi|1194686   122 DSNHLADTLSKLHINLVLTAHPTEVTRRTIINKHVELSDCLASLERKDNL 171

                    veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGv
                      +++ +   +   i  A+ tD+iRR++PtP DE + G + i   +W+ v
  gi|1194686   172 EHEREAILNRIAQLISQAWHTDDIRRSRPTPVDEAKWGYAVIENSLWHAV 221

                    PKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                    P+FLR      K   +   lP d   i+F+sWmGGDRDG nP vt  vt
  gi|1194686   222 PRFLREFSEHAKE-QLSLELPIDYSPIEFTSWMGGDRDG-NPFVTAQVTS 269

                    DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                     v    R mA  lY   ++ L  Elsm    dEL          a +d
  gi|1194686   270 QVLDHGRWMALDLYSRDIDTLCAELSMSDASDEL-------IELAGQD-- 310

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                                   EPYR +L   +  +  t     HL A+ i     +A
  gi|1194686   311 ------------FEPYRTVLKKLKGEVSET---VAHLGAK-IKHKRTDA 343

                    ..vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                    ++  t++ +   P+E+CY+sL  C  kv+ADG LLDl+     FGL L K
  gi|1194686   344 qdLVTDINQLKHPIEVCYRSLLKCNMKVVADGLLLDLMHRLNSFGLRLAK 393

                    LDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlg
                    LD+Rq+s R+ Dv   +t+ L++G Y +W E+ +q +LlaEL  +RPL++
  gi|1194686   394 LDVRQDSSRHSDVFSELTRYLGLGDYNQWQEQDKQAFLLAELNSRRPLIP 443

                    sDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRE
                           +v++vld+f v+A     +FG Yiisma + sD+LAv LL +E
  gi|1194686   444 KHWQPSPDVQEVLDTFDVIAKQDEKTFGLYIISMARTASDILAVQLLLKE 493

                    CgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYs
                     g    L+v PLFE L DL+     +  L    WY+ +i+  q+vm+GYs
  gi|1194686   494 SGCSFELPVAPLFETLDDLNNGSDVITTLLDNVWYRGHIQNTQNVMIGYS 543
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                    DsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPt
                    Ds KDAG ++A W  Y A + +++ A + G+ LvlFHGRGGtvGRGG P
  gi|1194686   544 DSAKDAGMMAAGWAQYEAMDKLVQLADERGIELVLFHGRGGTVGRGGAPA 593

                    HLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHG
                      A+ sqPP  ++G lRvt qGE+i f FG  ++  +sL  ++ A L
  gi|1194686   594 AQALHSQPPGSLKGGLRVTEQGEMIRFKFGLPDVALQSLNIYAGAVLQSN 643

                    mnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYG
                    + PP  PkP WR++m  +     E YR vv  +  Fv YFR+AtPElE
  gi|1194686   644 LLPPPEPKPQWREVMKLISEQSCEHYRNVVRHDENFVPYFRMATPELELS 693

                    kmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAi
                    k+ +GsRPaKR P GG+esLRAiPWiFaW q R  LP WLG     K A+
  gi|1194686   694 KLPLGSRPAKRNPNGGVESLRAIPWIFAWSQNRLMLPAWLGALTGLKKAL 743

                    dKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEe
                      D   l  L Em  +WPFFR  l++lEmvF K D  +   yD+ Lv +
  gi|1194686   744 --DQYGLETLNEMSLNWPFFRARLEMLEMVFSKADSWLSEHYDNALVEDM 791

                    LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLn
                     kP G  LR + +E  +l+  +   k lL   P++K  + LR++Y   Ln
  gi|1194686   792 YKPLGVTLRKELEEAIELVQSLSPQKSLLAAQPWIKESISLRNPYTDPLN 841

                    vfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPG
                    v+q   L+R R            s E  +E
  gi|1194686   842 VLQVELLRRAR------------SNEEHNEG----------D-------- 861

                    LEDtLiLtmKGiAAGmqntG<-*
                    ++  L++tm GiAAGm ntG
  gi|1194686   862 IDNALMITMTGIAAGMRNTG    881

gi|77362226|ref|YP_341800.1|: domain 1 of 1, from 1 to 881: score 694.8, E = 7.2e-206
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +  q  +L  G v            Ll + L+  ++D  G+ + +
  gi|7736222     1    -MSEQYAALR-GNVN----------LLGQLLgQTIKDAQGQAILDK 34

                    vqECYEls.AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    v E   ls+    G +  +K   L  +L +L   + + vA+++ H LnLA
  gi|7736222    35 VEEIRALSkSSRSGNENDRK--TLIKVLHALSDEELLPVARSFNHFLNLA 82

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnK...
                    n+AE  +   R          F D +       +  tlK L  k n ++
  gi|7736222    83 NVAEQFHTVSR----------FNDVGFCQLNP-LTQTLKTLATKANNgql 121

                    sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt
                      +   + L    + LvltAHPt   RR ++ K+  +  CLa L   D
  gi|7736222   122 NHNHLADTLSKLHINLVLTAHPTEVTRRTIINKHVELSDCLASLERTDNL 171

                    veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGv
                     ++++ +   +   i  A+ tD+iRR++PtP DE + G + i   +W+ v
  gi|7736222   172 AQEREAILNRIAQLISQAWHTDDIRRSRPTPVDEAKWGYAVIENSLWHAV 221

                    PKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                    P+FLR     +K   +   lP +   i+F+sWmGGDRDG nP vt  vt+
  gi|7736222   222 PRFLREFSQHVKE-HLSLELPINYSPIEFTSWMGGDRDG-NPYVTAQVTK 269

                    DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                    +v    R mA  lY   +E L  Elsm    dEL + A
  gi|7736222   270 EVLDHGRWMALDLYGRDLETLSTELSMSDASDELIALAGQ---------- 309

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE.e
                         EF       EPYR ++   + ++  t     HL A+   + sE +
  gi|7736222   310 -----EF-------EPYRCVIKTLKNQVLET---VMHLGAKIKNQRSEaQ 344

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                       t++ +   P+E+CY+sL  C  kv+ADG LLD+L     FGL L KL
  gi|7736222   345 DLITDINQIKHPIEVCYRSLLKCNMKVVADGLLLDVLHRLNSFGLRLAKL 394

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
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                    D+Rq+s R+ Dv   +t+ L++G Y +W E+ +q +Ll+EL  +RPL++
  gi|7736222   395 DVRQDSSRHGDVFSELTRYLGLGDYNQWQEQDKQAFLLTELNSRRPLIPK 444

                    DLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqREC
                          Ev++vld+f v+A     +FG Yiisma + sD+LAv LL +E
  gi|7736222   445 RWQPSPEVQEVLDTFDVIAQQDEQTFGLYIISMARTASDILAVQLLLKES 494

                    gvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsD
                    g    L+v PLFE L DL+     +  L   DWY+ +i+  q+vm+GYsD
  gi|7736222   495 GCSFKLPVAPLFETLDDLNDGHNVITTLLDNDWYRGQINNTQNVMIGYSD 544

                    sGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtH
                    s KDAG ++A W  Y A + +++ A k G+ LvlFHGRGGtvGRGG P
  gi|7736222   545 SAKDAGMMAAGWAQYEAMDKLVQLADKRGIELVLFHGRGGTVGRGGAPAA 594

                    LAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm
                     A+ sqPP  ++G lRvt qGE+i f FG  ++  +sL  ++ A L   +
  gi|7736222   595 QALHSQPPGSLKGGLRVTEQGEMIRFKFGLPDVALQSLNIYAGAVLQSNL 644

                    nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGk
                     PP  PkP WR++m  +     E YR vv  +  Fv YFR+AtPElE  k
  gi|7736222   645 LPPPEPKPQWREVMALISEESCEHYRNVVRHDENFVPYFRMATPELELSK 694

                    mniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid
                    + +GsRPaKR P GG+esLRAiPWiFaW q R  LP WLG     + A+
  gi|7736222   695 LPLGSRPAKRNPTGGVESLRAIPWIFAWSQNRLMLPAWLGALTGLQAALA 744

                    KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL
                    K    +  L+Em  +WPFFR  l++lEmvF K D  +   yD+ Lv +
  gi|7736222   745 K--YGVETLQEMSLQWPFFRSRLEMLEMVFSKADSWLSEHYDNALVEDMY 792

                    kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnv
                    kP G  LR +  E   l+  +   k lL   P++K  + LR++Y   Lnv
  gi|7736222   793 KPLGVTLRKELAEAISLVQSLSPQKSLLADQPWIKESIALRNPYTDPLNV 842

                    fqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGL
                    +q   L+R R            s +   E                   +
  gi|7736222   843 LQVELLRRAR------------SSDNGSEG----------D--------I 862

                    EDtLiLtmKGiAAGmqntG<-*
                    +  L++tm GiAAGm ntG
  gi|7736222   863 DNALMITMTGIAAGMRNTG    881

gi|219120583|ref|XP_002181027.1|: domain 1 of 1, from 72 to 1009: score 692.2, E = 4.4e-205
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       s DA     +P   ++ +  ++ D  ++   L+ i+q   G ++ E
  gi|2191205    72    SSDA---TSIPSNEADRDIQLRADIKVMGSLLgRIIQTHEGAEVLEK 115

                    vqECYElsAeYEGK...kDtk.......KLeELGakLtsLdPaDailvAk
                    v     l+  +  ++ ++D+++++  ++  + L a   s   a+   v +
  gi|2191205   116 VETMRGLAKTWRDQgagRDPStkqaadqTFQNLAAYAKSFTDAELFTVSR 165

                    ailHmLnLAnLAEEvelAyR.RRikkkkhGDFaDEasAttE...sDiEEt
                    a+ H L +An AE     +R+RR k+ +    +DE+s    +++  +
  gi|2191205   166 AFTHFLAIANAAES---HHRgRRLKQSR--LLSDESSGALYpkpDSVGGV 210

                    lKkLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnC
                    l  L  ++    + +++AL  q+ +LvltAHPt   RR +L K+ Ri
  gi|2191205   211 LPSLLAQG-HDADAIYDALTSQTTELVLTAHPTEVNRRTILNKKRRIQRI 259

                    La......qLsAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDE
                    L+  ++++qL A  v   ++ EL +AL REi   +  DE+ R +P P  E
  gi|2191205   260 LTmadqqrQLGASSVF--EQAELNDALYREISSIWLSDEVSRIKPSPETE 307

                    mRaGmsYiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmG
                       G   +   +W+ vP FLR+ D   +   +   lP d   i+F+sWmG
  gi|2191205   308 AEKGTLVLETVLWEAVPTFLRKLDATTREF-LGKPLPLDSSPIRFASWMG 356

                    GDRDGknPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndEL
                    GDRDG nP v P+ tR vCL  R  Aa l+   +  L  Els+  C  E+
  gi|2191205   357 GDRDG-NPNVKPDTTRQVCLRNRQKAATLFARNLRTLEAELSLTTCSREV 405
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                    RvRAEElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRER
                    R    E+   a+      y i     +   E       +  +     + R
  gi|2191205   406 R----EVVGAAREP----YRIFLQPMIRKMEA--TTDWAAQELAILQKRR 445

                    aRHLLAtGiseisE...eAvytkvEeFLEPLELCYksLCeCGDkviADGs
                    +    A Gi+ ++ ++ e +y + EeF   L   Y+sL e G  v A G
  gi|2191205   446 SGDKSASGIASVAStnvEGIYLDQEEFRAELLTIYRSLQETGNEVAASGI 495

                    LLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeK
                    L D++R  s FGL L+ LD+RqEs+R+ + lDAit+ L++GsY +W E+
  gi|2191205   496 LTDIIRNLSSFGLTLIPLDVRQESDRHEEALDAITRYLGLGSYIQWDEQT 545

                    RqEWLlaELkGKRPLlgsDLPktE......EvkDvldafrvLAELPiDsF
                    R  WL + ++ KRPLl + +    ++  ++   D l+  r++AE    s
  gi|2191205   546 RVSWLTTQISSKRPLLRAGVWYEHpdyfspTAIDTLEISRMIAEQHEGSL 595

                    GaYiismataPsDvLAvELLqRECgvkqtLrvvPLFEkLADLeAAPAave
                    GaY+is at+ sDvLAv LLq + gvk++Lrv PLFE L DL+ A  ++
  gi|2191205   596 GAYVISQATSASDVLAVLLLQLDAGVKKPLRVAPLFETLDDLNGAADTMR 645

                    kLFsiDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                    +LFs+  Y+  i GKqevm+GYsDs KDAGR++A W  Y  qE ++K AK
  gi|2191205   646 QLFSLPAYMGTIGGKQEVMIGYSDSAKDAGRMAATWAQYETQETLAKLAK 695

                    kyGvKLvlFHGRGGtvGRGGGP.tHLAiLsqPPDtinGslRvtvqGEviE
                    ++Gv ++ FHG+GGtvGRGG P+t  Ai++  P tinG  Rvt qGE+i
  gi|2191205   696 EFGVDMTFFHGKGGTVGRGGNPqTFTAIMAHAPKTINGHFRVTEQGEMIS 745

                    fsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEY
                    + FG  +   r++  +tAA L   +      k EWR +m  +  +  E Y
  gi|2191205   746 QNFGYADRAERTMDIYTAAVLAEKLSERPKVKDEWRSMMKILSDISCEAY 795

                    RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWi
                    R vv K+ RFv YFR+AtPElE   +niGsRPaKRk  GG+esLRAiPW
  gi|2191205   796 RQVVRKDERFVPYFRSATPELELSNLNIGSRPAKRKATGGVESLRAIPWN 845

                    FaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDL
                    FaWtqtRF LP WLGvG A    ++ D   l  L+E+Y+e   F   +DL
  gi|2191205   846 FAWTQTRFNLPTWLGVGDAIGQLLKSDRAPL--LRELYREARAFQTMVDL 893

                    lEmvFAKGDPGiAaLyDkLLvaE.eLkPFGksLRdkYvEtkdlLLkiAGH
                    +Emv AK +P iAa yD +Lv ++  k  Gk++R+    t++ +L +  H
  gi|2191205   894 VEMVLAKSEPAIAAHYDSVLVKDpKAKELGKEVRQLHMATEEAILDLTEH 943

                    kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                    k l E    L+  l +R++Y+  Ln++q  tL R+R
  gi|2191205   944 KKLGENNAVLQRALVVRNPYVDCLNILQVETLDRLRQ------------- 980

                    EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       +E   k d ++k            D L+ t+ G+A Gm ntG
  gi|2191205   981 --VEEG--KEDKVLK------------DALLTTITGVANGMGNTG    1009

gi|59936824|gb|AAX12115.1|: domain 1 of 1, from 1 to 492: score 690.6, E = 1.3e-204
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|5993682     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|5993682     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|5993682     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|5993682     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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                                                Y+HEt+WkGvPKFLR
  gi|5993682     1 ----------------------------------YFHETIWKGVPKFLR 15

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALKniGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|5993682    16 RVDTALKNIGINERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 64

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmAanlY  q+EDLmFElsmWRCndELR+RA+El+r +++d   K+Yi
  gi|5993682    65 ARMMAANLYCAQIEDLMFELSMWRCNDELRARADELHRSSKKD--AKHYI 112

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWK+vPP+EPYRviLGdvRD LYntRER+R LL  G s+i+EeA  t++
  gi|5993682   113 EFWKKVPPNEPYRVILGDVRDNLYNTRERSRELLSSGHSDIPEEATLTNL 162

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   E+ LEPLELCY+sLC CGD+viADG LLD+LRqvstFGLsLvKLDiRqEs
  gi|5993682   163 EQLLEPLELCYRSLCACGDRVIADGTLLDFLRQVSTFGLSLVKLDIRQES 212

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +R+tD lDAit  L+iGsYReWsEe+RqEWLl+EL GKRPL+g+DLP+tE
  gi|5993682   213 DRHTDALDAITSYLGIGSYREWSEERRQEWLLSELNGKRPLFGADLPMTE 262

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dv++af+v+AELP D FGaY+ismat+PsDvLAvELLqREC++k +L
  gi|5993682   263 EVADVMGAFQVIAELPGDNFGAYVISMATSPSDVLAVELLQRECHIKTPL 312

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAa+++LFsiDWY+ ri+GKqevm+GYsDsGKDAG
  gi|5993682   313 RVVPLFEKLADLEAAPAALARLFSIDWYRERINGKQEVMIGYSDSGKDAG 362

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWq+YkAqE+++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|5993682   363 RLSAAWQMYKAQEDLVKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 412

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PP+sP
  gi|5993682   413 PPDTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPISP 462

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L++emAvvAtEEYRs+v++EPRFv
  gi|5993682   463 KPEWRALLDEMAVVATEEYRSIVFQEPRFV---------------------- 492

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|5993682     - ------------------------------------------------- -

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|5993682     - ------------------------------------------------- -

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|5993682     - ------------------------------------------------- -

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|5993682     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|5993682     - -------------    -

gi|283896816|emb|CAX65709.1|: domain 1 of 1, from 1 to 503: score 689.7, E = 2.5e-204
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838968     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838968     - ------------------------------------------------- -
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                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|2838968    - ------------------------------------------------ -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|2838968    - ------------------------------------------------ -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|2838968    - ------------------------------------------------ -

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|2838968    - ------------------------------------------------ -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|2838968    - ------------------------------------------------ -

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|2838968    - ------------------------------------------------ -

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|2838968    - ------------------------------------------------ -

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  +tDv+DAit+ L+iGsYReWsEeKRqEWLl+EL GKRPL+g+DLPk
gi|2838968    1 --HTDVMDAITKYLGIGSYREWSEEKRQEWLLSELNGKRPLFGPDLPKSG 48

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                E++Dvld+++v+AELP+DsFGaY+ismataPsDvLAvELLqREC+vk++L
gi|2838968   49 EIADVLDTLHVIAELPSDSFGAYVISMATAPSDVLAVELLQRECHVKKPL 98

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                rvvPLFEkLADLeAAPAa+++LFs++WY+ ri+GKqevm+GYsDsGKDAG
gi|2838968   99 RVVPLFEKLADLEAAPAALARLFSVEWYRHRINGKQEVMIGYSDSGKDAG 148

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                R+sAAWqLYkAqEE+iKvAK yGvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|2838968  149 RFSAAWQLYKAQEELIKVAKLYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PP+ti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
gi|2838968  199 PPETIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 248

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                kPEWR Lm+emAvvAt EYRs+v+ EPRFvEYFRlAtPElEYG+mn GsR
gi|2838968  249 KPEWRALMDEMAVVATKEYRSIVFEEPRFVEYFRLATPELEYGRMNTGSR 298

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+K kPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++K i+nl
gi|2838968  299 PSKGKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLEKGIRNL 348

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                q L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+EeL+PFG++
gi|2838968  349 QTLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEELWPFGER 398

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR +Y+Etk+lLL++AGHkD+LEGDPYLKqrl +RdsYit Lnv+qA  L
gi|2838968  399 LRSNYEETKKLLLQVAGHKDILEGDPYLKQRLHIRDSYITALNVCQACAL 448

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                KRiRDP ++v +rPhlsK+  d   k+a+eLvkLn t+++aPGLEDtLiL
gi|2838968  449 KRIRDPGFQVKPRPHLSKDIMDSG-KPAEELVKLNTTSEYAPGLEDTLIL 497

                tmKGiAAGmqntG<-*
                tmKGiA
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  gi|2838968   498 TMKGIA-------    503

gi|283896794|emb|CAX65698.1|: domain 1 of 1, from 1 to 504: score 689.4, E = 3.1e-204
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838967     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838967     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838967     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838967     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838967     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838967     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838967     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838967     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838967     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDv+DAit  L+iGsYR+W+EeKRqEWLl+EL GKRPL+g+DL ktE
  gi|2838967     1 --HTDVMDAITNYLGIGSYRDWPEEKRQEWLLSELNGKRPLFGPDLLKTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E+++vld+f+vLAELP DsFGaY+ismataPsDvLAvELLqREC+vk++L
  gi|2838967    49 EIAEVLDTFHVLAELPADSFGAYVISMATAPSDVLAVELLQRECHVKKPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAa+++LFs+ WY+nri+GKqevm+GYsDsGKDAG
  gi|2838967    99 RVVPLFEKLADLEAAPAALARLFSVQWYRNRINGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   R+sAAWqLYkAqE++iKvAK +GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838967   149 RFSAAWQLYKAQEDLIKVAKSHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP+ti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2838967   199 PPETIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emAvvAt EYRs+v+ EPRFvEYFRlAtPE+EYG+ niGsR
  gi|2838967   249 KPEWRALMDEMAVVATKEYRSIVFEEPRFVEYFRLATPEMEYGRTNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGie+LRAiPWiFaWtqtRFHLPvWLG+GAAF h ++KDi+nl
  gi|2838967   299 PSKRKPSGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFEHVLNKDIRNL 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q L+EmY+eWPFFRvt+DL EmvFAKGDPGiAaLyDkLLv+ +L+ FG++
  gi|2838967   349 QTLQEMYNEWPFFRVTIDLAEMVFAKGDPGIAALYDKLLVSQDLWSFGER 398
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                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y Etk+ LLk+AGHkDlLEGDPYLKqrlR+RdsYit Lnv+qAYtL
  gi|2838967   399 LRANYDETKQRLLKVAGHKDLLEGDPYLKQRLRIRDSYITALNVCQAYTL 448

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP +++  rPhlsK+   +  k+a++LvkLn t+++aPGLEDtLiL
  gi|2838967   449 KRIRDPGFQMNTRPHLSKDIIMDSGKPAADLVKLNTTSEYAPGLEDTLIL 498

                    tmKGiAAGmqntG<-*
                    tmKGiA
  gi|2838967   499 TMKGIA-------    504

gi|192361093|ref|YP_001983406.1|: domain 1 of 1, from 3 to 871: score 688.7, E = 4.8e-204
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                  K    e L e   LL +   + +    G dL + v
  gi|1923610     3    ------------KLP--ETLRENVRLLGELLGETIHAHEGADLFDKV 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         +       +       L + L sLd  D + + +a+   LnLAn+
  gi|1923610    36 EKIRQVGKAINQAENGDS-APLVTMLSSLDDKDVLPIVRAFNQFLNLANI 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkl..nKsPe
                    A+                    E     Es+ ++ l+ L  +l ++K  +
  gi|1923610    85 ADQ------------------EYFSSAESEGDDKLQILLQQLaeEKGKD 115

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                         +    ++LvltAHPt   RR L+ K   i   La      +   +
  gi|1923610   116 ALAGVIGKLRIELVLTAHPTEVTRRTLIRKYDQIVDTLADRQNPSLLNFE 165

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    +  L   LHR +   + tDEiR  +Pt  DE + G + i   +W+ vP F
  gi|1923610   166 QDKLRGRLHRLVEEIWATDEIRAIRPTAVDEAKWGFAVIENSLWQAVPDF 215

                    LRRvD.tALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    +R  D+   + +G    lP      kF sWmGGDRDG nP vt  +tR+v
  gi|1923610   216 IRHLDrVCARHLG--RSLPSSLRPFKFYSWMGGDRDG-NPNVTHKITREV 262

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                     LL R mAa lY   +  L  +lsm   n+ELR+    ly  + +
  gi|1923610   263 LLLGRWMAAELYARDIYNLGGDLSMSEANSELRA----LY--PDSA---- 302

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                                PYR  + d R ++  t E a   L     e + + +
  gi|1923610   303 ------------TPYRDAMYDLRKRIQSTLEWAEARLQGRNIESPADLI- 339

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                    t  E+ L  L LC+ sL e     iA G LLD +R v  FG+ Lv LDiR
  gi|1923610   340 TSREDLLGILNLCFNSLNEVDLPHIANGPLLDTIRRVHCFGINLVPLDIR 389

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    q+ eR+   +D + + Le+G YR+WsEe Rq +Ll  L+ KRPL++   P
  gi|1923610   390 QDGERHVQAIDELVQYLELGNYRNWSEEERQSFLLDALQSKRPLMPHNWP 439

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                    + ++ ++vl + r++AE P +    Yiisma  PsDvLAv LL +ECg+
  gi|1923610   440 MSDDTAEVLATCRIIAEEPREILSHYIISMAQQPSDVLAVALLLKECGMT 489

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                      +++vPLFE L DL+ AP  +++L+ +DWY      +q +m+GYsDs K
  gi|1923610   490 WNMPIVPLFETLDDLDRAPSVMDRLWELDWYQEYSSHQQTIMIGYSDSAK 539

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG+lsA W  YkAqE ++  A ky v +vlFHGRGGtvGRGGGP   A+
  gi|1923610   540 DAGKLSATWAQYKAQEKLVALADKYKVSMVLFHGRGGTVGRGGGPVEKAM 589

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                     sqPP  ++G +Rvt qGE+i + FG   + F+sL  +  AtL   + P
  gi|1923610   590 ASQPPGSVKGRIRVTEQGEMIRYKFGLPRVAFKSLSSYLVATLRATLSPN 639

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                     +Pk EWR+L+e+m     E YRsvv     Fv YFR  tPE E   + +
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  gi|1923610   640 AAPKAEWRDLIERMGTASLEGYRSVVRGHKDFVPYFRNLTPEQELSLLAL 689

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRPaKRk  GG+esLRAiPW+FaWtq R  LP WLG   A  +A+  D
  gi|1923610   690 GSRPAKRKSTGGVESLRAIPWVFAWTQVRLNLPAWLGTRQAIEYALTNDP 739

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                         L Em  +WPFF   +DLlEmv  K D  i + y++ Lv  e +
  gi|1923610   740 ---ELLDEMMANWPFFSSFIDLLEMVVGKADGPICTYYEQQLVPAEYRGL 786

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G++LR +    ++lL  +     lL  DP L+q l +R +Y+  Ln +qA
  gi|1923610   787 GEQLRGDLASLEQLLNTLKKQDVLLSDDPMLRQSLEVRKPYVAPLNYLQA 836

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      LKR R                  En               ++P LE
  gi|1923610   837 ELLKRYR----------------SSEN---------------ISPDLERA 855

                    LiLtmKGiAAGmqntG<-*
                    L +tm GiAAGm ntG
  gi|1923610   856 LKVTMAGIAAGMRNTG    871

gi|88706831|ref|ZP_01104531.1|: domain 1 of 1, from 11 to 885: score 688.0, E = 8.3e-204
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         D   R L    vs          LL     + +   HGed    v
  gi|8870683    11    DNDHPYRSLR-NNVS----------LLGSMLGETMAQSHGEDFLASV 46

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls      +D +  e L a L + +      vA+a+   LnLAn+
  gi|8870683    47 ERIRLLSKSGSNGEDRS-WEQLEALLAGFETEQLGRVARAFAQFLNLANI 95

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE           + +  D    as t    +   +  L  k+   P+ +
  gi|8870683    96 AE-------QHHGLSREMDTVNSASRT----LTGVMDLLEDKG-LDPAAI 133

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      A+   s++LvltAHPt   RRsL+ K   i  CL qL    +t  ++
  gi|8870683   134 RAAVSDLSIELVLTAHPTEITRRSLIHKYEEIQRCLGQLESPGLTNYERS 183

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +D  L   i   + t E R  +P P DE R G + +   +W+ vP FLR
  gi|8870683   184 RMDRRLRELIAQLWHTHEFREHRPSPVDEARWGYAVVENSLWQAVPDFLR 233

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R D AL      ERlP d+  ++FssWmGGDRDG nP vt  vtR+v LL
  gi|8870683   234 RLDDALVA-ATGERLPLDAAPVQFSSWMGGDRDG-NPFVTAKVTREVLLL 281

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                     R  Aa lY+  v+ L+ Elsm  Cn  LR   E +  t
  gi|8870683   282 GRWQAAALYVKTVDRLVQELSMIECNAALR---EYVGDT----------- 317

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                            EPYR  + + R +L n       LL    ++  E     +
  gi|8870683   318 --------REPYRHAMKNLRRRLRNWLTALEALLDGRGAD--EGDLLQDA 357

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    Ee   PL LCY+sLC+CG   iADG LLDlLRq   FG+ Lv+LDiRq s
  gi|8870683   358 EEISKPLMLCYQSLCDCGMERIADGTLLDLLRQLRCFGVNLVRLDIRQHS 407

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+   l  it+ L++G Y +W Ee+R++W+  EL+ +RPL++      E
  gi|8870683   408 DRHSAALTEITEFLGLGRYVDWDEEQRRDWIRQELESRRPLIPQHWSPSE 457

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E ++vld   v+ E P D+   Yiisma   sDv+Av LL +  g   +L
  gi|8870683   458 ETREVLDCCAVVVEQPADALACYIISMARQASDVMAVRLLLKAAGGGDSL 507

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    ++ PLFE L DL+ AP  +  L +++    r+  +q vm+GYsDs KDAG
  gi|8870683   508 PIAPLFETLDDLDRAPQVITDLLAVEKALGRLPEQQMVMIGYSDSAKDAG 557
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                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     l+AAW  Y+AqE +  v  k Gv+L lFHGRGGt+GRGG P H A+Lsq
  gi|8870683   558 ILAAAWAQYRAQEALLEVCEKAGVRLQLFHGRGGTIGRGGAPAHDALLSQ 607

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  ++  lRvt qGE+i    G   L  ++L  +t A LE     P  P
  gi|8870683   608 PPGSLECGLRVTEQGEMIRTKLGMTGLAVKTLALYTSAILEARTAHPPTP 657

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                       WR+ m+++A    + YR+vv  +PRF  YFR AtPE E G + + sR
  gi|8870683   658 MAHWREAMDRLASHSCDAYRAVVRDDPRFLTYFREATPEGELGALPLASR 707

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+ Rk  GGie+LRAiPWiF+Wtq R  LP WLG GAA   A + + +
  gi|8870683   708 PTSRKKDGGIEALRAIPWIFSWTQNRLMLPSWLGAGAAL--ARELEAQGE 755

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      + Em++eWPFF   + +lEmv+ K D  i a yD  Lv  eL+  G++
  gi|8870683   756 TVITEMFREWPFFATRMQMLEMVYSKTDARISAHYDSKLVNPELRVIGEQ 805

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +       +L i     lLE   + +  l LR+ Y   Lnv+qA  L
  gi|8870683   806 LRSQLDNDVATVLSILKQEQLLEKLDWTRESLELRNIYTVPLNVLQAELL 855

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     R+R               Ad++  + + ++ +
  gi|8870683   856 ARLRQK--------------ADDD-TRQAIMISIA--------------- 875

                    tmKGiAAGmqntG<-*
                       G+AAGm ntG
  gi|8870683   876 ---GVAAGMRNTG    885

gi|283896798|emb|CAX65700.1|: domain 1 of 1, from 1 to 503: score 687.6, E = 1.1e-203
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838967     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838967     - ------------------------------------------------ -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838967     - ------------------------------------------------ -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838967     - ------------------------------------------------ -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838967     - ------------------------------------------------ -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838967     - ------------------------------------------------ -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838967     - ------------------------------------------------ -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838967     - ------------------------------------------------ -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838967     - ------------------------------------------------ -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDvlDAittHL++GsYReWsEe+RqEWLl+EL GKRPL+gsDLP+ E
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  gi|2838967     1 --HTDVLDAITTHLGLGSYREWSEERRQEWLLSELNGKRPLFGSDLPRSE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvld+f+v+AELP DsFGaY+ismat+PsDvLAvELLqRE  +k +L
  gi|2838967    49 EVADVLDTFKVIAELPADSFGAYVISMATSPSDVLAVELLQRESRIKAPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLe AP a+++LFsiDW + r++GKqevm+GYsDsGKDAG
  gi|2838967    99 RVVPLFEKLADLESAPTALARLFSIDWHRARVNGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWq+YkAqE+++KvA+++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838967   149 RLSAAWQMYKAQEDLVKVAQQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PP+sP
  gi|2838967   199 PPDTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPISP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L++emAvvAtEEYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|2838967   249 KPEWRALLDEMAVVATEEYRSIVFQEPRFVEYFRLATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++KDi+n+
  gi|2838967   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHILKKDIRNF 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY+eWPFFRvt+DL+EmvFAKG PGiAaLyD+LLv+EeL+P G++
  gi|2838967   349 HMLQEMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDRLLVSEELQPLGEK 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Et++lLL++AGHkDlLEGDPYLKqrlRLRd+Yitt+nv+qAYtL
  gi|2838967   399 LRANYEETQQLLLQVAGHKDLLEGDPYLKQRLRLRDAYITTMNVCQAYTL 448

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y+v lrPhlsKE  d   k a eLv Lnp++++aPGLEDtLiL
  gi|2838967   449 KRIRDPDYHVALRPHLSKEVMDTS-KLASELVTLNPASEYAPGLEDTLIL 497

                   tmKGiAAGmqntG<-*
                   tmKG+A
  gi|2838967   498 TMKGVA-------    503

gi|283896824|emb|CAX65713.1|: domain 1 of 1, from 1 to 503: score 686.0, E = 3.2e-203
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838968     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838968     - ---------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838968     - ---------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838968     - ---------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838968     - ---------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838968     - ---------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838968     - ---------------------------------------------------- -
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                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838968     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838968     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDvlDAitt L+iGsYReWsEe+RqEWLl+EL GKRPLlg+DLP+t+
  gi|2838968     1 --HTDVLDAITTYLGIGSYREWSEERRQEWLLSELNGKRPLLGPDLPMTD 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dv++afrv+AELP D FG+YiismataPsDvLAvELLqREC+vk +L
  gi|2838968    49 EVADVIGAFRVIAELPADNFGPYIISMATAPSDVLAVELLQRECHVKTPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADL+ APAav +LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|2838968    99 RVVPLFEKLADLQGAPAAVTRLFSVDWYRERINGKQEVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+  vAK++GvKL++FHGRGGtvGRGGGPtHLA L+q
  gi|2838968   149 RLSAAWQLYKAQEELTNVAKQFGVKLTMFHGRGGTVGRGGGPTHLATLAQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP tinGslRvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2838968   199 PPNTINGSLRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPMSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++emAvvAt EYRs+v++EPRFvEYFRlAtPE+EYGkmniGsR
  gi|2838968   249 KPEWRALLDEMAVVATKEYRSIVLQEPRFVEYFRLATPETEYGKMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGi+sLRAiPWiF+WtqtR HLPvWLG+GAAFKh ++KD +n+
  gi|2838968   299 PSKRKPSGGITSLRAIPWIFSWTQTRLHLPVWLGFGAAFKHVLEKDNRNM 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+EmY eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+ eL+PFG++
  gi|2838968   349 HVLQEMYSEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSPELWPFGEK 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR +Y+Etk lLL++AGHkDlLEGD YLKqrlRLR++YittLnv+qAYt+
  gi|2838968   399 LRTNYEETKRLLLQVAGHKDLLEGDLYLKQRLRLRQAYITTLNVCQAYTM 448

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDP+y+vtlrPhlsKE  d n k+a+eLvkLnpt+++aPGLE tLiL
  gi|2838968   449 KRIRDPDYHVTLRPHLSKEIMDWN-KPAAELVKLNPTSEYAPGLEGTLIL 497

                  tmKGiAAGmqntG<-*
                  tmKGiA
  gi|2838968   498 TMKGIA-------    503

gi|283896802|emb|CAX65702.1|: domain 1 of 1, from 1 to 503: score 682.0, E = 5.2e-202
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838968     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838968     - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838968     - ------------------------------------------------ -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838968     - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|2838968     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838968     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838968     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838968     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838968     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDvlDAitt L+iGsYReW+Ee+RqEWLl+EL GKRPL+g DLPktE
  gi|2838968     1 --HTDVLDAITTYLGIGSYREWPEERRQEWLLSELNGKRPLFGLDLPKTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvld+f+v+AELP D FGaYiismataPsD LAvELLqREC+vk +L
  gi|2838968    49 EVADVLDTFHVIAELPADNFGAYIISMATAPSDALAVELLQRECHVKTPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvP FEkLADLeAAPAa+++LFsiDWY+ ri+GKqevm+GYsDsGKDAG
  gi|2838968    99 RVVPPFEKLADLEAAPAALARLFSIDWYRQRINGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAA   YkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838968   149 RLSAAXXXYKAQEELIKVAKDFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP +P
  gi|2838968   199 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPNAP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L++emAvvAtEE Rs+++KEPRFvEYFRlAtPE+EYG+mniGsR
  gi|2838968   249 KPEWRALLDEMAVVATEEHRSIIFKEPRFVEYFRLATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRA PWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|2838968   299 PSKRKPSGGIESLRATPWIFAWTQTRFHLPVWLGFGAAFKHVLQKDIRNL 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+E+L+P G++
  gi|2838968   349 HMLQEMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEDLQPLGEK 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Et++lLL++AGH+DlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|2838968   399 LRANYEETQKLLLQVAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 448

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiR  +y+v lrPhlsKE  d   k+a+eLvkLnp++++aPGLEDtLiL
  gi|2838968   449 KRIRGLDYHVALRPHLSKEIMDSS-KPAAELVKLNPASEYAPGLEDTLIL 497

                   tmKGiAAGmqntG<-*
                   tmKGiA
  gi|2838968   498 TMKGIA-------    503

gi|114772589|ref|ZP_01449953.1|: domain 1 of 1, from 6 to 878: score 674.5, E = 9.2e-200
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       iDAqL+  v               Ll k   i  +L  e L  +
  gi|1147725     6    YIDAQLKHTVRDLGE-----------LLGK--TIKHELGQEWLDKI- 38

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    E   l        D++    L +    ++    ++vA+a+   LnLAn+
  gi|1147725    39 -EAIRLQGRAGHTGDSQANMALQSIFNDMNTDSLLVVARAFAQFLNLANI 87
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                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AE         ++ k+            +  +E  + +L   + +sPe +
gi|1147725    88 AE------QEFNSSKQ-----------LDDSVEVLFSHLRKAG-QSPEAI 119

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                +eA+    +DLvltAHPt   RR ++ K++ +  CL q     + +  K
gi|1147725   120 YEAVNSLNIDLVLTAHPTEVTRRTMIHKHTALAECLRQQHNDSLHPAQKL 169

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                 L E +   +   + t+EiR  +PtP DE   G s i   +W+ +P F+R
gi|1147725   170 QLAERIADLVEQSWHTEEIRDRRPTPVDEATWGFSVIENSLWDAIPDFMR 219

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                  D  L+      +lP d+  ++ ssWmGGDRDG nP vt  vt  v  L
gi|1147725   220 DLDLKLQQ-EYDIKLPIDAQPVQISSWMGGDRDG-NPFVTSKVTQTVLHL 267

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                aR  Aa l+   +  L  Elsm +C d +R      +
gi|1147725   268 ARRRAAKLFAKDISALQVELSMGKCDDNVR------QLVGDAA------- 304

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                         EPYR +L     +L  t++    LL   + + s
gi|1147725   305 ---------EPYRALLKPLVKRLRATKDGIDDLLNGRLYDQSK--WVNSQ 343

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                Ee L PL  CY+sL   G    A G LL  +R    FG+ L KLDiRq+s
gi|1147725   344 EELLTPLMQCYRSLLHSGLEQTAKGGLLNTIRRAHCFGIYLLKLDIRQDS 393

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk..
                 R+ D +  i   L iG Y +W E  +  +L  EL  KRPLl+ D   +
gi|1147725   394 GRHADAIAEICDYLSIGDYHSWNEAEKIAFLTKELGSKRPLLPNDWQAdw 443

                ..tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                ++ E+v++vld+ r +A    D+FG Yiisma   sDvLAv LL   C+v
gi|1147725   444 qpSEDVQEVLDTCRTVAANDRDAFGIYIISMASYASDVLAVQLLLQQCKV 493

                kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsG
                  ++ v PLFE L DL+  P  +++L +iD Y+n +   q++m+GYsDs
gi|1147725   494 TWPMSVAPLFETLDDLNHSPVVIKQLLAIDSYRNGLADGQHIMIGYSDSA 543

                KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                KDAG l+A W  Y AqE ++ +  +y   L+lFHGRGGt+GRGG P H A
gi|1147725   544 KDAGALAAGWAQYTAQEALVSICNQYDTSLTLFHGRGGTIGRGGLPAHSA 593

                iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP
                iLsqPP  ++G  Rvt qGE i + FG   L  rsL  ++ A +E  + P
gi|1147725   594 ILSQPPGSLDGGFRVTEQGETIRYKFGMPTLAKRSLGIYASAIIEAKLFP 643

                PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmn
                P +Pk  WR++++emA    + YR vv  +P Fv YFR AtPE E Gk+
gi|1147725   644 PPAPKSTWRDVLDEMAAQGRDNYRHVVRVDPDFVPYFRQATPEQELGKLP 693

                iGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                +GsRPaKR P GG+esLRAiPWiFaW qtR  LP WLGv  A     +KD
gi|1147725   694 LGSRPAKRNPQGGVESLRAIPWIFAWAQTRLVLPAWLGVMRAIMKTYKKD 743

                iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP
                      + Em  +WPFF   l +l+mvFAK D  iA  yD+ Lv +eLk
gi|1147725   744 P---NTIDEMIAQWPFFQSRLSMLDMVFAKADINIAKAYDDALVEDELKH 790

                FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfq
                FG+sLR + +  +  LL i     l+  DP     + +R  Y+  L  +q
gi|1147725   791 FGESLRHELQQSRADLLDITHKNNLMQDDPQGLNSMHIRADYLQPLHYLQ 840

                AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                   LKR R               + ++          L         +E
gi|1147725   841 IELLKRTR--------------QHGEDT--------DLS-------AIEK 861

                tLiLtmKGiAAGmqntG<-*
                 +++t+ GiA Gm ntG
gi|1147725   862 AMMVTITGIAIGMRNTG    878
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gi|283896820|emb|CAX65711.1|: domain 1 of 1, from 1 to 503: score 669.3, E = 3.3e-198
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2838968     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2838968     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2838968     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2838968     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2838968     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2838968     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2838968     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2838968     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2838968     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tD +DAit+ L+iGsYReWsEeKRqEWLl+EL GKRPL+g+DLPk +
  gi|2838968     1 --HTDAMDAITKYLGIGSYREWSEEKRQEWLLSELNGKRPLFGPDLPKSD 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++Dvld+++v+AELP+DsFGaY+ismataPsDvL vELLqREC++k++L
  gi|2838968    49 EIADVLDTLHVIAELPSDSFGAYVISMATAPSDVLVVELLQRECHLKKPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLeAAPAa+++LFs++WY+nrid Kqevm+GYsDsGKDAG
  gi|2838968    99 RVVPLFEKLADLEAAPAALARLFSVEWYRNRIDSKQEVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  R+sAAWq YkAqEE+iKvAK yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2838968   149 RFSAAWQPYKAQEELIKVAKLYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP+ti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|2838968   199 PPETIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+em vvAt EYRs+v+ EPRFvEYFRlAtPElEYG+mniGsR
  gi|2838968   249 KPEWRALMDEMDVVATKEYRSIVFEEPRFVEYFRLATPELEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|2838968   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLEKDIRNL 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+ +L+PF ++
  gi|2838968   349 QTLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSKDLWPFSER 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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                  LR + +Etk+lLLk+AGHkD+LEGDPYLKqrl + dsYit Lnv+qA tL
  gi|2838968   399 LRSNHEETKKLLLKVAGHKDILEGDPYLKQRLHICDSYITALNVCQACTL 448

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDP ++v +rPhlsK+      k+a+eLvkLn t+++aPGLEDtLiL
  gi|2838968   449 KRIRDPGFQVKPRPHLSKDIMVSG-KPAEELVKLNTTSEYAPGLEDTLIL 497

                  tmKGiAAGmqntG<-*
                  tmKG+A
  gi|2838968   498 TMKGVA-------    503

gi|219125106|ref|XP_002182829.1|: domain 1 of 1, from 1 to 877: score 667.8, E = 9.9e-198
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      iDA
  gi|2191251     1    MIDA------------------------------------------ 4

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                                         +kLt+   ++a+ v + ++ mLnL n
  gi|2191251     5 ----------------------ASKLTA---TEALGVTRVFSIMLNLVN- 28

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  A Ev+   R         D +      tE  i  t+  L    + +PeE+
  gi|2191251    29 AAEVQHRNRQIRAHESTKDPSGGPLPKTEDSIRGTMETLLESKQATPEEI 78

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                  F  L+ q v++vltAHPtq  R+sLL K  R+   La L   D+   +K
  gi|2191251    79 FAQLQKQKVEIVLTAHPTQVQRKSLLRKYRRVSEMLAYLERPDLDGFEKS 128

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                       L   +   +  DEiRR +PtPq E   G + +   +W+ vP +LR
  gi|2191251   129 SAQTSLQTILSSIWGADEIRRQKPTPQQEAAGGNAILESVLWDAVPAYLR 178

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                  + D   + + +   lP dv  ikF+sW+GGDRDG nP vtPEvtR+v L
  gi|2191251   179 KLDQQCR-LTLGQSLPVDVCPIKFASWIGGDRDG-NPNVTPEVTREVVLQ 226

                  aRmmAanlYisqvEDLmFElsm.WRCndELRvRAEElyrtaardkvvKyY
                   R+ Aa l +  + DL+ El+++ R    + + A+ ++    +
  gi|2191251   227 QRLRAARLLLKDMYDLISELAIsSRFSPAMDALADSVKDSQHKR------ 270

                  iEFWKqvPPtEPYRviLGdvRDKLYnt.RERaRHL..LAtGiseis....
                            E YR ++G    +L  t RE    L++L t  s +s++
  gi|2191251   271 ----------EKYRRVIGHLIKRLVKTaRECELELskLNTSASMVSqtlv 310

                  EeAv..ytkvE......eFLEPLELCYksLCeCGDkviADGsLLDlLRqv
                  EeAv+++ +v+  ++ ++ + PL + Y sL e G   +ADG L+D++R
  gi|2191251   311 EEAVdgWQDVDalddatDLIKPLRIMYDSLVETGFGLVADGLLVDIIRRL 360

                  stFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaE
                  + FG+sLv LDiR Es ++t+ lDAit+ L+iGsY eW Ee R  WL +E
  gi|2191251   361 YVFGMSLVPLDIREESTKHTEALDAITRWLGIGSYSEWTEEARLSWLTSE 410

                  LkGKRPLlg.sDLPktEEvkDvldafrv...LAELPiDsFGaYiismata
                  L+ KRPL+   +LPk      vl +++v +++A L   + GaY+is a +
  gi|2191251   411 LSNKRPLYRiRELPKLGFNDSVLKTLNVfgtIATLRPSCLGAYVISQAQT 460

                  PsDvLAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLFsiD
                   sDvLAv LLq+  g+++++++ +rvvPLFE L DL  AP  +e+LFsi
  gi|2191251   461 ASDVLAVMLLQKQYGMtdknRNMMRVVPLFETLNDLTNAPDKLEQLFSIP 510

                  WYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                   Y+  + GKqevmvGYsDs KDAGRl+A W  Y  qE ++KvA k+ + L
  gi|2191251   511 LYVGAVKGKQEVMVGYSDSAKDAGRLAACWAQYNSQERMVKVAAKHNIEL 560

                  vlFHGRGGtvGRGGGP.tHLAiLsqPPDtinGslRvtvqGEviEfsFGEE
                  + FHG+GGtvGRGG P+   Ai+s PP tinG  Rvt qGE+i + FG
  gi|2191251   561 TFFHGKGGTVGRGGNPsVYRAIMSHPPNTINGRFRVTEQGEMITQNFGAP 610

                  nLCFrsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvK
                   +  r+L  +tA          v P   WR+ m+++  v   EYR +v
  gi|2191251   611 SIAERTLDIYTAGVCREAFSERVEPSQAWRDQMQRISDVSCAEYRHLVRE 660
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                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                    EPRFv YFR AtPElE G +niGsRPaKR P GGiesLRAiPW FaWtqt
  gi|2191251   661 EPRFVPYFRQATPELELGSLNIGSRPAKRNPKGGIESLRAIPWTFAWTQT 710

                    RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                    R HL  WLGvGA        D   l+ L+ mY eWP+FR t+DL+ m+
  gi|2191251   711 RTHLSAWLGVGAGLTTT---DQSELKTLRAMYIEWPWFRETIDLIAMIVS 757

                    KGDPGiAaLyDkLLva..EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE
                    K D  i   yD+ Lv ++E L   G+++R+k v t++ +L +    D+
  gi|2191251   758 KTDFSISKNYDDQLVEkkEGLLKLGDEVREKMVQTRQAVLDVTESTDVAG 807

                    GDPYLKqr.lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                        L  ++  +R +Y+  +nv+qA  LKR+R  + k  l        Ad
  gi|2191251   808 AHVALMRGsSTIRHPYVDPVNVIQAELLKRLRVMDKKKSL-------LAD 850

                    EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    E   + +e++k            D Li+ + GiA Gm n G
  gi|2191251   851 EM--EEQEILK------------DALIISINGIAQGMRNSG    877

gi|254282267|ref|ZP_04957235.1|: domain 1 of 1, from 4 to 870: score 660.8, E = 1.2e-195
                    *->siDA.qLRllvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEa
                       +iD +qLR+     v            L +    i+ +  GedL
  gi|2542822     4    AIDNrQLRA----NVR----------FLGETLGNIVRESEGEDLFQT 36

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      s +      +  L+EL + L  Ld    + +A+a+   LnLAn
  gi|2542822    37 VEKIRLCSKD---SMASDTLDELYSLLQTLDDNTILSIASAFNQFLNLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +A+     y    +  k   F+  a At +  i +      l+  ++ eE
  gi|2542822    84 IADQ----YHSVSSATK-LHFS--ARATLDKAITD------LRDTRTSEE 120

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  AL   s+DLvltAHPt   RR L+ K+  i  CL qL     t eD
  gi|2542822   121 ITAALEALSIDLVLTAHPTEITRRTLIHKHREITRCLRQLDPP--TSEDE 168

                    kE.LDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    + ++   +   +   + t E R  +PtP DE R G + i   +W+ vP F
  gi|2542822   169 EAgVRRRIAELVTQIWHTHEFRTDRPTPVDEARWGFAVIENSLWDAVPAF 218

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    LR vD      G+        P i+ ssW+GGDRDG nP vt  vt +v
  gi|2542822   219 LRDVDHTCGVHGLPAPTAQWSP-IQISSWIGGDRDG-NPNVTASVTEEVL 266

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LLa   A  l+++ v  L+ Elsm  C   L         t
  gi|2542822   267 LLAQWQACDLFLQSVSALVEELSMTSCSAQLQ------RETGHAR----- 305

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                              EPYR +L   RD L   R     L      + +     t
  gi|2542822   306 -----------EPYRALLRPLRDTL---RSQLDALDDAIANNTPAPTALT 341

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +     +PL  CY sL eCG + iADG LLD +R  s FG  L+KLDiRq
  gi|2542822   342 Q-STLEDPLLACYASLNECGMQCIADGTLLDTIRRASCFGPHLIKLDIRQ 390

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    Es  +t  l  +t+ L+iG Y +W E +R E+L aEL  +RPL++ +
  gi|2542822   391 ESSQHTQALSELTRALDIGDYADWDERRRCEFLRAELLNRRPLIPREWHP 440

                    tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                         +vl +f+ +A  P ++ G+Y+isma  PsD+LAv LL +  g
  gi|2542822   441 GAVASEVLRTFETIASTPREALGSYVISMASEPSDILAVQLLLKATGCPI 490

                    tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                     ++v PLFE LADL+ AP  +  L   D Y  r      vm+GYsDs KD
  gi|2542822   491 DMPVAPLFETLADLDNAPRVIGELLEDDDYLRRTGAELVVMIGYSDSAKD 540

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
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                    AG l+A W  Y+AqE + Kv  ++ v L+lFHGRGGt+GRGG P   A+L
  gi|2542822   541 AGMLAAGWAQYRAQEALLKVCEQHRVGLTLFHGRGGTIGRGGAPAQQALL 590

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                    sqPP  ++  lRvt qGE+i    G   L   +   ++ A L   ++PP
  gi|2542822   591 SQPPHSLQNGLRVTEQGEMIRTKLGVKSLAINTFGQYASAVLRANLQPPP 640

                    sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                    +P PEWR+Lm+++       YR  v  EP Fv YFR AtPE E   + +G
  gi|2542822   641 APEPEWRRLMDRLGEDSCAAYRHWVREEPNFVSYFRQATPEQELASLPLG 690

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    sRP++R+  GGiesLRAiPWiFaW q R  LP WLG G A + AidK
  gi|2542822   691 SRPSRRRSDGGIESLRAIPWIFAWSQNRLMLPAWLGAGSALQSAIDKGH- 739

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     l  L+ m  +WPFF   l +lEmvFAK D  i  LyD++Lv +eLkP G
  gi|2542822   740 -LATLRTMATQWPFFAARLSMLEMVFAKADLSISELYDQMLVVDELKPIG 788

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    + LR+   E    LL +     lLE +P+    + LR+ Y   Ln +qA
  gi|2542822   789 NALRQALNEDCSTLLGLLEQETLLEHEPWGMESINLRNVYAYPLNLLQAE 838

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     L+R+R                  E                  P +E  L
  gi|2542822   839 LLRRVR------------------ET---------------HDPAVEQAL 855

                    iLtmKGiAAGmqntG<-*
                    ++t+ G+AAGm ntG
  gi|2542822   856 MVTIAGVAAGMRNTG    870

gi|40063490|gb|AAR38290.1|: domain 1 of 1, from 1 to 873: score 655.4, E = 5.4e-194
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                               + P   s+  +L +    L +    ++q      L Eav
  gi|4006349     1    --------MTPSSTSNTAQLRQNVRHLGEILGQVIQSQGDAGLFEAV 39

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          s +    +D    e L a Lt L+    + vA+a++H LnLAn+
  gi|4006349    40 EAIRLQSKQ---SRDDDDQEALRALLTQLNEKQILDVARAFSHFLNLANI 86

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE          + +   D++      t s +E  +++L        +
  gi|4006349    87 AE--------QHHTLA--DYSQSLFSATAS-LESAFQQLLKDH--EHNRL 123

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       LKn s+DLvltAHPt   RR L+ K++ i  CL+ L
  gi|4006349   124 NTVLKNLSIDLVLTAHPTEITRRTLIHKHGEINDCLTRLEILNDKAAASS 173

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                         L   i   + t+E R  +PtP DE R   + i   +W+ vP+FLR
  gi|4006349   174 KDHSRLKELISQIWHTEEFRSDRPTPIDEARWAFAVIENSLWDAVPQFLR 223

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     vD       +    P   P i+ ssW+GGDRDG nP vt  vtR+v LL
  gi|4006349   224 VVDDICERYALPIPPPNWSP-IRISSWIGGDRDG-NPNVTAKVTREVLLL 271

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    a   A  l  + +  L  Els+      L    EE    a
  gi|4006349   272 AQWQACTLLENDIATLYEELSVTTASTTL----EEATEGAL--------- 308

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             EPYR +L   RD+L       R  + + + + s       +
  gi|4006349   309 ---------EPYRFLLKPLRDRL----QGQRLNIEKALNDQSLAPAPLTL 345

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                     e ++PLE CY sL      v+A G LLD LR v  FG  L++LDiRqEs
  gi|4006349   346 SEIVDPLEACYESLQAVNLDVLARGYLLDTLRRVHCFGPYLIQLDIRQES 395

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     R+t  +  +t+ L +G YR+W E +R +WL  EL   RPL+++    t
  gi|4006349   396 ARHTQAIAELTEALALGDYRDWNEGQRCDWLRGELDNPRPLIPAGWKPTP 445
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                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E ++v+d+f v+AE P  + G+Y+isma   sDvLAv +L +  g    +
  gi|4006349   446 ETQEVIDTFLVIAETPQSALGSYVISMAAEASDVLAVQVLLKATGCTTNM 495

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                     v PLFE L DLe AP  ve L s   Y+ r d +  vm+GYsDs KDAG
  gi|4006349   496 LVAPLFETLDDLESAPRVVEELLSDNAYRDRCDHQIMVMIGYSDSAKDAG 545

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     l+A W  Y+AqE +  v Kk+ vKL lFHGRGG +GRGG P H A+Lsq
  gi|4006349   546 MLAAGWAQYRAQESLLGVCKKFAVKLQLFHGRGGSIGRGGAPAHDALLSQ 595

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  ++  lRvt qGE+i    G   L   +L R++ A L   + PP  P
  gi|4006349   596 PPGSLENGLRVTEQGEMIRTKLGLTPLAVNTLGRYASAILQANLTPPPEP 645

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                      EWR Lm+++A    E+YR  v  EP Fv YFR AtPE E   + +GsR
  gi|4006349   646 AGEWRVLMNRLAQHSCEDYRRWVRDEPNFVPYFRQATPEQELASLPLGSR 695

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P++R+  GGi sLRAiPWiFaW q R  LP WLG G A   A   D + +
  gi|4006349   696 PTRRRSDGGIASLRAIPWIFAWSQNRLMLPAWLGAGSALARAAA-DGREV 744

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      Lk m +eWPFF   l +lEmvFAK D  iA LyD+LLv+ eL   G
  gi|4006349   745 -VLKSMAREWPFFGARLSMLEMVFAKSDLTIAELYDHLLVSPELADLGAA 793

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++    +  LL i      LEGD + +  + LRd Y   Ln +qA  L
  gi|4006349   794 LRQQLSNDRAALLAILETGSELEGDNWGRESINLRDIYTAPLNLLQAELL 843

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    +R R         P    E A E                      L++
  gi|4006349   844 RRQR-------ANP----EEATER----------------------ALMV 860

                    tmKGiAAGmqntG<-*
                    t+ G+AAGm ntG
  gi|4006349   861 TIAGVAAGMRNTG    873

gi|18645092|gb|AAL76393.1|: domain 1 of 1, from 1 to 873: score 655.0, E = 6.8e-194
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                              + P   s+  +L +    L +    ++q      L Eav
  gi|1864509     1    --------MTPSSTSNTAQLRQNVRHLGEILGQVIQSQGDAGLFEAV 39

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          s +    +D    e L a Lt L+    + vA+a++H LnLAn+
  gi|1864509    40 EAIRLQSKQ---SRDDDDQEALRALLTQLNEKQILDVARAFSHFLNLANI 86

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE          + +   D++      t s +E  +++L        +
  gi|1864509    87 AE--------QHHTLA--DYSQSLFSATAS-LESAFQQLLNDH--EHNRL 123

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       LKn s+DLvltAHPt   RR L+ K++ i  CL+ L
  gi|1864509   124 NTVLKNLSIDLVLTAHPTEITRRTLIHKHGEINDCLTRLEILNDKAAASS 173

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                         L   i   + t+E R  +PtP DE R   + i   +W+ vP+FLR
  gi|1864509   174 KDHSRLKELISQIWHTEEFRSDRPTPIDEARWAFAVIENSLWDAVPQFLR 223

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     vD       +    P   P i+ ssW+GGDRDG nP vt  vtR+v LL
  gi|1864509   224 VVDDICERYALPIPPPNWSP-IRISSWIGGDRDG-NPNVTAKVTREVLLL 271

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    a   A  l  + +  L  Els+          A      a
  gi|1864509   272 AQWQACTLLENDIATLYEELSV--------TTASTTLEGATEG------- 306

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
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                          EPYR +L   RD+L       R  + + + + s   v   +
  gi|1864509   307 -------ALEPYRFLLKPLRDRL----QGQRLNIEKALNDQSLAPVPLTL 345

                      EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                       e ++PLE CY sL      v+A G LLD LR v  FG  L++LDiRqEs
  gi|1864509   346 SEIVDPLEACYESLQAVNLDVLARGYLLDTLRRVHCFGPYLIQLDIRQES 395

                      eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                       R+t  +  +t+ L +G YR+W E +R +WL  EL   RPL+++    t
  gi|1864509   396 ARHTQAIAELTEALALGDYRDWNEGQRCDWLRGELDNPRPLIPAGWKPTP 445

                      EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                      E ++v+d+f v+AE P  + G+Y+isma   sDvLAv +L +  g    +
  gi|1864509   446 ETQEVIDTFLVIAETPQSALGSYVISMAAEASDVLAVQVLLKATGCTTNM 495

                      rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                       v PLFE L DLe AP  ve L s   Y+ r d +  vm+GYsDs KDAG
  gi|1864509   496 LVAPLFETLDDLESAPRVVEELLSDNAYRDRCDHQIMVMIGYSDSAKDAG 545

                      RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                       l+A W  Y+AqE +  v Kk+ vKL lFHGRGG +GRGG P H A+Lsq
  gi|1864509   546 MLAAGWAQYRAQESLLSVCKKFAVKLQLFHGRGGSIGRGGAPAHDALLSQ 595

                      PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                      PP  ++  lRvt qGE+i    G   L   +L R++ A L   + PP  P
  gi|1864509   596 PPGSLENGLRVTEQGEMIRTKLGLTPLAVNTLGRYASAILQANLTPPPEP 645

                      kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                        EWR Lm+++A    E+YR  v  EP Fv YFR AtPE E   + +GsR
  gi|1864509   646 AGEWRVLMNRLAQHSCEDYRRWVRDEPNFVPYFRQATPEQELASLPLGSR 695

                      PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                      P++R+  GGi sLRAiPWiFaW q R  LP WLG G A   A   +   +
  gi|1864509   696 PTRRRSDGGIASLRAIPWIFAWSQNRLMLPAWLGAGSALARAAADEHEVV 745

                      qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                        Lk m +eWPFF   l +lEmvFAK D  iA LyD+LLv+ eL   G
  gi|1864509   746 --LKSMAREWPFFGARLSMLEMVFAKSDLTIAELYDHLLVSPELADLGAA 793

                      LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                      LR++    +  LL i      LE D + +  + LRd Y   Ln +qA  L
  gi|1864509   794 LRQQLSNDRAALLAILETGSELERDNWGRESINLRDIYTAPLNLLQAELL 843

                      KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                      +R R         P    E A E                       L++
  gi|1864509   844 RRQR-------ANP----EEATER----------------------ALMV 860

                      tmKGiAAGmqntG<-*
                      t+ G+AAGm ntG
  gi|1864509   861 TIAGVAAGMRNTG    873

gi|71083482|ref|YP_266201.1|: domain 1 of 1, from 1 to 895: score 627.8, E = 1e-185
                      *->siDAqLRl.LvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEa
                          i   L  + +P K     + ++Y   L D    +++   G++
  gi|7108348     1    MIKRDLYYeRIPTKSL--REDVRY---LGDVLGRVIKKQEGQSFFKL 42

                      vqECYEls.AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                      v +   ls+A+   K+       +  k+  L+P  +  +A+a+ H +n
  gi|7108348    43 VEDTRLLSkANLANKHVKDPFKNILNKIKNLNPENTFKLARAFNHFMNFI 92

                      nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                      nL E  + A R+  +           +      iEE + kL      + +
  gi|7108348    93 NLSETTD-ASRKLDEYEN-----NKKNSNKNIFIEEIFEKLFKDKKITNK 136

                      EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq..LsAKDvtv
                       +++  K   + +vltAHPt   RR L+qK  +i   L q++L+ K +
  gi|7108348   137 KIYDVAKKLNIGIVLTAHPTEVKRRTLIQKYNKIIKILEQrdLYKKNLSK 186

                      eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                         k LD  L  Ei   + tDE++R++PtP +E R G++ i + +W+ +P
  gi|7108348   187 --LKTLDKDLYNEITIIWNTDELKRSKPTPSEEARWGLAVIEDSLWDSIP 234
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                    KFLRRvDtA.LKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                    K  RR     LKn+G    lP +   i+F sWmGGDRDG nP vt  vt
  gi|7108348   235 KVYRRLNNIfLKNMG--KSLPRNFNPIEFGSWMGGDRDG-NPNVTAKVTS 281

                    DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                    +  LL+R  Aa lY  q+  L+  lsm +C   +      l  t +
  gi|7108348   282 EALLLSRWEAAKLYEKQLTNLIRSLSMKKCSTQI------LNITGKTF-- 323

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaR.HLLAtGiseisEe
                                 EPYRv L   RDKL  t    ++HL+ +    +
  gi|7108348   324 --------------EPYRVFLRPLRDKLRATHILIKeHLVNK--EPLDHK 357

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                        +  e L PL +   sL +     iA+G LLDl+R    FG+ L KL
  gi|7108348   358 KLLSNTGEILTPLRVVRDSLIQNQSENIAEGDLLDLIRRARCFGINLAKL 407

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    DiRqEs R+t  +  i +      Y  W E  +  +L + +k K+ L+
  gi|7108348   408 DIRQESSRHTKLISEIVKKKYNKDYFLWNESEKLAFLSSRIKSKKNLIKN 457

                    DLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqREC
                     L k  E k+v  +f+vL + P ++ GaY+ism+ a sD+L v  Lq+E
  gi|7108348   458 SLLKNKENKEVWSTFNVLVDQPKECLGAYVISMTSAASDILSVAYLQKEA 507

                    gvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsD
                    ++ + LrvvPLFE L DL+ A   ++ LFs+ WY+  i+ Kqe+m+GYsD
  gi|7108348   508 KIVNKLRVVPLFETLDDLRNAKSIMNSLFSLPWYRKSINYKQEIMIGYSD 557

                    sGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtH
                    s KDAG+lsA W  Yk q+Ei K AKky + ++ FHGRGG  GRGGGP
  gi|7108348   558 SSKDAGKLSASWHQYKLQDEILKLAKKYKIDITFFHGRGGSAGRGGGPIQ 607

                    LAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm
                      + sqP   +nG +R+t qGEvi + +G E L    L  +  A +   +
  gi|7108348   608 ATLKSQPANSVNGKIRITDQGEVIQQKYGYEPLAKYNLCSYIGAVVQATL 657

                    nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGk
                    nPP  Pk  W++L+e+m  +    YRs +     F+ YFR  tP    Gk
  gi|7108348   658 NPPPEPKIKWKQLIEKMSEISMKSYRSNINEKSDFIRYFRTVTPHKALGK 707

                    mniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid
                    + iGsRP+KRk    i+sLRAiPW+FaWtq R  LP WLG   A  +A
  gi|7108348   708 LSIGSRPSKRKNVDNIQSLRAIPWVFAWTQIRLFLPAWLGTTEALNYASS 757

                    KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL
                    K  K +  L +m k+WPFF  t+D+l+mv  K DP i  +y++ L    L
  gi|7108348   758 KVFKKI--LVDMEKNWPFFNSTMDILDMVISKVDPEISKVYENQLADKKL 805

                    kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnv
                    k  Gk+LR ++ Et + L k+     +       +  + +R+ Y   L +
  gi|7108348   806 KIVGKKLRSQF-ETLKRLNKVITPFQIRKQRKVFRTSVIIRNIYSEVLHI 854

                    fqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGL
                     q   +K       k tl+                   kLn  ++    L
  gi|7108348   855 TQSIVMK-------KLTLK-------------------KLN--KNKKQHL 876

                    EDtLiLtmKGiAAGmqntG<-*
                     D L+  + Gi A m+ntG
  gi|7108348   877 ADALMTSIAGISAAMKNTG    895

gi|221060224|ref|XP_002260757.1|: domain 1 of 1, from 61 to 1044: score 626.7, E = 2.2e-185
                    *->siDAqLRlLvPGKvsedekLieY......DALLlDkFL.DiLqDLHG
                       s + +L+ L+ GK+ e  + +++ ++ ++D   lD  L D+L+D
  gi|2210602    61    SGERKLKFLIEGKMVETKNAVDFikplkdDIKALDFLLfDMLKDNLP 107

                    edLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailH
                    + L E      +ls  Y   +  +  + L + +  Ld      +  a+ H
  gi|2210602   108 NKLFETLCTIHDLSEKYSENQTQENFNSLKSSIYNLDDEYLGTIVNAFGH 157

                    mLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkl
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                m  L n AE    A+R R +k    D +   +      + EtlK     l
gi|2210602   158 MCILSNFAE---WAHRGRRRKAF--DMSFTPNERIYGSVYETLKGTFHML 202

                nKs...PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLs
                 Ks+ + +E++e L nq++D vlt HPtq++R sLL+    +   L +L
gi|2210602   203 MKSgfdINEIYEQLCNQTIDFVLTTHPTQAIRTSLLKNYIQLAELLLKLD 252

                AKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEt
                  D     Kk L + L   + AA++tD iRR +PtP DE    +  +
gi|2210602   253 NTDKELYKKKILYDNLKTYLLAAWKTDVIRRIKPTPIDEAISLVDIVENC 302

                vWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvt
                ++  +P  +R +D       +   l  +  +  FssW GGDRDG nP v
gi|2210602   303 IFYRIPNIIRYIDNVFYEYNLPP-LKLESKICLFSSWAGGDRDG-NPFVL 350

                PEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRA...EEly
                PE tR vC + ++    l+i  vE L+ +l +  C +  +   +  E+
gi|2210602   351 PETTRYVCYMNKIRGCELFIPMVEKLIRDLTLHHCTEHFKTYVkllEDEV 400

                rtaardkvvKyYiEFWKqvPP......tEPYRviLGdvRDKLYntRERaR
                +    dk  Ky    +    P ++++++E YR  L  v  KL  t    +
gi|2210602   401 SQYIFDKDKKYLAQKFLWFSPfsktnkNEIYRSALLVVWAKLKSTVQVYK 450

                HLLAtGiseis.EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDl
                 L+ +   +   E  ++   EeF E L  CYksL + G   iA+G L D+
gi|2210602   451 ALISHQPVDTNfEKLMFHSSEEFEEILMECYKSLTDSGNALIAEGYLKDV 500

                LRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEW
                +R v  FGL L+KLDiRqEs ++ + +D i + L+   Y   sEe + ++
gi|2210602   501 IRNVKIFGLHLMKLDIRQESKKHVEAMDYICEKLQTAKYSLLSEEEKIDF 550

                LlaELkGKRPLlgsDLPktEEv....kDvldafrvLAELPiDsFGaYiis
                L   L+  RPL++  + + E+v+++   v+ +f v   +   + GaYi+s
gi|2210602   551 LTKILQSNRPLIPKNIEQEEDVpndfLNVIKTFDVCSQIEESALGAYIVS 600

                mataPsDvLAvELLqREC...gvkqtLrvvPLFEkLADLeAAPAavekLF
                m+   sD+L vE+ q+E +++  ++t rvvPL E +  L+     +e L
gi|2210602   601 MCNHASDILLVEVFQKELkknAKRKTQRVVPLLETIQSLQMSCTILENLI 650

                siDWYinri....dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvA
                   WY+ +++++ d Kqevm+GYsDsGKD GR+  AW L+kAqE ++++
gi|2210602   651 QNPWYRTHLrthfDNKQEVMIGYSDSGKDGGRFTSAWELFKAQEKLVQIG 700

                KkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviE
                K+y v +  FHGRGG v RGGGP HLAiLsqP  ti+  lRvt+qGEvi
gi|2210602   701 KQYSVEVRFFHGRGGSVSRGGGPQHLAILSQPINTIKNYLRVTIQGEVIT 750

                fsFGEEnLCFrsLqRFtAAtLEHG.mnPPvsPkPEWRkLmeemAvvAtEE
                + F    +  rs+  +  A L    ++  vs k EWR+Lm+em  + t E
gi|2210602   751 QNFCLKGMMLRSIETYISALLKCSlLKNTVSVKDEWRELMDEMSEITTKE 800

                YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPW
                YR vv+    Fv YFR AtP +E Gk+n+GsRP+KRk  G +esLRAiPW
gi|2210602   801 YRQVVYENKDFVNYFRCATPQIEIGKLNLGSRPSKRK-QGNVESLRAIPW 849

                iFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlD
                +F+Wtq R HLPvWLG+   + h i+K+   l  +++mYk+WPF
gi|2210602   850 VFSWTQNRMHLPVWLGIEKLYDHLIKKE--KLWLIQDMYKNWPFCTSFFN 897

                LlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGH
                L+ mv AK    i   yD +Lv EeLk  G  LR+k +   +l   +
gi|2210602   898 LISMVMAKASLQITEEYD-ILVPEELKYIGIMLREKLKKAMELTALVTNE 946

                kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRD..PsykvtlrPhl
                k   + D   K  +  R  ++   n +q   LKR+R+++ +++      l
gi|2210602   947 KIFCDNDILTKRSIESRTKWVVVCNLIQIQALKRLRErqREWELAQGKDL 996

                sKEyAd....EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqnt
                sK   d++++E+ + + +  + n  + +aP  +D  +  ++G
gi|2210602   997 SKKNSDtptgEEQQIPIQSAHPN-NDPIAP--DDSPLTPIQGHTNDEEHK 1043
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                  G<-*

  gi|2210602  1044 L    1044

gi|270239854|emb|CBI27087.1|: domain 1 of 1, from 16 to 987: score 621.5, E = 8.4e-184
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                     s D   RlL  G     +++++ +  +   F++ +     e  +
  gi|2702398    16    SFDDDCRLL--GSLL--NEVLQRE--VGSNFMEKV-----ERNRILA 51

                  qECYElsAeYEGKkDtkKLeE..LGakLtsLdPaDailvAkailHmLnLA
                  q    + A   G +Dt  L E++L + +  ++  +a+ +A+a++H LnL
  gi|2702398    52 QSACNMRAS--GIEDTAELLEkqLISEISQMNLEEALTLARAFSHYLNLM 99

                  nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                   +AE     +R R  +           A      ++ + +L   +  sPe
  gi|2702398   100 GIAET---HHRLRKARNV---------AHMSKSCDDIFNQLLQGG-VSPE 136

                  EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                  E ++ +  q v++vltAHPtq  RR L  K+ Ri   L       +  eD
  gi|2702398   137 ELYNTVCKQEVEIVLTAHPTQINRRTLQYKHIRIAHLLDYNDRPNLGHED 186

                  KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                  ++ L E L REi   + tDE+RR +Pt  DE RaG+  +   +W+ vP +
  gi|2702398   187 REMLIEDLVREITSIWQTDELRRQKPTVVDEARAGLNIVEQSLWRAVPHY 236

                  LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                  LRRv  ALK       lP     ikF sWmGGDRDG nP vt EvtRDv
  gi|2702398   237 LRRVSNALKK-HTGKSLPLTCTPIKFGSWMGGDRDG-NPNVTAEVTRDVS 284

                  LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyr..........
                  LL+R mA  lYi  v+ L FElsm RC d L   A E+  +++++ ++++
  gi|2702398   285 LLSRWMAIDLYIREVDSLRFELSMNRCSDSLSRLAHEILEketssvdrne 334

                  ................................taardkvvKy......
                  +++++ ++++ ++ ++ +++ +++ + + + ++ t  +d   Ky++ + +
  gi|2702398   335 srnqplnrsqlkpysqlgptlprqlpagadlpscTECKDGESKYpklefp 384

                  ...Yi.....................EFWK...................
                  +++Y++ ++++ +  ++++++ ++++++F K+ ++++  +++++++  ++
  gi|2702398   385 gtdYMplnrqdvkaasssdtsfqdsnkDFGKtygngtvanssnsqsaatp 434

                  ..................................qvPPtEPYRviLGd
                  ++ + ++++  ++++  ++++ ++++ ++  +++ +q P   PYR++LG+
  gi|2702398   435 rtvsfssgqllsqrklfsesqlgrssfqkllepslpQRPGIAPYRIVLGN 484

                  vRDKLYntRERaRHLLAtGiseisEeAvytkvEeFLEPLELCYksLCeCG
                  v+DKL  t  R   LL     e      y   +e LEPL LC  s+  CG
  gi|2702398   485 VKDKLMKTQRRLELLLEDLPCEHDPGDYYETADELLEPLLLCHESMQSCG 534

                  DkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs
                    ++ADG L Dl+R v tF + L+KLD+RqEs R+ + lDAit  L++G
  gi|2702398   535 SGILADGRLADLIRRVATFRMVLMKLDLRQESARHAETLDAITSYLDMGI 584

                  YReWsEeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiD
                  Y eW Ee++ ++L  ELkGKRPL+++ +    +vk+vld+frv AE+ +D
  gi|2702398   585 YSEWDEERKLDFLTRELKGKRPLVPPTIEVVADVKEVLDTFRVAAEIGSD 634

                  sFGaYiismataPsDvLAvELLqRECgvkq...........tLrvvPLFE
                  sFGaY+isma   sDvLAvELLq++  +   ++ +++ +++tLrvvPLFE
  gi|2702398   635 SFGAYVISMASNASDVLAVELLQKDARLAVcgelgrpcsggTLRVVPLFE 684

                  kLADLeAAPAavekLFsiDWYinri....dGKqevmvGYsDsGKDAGRls
                   + DL+ A A + kL siDWY+ +i ++++G qevmvGYsDsGKDAGR+
  gi|2702398   685 TVKDLRGAGAVIRKLLSIDWYREHIiknhNGHQEVMVGYSDSGKDAGRFT 734

                  AAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPD
                  AAW LYkAqE+++    +yG+K++lFHGRGG +GRGGGPt LAi sqPP
  gi|2702398   735 AAWELYKAQEDVVAACNEYGIKVTLFHGRGGSIGRGGGPTYLAIQSQPPG 784

                  tinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE
                   + G lR t qGE++   FG  +   r L  +t A L   m PP+ P+ E
```

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  gi|2702398   785 SVMGTLRSTEQGEMVQAKFGLPHTAVRQLEIYTTAVLLATMRPPLPPREE 834

                   .WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPa
                   +WR+Lmee+  +    YRs v+  P F  YF  AtP  E G +niGsRP+
  gi|2702398   835 kWRNLMEEISKISGQCYRSTVYENPEFLAYFHEATPQAELGFLNIGSRPT 884

                   KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqk
                   +Rk s Gi  LRAiPW+FaWtqtRF LP WLGvG   K   +K  K
  gi|2702398   885 RRKSSTGIGHLRAIPWVFAWTQTRFVLPAWLGVGSGLKGVCEKGHKE--D 932

                   LkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLR
                   L  mYkeWPFF  t+DL+Emv                        + LR
  gi|2702398   933 LIAMYKEWPFFQSTIDLIEMV-----------------------EILR 957

                   dkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKR
                                                RLR
  gi|2702398   958 ------------------------------RLR----------------- 960

                   iRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtm
                    RD               d+n          n        L D L++t+
  gi|2702398   961 -RD----------------DDN----------N-------KLRDALLITI 976

                   KGiAAGmqntG<-*
                    GiAAGm ntG
  gi|2702398   977 NGIAAGMRNTG    987

gi|156102026|ref|XP_001616706.1|: domain 1 of 1, from 58 to 1050: score 606.1, E = 3.6e-179
                   *->siDAq....LRlLvPGKvsedekLieY......DALLlDkFL.DiLq
                      s D q++++L+ L+ GK+ e  + +++ ++ ++D   lD  L D+L+
  gi|1561020    58    SQDSQderkLKFLIEGKMVETKNAVDFikplkdDIKALDFLLfDMLK 104

                   DLHGedLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAk
                   D   + L E      +ls  Y   +  +    L   +  L+      +
  gi|1561020   105 DNLPNKLFETLCAIHDLSERYSENQTEENFKALKNSIYNLEDHYLGTIVN 154

                   ailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkL
                   a+ Hm  L n AE    A+R R +k    D +   +      + EtlK
  gi|1561020   155 AFGHMCVLSNFAE---WAHRGRRRKAF--DMSFTPNERIYGSVYETLKGT 199

                   vlklnKs...PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL
                      l Ks+ +   ++e L nq++D vlt HPtq++R sLL+    +   L
  gi|1561020   200 FHMLIKSgfdIHQIYEQLCNQTIDFVLTTHPTQAIRTSLLKNYIQLAELL 249

                   aqLsAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsY
                    +L   D     Kk L + L   + AA++tD iRR +PtP DE    +
  gi|1561020   250 LKLDSTDKELYKKKLLYDNLKTYLLAAWKTDVIRRIKPTPIDEAISLVDI 299

                   iHEtvWkGvPKFLRRvDtALKniGinE.RlPYdvPLikFssWmGGDRDGk
                   +   ++  +P  +R +D      G n + +  d  +  FssW GGDRDG
  gi|1561020   300 VENCIFYRIPNIIRYIDNVF--YGYNLpPVKLDSKICLFSSWAGGDRDG- 346

                   nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEE
                   nP v PE tR vC + ++    l+i  vE L+ +l +  C +  +
  gi|1561020   347 NPFVLPETTRYVCYMNKIRGCELFIPMVEKLIRDLTLHHCTQHFKTYVKL 396

                   lyrtaardkv...vKyYiEFWKqvPP......tEPYRviLGdvRDKLYnt
                   l     +   +++ Ky    +    P +++++ E YR  L  v  KL
  gi|1561020   397 LEDEVSQYIFdpdRKYLAQKFHWFSPfsksnkSEIYRRALLVVWAKLKSV 446

                   RERaRHLLAtGise.isEeAvytkvEeFLEPLELCYksLCeCGDkviADG
                       + L+     ++  E  ++   +eF E L  CYksLC+ G   iA+G
  gi|1561020   447 IQVYKSLISNQPVDpHFEKLMFNSSDEFEEILMECYKSLCDSGNTLIAEG 496

                   sLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEe
                    L D++R v  FGL L+KLDiRqEs ++   +D i + L iG Y   sEe
  gi|1561020   497 YLKDVIRNVKIFGLHLMKLDIRQESVKHIQAMDYICEKLHIGRYSLLSEE 546

                   KRqEWLlaELkGKRPLlgsDLPktEEv....kDvldafrvLAELPiDsFG
                    R ++L   L+  RPL++  + + E+v+++   v+++f v   +   + G
  gi|1561020   547 ERIDFLTEVLQSNRPLIPNNIEQEEDVpsdfLNVINTFDVCSQIEESALG 596
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                    aYiismataPsDvLAvELLqREC...gvkqtLrvvPLFEkLADLeAAPAa
                    aY++sm+   sD+L vE+ q+E +++  ++t rvvPL E +  L+
  gi|1561020   597 AYVVSMCNNASDILLVEVFQKELkknAQRKTQRVVPLLETIQSLQMSCTI 646

                    vekLFsiDWYinri....dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEE
                    +e L    WY+ +++++ d Kqe+m+GYsDsGKD GR+  AW L+kAqE
  gi|1561020   647 LENLIKNPWYRTHLrthfDNKQEIMIGYSDSGKDGGRFTSAWELFKAQEK 696

                    iiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvq
                    ++ + K+y v +  FHGRGG v RGGGP HLAiLsqP  ti+  lRvt+q
  gi|1561020   697 LVHIGKQYSVEVRFFHGRGGSVSRGGGPQHLAILSQPINTIKNYLRVTIQ 746

                    GEviEfsFGEEnLCFrsLqRFtAAtLEHG.mnPPvsPkPEWRkLmeemAv
                    GEvi + F    +  rs+  +  A L    ++  v  k EWR+Lm+em
  gi|1561020   747 GEVITQDFCLKGMMLRSIETYISALLKCSlLKNKVLVKDEWRELMDEMSQ 796

                    vAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesL
                      t EYR vv+    Fv YFR AtP +E Gk+n+GsRP+KRk  G +esL
  gi|1561020   797 LTTKEYRHVVYENDDFVKYFRCATPQIEIGKLNLGSRPSKRK-QGNVESL 845

                    RAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFF
                    RAiPW+F+Wtq R HLPvWLG+     + +++D   l  L++mY++WPF
  gi|1561020   846 RAIPWVFSWTQNRMHLPVWLGIEKLHDYLVERD--KLPLLQDMYRNWPFC 893

                    RvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLL
                         L+ mv AK    iA  yD +Lv EeLk  G  LR+k +   +l
  gi|1561020   894 TSFFNLISMVMAKASLQIAEEYD-VLVPEELKYIGTMLRQKLKKAMELTA 942

                    kiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRD..Psykvt
                     +   k   + D   K  +  R  ++   n +q   LKR+R+++ +++
  gi|1561020   943 LVTNEKTFCDNDLLTKRSIESRTKWVAVCNLIQIQALKRLRErqREWELA 992

                    lrPhlsKE..yAdEnskkadeLvk....LnptervaPGLEDt.LiLtmKG
                        l++E++ A+E    a++ + ++++L  +e   P  ED +L +
  gi|1561020   993 QEGRLAQEggLAQEGGLAAEGGLAqeggLA-AEGGHPTCEDHkLSVSSAK 1041

                    iAAGmqntG<-*
                         q  G
  gi|1561020  1042 DELESQYGG    1050

gi|254455801|ref|ZP_05069230.1|: domain 1 of 1, from 1 to 895: score 605.0, E = 7.9e-179
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           q R L   ++    kL++     l   L+ +L+D  G+   E
  gi|2544558     1    ---MQKRDLYYERIP--TKLLRENVRYLGNILgKVLKDQEGDKFFEL 42

                    vqECYEls....AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmL
                    v     ls+ ++ +   K+  +K+      + +L+   +  + +a++H +
  gi|2544558    43 VEKIRKLSkvnkTNLNSKHSYRKIIR---TIKGLNSKNTFKLTRAFSHFM 89

                    nLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnK
                    nL nLAE ++ A R  ++                  iEE +  L    n
  gi|2544558    90 NLINLAESID-ASRSLNEYEN----NKKKINKSNLFIEEIFEDLFNNKNI 134

                    sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt
                    s   +++  Kn  + +vltAHPt   RR L+qK  +i   L q
  gi|2544558   135 SDSKIYNHAKNLNIGIVLTAHPTEVKRRTLIQKYHKITEILEQRDLLKNY 184

                    veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGv
                    +   k LD  L  E    + tD+++R +P P DE R G++ i + +W+ +
  gi|2544558   185 PSKLKLLDKKLFDEFTIIWNTDDLKRVKPSPFDEARWGLAIIEDSLWDTI 234

                    PKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                    PK  RR         +   lP +   i+F sWmGGDRDG nP vt  vt+
  gi|2544558   235 PKVYRRLNSIFVQ-NMDKGLPKNFNPIEFGSWMGGDRDG-NPNVTAKVTK 282

                    DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                    +v LL+R  Aa lY   +  ++   sm +C   +      l++t ++
  gi|2544558   283 EVILLSRWEAAKLYEKTLTKIIRSYSMEKCSKQI------LKKTGKSY-- 324

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYnt.RERaRHLLAtGiseisEe
                                 EPYRv L   RDK+  t+R    HL+ +    +
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  gi|2544558   325 --------------EPYRVFLRPLRDKMRIThRMIEQHLVNK--KPLDQK 358

                   AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                        Ee L PL +  +sL +     +A G LLDl+R    FG+ L KL
  gi|2544558   359 KLLNSKEEILKPLRVVRQSLEQNNNENLASGELLDLMRRAKCFGINLAKL 408

                   DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                   DiRqEs R+   +    +      Y ++sE  +  +L + L   + ++
  gi|2544558   409 DIRQESSRHSQLISEFVKKKYNKDYSKFSEIEKINFLKTKLNSSKNVINK 458

                   DLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqREC
                      k  E  +v  +f++LAE P+++ GaY+ism+ a sD+L v  Lq+E
  gi|2544558   459 FKFKNRENSEVWSTFNILAEEPSECLGAYVISMTSAASDILSVYFLQKEA 508

                   gvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsD
                   ++k+ LrvvPLFE L DL  A   +e LFs  WY+  i+ Kqevm+GYsD
  gi|2544558   509 KIKNKLRVVPLFETLDDLINAKSIMESLFSHKWYRKLINHKQEVMIGYSD 558

                   sGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtH
                   s KDAG++ A W  YkAqEEi+K  Kk+ + ++ FHGRGG  GRGGGP
  gi|2544558   559 SSKDAGKICASWHQYKAQEEIVKLGKKFNIEITFFHGRGGSAGRGGGPIQ 608

                   LAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm
                     + s PP  +nG +R+t qGEvi + +G E L    L  +  A  E  +
  gi|2544558   609 ATMRSLPPNSVNGRIRITDQGEVIQQKYGYEPLAKYNLCSYIGAVSEATL 658

                   nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGk
                    PP  Pk  WR L+e+mA +    YR  + +   F+ YF+  tP +  Gk
  gi|2544558   659 IPPPQPKDSWRALIEKMAEISKSSYRKNINQSSDFIKYFKTVTPHVSLGK 708

                   mniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid
                   + iGsRP+KRk    i+sLRAiPWiFaWtq R  LP WLG   A ++A
  gi|2544558   709 LSIGSRPSKRKNVDNIQSLRAIPWIFAWTQIRLMLPAWLGSAEALRYA-- 756

                   KDiKnlqk.LkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEe
                     iK + k+L +m ++WPFF   lD+l+mv  K DP +  +y++ L  E
  gi|2544558   757 -NIKEFRKtLYDMERNWPFFNSMLDILDMVISKVDPDVSKIYEEYLADEK 805

                   LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLn
                   Lk  Gk+LR ++   k+l  +i    ++       +  + +R+ Y   Ln
  gi|2544558   806 LKRVGKRLRFQFDVIKKLNKEITP-NEISKLRKQFRTSVIVRNIYTEVLN 854

                   vfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPG
                   ++q   +K+i+      t++ ++ K y             Ln
  gi|2544558   855 IIQPIVIKKIK------TIKNKVDKKY-------------LN-------- 877

                   LEDtLiLtmKGiAAGmqntG<-*
                     D L+  + Gi A m+ntG
  gi|2544558   878 --DALLTSIAGISAAMKNTG    895

gi|224000774|ref|XP_002290059.1|: domain 1 of 1, from 1 to 843: score 602.2, E = 5.5e-178
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       +D   R+  P
  gi|2240007     1    -MD---RAANP---------------------------------- 7

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                                Dt   eE+      ++P D++ v k+++  LnL n
  gi|2240007     8 -------------DDTAPFEEMKKLAYDINPRDTLGVMKTFSIALNLVNA 44

                   AEEvelAyRRRikkkkhGDFaDEasA.ttEsDiEEtlKkLvlklnKsPeE
                   AE  +     R++ +k  D    +  +  E  i  t+  L        +
  gi|2240007    45 AEVHHRIRLVRVSELK-DDVNHIGPLpMVEDSIRGTMEILLEGDCDDKDK 93

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    Fe L  q  ++vltAHPt   R+ ++ K  +i   La +   D+ + ++
  gi|2240007    94 LFERLTTQKCEIVLTAHPTEVNRKTIISKYRKISELLAYMERPDLHPFER 143

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    E    L   i A +  DEiRR +Pt q E   G + i   +W+ vP +L
  gi|2240007   144 AEAVNNLRGIISAIWGADEIRRVKPTVQKEAAGGCAVIESVLWDAVPSYL 193
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                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R+ D A   + +  + P d+  ikF+sW+GGDRDG nP  tPEvt +v
  gi|2240007   194 RKLD-AQCRVTLGKKFPVDATPIKFASWIGGDRDG-NPNCTPEVTLEVVT 241

                    LaRmmAanlYisqvEDLmFElsm.WRCndELRvRAEElyrtaardkvvKy
                      R+ Aa ++++ +  L  El+++ R   EL + A  +++
  gi|2240007   242 RQRLRAAKMFLNDLNMLYSELAIsSRFSKELEALAASVKKSDDNR----- 286

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv.y
                                E YR ++G  R +L  t       L + + + sE+  +
  gi|2240007   287 ----------EKYRRVIGHLRRRLVRTVKECEAKL-HTLTDTSEDVEpI 324

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     k Ee + PL + Y sL e G   +ADG + D++R v  FG+ Lv LDiR
  gi|2240007   325 IKSEELMTPLRIMYDSLVETGFELVADGHVSDIIRRVAVFGMTLVPLDIR 374

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD..
                     Es R+t  +DAit+HL+iGsY+eW Ee R  WL +EL  KRPL+   +
  gi|2240007   375 EESTRHTIAIDAITRHLGIGSYKEWDEEARLNWLQSELNNKRPLFRIRdi 424

                    ....LPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLq
                    +++ L    + +  l  f+v  EL ++s GaY+is a + sDvL v LLq
  gi|2240007   425 ednlLGLDPDNRKTLMVFKVASELDSESLGAYVISQANTASDVLLVMLLQ 474

                    RECgvkqt....LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqe
                    +  g+ + +++ +rvvPLFE L DL   PA +e+LFsi  Y   i+GKqe
  gi|2240007   475 KQFGMTEKngklMRVVPLFETLTDLTNSPAQLERLFSITNYLGAINGKQE 524

                    vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                    vmvGYsDs KDAGRl+A W  Y AqE ++ vA +yGv L+ FHG+GGtvG
  gi|2240007   525 VMVGYSDSAKDAGRLAACWAQYTAQEAMANVADRYGVELTFFHGKGGTVG 574

                    RGGGPt.HLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                    RGG P    AiLs PP tinG  Rvt qGE+i + FG  ++  r+L  +t
  gi|2240007   575 RGGNPAlYRAILSHPPNTINGRFRVTEQGEMIRQNFGSLEIAERTLDIYT 624

                    AAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlA
                    AA L       v Pk EWR+ me++  v    YR  v  +PRFv YFR A
  gi|2240007   625 AALLRESFTKRVEPKQEWRDQMERVSEVSCAAYRHTVRDDPRFVPYFRQA 674

                    tPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvG
                    tPElE G++niGsRPaKR P GG++sLRAiPW FaW qtR HL  WLGvG
  gi|2240007   675 TPELELGRLNIGSRPAKRNPKGGVDSLRAIPWTFAWAQTRMHLSAWLGVG 724

                    AAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyD
                       +  +    + ++ L+EmY++WP+FR  + L+ m   K D  i   yD
  gi|2240007   725 DGLRSDVSDQCRYMKTLQEMYEQWPWFREIISLISMLVSKTDFSITKNYD 774

                    kLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr.lRLR
                    +LLv  +L+  G+++R+k vEt++ ++ + G  D+      L   +  +R
  gi|2240007   775 DLLVDSNLRSLGDEVRNKLVETRQAVIDVSGATDISGPHVQLMRAsSTIR 824

                    dsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLn
                    ++Y+  +nv+qA  LK +R
  gi|2240007   825 NPYVDSINVVQAEILKVLR------------------------------ 843

                    ptervaPGLEDtLiLtmKGiAAGmqntG<-*

  gi|2240007     - ----------------------------    -

gi|124808830|ref|XP_001348420.1|: domain 1 of 1, from 29 to 1008: score 581.6, E = 8.4e-172
                    *->siDAqLRlLvPGKvsedekLieY......DALLlDkFL.DiLqDLHG
                         D +L+ L+ GK+ e    +++ ++ ++D   lD  L D+L+D
  gi|1248088    29    --DEKLKFLIEGKMIEKKGCVDFikplkdDIKALDFLLfDMLKDNLP 73

                    edLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailH
                    ++L E+     +ls  Y           L   +  L       +  a+ H
  gi|1248088    74 NNLFEILCTIHDLSETYSENPNDDNFLSLKNCIYNLKDEYLGTIVNAFGH 123

                    mLnLAnLAEEvelAyRRRikkkkhGDFa..DEasAttEsDiEEtlKkLvl
                    m  + n AE    A+R R +k     F ++D         +  t+  L+
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  gi|1248088   124 MCVISNFAE---WAHRGRRRKAFDKSFIpnDKIYGSVNETLKGTFNILIQ 170

                    klnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsA
                     +    ++++e L nq+++ vlt HPtq++R sLL+   R+   L +L
  gi|1248088   171 NG-FQLNDIYEQLCNQTIEFVLTTHPTQAIRTSLLKNYIRLGELLLKLDN 219

                    KDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtv
                     D     Kk L + L   +   ++tD iRR +PtP DE    +  +   +
  gi|1248088   220 TDKELYKKKLLYDNLKTNLLSSWKTDVIRRIKPTPIDEAISLVDIVENCI 269

                    WkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtP
                    +  +P  +R +D  L    +   +  +  +  FssW GGDRDG nP v P
  gi|1248088   270 FYRIPNIIRYIDNVLFEYNLPP-VKLNSKVCIFSSWAGGDRDG-NPFVLP 317

                    EvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRA...EElyr
                    E t+ vC + ++    l+i  +E L+ +l +  C +  R   +  E+  +
  gi|1248088   318 ETTKYVCYMNKIRGCELFIPMIEILIRDLTLHHCTQHFRSYVkllEDEVS 367

                    taardkvvKyYiEFWKqvPP......tEPYRviLGdvRDKLYntRERaRH
                        dk  Ky    ++   P +++++ E YR  L  v  KL    E  +
  gi|1248088   368 EYIFDKDHKYLAKKFQWFSPfsksnkKEIYRRALLIVWAKLKSVVEVYKS 417

                    LLA.tGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlL
                    L+ ++ + e     ++ + +eF E L  CYksL e G   iA+G L D++
  gi|1248088   418 LISnQRVDEDFKKLMFHNSDEFEEILLECYKSLVESGNTLIAEGYLKDVI 467

                    RqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWL
                    R v  FGL L+KLDiRqEse++   +  i + L++  Y    Ee++  +L
  gi|1248088   468 RNVKIFGLHLMKLDIRQESEKHISTMNYICQKLNMKKYSLLNEEQKINFL 517

                    laELkGKRPLlgsDLPktEEv....kDvldafrvLAELPiDsFGaYiism
                       L   RPL++  +   E+v+++   v+ +f v   +   + GaYi+sm
  gi|1248088   518 TDILNSNRPLIPKNIEEEEDVpndfINVIKTFDVCSQIEDSALGAYIVSM 567

                    ataPsDvLAvELLqRECg...vkqtLrvvPLFEkLADLeAAPAavekLFs
                    +t  sD+L vE+ q+E ++++ ++t rvvPL E +  L+     +e L
  gi|1248088   568 CTNASDILLVEVFQKEMKkgtQRKTQRVVPLLETIQSLQNSSIILENLLK 617

                    iDWYinri....dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                      WY+ +++++ + Kqe+m+GYsDsGKD GRl  AW L+kAqE ++ + K
  gi|1248088   618 NPWYRKHLttnfEDKQEIMIGYSDSGKDGGRLTSAWELFKAQEKLVHIGK 667

                    kyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf
                    ky v +  FHGRGG v RGGGP HLAiLsqP  ti+  lRvt+qGEvi +
  gi|1248088   668 KYSVEIRFFHGRGGSVSRGGGPQHLAILSQPINTIKNYLRVTIQGEVITQ 717

                    sFGEEnLCFrsLqRFtAAtLEHG.mnPPvsPkPEWRkLmeemAvvAtEEY
                     F    +  rs+  +  A L    ++  +  k EWR+Lm+e+  + t EY
  gi|1248088   718 DFCLKGMALRSVEIYMSALLKCSlLKNTLVIKKEWRDLMDEISEISTKEY 767

                    RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWi
                    R vv+    Fv YFR AtPE+E Gk+n+GsRP+KRk  G +esLRAiPW+
  gi|1248088   768 RKVVYENKDFVKYFRCATPEIEIGKLNLGSRPSKRK-EGNVESLRAIPWV 816

                    FaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDL
                    F+Wtq R HL vWLG+   + + i+     l  +++mY  WPF      L
  gi|1248088   817 FSWTQNRMHLSVWLGIEKIYDYLINNN--KLHIIQDMYTHWPFCTSFFNL 864

                    lEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHk
                    + mv AK    i   yD +Lv EeLk  G  LR+k +   +l   +   k
  gi|1248088   865 ISMVMAKASIQISQEYD-ILVPEELKYIGVLLREKLKKSMELTFLVTNEK 913

                    DlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKE
                       + D   K  +  R  ++t  n +q   LKR+R+ + k     +   +
  gi|1248088   914 KFCDNDQLTKRSIECRTKWVTVCNLIQIQALKRLREKESKQKNENKDQLD 963

                    yAdEns.kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      d  s        k+     v P  E t +  +K     + n
  gi|1248088   964 NKDNSSyTNITHNYKIYENTLVTPTSEYTNVENIKQDNNQLNNSM    1008

gi|51701320|sp|Q6R2V6.1|CAPP2_CHLRE: domain 1 of 1, from 1 to 1221: score 572.7, E = 4.1e-169
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                *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedL...
                     D        G v +d   +e D  Ll   L+D L    Ge + ++
gi|5170132     1    MTDSTYDF---GAVRDDLTPLEDDCKLLGSLLdDCLRVEIGETMfkk 44

                ....kEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkail
                 ++ +   q    ls   +          L   L  Ld  +a+ + +a
gi|5170132    45 ieriRALAQCASNLSIKGDAGASDMLSHRLAEELMNLDMDEAVPLTRACG 94

                HmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlk
                H LnL  +AE  +   R R  +                  +  + +L+
gi|5170132    95 HYLNLSGIAELHHGVRRDRATREP-----------NPNSCDAVFARLITE 133

                lnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK
                +   PeE + A+  q v++vltAHPtq  RR L  K++Ri   L q
gi|5170132   134 G-VDPEELYRAVSEQNVEVVLTAHPTQVNRRTLQYKHTRIAALLQQHDRS 182

                DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvW
                D+t e+++ +   L RE+ A + tDE+RR +PtP DE R G+  +   +W
gi|5170132   183 DLTAEERRNMVSELQREVAALWQTDELRRQKPTPLDEARGGLHIVEQSLW 232

                kGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPE
                  vP+++RR   ALK       lP ++   +F sWmGGDRDG nP vt
gi|5170132   233 AAVPQYMRRLSAALKK-HTGHDLPLQATPFRFGSWMGGDRDG-NPNVTAK 280

                vtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndEL.....RvRAE...
                vt  v  LaR mAa lY+  ++ L FElsm  C   + +  +R+ AE+++
gi|5170132   281 VTAHVTALARWMAADLYLREIDTLRFELSMNQCSAAVwkmarRIIAEght 330

                ..................................................
                ++ +  + +     +++ ++  +++++  +       +++   +++++++
gi|5170132   331 kragvvrakaaaalhqtatdaashggsaasaaaaaaaggdvvadgtsggg 380

                ..................................................
                     ++      ++  + ++ ++++++++++ ++ +   ++++   ++
gi|5170132   381 aaaaagpaaaaaaddaftfsrlgrprperpstdvrsvgvlaggegaafpg 430

                ..................................................
                +   ++++ + ++  + + +++ ++++ +++++ + +++++ ++ ++ +
gi|5170132   431 gmilgtqpvsahtaaevsvphelpgqdveggsemdfnesrrasdagdlga 480

                ........................................El........
                ++++  ++++ + + +++ ++ +++ +      +++++++E++++++  +
gi|5170132   481 sqhpmlggpsagasaeptahgytttataaaaaadgtqpepEVpgtpsyad 530

                ............................yrtaar................
                ++++++ +  +++ ++++++ ++  +   +taa+++ +++++++ ++  +
gi|5170132   531 pgtpdrlgalpgpftpgptpfreaanaaMSTAASggaggggggganraas 580

                ...............dkvvKyYiEFWK..qvPPtEPYRviLGdvRDKLYn
                + +++++ ++++   +++    + F + +  P   PYR++LG vRD+L
gi|5170132   581 glggdptftrrslmaQRLGTSSVQFARahEHPGFHPYRIVLGHVRDRLAA 630

                tRERaRHLL.........AtGisei......sEeAvytkvEeFLEPLELCY
                tR R   LL+++++ ++A+G    ++++++     y   +e  EPL  CY
gi|5170132   631 TRRRMEDLLsgrepageAHGGVGAgggggggGAAPWYESEDELAEPLMACY 680

                ksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAit
                 sL eCG  viADG LLDl+R v+tFG+ L+KLD+RqEs R+ + lDA+t
gi|5170132   681 WSLWECGGGVIADGRLLDLIRRVYTFGMCLMKLDLRQESTRHAEALDAVT 730

                tHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrv
                  L++GsY eWsE+++ EWL  EL+G+RPL+++D+P+  Ev++vld+f+v
gi|5170132   731 SYLGLGSYLEWSEDQKIEWLTKELQGRRPLIPADMPMSAEVREVLDTFKV 780

                LAELPiDsFGaYiismataPsDvLAvELLqRECgvkq.............
                 A L  D  GaY+ism+   sDv+AvELLqRE  ++ + + +++++++++
gi|5170132   781 AAHLGRDNLGAYVISMTKGASDVMAVELLQREARMQVgaeaggrggggpe 830

                ...tLrvvPLFEkLADLeAAPAavekLFsiDWYinridG....KqevmvG
                ++++LrvvPLFE L DL+AA   + +L    WY+ ++   +++ qevm+G
gi|5170132   831 dggSLRVVPLFETLEDLDAAEDVMTRLLTNPWYREHLRAvhgdAQEVMLG 880
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                    YsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGG
                    YsDsGKDAGRl+A W LYk qE ++ + K   vKL+lFHGRGGtvGRGGG
  gi|5170132   881 YSDSGKDAGRLAANWALYKCQERLVAITKANNVKLTLFHGRGGTVGRGGG 930

                    PtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLE
                    PtH+Ai sqPP  ++G  R+t qGE++   FG   +    L  +t A L
  gi|5170132   931 PTHIAIQSQPPGSVEGTFRITEQGEMVQAKFGISGVALSQLETYTTAVLL 980

                    HGmnPPvsP.kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPEl
                      m PP  P++ EWR +me +  v  E YR +v   P F  YF+ AtPE
  gi|5170132   981 ATMRPPSPPrREEWRAVMEMLSRVSCESYRNIVHHSPLFLRYFKHATPEA 1030

                    EYGkmniGsRPaKRkP.sGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAF
                    E G + iGsRPa+R+ +   i +LRAiPWiFaWtq R  LP WLG+GAA
  gi|5170132  1031 ELGNLYIGSRPARRRNkDASISTLRAIPWIFAWTQNRLILPSWLGIGAAL 1080

                    KhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL
                      A+ +    l  L+ mY+eWPFF  t+DL+Em+ AK DP iAaLy+++L
  gi|5170132  1081 TAAMTQGH--LPTLQAMYREWPFFGSTVDLIEMILAKTDPRIAALYEEVL 1128

                    vaE.eLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsY
                    v ++e k  G +LR++ +  +  +Lk+ GH  lL   P L + + +R ++
  gi|5170132  1129 VNDpEEKKLGAELRERLQRCQGAILKVTGHENLLSNNPTLSKLISMRSPF 1178

                    ittLnvfqAYtLKRiR.DPsykvtlrPhlsKEyAdEnskkadeLvkLnpt
                    +  +n++q   L+R+R+DP+                n       ++L
  gi|5170132  1179 VDPINILQVEVLRRLRqDPN----------------N-------MRLR-- 1203

                    ervaPGLEDtLiLtmKGiAAGmqntG<-*
                            D L++ + GiAAGm ntG
  gi|5170132  1204 --------DALLISINGIAAGMRNTG    1221

gi|83282693|ref|XP_729881.1|: domain 1 of 1, from 15 to 987: score 567.8, E = 1.2e-167
                    *->siDAqLRlLvPGKvsedekLieY......DALLlDkFL.DiLqDLHG
                         D +LR L+ GK+ e +  +++ ++ ++D   lD  L D+L+
  gi|8328269    15    --DGKLRFLIEGKMMETQYSVDFikplkgDIKALDFLLfDMLKNNLP 59

                    edLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailH
                    ++L E+     +ls  Y      +  e L   +  L       +  a+ H
  gi|8328269    60 PNLYEILCTIHDLSEKYSENPTNENFELLKNCVYNLKDEYLGTIVNAFGH 109

                    mLnLAnLAEEvelAyRRRikkkkhGDFa..DEasAttEsDiEEtlKkLvl
                    m  L n AE    A+R R +k     F ++D         +  t+  L+
  gi|8328269   110 MCVLSNFAE---WAHRGRRRKAFEKAFIpnDKIYGAVYETLRGTFNILIN 156

                    klnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsA
                     +    +++++ + nq+++ vlt HPtq++R sLL+    +   L +L
  gi|8328269   157 NG-ININDIYDQICNQTIEFVLTTHPTQAIRTSLLKNYIQLGELLLKLDN 205

                    KDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtv
                           Kk L + L   +   ++tD iRR +PtP DE    +  +   +
  gi|8328269   206 TNKELYKKKLLCDNLKAYLLSSWKTDVIRRIKPTPIDEAITLLDIVENCI 255

                    WkGvPKFLRRvDtALKniGinERlPYdvPLik.......FssWmGGDRDG
                    +  +P  +R +D  L         l Y+ P ik +++   FssW GGDRDG
  gi|8328269   256 FYRIPNIIRYIDNVL--------LEYNMPPIKlkskiclFSSWAGGDRDG 297

                    knPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCn.......d
                     nP v PE t  vC + ++    l+i  +E L+ +l +  C  + ++
  gi|8328269   298 -NPFVLPETTEYVCYMNKIRGCELFIPMIEKLIRDLTIHQCTvhfknyvK 346

                    ELRvRAEElyrtaardkvvKyYiEF..WKqvPPtEPYRviLGdvRDKLYn
                     L     ++     + ++ K +  F+++ +    E YR +L  v  KL
  gi|8328269   347 NLEHNISDIIFDKDQYRLGKKFQWFspFSKYNKKEIYRRVLLIVLTKLKS 396

                    tRERaRHLLAtGiseis.EeAvytkvEeFLEPLELCYksLCeCGDkviAD
                         + L+     +      ++   EeF E L  CYksL e G   iA+
  gi|8328269   397 VVYVYKALISGDSVDPDfQKLMFKSTEEFEEILLECYKSLIESGNALIAE 446

                    GsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsE
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                    G L D++R v  FGL L+KLDiRqEse++   +  i + L+i  Y    E
  gi|8328269   447 GYLKDVIRNVNIFGLHLMKLDIRQESEKHIQAMNYICEKLNIKKYELLNE 496

                    eKRqEWLlaELkGKRPLlgsDLPktEEvk....DvldafrvLAELPiDsF
                    e R  +L   L+  RP+++  + +  +v ++   ++ +f +   +  D+
  gi|8328269   497 EERITFLTDILESNRPIIPNNIEQEPDVSsdflNIIKTFDMCSKMEEDAL 546

                    GaYiismataPsDvLAvELLq...RECgvkqtLrvvPLFEkLADLeAAPA
                    GaYiism+   sD+L vE+ q++ +    ++t rvvPL E +  L+
  gi|8328269   547 GAYIISMCQNASDILLVEVFQtsfKKNIHRKTQRVVPLLETIQALQMSST 596

                    avekLFsiDWYinri....dGKqevmvGYsDsGKDAGRlsAAWqLYkAqE
                     +e L    WY+n+++++ d  qe+m+GYsDsGKD GRl  AW L+kAqE
  gi|8328269   597 ILENLIKNKWYRNHLknnfDNIQEIMIGYSDSGKDGGRLTSAWELFKAQE 646

                    EiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtv
                     +++v  ky + +  FHGRGG v RGGGP HLAiLsqP  ti+   R+t+
  gi|8328269   647 KLVQVGAKYSIEIRFFHGRGGSVSRGGGPQHLAILSQPINTIKNYTRITI 696

                    qGEviEfsFGEEnLCFrsLqRFtAAtLEHG.mnPPvsPkPEWRkLmeemA
                    qGEvi + FG   +  rs+  +  A L    ++  v  k EWR+Lm+++
  gi|8328269   697 QGEVITQDFGLKGMALRSVETYISALLKCSlLKNRVLIKQEWRDLMDDIS 746

                    vvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGies
                       t EYR +v+  P Fv YFR AtPE+E Gk+n+GsRP+KRk  G +es
  gi|8328269   747 ELTTKEYRKIVYENPDFVKYFRYATPEIEIGKLNLGSRPSKRK-KGNVES 795

                    LRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPF
                    LRAiPW+F+Wtq R HL vWLG+   +++ +  D   lq L++mYk+WPF
  gi|8328269   796 LRAIPWVFSWTQNRMHLSVWLGIEEIYQYIM--DNNKLQILQDMYKNWPF 843

                    FRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlL
                          L+ mv AK    iA  yD +Lv   Lk  G +LR+k +   +l
  gi|8328269   844 CTSFFNLISMVMAKASIKIAEEYD-ILVPNHLKYIGVQLREKLKKSMELT 892

                    LkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtl
                    L +   +   + D   K  +  R  ++t  n +q   LKR+R+ +    l
  gi|8328269   893 LLVTNEQNFCDNDQITKRSIETRTKWVTVCNLIQIQALKRLREKEENADL 942

                    rPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqnt
                     P  s +  d n    d+    n  +       D L+L    i     n
  gi|8328269   943 DPNHSED--DGN---NDDNNNGN-DSMTLKVSKDKLLLNQISIKNEAINK 986

                    G<-*

  gi|8328269   987 D    987

gi|68071185|ref|XP_677506.1|: domain 1 of 1, from 15 to 993: score 567.4, E = 1.7e-167
                    *->siDAqLRlLvPGKvsedekLieY......DALLlDkFL.DiLqDLHG
                         D +LR L+ GK+ e +  +++ ++ ++D   lD  L D+L+
  gi|6807118    15    --DGKLRFLIEGKMMETQYPVDFikplkgDIKALDFLLfDMLKNNLP 59

                    edLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailH
                    ++L E+     +ls  Y      +  e L   +  L       +  a+ H
  gi|6807118    60 PNLYEILCTIHDLSEKYSENPTNENFELLKNCVYNLKDEYLGTIVNAFGH 109

                    mLnLAnLAEEvelAyRRRikkkkhGDFa..DEasAttEsDiEEtlKkLvl
                    m  L n AE    A+R R +k     F ++D         +  t+  L+
  gi|6807118   110 MCVLSNFAE---WAHRGRRRKAFEKTFIpnDKIYGAVYETLRGTFNILIN 156

                    klnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsA
                     +    +++++ + nq+++ vlt HPtq++R sLL+    +   L +L
  gi|6807118   157 NG-ININDIYDQICNQTIEFVLTTHPTQAIRTSLLKNYIQLGELLLKLDN 205

                    KDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtv
                           Kk L + L   +   ++tD iRR +PtP DE    +  +   +
  gi|6807118   206 TNKELYKKKLLCDNLKAYLLSSWKTDVIRRIKPTPIDEAISLLDIVENCI 255

                    WkGvPKFLRRvDtALKniGinERlPYdvPLik.......FssWmGGDRDG
                    +  +P  +R +D  L        l Y+ P ik +++   FssW GGDRDG
  gi|6807118   256 FYRIPNIIRYIDNVL--------LEYNMPPIKlkskiclFSSWAGGDRDG 297
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                    knPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCn.......d
                     nP v PE t  vC + ++    l+i  +E L+ +l +  C  + ++
  gi|6807118   298 -NPFVLPETTQYVCYMNKIRGCELFIPMIEKLIRDLTIHQCTvhfknyvK 346

                    ELRvRAEElyrtaardkvvKyYiEF..WKqvPPtEPYRviLGdvRDKLYn
                     L     ++     + ++ K +  F+++ +    E YR +L  v  KL
  gi|6807118   347 NLEHNISDIIFDKDKYRLGKKFQWFspFSKYNKKEIYRRVLLIVLTKLKS 396

                    tRERaRHLLA.tGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviAD
                         + L+ +  +     + ++   EeF E L  CYksL e G   iA+
  gi|6807118   397 VVYVYKALISgESVDPDFKNLMFKSTEEFEEILLECYKSLIESGNALIAE 446

                    GsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsE
                    G L D++R v  FGL L+KLDiRqEse++   +  i + L+i  Y    E
  gi|6807118   447 GYLKDVIRNVNIFGLHLMKLDIRQESEKHIQAMNYICEKLNIKKYELLNE 496

                    eKRqEWLlaELkGKRPLlgsDLPktEEv....kDvldafrvLAELPiDsF
                    e R  +L   L+  RP+++  + +  +v+++   ++ +f +   L   +
  gi|6807118   497 EERITFLTDILESNRPIIPNNIEQEPDVpsdfLNIIKTFDMCSKLEESAL 546

                    GaYiismataPsDvLAvELLq...RECgvkqtLrvvPLFEkLADLeAAPA
                    GaYiism+   sD+L vE+ q++ +    ++t rvvPL E +  L+
  gi|6807118   547 GAYIISMCQNASDILLVEVFQtsfKKNIHRKTQRVVPLLETIQSLQMSST 596

                    avekLFsiDWYinri....dGKqevmvGYsDsGKDAGRlsAAWqLYkAqE
                     +e L    WY+n+++++ d  qe+m+GYsDsGKD GRl  AW L+kAqE
  gi|6807118   597 ILENLIKNKWYRNHLknnfDNIQEIMIGYSDSGKDGGRLTSAWELFKAQE 646

                    EiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtv
                     ++++  ky + +  FHGRGG v RGGGP HLAiLsqP  ti+  +R+t+
  gi|6807118   647 KLVQIGAKYFIEIRFFHGRGGSVSRGGGPQHLAILSQPINTIKNYIRITI 696

                    qGEviEfsFGEEnLCFrsLqRFtAAtLEHG.mnPPvsPkPEWRkLmeemA
                    qGEvi + FG   +  rs+  +  A L    ++  vs k EWR+Lm+++
  gi|6807118   697 QGEVITQDFGLKGMALRSVETYISALLKCSlLKNKVSIKQEWRDLMDDIS 746

                    vvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGies
                       t EYR +v+  P Fv YFR AtPE+E Gk+n+GsRP+KRk  G +es
  gi|6807118   747 ELTTKEYRKIVYENPDFVKYFRFATPEIEIGKLNLGSRPSKRK-KGNVES 795

                    LRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPF
                    LRAiPW+F+Wtq R HL vWLG+   +++ ++     lq L++mY +WPF
  gi|6807118   796 LRAIPWVFSWTQNRMHLSVWLGIEEIYQYVMNNN--KLQILQDMYTNWPF 843

                    FRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlL
                          L+ mv AK    iA  yD +Lv  +Lk  G +LR+k +   +l
  gi|6807118   844 CTSFFNLISMVMAKASIKIAEEYD-ILVPNNLKYIGVQLREKLKKSMQLT 892

                    LkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtl
                    L +   +   + D   K  +  R  ++t  n +q   LKR+RD +    l
  gi|6807118   893 LLVTNEQNFCDNDQITKRSIETRTKWVTVCNLIQIQALKRLRDKEGNTHL 942

                    rP...hlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGm
                     P++   sK   +   k + +   Ln   +++   E+        i  G
  gi|6807118   943 DPnniNFSKHDNNMTLKVSKDKSLLN---QISIKNEEINKDDDNNINDGR 989

                    qntG<-*
                     n
  gi|6807118   990 TNNS    993

gi|145641160|ref|ZP_01796740.1|: domain 1 of 1, from 1 to 758: score 554.2, E = 1.5e-163
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1456411     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1456411     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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                              k                  t+ kL   l
gi|1456411     1 -------------MHK------------------TVEKLLIEL------- 12

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                             vltAHPt   RRsL+ K+  i  CL++L   D+t  ++
gi|1456411    13 -----------VLTAHPTETTRRSLIHKHIEINKCLSKLEHHDLTEKERN 51

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ++  L R i  A+ t EiR  +PtP DE + G + +   +W+ vP FLR
gi|1456411    52 IIERLLLRLIAEAWHTNEIRTVRPTPFDEAKWGFAMLENSLWQAVPEFLR 101

                  RvDtALKniGinERlPYdvPL....ikFssWmGGDRDGknPRvtPEvtRD
                         n    E l Yd P++ ++++ ssWmGGDRDG nP vt  +t+
gi|1456411   102 QL-----NETTREFLGYDLPVglkpVRISSWMGGDRDG-NPFVTAQITKK 145

                  vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                  v   aR  Aa l+++ +  L  Elsm +C dE R            dk
gi|1456411   146 VLYFARWKAADLFLQDISKLADELSMMKCSDEFR------------DKYG 183

                  KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                   +           EPYR ++ + R +L  t       L      +sE  +
gi|1456411   184 EHL----------EPYRFVVKNLRNQLTATLAYFDDHLSNRTPRVSESEI 223

                  ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    +  +  EPL  CY+sL +CG ++iA GsLL +L  +s FG+ L ++Di
gi|1456411   224 ILEDNQLWEPLYDCYQSLIQCGMRIIANGSLLNILHRISCFGVTLSQMDI 273

                  RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                  RqEs R+tD +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
gi|1456411   274 RQESTRHTDAIAEITRYIGLGDYSQWMEDDKQAFLIRELSSRRPLIPQNW 323

                  PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                      E k++ld+ +v+A         Y+isma + sDvLAv LL +E gv
gi|1456411   324 TPSPETKEILDTCKVIAQQKQGVIACYVISMAHSASDVLAVHLLLKEAGV 373

                  kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsG
                     ++vvPLFE L DL+AA   + +LF + WY+  i+ +q vm+GYsDs
gi|1456411   374 PYHIPVVPLFETLEDLDAAEKVMTQLFNVGWYRGVINNRQMVMIGYSDSA 423

                  KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                  KDAG ++A W  Y+AqE ++    k G+ L+lFHGRGGt+GRGG P H A
gi|1456411   424 KDAGMMAASWAQYRAQEALVNLTEKLGIELTLFHGRGGTIGRGGAPAHAA 473

                  iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP
                  +LsqPP  ++  lRvt qGE+i f  G   +   +   ++ A LE  + P
gi|1456411   474 LLSQPPRSLKNGLRVTEQGEMIRFKLGLPAVAVETFDLYASAILEANLLP 523

                  PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmn
                  P  PkPEWR +m+e+  +  + YR vv  +  Fv YFR+AtPE E  k+
gi|1456411   524 PPEPKPEWRTIMDELSTISCDIYRGVVRGDKDFVPYFRSATPEQELSKLP 573

                  iGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                  +GsRPaKR P GG+esLRAiPWiFaW q R  LP WLG GAA +  i++
gi|1456411   574 LGSRPAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGAAIRQVIEQG 623

                  iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP
                     +  ++ m ++WPFF   + +lEmvF K D  +   yD+ Lv  eL+
gi|1456411   624 KGDI--IHKMCENWPFFSTRIGMLEMVFSKSDTWLSQQYDQRLVKKELWY 671

                  FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfq
                   G++LR + ++  + +L +    +l+   P++   + LR+ Y   Ln +q
gi|1456411   672 LGENLRKQLEDDIQTVLSLSHQSELMSDLPWIADSIALRNIYTDPLNLLQ 721

                  AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                     L R R                  En             e+v P +E
gi|1456411   722 VELLHRFR-----------------EN------------PEQVNPDVEQ 741

                  tLiLtmKGiAAGmqntG<-*
                   L++t+ GiAAGm ntG
gi|1456411   742 ALMITITGIAAGMRNTG    758
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gi|154146762|emb|CAM84068.1|: domain 1 of 1, from 1 to 439: score 538.3, E = 9.3e-159
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDv+DAittHL+iGsYR+W+E+KR EWL++EL+GKRPLl++DLP+tE
  gi|1541467      1 --HTDVIDAITTHLGIGSYRSWPEDKRVEWLVSELRGKRPLLPPDLPMTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++Dv++a+rv+AELP+DsFG+Yiism+taPsDvLAvELLqRECg++q+L
  gi|1541467     49 EIADVIGAMRVIAELPSDSFGPYIISMCTAPSDVLAVELLQRECGIRQSL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +vvPLFE+LADL+AAPA+vekLFs+DWYi +i GKq+vmvGYsDsGKDAG
  gi|1541467     99 PVVPLFERLADLQAAPASVEKLFSTDWYIDHIKGKQQVMVGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLY+AqEE++KvAKkyGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1541467    149 RLSAAWQLYVAQEEMAKVAKKYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGs+RvtvqGEviEf+FGE++LCF+sLqRFtAAtLEHGm+PPvsP
  gi|1541467    199 PPDTINGSIRVTVQGEVIEFMFGEDHLCFQSLQRFTAATLEHGMHPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWRkLm+emAvvAtEEYRsvvvKEPRFvEYFR+AtPE+EYGkmniGsR
  gi|1541467    249 KPEWRKLMDEMAVVATEEYRSVVVKEPRFVEYFRSATPETEYGKMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKRkP+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+AidKDiKn+
  gi|1541467    299 PAKRKPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKWAIDKDIKNF 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  qkLkEmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva+eLkPFGk+
  gi|1541467    349 QKLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADELKPFGKQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR+kYvEt++lLL+iAGHkD+LEGDPYLK +lRLR++Yitt
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  gi|1541467   399 LREKYVETQQLLLQIAGHKDILEGDPYLKEGLRLRNPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146754|emb|CAM84064.1|: domain 1 of 1, from 1 to 439: score 538.2, E = 1e-158
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDv+DAittHL+iGsYR+W+E+KR E+L++ELkGKRPLl++DLP+tE
  gi|1541467     1 --HTDVIDAITTHLGIGSYRSWPEDKRVEFLVTELKGKRPLLPADLPMTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dv++a++v+AELP+DsFG+Yiism+taPsDvLAvELLqRECg+kqtL
  gi|1541467    49 EIADVIGAMKVIAELPSDSFGPYIISMCTAPSDVLAVELLQRECGIKQTL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLFE+LADL+ APA+vekLFs+DWYin+i+GKq+vmvGYsDsGKDAG
  gi|1541467    99 PVVPLFERLADLQGAPASVEKLFSTDWYINHINGKQQVMVGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLY+AqEE++KvAKkyGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYVAQEEMAKVAKKYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGs+RvtvqGEviEf+FGEEnLCF+sLqRFtAAtLEHGm+PPvsP
  gi|1541467   199 PPDTINGSIRVTVQGEVIEFMFGEENLCFQSLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFR+AtPE+EYGkmniGsR
  gi|1541467   249 KPEWRKLMEEMAVVATEEYRSVVVKEPRFVEYFRSATPETEYGKMNIGSR 298
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                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkP+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+AidKDiKn+
  gi|1541467   299 PAKRKPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKWAIDKDIKNF 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    qkLkEmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLvaEeLkPFGks
  gi|1541467   349 QKLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVAEELKPFGKS 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRdkYvEt++lLL+iAGHkD+LEGDPYLK +l+LR++Yitt
  gi|1541467   399 LRDKYVETQQLLLQIAGHKDILEGDPYLKEGLKLRNPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146800|emb|CAM84087.1|: domain 1 of 1, from 1 to 439: score 537.9, E = 1.3e-158
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDv+DAittHL+iGsYR+W+E+KR E+L++ELkGKRPLl++DLP+tE
  gi|1541468     1 --HTDVIDAITTHLGIGSYRSWPEDKRVEFLVSELKGKRPLLPADLPMTE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dv++a++v+AELP+DsFG+Yiism+taPsDvLAvELLqRECg+kqtL
  gi|1541468    49 EIADVIGAMKVIAELPSDSFGPYIISMCTAPSDVLAVELLQRECGIKQTL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFE+LADL+ APA+vekLFs+DWYin+i+GKq+vmvGYsDsGKDAG
  gi|1541468    99 PVVPLFERLADLQGAPASVEKLFSTDWYINHINGKQQVMVGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLY+AqEE++KvAKkyGvKL+lFHGRGGtvGRGGGPtHLAiLsq
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  gi|1541468   149 RLSAAWQLYVAQEEMAKVAKKYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGs+RvtvqGEviEf+FGE+nLCF+sLqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTINGSIRVTVQGEVIEFMFGEDNLCFQSLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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  gi|1541468   249 KPEWRKLMEEMAVVATEEYRSVVVKEPRFVEYFRSATPETEYGKMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKRkP+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+AidKDiKn+
  gi|1541468   299 PAKRKPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKWAIDKDIKNF 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   qkLkEmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva+eLkPFGks
  gi|1541468   349 QKLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADELKPFGKS 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LRdkYvEt++lLL+iAGHkD+LEGDPYLK +lRLR++Yitt
  gi|1541468   399 LRDKYVETQQLLLQIAGHKDILEGDPYLKEGLRLRNPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - -------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146808|emb|CAM84091.1|: domain 1 of 1, from 1 to 439: score 537.0, E = 2.3e-158
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - -------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - -------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - -------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - -------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - -------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - -------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - -------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - -------------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDv+DAittHL+iGsYR+W+E+KR E+L++ELkGKRPLl++DLP+tE
  gi|1541468     1 --HTDVIDAITTHLGIGSYRSWPEDKRVEFLVSELKGKRPLLPPDLPMTE 48
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                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dv++a++v+AELP+DsFG+Yiism+taPsDv AvELLqRECg+kqtL
  gi|1541468    49 EIADVIGAMKVIAELPSDSFGPYIISMCTAPSDVFAVELLQRECGIKQTL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLFE+LADL+ APA+vekLFs+DWYin+i+GKq+vmvGYsDsGKDAG
  gi|1541468    99 PVVPLFERLADLQGAPASVEKLFSTDWYINHINGKQQVMVGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLY+AqEE++KvAKkyGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYVAQEEMAKVAKKYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGs+RvtvqGEviEf+FGEEnLCF+sLqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTINGSIRVTVQGEVIEFMFGEENLCFQSLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFR+AtPE+EYGkmniGsR
  gi|1541468   249 KPEWRKLMEEMAVVATEEYRSVVVKEPRFVEYFRSATPETEYGKMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKRkP+GGi++LRAiPWiF+WtqtRFHLPvWLGvG AFK+AidKDiKn+
  gi|1541468   299 PAKRKPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGGAFKWAIDKDIKNF 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   qkLkEmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLvaEeLkPFGks
  gi|1541468   349 QKLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDDLLVAEELKPFGKS 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LRdkYvEt++lLL+iAGHkD+LEGDPYLK +lRLR++Yitt
  gi|1541468   399 LRDKYVETQQLLLQIAGHKDILEGDPYLKEGLRLRNPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146746|emb|CAM84060.1|: domain 1 of 1, from 1 to 439: score 535.9, E = 5e-158
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
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  gi|1541467     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDv+DAittHL+iGsYR+W+EeKR EWL+ ELkGKRPLl++DLP+tE
  gi|1541467     1 --HTDVIDAITTHLGIGSYRSWPEEKRVEWLVGELKGKRPLLPPDLPMTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dv++a++vLAELP+DsFG+Yiism+taPsDvLAvELLqRECg+kqtL
  gi|1541467    49 EIADVVGAMHVLAELPSDSFGPYIISMCTAPSDVLAVELLQRECGIKQTL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLFE+LADL+ APA+vekLFs+DWYin+i+GKq+vmvGYsDsGKDAG
  gi|1541467    99 PVVPLFERLADLQNAPASVEKLFSTDWYINHINGKQQVMVGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLY+AqEE++KvAKkyGvKL+lFHGRGGtvGRGGGP HLAiLsq
  gi|1541467   149 RLSAAWQLYVAQEEMAKVAKKYGVKLTLFHGRGGTVGRGGGPSHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGs+RvtvqGEviEf+FGEEnLCF+sLqRFtAAtLEHGm+PPvsP
  gi|1541467   199 PPDTINGSIRVTVQGEVIEFMFGEENLCFQSLQRFTAATLEHGMHPPVSP 248

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  gi|1541467   249 KPEWRKLMEEMAVVATEEYRSVVVKEPRFVEYFRSATPETEYGKMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKRkP+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+AidKDiKn+
  gi|1541467   299 PAKRKPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKWAIDKDIKNF 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   qkLkEmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva+eLkPFGks
  gi|1541467   349 QKLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADELKPFGKS 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LRdkYvEt++lLL+iAGHk++LEGD YLKq+lRLR++Yitt
  gi|1541467   399 LRDKYVETQQLLLQIAGHKEILEGDLYLKQGLRLRNPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146724|emb|CAM84049.1|: domain 1 of 1, from 1 to 439: score 535.4, E = 6.8e-158
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------ -
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                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDv+DAittHL+iGsYR+W+E+KR E+L++ELkGKRPLl++DLP+tE
  gi|1541467     1 --HTDVIDAITTHLGIGSYRSWPEDKRVEFLVSELKGKRPLLPPDLPMTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++Dv++a++v+AELP+DsFG+Yiism+taPsDv AvELLqRECg+kqtL
  gi|1541467    49 EIADVIGAMKVIAELPSDSFGPYIISMCTAPSDVFAVELLQRECGIKQTL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +vvPLFE+LADL+ APA+vekLFs+DWYin+i+GKq+vmvGYsDsGKDAG
  gi|1541467    99 PVVPLFERLADLQGAPASVEKLFSTDWYINHINGKQQVMVGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
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  gi|1541467   149 RLSAAWQLYVAQEEMAKVAKKYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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  gi|1541467   199 PPDTINGSIRVTVQGEVIEFMFGEENLCFQSLQRFTAATLEHGMHPPVSP 248

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  gi|1541467   249 KPEWRKLMEEMAVVATEEYRSVVVKEPRFVEYFRSATPETEYGKMDIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
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  gi|1541467   299 PAKRKPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKWAIDKDIKNF 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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  gi|1541467   349 QKLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADELKPFGKS 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LRdkYvEt++lLL+iAGHkD+LEGDPYLK +lRLR++Yitt
  gi|1541467   399 LRDKYVETQQLLLQIAGHKDILEGDPYLKEGLRLRNPYITT--------- 439

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146788|emb|CAM84081.1|: domain 1 of 1, from 1 to 439: score 535.0, E = 9e-158
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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  gi|1541467     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDv+DAittHL+iGsYR+W+E+KR E+L +ELkGKRPLl++DLP+tE
  gi|1541467     1 --HTDVIDAITTHLGIGSYRSWPEDKRVEFLESELKGKRPLLPPDLPMTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dv++a+rv+AELP+DsFG+Yiism+taPsDv AvELLqRECg+kqtL
  gi|1541467    49 EIADVIGAMRVIAELPSDSFGPYIISMCTAPSDVFAVELLQRECGIKQTL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLFE+LADL+AAPA+vekLFs+DWYin+i+GKq+vmvGYsDsGKDAG
  gi|1541467    99 PVVPLFERLADLQAAPASVEKLFSTDWYINHINGKQQVMVGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLY+AqEE++KvAKkyGvKL+lFHGRGGtvGRGGGPtHLA+Lsq
  gi|1541467   149 RLSAAWQLYVAQEEMAKVAKKYGVKLTLFHGRGGTVGRGGGPTHLAVLSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGs+RvtvqGEviEf+FGEEnLCF+sLqRFtAAtLEHGm+PPvsP
  gi|1541467   199 PPDTINGSIRVTVQGEVIEFMFGEENLCFQSLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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  gi|1541467   249 KPEWRKLMEEMAVVATEEYRSVVVKEPRFVEYFRSATPETEYGEMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKRkP+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+AidKDiKn+
  gi|1541467   299 PAKRKPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKWAIDKDIKNF 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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  gi|1541467   349 QKLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADELKPFGKS 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LRdkYvEt++lLL+iAGHkD+LEGDPYLK +lRLR++Yitt
  gi|1541467   399 LRDKYVETQQLLLQIAGHKDILEGDPYLKEGLRLRNPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146830|emb|CAM84102.1|: domain 1 of 1, from 1 to 439: score 534.6, E = 1.2e-157
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                *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

gi|1541468     -    ---------------------------------------------- -

                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|1541468     - ---------------------------------------------- -

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1541468     - ---------------------------------------------- -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1541468     - ---------------------------------------------- -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1541468     - ---------------------------------------------- -

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gi|1541468     - ---------------------------------------------- -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1541468     - ---------------------------------------------- -

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1541468     - ---------------------------------------------- -

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1541468     - ---------------------------------------------- -

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  +tDv+DAittHL+iGsYR+W+E+KR E+L++ELkGKRPLl++DLP+tE
gi|1541468      1 --HTDVIDAITTHLGIGSYRSWPEDKRVEFLVSELKGKRPLLPPDLPMTE 48

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                E++Dv++a++v+AELP+DsFG+Yiism+taPsDvLAvELLqRECg+kqtL
gi|1541468     49 EIADVIGAMKVIAELPSDSFGPYIISMCTAPSDVLAVELLQRECGIKQTL 98

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                +vvPLFE+LADL+ APA+vekLFs+DWYin+i GKq+vmvGYsDsGKDAG
gi|1541468     99 PVVPLFERLADLQGAPASVEKLFSTDWYINHIGGKQQVMVGYSDSGKDAG 148

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLY+AqEE++KvAKkyGvKL+lFHGRGGtvGRGGGPtHLAiLsq
gi|1541468    149 RLSAAWQLYVAQEEMAKVAKKYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PPDtinGs+RvtvqGEviEf+FGE+nLCF+sLqRFtAAtLEHGm+PPvsP
gi|1541468    199 PPDTINGSIRVTVQGEVIEFMFGEDNLCFQSLQRFTAATLEHGMHPPVSP 248

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFR+AtPE+EYGkmniGsR
gi|1541468    249 KPEWRKLMEEMAVVATEEYRSVVVKEPRFVEYFRSATPETEYGKMNIGSR 298

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                PaKRkP+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+AidKDiKn+
gi|1541468    299 PAKRKPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKWAIDKDIKNF 348

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                qkLkEmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva+eLkPFGks
gi|1541468    349 QKLKEMYNEWPFFRVTLDLLEMVFAKGDPGIASLYDELLVADELKPFGKS 398

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LRdkYvEt++lLL+iAGHkD+LEGDPYLK +lRLR++Yitt
gi|1541468    399 LRDKYVETQQLLLQIAGHKDILEGDPYLKEGLRLRNPYITT--------- 439
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                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------ -

                  tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146878|emb|CAM84126.1|: domain 1 of 1, from 1 to 439: score 524.3, E = 1.5e-154
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------ -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------ -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDvlDAittHL+iGsYR+W+E+KR EWL++EL+GKRPLl++DLP+tE
  gi|1541468     1 --HTDVLDAITTHLGIGSYRSWPEDKRVEWLVSELSGKRPLLPPDLPMTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++Dv++a++v+AELP+DsFG+Yiism+taPsDv AvELLqRECg+k+tL
  gi|1541468    49 EIADVIGAMKVIAELPSDSFGPYIISMCTAPSDVFAVELLQRECGIKKTL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +vvPLFE+LADL+AAPA+vekLFs+DWYi +i GKq+vmvGYsDsGKDAG
  gi|1541468    99 PVVPLFERLADLQAAPASVEKLFSTDWYIGHIGGKQQVMVGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLY+AqEE++KvAKkyGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYVAQEEMAKVAKKYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGs+RvtvqGEviEf+FGE+nLCF+sLqRFtAAtLEHG++PPvsP
  gi|1541468   199 PPDTINGSIRVTVQGEVIEFMFGEDNLCFQSLQRFTAATLEHGIHPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFR+AtPE+EYGkmniGsR
  gi|1541468   249 KPEWRKLMEEMAVVATEEYRSVVVKEPRFVEYFRSATPETEYGKMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
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                    PaKRkP+GGi++LRAiPWiF+WtqtRFHLPvWLGvG AFK+AidKDiKn+
  gi|1541468   299 PAKRKPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGGAFKWAIDKDIKNF 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    qkLkEmY+eWPFFRvtlDLlEmvFAKGDP iA+LyD+LLvaEeLkPFGk+
  gi|1541468   349 QKLKEMYNEWPFFRVTLDLLEMVFAKGDPAIAGLYDELLVAEELKPFGKQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR+kYvEt++lLL+iAGHkD+LEGDPYLK +lRLR++Yitt
  gi|1541468   399 LREKYVETQQLLLQIAGHKDILEGDPYLKEGLRLRNPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146834|emb|CAM84104.1|: domain 1 of 1, from 1 to 439: score 523.3, E = 3.1e-154
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDvlDAittHL+iGsYR+W+Ee+R+EWL++ELk KRPLl++DLP+tE
  gi|1541468     1 --HTDVLDAITTHLGIGSYRSWPEEQRMEWLVSELKSKRPLLPPDLPQTE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dv++a++vLAELP+DsFG+Yiism+taPsDvLAvELLqRECg+kqtL
  gi|1541468    49 EIADVIGAMHVLAELPSDSFGPYIISMCTAPSDVLAVELLQRECGIKQTL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFE+LADL+AAP +ve+LFs+DWYi +i GKq+vmvGYsDsGKDAG
  gi|1541468    99 PVVPLFERLADLQAAPESVERLFSTDWYIDHIKGKQQVMVGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLY+AqEE++KvAK+yGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYVAQEEMAKVAKRYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 198
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                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGs+RvtvqGEviEf+FGE+nLCF+sLqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTINGSIRVTVQGEVIEFMFGEDNLCFQSLQRFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWRkLm+emAvvAtEEYRsvvvKEPRFvEYFR+AtPE+EYGkmniGsR
  gi|1541468   249 KPEWRKLMDEMAVVATEEYRSVVVKEPRFVEYFRSATPETEYGKMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkP+GGi++LRAiPWiF+WtqtRFHLPvWLGvG AFK+AidKDiKn+
  gi|1541468   299 PAKRKPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGGAFKWAIDKDIKNF 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    qkLkEmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLvaEeLkPFGk+
  gi|1541468   349 QKLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVAEELKPFGKQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRdkYvE ++lLL+iAGHkD+LEGDPYLKq +RLR++Yitt
  gi|1541468   399 LRDKYVEAEKLLLQIAGHKDILEGDPYLKQAVRLRNPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146768|emb|CAM84071.1|: domain 1 of 1, from 1 to 439: score 516.3, E = 3.9e-152
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDvlDAittHL+iGsYR+W+E+KR EWL+ EL+GKRPLl++DLP+tE
  gi|1541467     1 --HTDVLDAITTHLGIGSYRSWPEDKRVEWLVMELRGKRPLLPPDLPMTE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
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                   Ev+Dv++a+rv+AELP+DsFG+Yiism+taPsDvLAvELLqRECg++qtL
  gi|1541467    49 EVADVIGAMRVIAELPSDSFGPYIISMCTAPSDVLAVELLQRECGIRQTL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLFE+LADL+AAPA+ve LFs+DWYi +i GKq+vmvGYsDsGKDAG
  gi|1541467    99 PVVPLFERLADLQAAPASVECLFSTDWYIDHIKGKQQVMVGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLY+AqEE++KvAKkyGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYVAQEEMAKVAKKYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGs+RvtvqGEviEf+FGE+nLCF+sLqRFtAAtLEHGm+PPvsP
  gi|1541467   199 PPDTINGSIRVTVQGEVIEFMFGEDNLCFQSLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR+Lm+emAvvAtEEYRsvvvKEPRFvEYFR+AtPE+EYGkmniGsR
  gi|1541467   249 KPEWRRLMDEMAVVATEEYRSVVVKEPRFVEYFRSATPETEYGKMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKRkP+GGi++LRAiPW+F+WtqtRFHLPvWLGvGAAFK+AidKDiKn+
  gi|1541467   299 PAKRKPGGGITTLRAIPWMFSWTQTRFHLPVWLGVGAAFKWAIDKDIKNF 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q+Lk mY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva+eLkPFGk+
  gi|1541467   349 QMLKQMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADELKPFGKQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LRdkYvEt++lLL+iAGHkD+LEGD YLK  lRL ++Yitt
  gi|1541467   399 LRDKYVETQQLLLQIAGHKDILEGDVYLKEELRLHNPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - -------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146820|emb|CAM84097.1|: domain 1 of 1, from 1 to 439: score 514.5, E = 1.3e-151
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - -------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - -------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - -------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - -------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - -------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - -------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - -------------------------------------------------- -
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                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDv+DAitt L+iGsYR+W+Ee+R+EWL++EL+GKRPLl++DLP+tE
  gi|1541468     1 --HTDVIDAITTYLGIGSYRDWPEEQRMEWLVSELQGKRPLLPPDLPQTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++Dv++a+rvLAELP+DsFG+Yiism+taPsDvLAvELLqRECg++qtL
  gi|1541468    49 EIADVIGAMRVLAELPSDSFGPYIISMCTAPSDVLAVELLQRECGIRQTL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +vvPLFE+LADL+AAPA+vekLFs+DWY  +i+GKq+vmvGYsDsGKDAG
  gi|1541468    99 PVVPLFERLADLQAAPASVEKLFSTDWYFQHINGKQQVMVGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLY+AqEE++KvAK++GvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYVAQEEMAKVAKRFGVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGs+RvtvqGEviEf+FGEE+LCF+sLqRFtAAtLEHGm+PPv+P
  gi|1541468   199 PPDTINGSIRVTVQGEVIEFMFGEEHLCFQSLQRFTAATLEHGMHPPVAP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWRkLm++mAvvAtEEYRsvvvKE RFvEYFR+AtPE+EYGkmniGsR
  gi|1541468   249 KPEWRKLMDDMAVVATEEYRSVVVKEERFVEYFRSATPETEYGKMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKRkP+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+AidKDiKn+
  gi|1541468   299 PAKRKPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKYAIDKDIKNF 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q+LkEmY+eWPFFRvtlDLlEmvFAKGDP iAaLyD+LLva+eLkPFGk+
  gi|1541468   349 QMLKEMYNEWPFFRVTLDLLEMVFAKGDPYIAALYDELLVADELKPFGKQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LRdkY Et +lLL+iAGHkD+LE DPYLKq+lRLR++Yitt
  gi|1541468   399 LRDKYMETLQLLLQIAGHKDILEADPYLKQGLRLRNPYITT--------- 439

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------ -

                  tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|167470809|ref|ZP_02335513.1|: domain 1 of 1, from 1 to 773: score 513.3, E = 3.1e-151
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      +  q  ++    vs          +L     D +++  Ge + + v
  gi|1674708     1    -MNEQYSAMR-SNVS----------MLGTLLGDTIKEALGEHILDRV 35

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       ls       ++++ +EL + L  L   + + vA+a++  LnL n
  gi|1674708    36 ETIRKLSKSSRAGNEASR-QELLTTLQNLSNDELLPVARAFSQFLNLTNT 84

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AE  +       +   hG+ a   +A     +   + +L  k   s +++
  gi|1674708    85 AEQYH-------SISPHGEAASNPEA-----LAQLFTRLKDKK-LSDQDM 121

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    A+   s++LvltAHPt   RR L+ K   +  CL+qL   D+   ++
  gi|1674708   122 RSAVDDLSIELVLTAHPTEITRRTLIHKLVEVNTCLSQLDHNDLADYERN 171

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   +   L   +   + tDEiR+ +P P DE + G + +   +W+GvP FLR
  gi|1674708   172 KIMRRLRQLVAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWEGVPAFLR 221

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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                      L n  +  RlP ++  i+F+sWmGGDRDG nP vt E+tR v LL
  gi|1674708   222 EFNEQLEN-SLDYRLPVEAVPIRFTSWMGGDRDG-NPNVTAEITRHVLLL 269

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   +R  A+ l++  +  L+ Elsm  C  ELR    El
  gi|1674708   270 SRWKATDLFLRDIQVLVSELSMSECTPELR----ELAGGEEVL------- 308

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                            EPYR ++ +vR +L nt       L +G   ++
  gi|1674708   309 ---------EPYRQLMKNVRTQLTNTQAYLEARL-KGERVLPPHDLLVSN 348

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   ++  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++D+RqEs
  gi|1674708   349 DQLWEPLYACYQSLKACGMEIIANGQLLDTLRRVRCFGVPLVRIDVRQES 398

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    R+tD +  +t+ L++G Y +WsE  +q +L+ EL  KRPL++
  gi|1674708   399 TRHTDAIAELTRYLGLGDYESWSESDKQAFLVRELNSKRPLVPLKWEPSA 448

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E ++vl++ rv+AE P  s  aY+isma  PsDvLAv LL +E g   tL
  gi|1674708   449 ETQEVLETCRVIAEAPQGSIAAYVISMAKVPSDVLAVHLLLKEAGCPFTL 498

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs KDAG
  gi|1674708   499 PVAPLFETLDDLNNADDVMTQLLGIDWYRGLIQGKQMVMIGYSDSAKDAG 548

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG +GRGG P H A+Lsq
  gi|1674708   549 VMAASWAQYRAQDALIKTCEKAGITLTLFHGRGGSIGRGGAPAHAALLSQ 598

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP  P
  gi|1674708   599 PPGSLKGGLRVTEQGEMIRFKFGLPEVTISSLALYAGAILEANLLPPPEP 648

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   k EW ++m+ +     + YRs v   P Fv YFR AtPElE Gk+ +GsR
  gi|1674708   649 KKEWIEVMDLLSDASCDMYRSYVRENPEFVRYFRAATPELELGKLPLGSR 698

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKR+P GG+esLRAiPWiFaWtq R  LP WLG GA  + Aid   + +
  gi|1674708   699 PAKRRPDGGVESLRAIPWIFAWTQNRLMLPAWLGAGAGLQRAIDAGKQDV 748

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L  m ++WPFF   + +lEmv  K
  gi|1674708   749 --LATMCRDWPFFSKGIGMLEMVSPK------------------------ 772

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|1674708     - ------------------------------------------------- -

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                                          +
  gi|1674708   773 ----------------------P-------------------------- 773

                   tmKGiAAGmqntG<-*

  gi|1674708     - -------------    -

gi|629595|pir||PC2167: domain 1 of 1, from 1 to 453: score 512.9, E = 4.2e-151
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|629595|     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|629595|     - ------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|629595|     - ------------------------------------------------- -
```

```
                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                                                iR CL+qL+AKD+t++DK+
  gi|629595|     1 ------------------------------IRDCLTQLYAKDITPDDKQ 19

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                  ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|629595|    20 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 69

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|629595|     - ------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|629595|     - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   FWKq+P +EPYR iLGdvRDKLYntRERaR LL  G+s+i+E+ v+  v
  gi|629595|    70 -FWKQIPSNEPYRAILGDVRDKLYNTRERARQLLSSGVSDIPEDSVFASV 118

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                  ++FLEPLELCY+sLC+CGD+  ADGsLLD+LRq s FGL+LvKLDiRqEs
  gi|629595|   119 DQFLEPLELCYRSLCDCGDRPTADGSLLDFLRQASAFGLALVKLDIRQES 168

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  +R+tDvlDAit+HL+iGsY+eWsE+KRqEWLl+EL+GKRPL+g DLPktE
  gi|629595|   169 DRHTDVLDAITQHLGIGSYKEWSEDKRQEWLLSELSGKRPLFGHDLPKTE 218

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++Dvld+f+v+ ELP DsFGaYiismataPsDvLAvELLqRECg+ ++L
  gi|629595|   219 EIADVLDTFKVISELPHDSFGAYIISMATAPSDVLAVELLQRECGIIHPL 268

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLe APA+v++LFsi+WY+nri+GKqevm+GYsDsGKDAG
  gi|629595|   269 RVVPLFEKLADLENAPASVARLFSIEWYRNRINGKQEVMIGYSDSGKDAG 318

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYk qEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|629595|   319 RLSAAWQLYKTQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 368

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+G lRvtvqGEviE+sFGEE+LCFr+L  FtA tLEHG++PPvsP
  gi|629595|   369 PPDTIHGQLRVTVQGEVIEQSFGEEHLCFRTLHGFTARTLEHGIDPPVSP 418

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+emAv+AtEEYRsvv+KEPRFvEYFRl
  gi|629595|   419 KPEWRVLMDEMAVIATEEYRSVVFKEPRFVEYFRL--------------- 453

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|629595|     - ------------------------------------------------- -

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|629595|     - ------------------------------------------------- -

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|629595|     - ------------------------------------------------- -

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|629595|     - ------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|629595|     - -------------    -

gi|66357588|ref|XP_625972.1|: domain 1 of 1, from 55 to 1148: score 507.9, E = 1.4e-149
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
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                  +++  +  Lv        k i           + +     + ++  +
gi|6635758    55    ALELHMFGLVTSHWRSSRKYILHGNKQKNNIDEGVLSPSNDGVRK-I 100

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   +   ls ++   +D++ L+ L  ++  Ld +   lv + +  m  + n
gi|6635758   101 FDILKLSMNFAENEDSSSLNQLWERIKHLDSGMLTLVVSLFNQMCMITNY 150

                  AEEvelAyRRRi......kkkkhGDFaDEasAttEsDi......EEtlKk
                  AE  +     R  +++ ++ +         +   +sDi   ++   t+Kk
gi|6635758   151 AESAQRIRQCRQfereipSILSESQIFSKNNQSPDSDIifahslRVTIKK 200

                  LvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq
                  L   +  s e ++  +  q vDLv+tAHPtq+ R s+++   +i   +
gi|6635758   201 LLQAG-FSKEHIYKLICEQEVDLVVTAHPTQAQRISVIKCCQKIGEIMIY 249

                  LsAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiH
                  L   D+t+ +       L R +   +  D +RRa+PtP DE+   +  i
gi|6635758   250 LDRDDLTPFEINNAKYELQRAMAMLWNVDTLRRARPTPLDEVQNTINTIE 299

                  EtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPR
                  Etv+   P FLR++D  L   G+ + lP    L k+ssW+GGDRDG nP
gi|6635758   300 ETVFSTLPTFLRKIDEILNEFGM-DPLPPTKTLFKYSSWVGGDRDG-NPY 347

                  vtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE....
                  vt  vtR   +  R+ A nl++ ++EDLm+E+ +    + LR   ++ ++
gi|6635758   348 VTAKVTRLSVINMRLRACNLFLHKIEDLMYEIPIISSHEKLREYVDnlpd 397

                  .Elyrtaard............kvvKyYiEFWKqvPPtEPYRviLGdvRD
                   E y  + +  ++ ++++ +++  +     F   +P  E YR iL  vR
gi|6635758   398 iEFYIRPVSScdtlnnsgcttsDATVGLRPFMGFIPEYELYRRILHHVRI 447

                  KLYntRERaRHLLAtGiseisE...eAvytkvEeFLEPLELCYksLCeCG
                  +L   R+     L  G s  sE+++   y   E+ LEPL L Y +L +
gi|6635758   448 RLIASRDYYLDALNFGHSVNSEtrrALAYHSTEQILEPLILMYNALEDYD 497

                  Dkv...........................iADGsLLDlLRqvstFGLs
                    ++++ ++++ ++++ + +  +++++ + ++  G LLD++Rq+s FGLs
gi|6635758   498 HEIktnfedghlpgtnisvpwisesgsvsakLGRGLLLDVIRQISAFGLS 547

                  LvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRP
                   ++LDiRqE+ ++   +D i   LeiG Y e+sEe +qE+Ll  Lk KRP
gi|6635758   548 FMRLDIRQEASKHEKAMDEICNYLEIGNYSEFSEEEKQEFLLNCLKSKRP 597

                  LlgsDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                  L++  L    E  ++ld+f     L  ++ G+Yiism+  PsD+L v +
gi|6635758   598 LIPYRLNWSKETTEILDTFYECSHLGAEALGSYIISMCMKPSDILCVHVF 647

                  qRE.................................Cg.............
                  q+E  ++ + +++ + + ++ ++  ++++++ +++C +++  + + ++ +
gi|6635758   648 QKEyfstisadsefhaeihdlnkfikrrsssissnCNsngvvnvevsnvd 697

                  ............................vkqtLrvvPLFEkLADLeAAPA
                  +++++++++ +++ +++++++    ++   + +rvvPL E +  L+ A
gi|6635758   698 nndsrqnggispsindspkssaailssiASKRMRVVPLLETVEALNNAEK 747

                  avekLFsiDWYinrid....GKqevmvGYsDsGKDAGRlsAAWqLYkAqE
                  ++e L s +WY n + + ++G  evm+GYsDs KD GRl   WqLY AqE
gi|6635758   748 TLETLLSNEWYLNYVKtvdgGIVEVMIGYSDSSKDGGRLTSGWQLYNAQE 797

                  EiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtv
                   +  +A+++Gv +v FHGRGG +GRGGGP HLAiLsqPP ti   +R+tv
gi|6635758   798 RLSNIARRFGVEMVFFHGRGGSIGRGGGPQHLAILSQPPNTITSLMRITV 847

                  qGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP.............
                  qGE i +sFG  ++ F++   ++ A LE  +     P++++ +++++ +
gi|6635758   848 QGEAITQSFGLSEIAFKTWEIYCSAILESRITALDIPnnnqcepngnlgy 897

                  ....kPEWRkLmeemAvvAtEEYRsvvvKE.......PRFvEYFRlAtPE
                  +++ k  WR+L+++m  +   EYR +v+ E++++ ++  Fv YFR+ tPE
gi|6635758   898 gtkvKESWRELLDQMSDISMKEYRKIVFGEgnsdftsDEFVAYFRSVTPE 947
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                    lEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAF
                     E   +n+GsRP+KRk sGGie+LRAiPW+FaWtq R HLPvWLG+ AA
  gi|6635758   948 KEISELNLGSRPSKRK-SGGIETLRAIPWVFAWTQIRSHLPVWLGLSAAL 996

                    KhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL
                       ++K  K l  + EmY++WPF +   DL+ m+  K D  i  Ly ++L
  gi|6635758   997 EE-MKKQNK-LNLVTEMYENWPFVKSFFDLVSMILLKADVHIFELYNRIL 1044

                    vaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYi
                       +L+  G+ L  k ++t +l++++   k lL+ D   ++ + LR s++
  gi|6635758  1045 APPDLQKIGDLLISKLKDTIKLVMEVTKEKQLLDSDFVTRKAILLRFSWL 1094

                    ttLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpter
                         +q   + R R    k+      s E  + +         L
  gi|6635758  1095 APCHLVQIECINRRR----KILCSSVNSSEINEIE---------LS---- 1127

                    vaPGLEDtLiLtmKGiAAGmqntG<-*
                        +E  L + ++ i AGm+ tG
  gi|6635758  1128 ---KIENALKISIQSISAGMKFTG    1148

gi|67594757|ref|XP_665868.1|: domain 1 of 1, from 55 to 1148: score 507.0, E = 2.5e-149
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       +++  +  Lv        k i           + +     + ++  +
  gi|6759475    55    ALELHMFGLVTSHWRSSRKYILHGNKQKNNIEEGVSSPSNDGVRK-I 100

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     +   ls ++   +D++ L+ L  ++  Ld +   lv + +  m  + n
  gi|6759475   101 FDILKLSMNFAENEDSSSLNQLWERIKNLDSGMLTLVVSLFNQMCMITNY 150

                    AEEvelAyRRRi......kkkkhGDFaDEasAttEsDi......EEtlKk
                    AE  +     R  +++ ++ +         +   +sDi   ++   t+Kk
  gi|6759475   151 AESAQRIRQCRQfereipSILSESQIFSKNNQSPDSDIifahslKVTIKK 200

                    LvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq
                    L   +  s e ++  +  q vDLv+tAHPtq+ R s+++   +i   +
  gi|6759475   201 LLQAG-FSKEHIYKLICEQEVDLVVTAHPTQAQRISVIKCCQKIGEIMIY 249

                    LsAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiH
                    L   D+t+ +       L R +   +  D +RRa+PtP DE+   +  i
  gi|6759475   250 LDRDDLTPFEINNAKYELQRAMAMLWNVDTLRRARPTPLDEVQNTINTIE 299

                    EtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPR
                    Etv+   P FLR++D  L   G+ + lP    L k+ssW+GGDRDG nP
  gi|6759475   300 ETVFSTLPTFLRKIDEILNEFGM-DPLPPTKTLFKYSSWVGGDRDG-NPY 347

                    vtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE....
                    vt  vtR   +  R+ A nl++ ++EDLm+++ +    + LR   ++ ++
  gi|6759475   348 VTAKVTRLSVINMRLRACNLFLHKIEDLMYDIPIISSHEKLREYVDnlpd 397

                    .Elyrtaard............kvvKyYiEFWKqvPPtEPYRviLGdvRD
                     E y  + +  ++ ++++ +++  +     F   +P  E YR iL  vR
  gi|6759475   398 iEFYIRPVSScdtlnnsgcttsDATVGLRPFMGFIPEYELYRRILHHVRI 447

                    KLYntRERaRHLLAtGiseisE...eAvytkvEeFLEPLELCYksLCeCG
                    +L   R+     L  G s  sE+++   y   E+ LEPL L Y +L +
  gi|6759475   448 RLIASRDYYLDALNFGHSVNSEtrrALAYHSTEQILEPLILMYNALEDYD 497

                    Dkv.........................iADGsLLDlLRqvstFGLs
                      ++++ ++++ ++++ + +  +++++ + ++  G LLD++Rq+s FGLs
  gi|6759475   498 HEIktnfedghlpgtnisvpwisesgsvsakLGRGLLLDVIRQISAFGLS 547

                    LvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRP
                     ++LDiRqE+ ++   +D i   LeiG Y e+sEe +qE+Ll  Lk KRP
  gi|6759475   548 FMRLDIRQEASKHEKAMDEICNYLEIGNYSEFSEEEKQEFLLNCLKSKRP 597

                    LlgsDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                    L++  L    E  ++ld+f     L  ++ G+Yiism+  PsD+L v +
  gi|6759475   598 LIPYRLNWSKETTEILDTFYECSHLGAEALGSYIISMCMKPSDILCVHVF 647

                    qRE.............................Cg.............
                    q+E  ++ + +++ + + ++ ++  ++++++ +++C +++  + + ++ +
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  gi|6759475   648 QKEyfstisadsefhaeihdlnkfikrrsssisnnCNsngvvsveasnvn 697

                    ............................vkqtLrvvPLFEkLADLeAAPA
                    +++++++++ +++ +++++++    ++   + +rvvPL E +  L+ A
  gi|6759475   698 nndsrqnggispsindspkssaailssiASKRMRVVPLLETVEALNNAEK 747

                    avekLFsiDWYinrid....GKqevmvGYsDsGKDAGRlsAAWqLYkAqE
                    ++e L s +WY n + + ++G  evm+GYsDs KD GRl   WqLY AqE
  gi|6759475   748 TLETLLSNEWYLNYVKtvdgGIVEVMIGYSDSSKDGGRLTSGWQLYNAQE 797

                    EiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtv
                     +  +A+++Gv +v FHGRGG +GRGGGP HLAiLsqPP ti   +R+tv
  gi|6759475   798 RLSNIARRFGVEMVFFHGRGGSIGRGGGPQHLAILSQPPNTITSLMRITV 847

                    qGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP.............
                    qGE i +sFG  ++ F++   ++ A LE  +     P++++ +++++ +
  gi|6759475   848 QGEAITQSFGLSEIAFKTWEIYCSAILESRITALDIPnnnqcepngnlgy 897

                    ....kPEWRkLmeemAvvAtEEYRsvvvKE.......PRFvEYFRlAtPE
                    +++ k  WR+L+++m  +   EYR +v+ E++++ ++  Fv YFR+ tPE
  gi|6759475   898 gtkvKESWRELLDQMSDISMKEYRKIVFGEgnsdftsDEFVAYFRSVTPE 947

                    lEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAF
                     E   +n+GsRP+KRk sGGie+LRAiPW+FaWtq R HLPvWLG+ AA
  gi|6759475   948 KEISELNLGSRPSKRK-SGGIETLRAIPWVFAWTQIRSHLPVWLGLSAAL 996

                    KhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL
                       ++K  K l  + EmY++WPF +   DL+ m+  K D  i  Ly ++L
  gi|6759475   997 EE-MKKQNK-LNLVTEMYENWPFVKSFFDLVSMILLKADVHIFELYNRIL 1044

                    vaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYi
                       +L+  G+ L  k ++t +l++++   k lL+ D   ++ + LR s++
  gi|6759475  1045 APPNLQKIGDLLISKLKDTIKLVMEVTREKQLLDSDFVTRKAILLRFSWL 1094

                    ttLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpter
                         +q   + R R    k+      s E  d +         L
  gi|6759475  1095 APCHLVQIECINRRR----KILCSSVNSSEINDIE---------LS---- 1127

                    vaPGLEDtLiLtmKGiAAGmqntG<-*
                        +E  L + ++ i AGm+ tG
  gi|6759475  1128 ---KIENALKISIQSISAGMKFTG    1148

gi|194689768|gb|ACF78968.1|: domain 1 of 1, from 1 to 435: score 505.8, E = 5.7e-149
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1946897     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1946897     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1946897     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1946897     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1946897     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1946897     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1946897     - ---------------------------------------------- -
```

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                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1946897     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1946897     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1946897     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                                      mataPsDvLAvELLqRECgv+q+L
  gi|1946897     1 -------------------------MATAPSDVLAVELLQRECGVRQPL 24

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +vvPLFE+LADL+ APA+ve+LFs+DWY+ ri GKq+vmvGYsDsGKDAG
  gi|1946897    25 PVVPLFERLADLQSAPASVERLFSVDWYMDRIKGKQQVMVGYSDSGKDAG 74

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLY+AqEE+++vAK+yGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1946897    75 RLSAAWQLYRAQEEMAQVAKRYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 124

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGs+RvtvqGEviEf FGEE+LCF++LqRFtAAtLEHGm+PPvsP
  gi|1946897   125 PPDTINGSIRVTVQGEVIEFCFGEEHLCFQTLQRFTAATLEHGMHPPVSP 174

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWRkLm+emAvvAtEEYRsvvvKE RFvEYFR+AtPE+EYG+mniGsR
  gi|1946897   175 KPEWRKLMDEMAVVATEEYRSVVVKEARFVEYFRSATPETEYGRMNIGSR 224

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+AidKD++n+
  gi|1946897   225 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKFAIDKDVRNF 274

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q LkEmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLvaEeLkPFGk+
  gi|1946897   275 QVLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVAEELKPFGKQ 324

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LRdkYvEt++lLL+iAGHkD+LEGDP+LKq+l LR++YittLnvfqAYtL
  gi|1946897   325 LRDKYVETQQLLLQIAGHKDILEGDPFLKQGLVLRNPYITTLNVFQAYTL 374

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDP++kvt++P+lsKE+AdEn  k+++LvkLnp+++++PGLEDtLiL
  gi|1946897   375 KRIRDPNFKVTPQPPLSKEFADEN--KPAGLVKLNPASEYPPGLEDTLIL 422

                  tmKGiAAGmqntG<-*
                  tmKGiAAGmqntG
  gi|1946897   423 TMKGIAAGMQNTG    435

gi|154146850|emb|CAM84112.1|: domain 1 of 1, from 1 to 439: score 504.3, E = 1.6e-148
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------ -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|1541468     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDvlDAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
  gi|1541468     1 --HTDVLDAITTHLGIGSYREWPEEKRQEWLLSELRGKRPLLGPDLPQTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v ++L
  gi|1541468    49 EIADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECHVPHPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAav++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|1541468    99 RVVPLFEKLADLEAAPAAVARLFSVDWYMERINGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYKAQEELVKVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEv+E sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTIHGSLRVTVQGEVVEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+e+AvvAt+EYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPEWRALMDELAVVATDEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhAi+KDi+n+
  gi|1541468   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAINKDIRNI 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva++LkPFG++
  gi|1541468   349 QTLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADDLKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Yv+t++lLL++AGHkD+LEGDPYLKqrlRLRd+Yitt
  gi|1541468   399 LRNNYVDTQQLLLQVAGHKDILEGDPYLKQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146844|emb|CAM84109.1|: domain 1 of 1, from 1 to 439: score 504.3, E = 1.7e-148
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------ -
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                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1541468    - ------------------------------------------------- -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1541468    - ------------------------------------------------- -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1541468    - ------------------------------------------------- -

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1541468    - ------------------------------------------------- -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1541468    - ------------------------------------------------- -

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1541468    - ------------------------------------------------- -

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1541468    - ------------------------------------------------- -

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  +tDvlDAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
gi|1541468    1 --HTDVLDAITTHLGIGSYREWPEEKRQEWLLSELRGKRPLLGPDLPQTE 48

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
gi|1541468   49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECHVRHPL 98

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                rvvPLFEkLADLeAAPAav++LFs+DWY+ ri+GKqev++GYsDsGKDAG
gi|1541468   99 RVVPLFEKLADLEAAPAAVARLFSVDWYMERINGKQEVVIGYSDSGKDAG 148

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLYkAqEE++KvAK+y vKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1541468  149 RLSAAWQLYKAQEELVKVAKRYSVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
gi|1541468  199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                kPEWR Lm+e+AvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
gi|1541468  249 KPEWRALMDELAVVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhAidKDi+n+
gi|1541468  299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAIDKDIRNI 348

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                q+L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva++LkPFG++
gi|1541468  349 QMLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADDLKPFGEQ 398

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR++Yv+t++lLL++AGHkD+LEGDPYLKqrlRLRd+ itt
gi|1541468  399 LRNNYVDTQQLLLQVAGHKDILEGDPYLKQRLRLRDPHITT--------- 439

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

gi|1541468    - ------------------------------------------------- -

                tmKGiAAGmqntG<-*

gi|1541468    - -------------    -
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gi|154146842|emb|CAM84108.1|: domain 1 of 1, from 1 to 439: score 501.7, E = 9.7e-148
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDv+DAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
  gi|1541468      1 --HTDVVDAITTHLGIGSYREWPEEKRQEWLLSELRGKRPLLGPDLPQTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541468     49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECHVRHPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLeAAPAav++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|1541468     99 RVVPLFEKLADLEAAPAAVARLFSVDWYMERINGKQEVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468    149 RLSAAWQLYKAQEELVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+G lRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541468    199 PPDTIHGLLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+e+AvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468    249 KPEWRALMDELAVVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+n+
  gi|1541468    299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMKKDIRNI 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q+L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva++LkPFG++
  gi|1541468    349 QMLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADDLKPFGEQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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                    LR++Yv+t++lLL++AGHkD+LEGDPYL+qrlRLRd+Yitt
  gi|1541468   399 LRNNYVDTQQLLLQVAGHKDILEGDPYLRQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ---------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146896|emb|CAM84135.1|: domain 1 of 1, from 1 to 439: score 499.8, E = 3.5e-147
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ---------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ---------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ---------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ---------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ---------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ---------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ---------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ---------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDv+DAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
  gi|1541468     1 --HTDVVDAITTHLGIGSYREWPEEKRQEWLLSELRGKRPLLGPDLPQTE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541468    49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECQVRHAL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAav++LFs+DWY+ ridGKqevm+GYsDsGKDAG
  gi|1541468    99 RVVPLFEKLADLEAAPAAVARLFSVDWYMDRIDGKQEVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYKAQEELVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+e+AvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPEWRALMDELAVVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298
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                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+n+
  gi|1541468   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMKKDIRNI 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva+eLkPFG++
  gi|1541468   349 QMLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADELKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y +t++lLL++AGHkD+LEGDPYL+qrlRLRd+Yitt
  gi|1541468   399 LRNNYMDTQQLLLQVAGHKDILEGDPYLRQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146722|emb|CAM84048.1|: domain 1 of 1, from 1 to 439: score 499.8, E = 3.7e-147
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDvlDAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlgsDLP+ E
  gi|1541467     1 --HTDVLDAITTHLGIGSYREWPEEKRQEWLLSELRGKRPLLGSDLPQSE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541467    49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECQVRHPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADL  APAave+LFs+DWY+ ri GKqevm+GYsDsGKDAG
  gi|1541467    99 RVVPLFEKLADLITAPAAVERLFSVDWYMDRICGKQEVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
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                    RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYKAQEEMVKVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541467   199 PPDTINGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAvvAtEEYRs+v+KEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWRALMDEMAVVATEEYRSIVFKEPRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+n+
  gi|1541467   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVMNKDIRNV 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva++LkPFG++
  gi|1541467   349 QMLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDQLLVADDLKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y Et++lLL++AGHkD+LEGDPYLKqrlRLRd+Yitt
  gi|1541467   399 LRNNYMETQQLLLQVAGHKDILEGDPYLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------ -

                    tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146786|emb|CAM84080.1|: domain 1 of 1, from 1 to 439: score 499.5, E = 4.4e-147
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------ -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------ -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------ -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------ -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------ -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------ -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------ -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------ -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDvlDAittH++iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
  gi|1541467     1 --HTDVLDAITTHVGIGSYREWPEEKRQEWLLSELRGKRPLLGPDLPQTE 48
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                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl+afrvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541467     49 EVADVLGAFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECHVRHPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFE+LADLeAAPAav++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|1541467     99 RVVPLFERLADLEAAPAAVARLFSVDWYMDRINGKQEVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467    149 RLSAAWQLYKAQEELVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541467    199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+e+AvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467    249 KPEWRALMDELAVVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+n+
  gi|1541467    299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMKKDIRNI 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva++LkPFG++
  gi|1541467    349 QMLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADDLKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Yv+t++lLL++AGHk++LEG PYLKqrlRLRd+Yitt
  gi|1541467    399 LRNNYVDTQQLLLQVAGHKEILEGGPYLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146880|emb|CAM84127.1|: domain 1 of 1, from 1 to 439: score 499.4, E = 4.6e-147
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
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  gi|1541468     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDvlDA+ttHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
  gi|1541468     1 --HTDVLDAVTTHLGIGSYREWPEEKRQEWLLSELRGKRPLLGPDLPQTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541468    49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECHVRHPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAav++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|1541468    99 RVVPLFEKLADLEAAPAAVARLFSVDWYMDRINGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYKAQEELVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+++AvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPEWRALMDDLAVVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhAi+KDi+n+
  gi|1541468   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAINKDIRNI 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLv+++LkPFG++
  gi|1541468   349 QALREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVTDDLKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y +t++lLL++AGHk++LEGDPYLKqrlRLRd+Yitt
  gi|1541468   399 LRNNYLDTQQLLLQVAGHKEILEGDPYLKQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146910|emb|CAM84142.1|: domain 1 of 1, from 1 to 439: score 499.4, E = 4.9e-147
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541469     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541469     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541469     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541469     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541469     - ------------------------------------------------ -
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                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541469     - ------------------------------------------------ -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541469     - ------------------------------------------------ -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541469     - ------------------------------------------------ -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541469     - ------------------------------------------------ -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDvlDAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
  gi|1541469      1 --HTDVLDAITTHLGIGSYREWPEEKRQEWLLSELRGKRPLLGADLPQTE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl++fr+LAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541469     49 EVADVLGTFRILAELPPDSFGAYIISMATAPSDVLAVELLQRECHVRHPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAav++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|1541469     99 RVVPLFEKLADLEAAPAAVARLFSVDWYMGRINGKQEVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541469    149 RLSAAWQLYKAQEELVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541469    199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+e+AvvAtE YRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541469    249 KPEWRALMDELAVVATEAYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+n+
  gi|1541469    299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMKKDIRNI 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva++LkPFG++
  gi|1541469    349 QTLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADDLKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Yv+t++lLL++AGHkD+LEGDPYLKqrlRLRd+Yitt
  gi|1541469    399 LRNNYVDTQQLLLQVAGHKDILEGDPYLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541469     - ------------------------------------------------ -

                    tmKGiAAGmqntG<-*

  gi|1541469     - -------------    -

gi|154146796|emb|CAM84085.1|: domain 1 of 1, from 1 to 439: score 499.2, E = 5.4e-147
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------ -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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gi|1541467     - ------------------------------------------------- -

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1541467     - ------------------------------------------------- -

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1541467     - ------------------------------------------------- -

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1541467     - ------------------------------------------------- -

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1541467     - ------------------------------------------------- -

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1541467     - ------------------------------------------------- -

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1541467     - ------------------------------------------------- -

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +tDvlDAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLl +DLP+tE
gi|1541467     1 --HTDVLDAITTHLGIGSYREWAEEKRQEWLLSELRGKRPLLAPDLPQTE 48

                 EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                 Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
gi|1541467    49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECHVRHPL 98

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                 rvvPLFEkLADLeAAPAav++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
gi|1541467    99 RVVPLFEKLADLEAAPAAVARLFSVDWYMDRINGKQEVMIGYSDSGKDAG 148

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 RlsAAWqLYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1541467   149 RLSAAWQLYKAQEELVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                 PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
gi|1541467   199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                 kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                 kPEWR Lm+e+AvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
gi|1541467   249 KPEWRALMDELAVVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                 PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                 P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+n+
gi|1541467   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMKKDIRNI 348

                 qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                 q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLv+++LkPFG++
gi|1541467   349 QTLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVSDDLKPFGEQ 398

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                 LR++Yv+t++lLL++ GHkD+LEGDPYL+qrlRLRd+Yitt
gi|1541467   399 LRNNYVDTQQLLLQVTGHKDILEGDPYLRQRLRLRDPYITT--------- 439

                 KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

gi|1541467     - ------------------------------------------------- -

                 tmKGiAAGmqntG<-*

gi|1541467     - -------------    -
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gi|154146752|emb|CAM84063.1|: domain 1 of 1, from 1 to 439: score 498.9, E = 6.9e-147
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDv+DAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
  gi|1541467     1 --HTDVVDAITTHLGIGSYREWPEEKRQEWLLSELRGKRPLLGPDLPQTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541467    49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECHVRHPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLeAAPAav++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|1541467    99 RVVPLFEKLADLEAAPAAVARLFSVDWYMDRINGKQEVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYKAQEELVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541467   199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+e+A+vAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWRALMDELAIVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+n+
  gi|1541467   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMKKDIRNI 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q L+EmY+eWPFFRvtlDLlEmvFAKGDP iA+LyD+LLva++LkPFG++
  gi|1541467   349 QTLREMYNEWPFFRVTLDLLEMVFAKGDPSIAGLYDELLVADDLKPFGEQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Yv+t++lLL++AGHkD+LEGDPYL+qrlRLRd+Yitt
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  gi|1541467   399 LRNNYVDTQQLLLQVAGHKDILEGDPYLRQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146922|emb|CAM84148.1|: domain 1 of 1, from 1 to 439: score 498.7, E = 7.7e-147
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541469     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541469     - ------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541469     - ------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541469     - ------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541469     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541469     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541469     - ------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541469     - ------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541469     - ------------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDv+DAittHL+iG YR+W+EeKR +WLl+EL+GKRPLl++DLP+tE
  gi|1541469     1 --HTDVVDAITTHLGIGPYRSWPEEKRFDWLLSELRGKRPLLPADLPMTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dv++a+rvLAELP DsFG+Yiism+taPsDvLAvELLqRECg++q+L
  gi|1541469    49 EIADVVGAMRVLAELPPDSFGPYIISMCTAPSDVLAVELLQRECGIRQPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLFE+LADL+ APA+vekLFs DWY nri+GKq+vmvGYsDsGKDAG
  gi|1541469    99 PVVPLFERLADLQGAPASVEKLFSADWYFNRIQGKQQVMVGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLY+AqEE++KvAKk+ vKL+lFHGRG tvGRGGGPtHLAiLsq
  gi|1541469   149 RLSAAWQLYVAQEEMAKVAKKFSVKLTLFHGRGDTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGs+RvtvqGEviEf FGEEnLCF++LqRFtAAtLEHGm+PPvsP
  gi|1541469   199 PPDTINGSIRVTVQGEVIEFCFGEENLCFQTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR LmeemAvvAt EYRsvvv+EPRFvEYFR+AtPE+EYGkmniGsR
  gi|1541469   249 KPEWRALMEEMAVVATKEYRSVVVQEPRFVEYFRSATPETEYGKMNIGSR 298
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                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKRkP+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+AidKDiKn+
  gi|1541469   299 PAKRKPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKFAIDKDIKNF 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  qkLkEmY+eWPFFR tlDLlEmvFAKGDPGiA+LyD+LLva++LkPFGk+
  gi|1541469   349 QKLKEMYNEWPFFRGTLDLLEMVFAKGDPGIAGLYDELLVADDLKPFGKQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LRdkYvEt +lLL+iAGHkD+LEGDPYLKq+lRLR++Yitt
  gi|1541469   399 LRDKYVETLQLLLQIAGHKDILEGDPYLKQGLRLRNPYITT--------- 439

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541469     - ------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|1541469     - -------------    -

gi|154146854|emb|CAM84114.1|: domain 1 of 1, from 1 to 439: score 497.5, E = 1.8e-146
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDv+DAittHL+iGsYR W EeKRqEWLl+EL+GKRPLlg+D+P+tE
  gi|1541468     1 --HTDVIDAITTHLGIGSYRGWDEEKRQEWLLSELRGKRPLLGADMPQTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541468    49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECHVRHPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLeAAPA+ve+LFs+DWY+ +i+GKqevm+GYsDsGKDAG
  gi|1541468    99 RVVPLFEKLADLEAAPASVERLFSVDWYMDHINGKQEVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
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  gi|1541468   149 RLSAAWQLYKAQEEMVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPv+P
  gi|1541468   199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVAP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+e+AvvAtEEYRs+v++EPRFvEYFR AtPE+EYG+mniGsR
  gi|1541468   249 KPEWRALMDELAVVATEEYRSIVFREPRFVEYFRRATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhA++KDi+n+
  gi|1541468   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGVGAAFKHAMKKDIRNI 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q+L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLv+++LkPFG++
  gi|1541468   349 QMLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVSDDLKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Yv+t++lLL++AGHkD+LEGDPYL+qrlRLRd+Yitt
  gi|1541468   399 LRNNYVDTQQLLLQVAGHKDILEGDPYLRQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - -------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146848|emb|CAM84111.1|: domain 1 of 1, from 1 to 439: score 496.8, E = 2.8e-146
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - -------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - -------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - -------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - -------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - -------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - -------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - -------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - -------------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDvlDAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DL +tE
  gi|1541468     1 --HTDVLDAITTHLGIGSYREWAEEKRQEWLLSELRGKRPLLGPDLAQTE 48
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                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541468    49 EVTDVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECHVRHPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAav++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|1541468    99 RVVPLFEKLADLEAAPAAVARLFSVDWYMDRINGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYKAQEELVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+e+AvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPEWRALMDELAVVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+n+
  gi|1541468   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMKKDIRNI 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva++LkPFG++
  gi|1541468   349 QTLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADDLKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Yv+t++lLL++AGHk++LEGDPYLKqrlRLRd+Yitt
  gi|1541468   399 LRNNYVDTQQLLLQVAGHKEILEGDPYLKQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146718|emb|CAM84046.1|: domain 1 of 1, from 1 to 439: score 495.1, E = 9.7e-146
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
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  gi|1541467     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     + DvlDA+ttHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
  gi|1541467     1 --HNDVLDAVTTHLGIGSYREWPEEKRQEWLLSELRGKRPLLGPDLPQTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541467    49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECHVRHPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAav++LFs+DWY+ ridGKqevm+GYsDsGKDAG
  gi|1541467    99 RVVPLFEKLADLEAAPAAVARLFSVDWYMDRIDGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYKAQEELVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541467   199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+e+AvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWRALMDELAVVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD++n+
  gi|1541467   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHTIKKDVRNI 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva++LkPFG++
  gi|1541467   349 QTLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADDLKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y +t++lLL++AGHk++LEGDPYLKqrlRLRd+Yitt
  gi|1541467   399 LRNNYLDTQQLLLQVAGHKEILEGDPYLKQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146862|emb|CAM84118.1|: domain 1 of 1, from 1 to 439: score 493.8, E = 2.3e-145
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------ -
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                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDv+DAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
  gi|1541468     1 --HTDVVDAITTHLGIGSYREWPEEKRQEWLLSELRGKRPLLGPDLPQTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541468    49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECQVRHPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLeAAPAav++LFs+DW + ridGKqevm+GYsDsGKDAG
  gi|1541468    99 RVVPLFEKLADLEAAPAAVARLFSVDWCMDRIDGKQEVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+++vA++yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYKAQEELVQVARRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+e+AvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPEWRALMDELAVVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+n+
  gi|1541468   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMKKDIRNI 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q+L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva+eLkPFG++
  gi|1541468   349 QMLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADELKPFGEQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y +t++lLL++AGHkD+LEGDPYL+qrlRLRd+Yitt
  gi|1541468   399 LRNNYMDTQQLLLQVAGHKDILEGDPYLRQRLRLRDPYITT--------- 439

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|209881885|ref|XP_002142380.1|: domain 1 of 1, from 76 to 1164: score 491.0, E = 1.6e-144
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                     s + q   L P ++                     +  G+d   ++
  gi|2098818    76    SSESQTPELSPARIP-----------------SSCNEKEGKDGMSII 105

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   +    s e+     ++ Le L  ++  Ld +   lv + +  m  + n
  gi|2098818   106 FDILKASMEFVESDNSESLEKLWNQIRVLDSGMLSLVVSLFNQMCMISNY 155

                  AEEvelAyRRR.....ikkkkhGDFaDEasAttEsDiEEtlKkLvlklnK
                  AE  +   RRR+ ++   ++   +  DEa       +  t+K L   +
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gi|2098818   156 AEAAQRIRRRRhfekvLALRNENEDQDEAFRLSTHSLRNTIKDLLNAG-Y 204

                  sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt
                    + ++  +  q +DLv+tAHPtq+ R s+++    i   + qL   D+t
gi|2098818   205 EKQIIYKLICEQEIDLVVTAHPTQAQRISVVKCCQNIAELILQLDRSDLT 254

                  veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGv
                  + + k+    + R +   +  D +RRa+PtP DE+   +  i Etv++
gi|2098818   255 PTEIKDAKNTIQRCLAMLWNSDTLRRARPTPLDEVQNTVNTICETVFNTL 304

                  PKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                  P+FLR +D  L   G+ + lP    L kFssW+GGDRDG nP vt  +tR
gi|2098818   305 PQFLRNIDMILDDNGM-DPLPPTKTLFKFSSWVGGDRDG-NPYVTAKITR 352

                  DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEl........y
                        R+ A  ++++ ++ Lm+++ +      L+   + l++ +   +
gi|2098818   353 LAVTNMRLKACSIFLESIDKLMYDIPIVSNHKKLKNYVDNLpnisfylnN 402

                  rtaard.....kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRH
                   t+a ++++++  +     F   +   E YR +L  +R +L  tR+
gi|2098818   403 NTPANNgdttnDATVCLRPFMGFIAEHELYRRVLAHIRVRLIATRDYYLD 452

                  LLAtGi...seisEeAvytkvEeFLEPLELCYksLCeC.........GDk
                   L  G   +sei     y    + LEPL + + +L + +++ +++ + Dk
gi|2098818   453 TLNSGHcvqSEIRRSLAYHSTQQLLEPLLVMFEALEDYdkdikenieEDK 502

                  viAD.....................GsLLDlLRqvstFGLsLvKLDiRqE
                  v A +++++ +  ++++  + + ++G LLDl+Rqvs FGLsL++LDiRqE
gi|2098818   503 VSASssnntipwlshsnyataklgrGLLLDLIRQVSAFGLSLMRLDIRQE 552

                  seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                  + ++   +D + + +++GsY e+ Ee +q +L   L  KRPL++  L  t
gi|2098818   553 ASKHEKAMDEVCKYIGVGSYSEFTEEEKQNFLFKCLASKRPLIPHRLNWT 602

                  EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqREC.....
                   E  ++l++fr    L  ++ G+Yiism+  PsD+L v + q+E   + +
gi|2098818   603 PETVEILETFRECSHLGAEALGSYIISMCMKPSDILCVHVFQKEYfatis 652

                  .....................................gvkqtL.........
                   +++  ++ ++ ++  ++++++++ + +++ ++++++  +L+++++++++
gi|2098818   653 aesevysklsdlntllnsrnsqdslnmtnnlqskgQIYSPLnnnspksst 702

                  ...........rvvPLFEkLADLeAAPAavekLFsiDWYinrid....GK
                  +  ++  +++ rvvPL E +  L+ A  ++e L s +WY n +++ ++G
gi|2098818   703 silpslaskrmRVVPLLETVEALNNAQKTLEVLLSNEWYLNYVNsvdkGI 752

                  qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                   evm+GYsDs KD GRl+ AWqLY AqE +  +  +yGv++v FHGRGG
gi|2098818   753 VEVMIGYSDSSKDGGRLASAWQLYNAQECLSNISHRYGVQIVFFHGRGGS 802

                  vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                  vGRGGGP HLAiLsqPP ti   +R+tvqGEv+ +sFG  ++ +++   +
gi|2098818   803 VGRGGGPQHLAILSQPPNTITSFMRITVQGEVMTQSFGLAEIAYKTWEIY 852

                  tAAtL.................EH.........................
                  t A L+ + +  + +++ ++ +H ++++++  ++++++++ ++++++
gi|2098818   853 TSAVLtarcsvldlentceefDHlenknkpiinettdksdlndtnqnyly 902

                  ......GmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPR.......F
                  +  ++   n  v   P WR+Lm++m  v   EYR +v+ E  ++ ++++F
gi|2098818   903 kylskmKFNKNVVVSPKWRELMNKMSEVSMKEYRRIVFGEDNkdftsddF 952

                  vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                  v YFR+ tPE E   +niGsRP+KRk  GGie+LRAiPW+FaWtq R HL
gi|2098818   953 VNYFRSVTPEKEISELNIGSRPSKRK-EGGIETLRAIPWVFAWTQIRSHL 1001

                  PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                  PvWLG+ AA      K i  l  + +mY++WPF +    L+ m+  K D
gi|2098818  1002 PVWLGLSAALEEM--KRIDELGEIADMYQQWPFMKSFFNLVSMILLKTDV 1049

                  GiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLK
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                   i  Ly k L  E+L+  G+ L +k ++t +l++++   k lL+ D   +
  gi|2098818  1050 HIFQLYSKTLAPENLQHLGNLLSQKLKDTTKLVMEVTKEKQLLDSDCVTR 1099

                   qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                     + LR +++   n +q   + R R        +  +s    +++ k
  gi|2098818  1100 RAILLRFAWLAPCNLVQIECINRRR--------KLCISNSNIQDP-KTQL 1140

                   eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   eL k+             L + ++ iAAGmq  G
  gi|2098818  1141 ELEKIE----------NALKISIQSIAAGMQFSG    1164

gi|154146782|emb|CAM84078.1|: domain 1 of 1, from 1 to 439: score 490.4, E = 2.4e-144
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     + DvlDA+ttHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
  gi|1541467     1 --HADVLDAVTTHLGIGSYREWPEEKRQEWLLSELRGKRPLLGPDLPQTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541467    49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECHVRHPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAav++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|1541467    99 RVVPLFEKLADLEAAPAAVARLFSVDWYMDRINGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqE++++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYKAQEDLVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541467   199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+++A+vAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWRALMDKLAIVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298
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                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G A KhAi+KDi+n+
  gi|1541467   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGVASKHAINKDIRNI 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva++LkPFG++
  gi|1541467   349 QTLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADDLKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Yv+t++lLL++AGHkD+LEGDPYLKqrlRLRd+Yitt
  gi|1541467   399 LRNNYVDTQQLLLQVAGHKDILEGDPYLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146916|emb|CAM84145.1|: domain 1 of 1, from 1 to 439: score 490.0, E = 3.3e-144
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541469     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541469     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541469     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541469     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541469     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541469     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541469     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541469     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541469     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tD +DAittHL+iGsY++W+EeKRqEWLl+EL+GKRPLl +D+P+ E
  gi|1541469     1 --HTDAIDAITTHLGIGSYKSWPEEKRQEWLLSELQGKRPLLVPDMPQNE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+ v+++f+vLAELP+DsFG+YiismataPsDvLAvELLqREC+vk +L
  gi|1541469    49 EVAAVIGTFKVLAELPSDSFGPYIISMATAPSDVLAVELLQRECHVKPPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFE+LADL+ APA+ve+LFs+DWY+nri+GKq+vmvGYsDsGKDAG
  gi|1541469    99 PVVPLFERLADLQNAPASVERLFSVDWYKNRINGKQQVMVGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
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                    RlsAAW LY AqE ++KvAKkyGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1541469   149 RLSAAWALYTAQEQMAKVAKKYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGs+RvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541469   199 PPDTINGSIRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWRkLm+em vvAt+ YRsvv+KEPRF+EYFR+AtPE+EYG+mniGsR
  gi|1541469   249 KPEWRKLMDEMTVVATDAYRSVVFKEPRFIEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+ +GGie+LRAiPWiF+WtqtRFHLPvWLGvGAAFK AidKDiKn+
  gi|1541469   299 PAKRRAGGGIETLRAIPWIFSWTQTRFHLPVWLGVGAAFKSAIDKDIKNF 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    qkLkEmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG++
  gi|1541469   349 QKLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVAEELKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR kYvEt++lLL+iAGHk++LEGDPYLKqrlRLRd+Yitt
  gi|1541469   399 LRSKYVETQQLLLQIAGHKEILEGDPYLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541469     - ------------------------------------------------ -

                    tmKGiAAGmqntG<-*

  gi|1541469     - -------------    -

gi|154146882|emb|CAM84128.1|: domain 1 of 1, from 1 to 439: score 489.1, E = 6e-144
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------ -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------ -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------ -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------ -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------ -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------ -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------ -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------ -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDvlDAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+D P+tE
  gi|1541468     1 --HTDVLDAITTHLGIGSYREWPEEKRQEWLLSELRGKRPLLGADHPQTE 48
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                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541468     49 EVADVLGTFRVLAELPADSFGAYIISMATAPSDVLAVELLQRECHVRHPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLe APAa+++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|1541468     99 RVVPLFEKLADLESAPAAMARLFSVDWYMDRINGKQEVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468    149 RLSAAWQLYKAQEELVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541468    199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468    249 KPEWRALMDEMAVVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+n+
  gi|1541468    299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIMKKDIRNI 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLv+++LkPFG++
  gi|1541468    349 HMLREMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDELLVTDDLKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y +t++lLL++AGHkD LEGDPYLKqrlRLRd+Yitt
  gi|1541468    399 LRNDYLDTRQLLLQVAGHKDALEGDPYLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146852|emb|CAM84113.1|: domain 1 of 1, from 1 to 439: score 487.7, E = 1.6e-143
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
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  gi|1541468     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDv+DAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
  gi|1541468     1 --HTDVVDAITTHLGIGSYREWPEEKRQEWLLSELRGKRPLLGPDLPQTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl++frvLAELP DsFGaYiismata sDvLAvELL REC+v+++L
  gi|1541468    49 EVADVLGTFRVLAELPPDSFGAYIISMATALSDVLAVELLLRECHVRHPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLAD eAAPAav++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|1541468    99 RVVPLFEKLADPEAAPAAVARLFSVDWYMDRINGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYKAQEELVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+e+AvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPEWRALMDELAVVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+n+
  gi|1541468   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMKKDIRNI 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva++LkPFG++
  gi|1541468   349 QILREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADDLKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Yv+t++lLL++AGHkD+LEGDPYL+qrlRLRd+Yitt
  gi|1541468   399 LRNNYVDTQQLLLQVAGHKDILEGDPYLRQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146838|emb|CAM84106.1|: domain 1 of 1, from 1 to 439: score 485.2, E = 8.8e-143
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------ -
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                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------ -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------ -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------ -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------ -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tD lDA+ttHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
  gi|1541468      1 --HTDALDAVTTHLGIGSYREWPEEKRQEWLLSELRGKRPLLGPDLPQTE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541468     49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECQVRHPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAav++LFs+DWY+ ri GKqevm+GYsDsGKDAG
  gi|1541468     99 RVVPLFEKLADLEAAPAAVARLFSVDWYMDRIGGKQEVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468    149 RLSAAWQLYKAQEELVKVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDt+nGslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+P vsP
  gi|1541468    199 PPDTVNGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPTVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWRkLm+e+AvvAtE YRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468    249 KPEWRKLMDELAVVATEAYRSIVLREPRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+n+
  gi|1541468    299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMNKDIRNI 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva++LkPFG++
  gi|1541468    349 QMLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADDLKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR+ Y Et++lLL++AGHk++LEGDPYLKqrlRLRd+Yitt
  gi|1541468    399 LRNSYAETQQLLLQVAGHKEILEGDPYLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------ -

                    tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146832|emb|CAM84103.1|: domain 1 of 1, from 1 to 439: score 485.1, E = 9.7e-143
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------ -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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gi|1541468     - ------------------------------------------------- -

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1541468     - ------------------------------------------------- -

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1541468     - ------------------------------------------------- -

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1541468     - ------------------------------------------------- -

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1541468     - ------------------------------------------------- -

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1541468     - ------------------------------------------------- -

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1541468     - ------------------------------------------------- -

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +tD lDAittHL+iGsYReW+E++RqEWLl+EL+G+RPLlg+DLP+tE
gi|1541468     1 --HTDALDAITTHLGIGSYREWPEQRRQEWLLSELRGRRPLLGPDLPQTE 48

                 EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                 Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
gi|1541468    49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECHVRHPL 98

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                 rvvPLFE+LADLeAAPAav++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
gi|1541468    99 RVVPLFERLADLEAAPAAVARLFSVDWYMDRINGKQEVMIGYSDSGKDAG 148

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 RlsAAWqLYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1541468   149 RLSAAWQLYKAQEELVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                 PPDti+G lRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
gi|1541468   199 PPDTIHGPLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                 kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                 kPEWR Lm+emAvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
gi|1541468   249 KPEWRALMDEMAVVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                 PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                 P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KDi+n+
gi|1541468   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVINKDIRNV 348

                 qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   L+EmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLv ++L+PFG++
gi|1541468   349 HTLREMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDELLVVDDLRPFGEQ 398

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                 LR++Y Et++lLL++AGHkD+LEGDPYLKqrlRLRd+Yitt
gi|1541468   399 LRNNYLETQQLLLQVAGHKDVLEGDPYLKQRLRLRDPYITT--------- 439

                 KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

gi|1541468     - ------------------------------------------------- -

                 tmKGiAAGmqntG<-*

gi|1541468     - -------------    -
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gi|154146874|emb|CAM84124.1|: domain 1 of 1, from 1 to 439: score 484.7, E = 1.3e-142
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDvlDAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg DLP+ E
  gi|1541468      1 --HTDVLDAITTHLGIGSYREWPEEKRQEWLLSELRGKRPLLGTDLPQNE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541468     49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECHVRHPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLeAAPAav++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|1541468     99 RVVPLFEKLADLEAAPAAVARLFSVDWYMDRINGKQEVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468    149 RLSAAWQLYKAQEELVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541468    199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+emAvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468    249 KPEWRALMDEMAVVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF h ++ Di+n+
  gi|1541468    299 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFEHVMKEDIRNI 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+EmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLv++++kPFG++
  gi|1541468    349 HMLREMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDELLVTDDIKPFGEQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR+ Y +t++lLL++AGHkD+LEGDPYLKqrlRLRd+Yitt
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  gi|1541468   399 LRNTYLDTQQLLLQVAGHKDILEGDPYLKQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146904|emb|CAM84139.1|: domain 1 of 1, from 1 to 439: score 484.1, E = 1.9e-142
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541469     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541469     - ------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541469     - ------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541469     - ------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541469     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541469     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541469     - ------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541469     - ------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541469     - ------------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDvlDAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
  gi|1541469     1 --HTDVLDAITTHLGIGSYREWAEEKRQEWLLSELRGKRPLLGADLPQTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl++frvLAELP DsFGaY+ismataPsDvLAvELLqREC v+++L
  gi|1541469    49 EVADVLGTFRVLAELPADSFGAYVISMATAPSDVLAVELLQRECRVRHPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAav++LFs+DWY+ ri GKqevm+GYsDsGKDAG
  gi|1541469    99 RVVPLFEKLADLEAAPAAVARLFSVDWYMDRIGGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+++vA +yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541469   149 RLSAAWQLYKAQEELVQVAERYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541469   199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm++mAvv tEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541469   249 KPEWRALMDDMAVVTTEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298
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                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+n+
  gi|1541469   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVMKKDIRNI 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLva+eLkPFG++
  gi|1541469   349 HTLREMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDELLVADELKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y++t++lLL++AGHkD+LEGDPYLKqrlRLRd+Yitt
  gi|1541469   399 LRKNYEDTQQLLLQVAGHKDILEGDPYLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541469     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541469     - -------------    -

gi|154146758|emb|CAM84066.1|: domain 1 of 1, from 1 to 439: score 484.1, E = 1.9e-142
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDvlDAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
  gi|1541467     1 --HTDVLDAITTHLGIGSYREWAEEKRQEWLLSELRGKRPLLGPDLPQTE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541467    49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECHVHHPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAav++LFs+DWY+ ri GKqevm+GYs sGKDAG
  gi|1541467    99 RVVPLFEKLADLEAAPAAVARLFSVDWYMERISGKQEVMIGYSGSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
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  gi|1541467   149 RLSAAWQLYKAQEELVRVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDt++GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541467   199 PPDTVHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+e+AvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWRALMDELAVVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGie+LRAiPWiFaWtqtRFHLPvWLG+GAAFKhA+ KDi+n+
  gi|1541467   299 PSKRKPSGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMSKDIRNI 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q L+EmY+eWPFFRvtlDLlEmvFAKGDP iA+LyD+LLva++LkPFG+
  gi|1541467   349 QTLREMYNEWPFFRVTLDLLEMVFAKGDPSIAGLYDELLVADDLKPFGEH 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Yv+t++lLL++AGHkD+LEGDPYL+qrlRLRd+Yitt
  gi|1541467   399 LRNNYVDTQQLLLQVAGHKDILEGDPYLRQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|222617602|gb|EEE53734.1|: domain 1 of 1, from 16 to 946: score 481.5, E = 1.1e-141
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       + +   RlL  G    d  L e    L  +F+ +L     e +
  gi|2226176    16    AFEDDCRLL--GSLLHDVLLRE----LGPRFIHLL-----ERITILA 51

                    qECYElsAeYEGKkDtkKLeE..LGakLtsLdPaDailvAkailHmLnLA
                    q    +     G +Dt  + E++LGa L ++   D++ +A+a++H LnL
  gi|2226176    52 QSAVNMRSA--GVEDTAVVVEkqLGAELAAMSLEDSLCLARAFSHHLNLM 99

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                     +A+  +     R++k +   FaD +        ++t+ kL+  +  sPe
  gi|2226176   100 TIADTYH-----RVRKAR--NFADLSKSC-----DDTFAKLIQSG-VSPE 136

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    E ++ +  q                LL  n R           D+  eD
  gi|2226176   137 ELYDTVCKQH----------------LLEFNERA----------DLSLED 160

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    K+ L E L REi A + tDE+RR +PtP DE RaG+  +   +Wk +P +
  gi|2226176   161 KEILIEDLVREITAIWQTDELRRHKPTPVDEARAGLHIVEQSLWKAIPHY 210

                    LRRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    LRRv  AL+Kn G    lP     ikF sWmGGDRDG nP vt  vtRDv
  gi|2226176   211 LRRVSNALkKNTG--KPLPLTCTPIKFGSWMGGDRDG-NPNVTAKVTRDV 257

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEl...........
                     +L+  mA  lYi  ++ L FEls+ RC + L   A ++  +++ +++++
  gi|2226176   258 SILSQWMAIDLYIRELDTLSFELSINRCSEKLANLANDIllkesasedqk 307

                    .....yrtaardkvvKyYiEFWKqvPPtEPYRviL....GdvRDKLYntR
                    +++ ++  ++ +   ++ +    q+P         + ++G+   ++
  gi|2226176   308 tntwnQTGPQNNLKLQHSLALPAQLPSGADLPSCTecndGESQIRMSKLP 357

                    ERaRHLLAtGiseisEeA.....................vytk.......
                       +H LA  i e  E+ + +++++++ ++++++++ ++++t+++ ++++
  gi|2226176   358 GNPKHKLALNITEKREDSplpspshrpmgrtpsggqlrkMFTEsqigrss 407

                    vEeFLEPL......ELCYksLC.......eCGDkviADGsLLDlLRqvst
                      + LEP  +++++   Y+ + ++ ++++ CG  v+ADG L Dl+R v t
  gi|2226176   408 FRKLLEPSiserpgSTPYRVVLgdvkekqSCGSSVLADGRLADLIRRVAT 457
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                    FGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELk
                    FG+ L+KLD+RqEs R+t+ lDAit  L++G Y eW E+K+ ++L  ELk
  gi|2226176   458 FGMVLMKLDVRQESGRHTETLDAITSYLDLGVYSEWDEQKKLDFLTRELK 507

                    GKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLA
                    GKRPL+++ +  t +v++vld+frv AEL +D+ GaY+isma +   +L
  gi|2226176   508 GKRPLVPPYIQVTADVQEVLDTFRVAAELGSDALGAYVISMA-SNCVILF 556

                    vELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri....
                    v          + LrvvPLFE + DL+ A  a+ kL siDWY+ +i +++
  gi|2226176   557 V----------NRLRVVPLFETVNDLREAGPAIRKLLSIDWYRDHIiknh 596

                    dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    +G qevmvGYsDsGKDAGR+ AAW LYkAqE+++     +G+K++lFHGR
  gi|2226176   597 NGHQEVMVGYSDSGKDAGRFTAAWELYKAQEDVVAACNAFGIKVTLFHGR 646

                    GGtvGRGGGP......tHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                    GG +GRGGGP+ ++++     Ls     ++G+      G+   +     +
  gi|2226176   647 GGSIGRGGGPdlsrhsVAATRLSDGNSSVDGA-----RGDGAGQVRAAAD 691

                    LCFrs..LqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsv..
                    +C  ++++    AA      +   +     R++          E R+v++
  gi|2226176   692 VCPAAgdIHDGGAAG-----DAAAAAAAAGRQVAGGDGGDIAGELRAVpe 736

                    .vvKEPRFvEYFRlA.tPElEYGkmniGsRPaKRkPsGGiesLRAiPWiF
                    + v+EP         +      G +niGsRPaKR+   Gi  LRAiPW+F
  gi|2226176   737 hGVREPGVHQVLPGGdAAGRSLGYLNIGSRPAKRRTTPGISNLRAIPWVF 786

                    aWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLl
                    aWtqtR  LP WLGvG   + A dK       L+ mY+eWPFF  t+DL+
  gi|2226176   787 AWTQTRLVLPAWLGVGRGLQDACDKGHT--HELRAMYEEWPFFQSTVDLI 834

                    EmvFAKGDPGiAaLyDkLLvaEe.LkPFGksLRdkYvEtkdlLLkiAGHk
                    Emv AK D  +A  yD++Lv + + +  G +LR++   t++ +L + GHk
  gi|2226176   835 EMVVAKADAPMAKHYDDVLVHDAgRRTLGAELRQELARTENCVLAVSGHK 884

                    DlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKE
                     l      L++ +  R  Y+  +n++q   L+R+R
  gi|2226176   885 KLSANNRSLRKLIDSRLTYLNPMNMLQVEVLRRLRQ-------------- 920

                    yAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      d+n        kL           D L++t+ GiAAGm ntG
  gi|2226176   921 -DDDN-------RKLR----------DALLITINGIAAGMRNTG    946

gi|154146756|emb|CAM84065.1|: domain 1 of 1, from 1 to 439: score 480.5, E = 2.3e-141
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|1541467     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDvlDAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg DLP+tE
  gi|1541467     1 --HTDVLDAITTHLGIGSYREWAEEKRQEWLLSELRGKRPLLGQDLPQTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541467    49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECHVRHPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAav++LFs+DWY+ ri+GKqevm GYsDsGKDAG
  gi|1541467    99 RVVPLFEKLADLEAAPAAVARLFSVDWYMDRINGKQEVMTGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYKAQEELVRVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDt++GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541467   199 PPDTVHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+e+AvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG mniGsR
  gi|1541467   249 KPEWRALMDELAVVATEEYRSIVFREPRFVEYFRSATPETEYGGMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+n+
  gi|1541467   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHSMKKDIRNI 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q+ +EmY+eWPFFRvtlDLlEmvFAKGDP iA+LyD+LLva++LkPFG++
  gi|1541467   349 QMHREMYNEWPFFRVTLDLLEMVFAKGDPSIAGLYDELLVADDLKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Yv+t++lLL++AGHkD+LEGDPYL+qrlRLRd+ itt
  gi|1541467   399 LRNNYVDTQQLLLQVAGHKDILEGDPYLRQRLRLRDPHITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146736|emb|CAM84055.1|: domain 1 of 1, from 1 to 439: score 480.4, E = 2.5e-141
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------ -
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                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt.
                    +tD lDAittHL+iGsYReWsEe+RqEWLl+EL+GKRPLlgsDLP+t+
  gi|1541467      1 --HTDALDAITTHLGIGSYREWSEERRQEWLLSELRGKRPLLGSDLPQTs 48

                  EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                  EEv+Dvl++frvLAELP DsFGaYiisma aPsDvLAvELLqREC+v+++
  gi|1541467     49 EEVADVLGTFRVLAELPADSFGAYIISMAAAPSDVLAVELLQRECQVRHP 98

                  LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                  LrvvPLFEkLADLeAAPAav++LFs+DWY+ ri GKqevm+GYsDsGKDA
  gi|1541467     99 LRVVPLFEKLADLEAAPAAVARLFSVDWYMDRIGGKQEVMIGYSDSGKDA 148

                  GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                  GRlsAAWqLY+AqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLs
  gi|1541467    149 GRLSAAWQLYRAQEEMVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILS 198

                  qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                  qPPDtinGslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvs
  gi|1541467    199 QPPDTINGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVS 248

                  PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                  PkPEWRkLm+emAvvAtE YRs+v+KEPRFvEYFR+AtPE+EYG+mniGs
  gi|1541467    249 PKPEWRKLMDEMAVVATEAYRSIVFKEPRFVEYFRSATPETEYGRMNIGS 298

                  RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                  RP+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+n
  gi|1541467    299 RPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVMNKDIRN 348

                  lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                  +q+L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva++LkPFG+
  gi|1541467    349 VQMLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDQLLVADDLKPFGE 398

                  sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                  +LR++Y +t++lLL++AGHkD+LEGDPYLKqrlRLRd+Yit
  gi|1541467    399 QLRNNYLDTRQLLLQVAGHKDILEGDPYLKQRLRLRDPYIT--------- 439

                  LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi

  gi|1541467     - ------------------------------------------------- -

                  LtmKGiAAGmqntG<-*

  gi|1541467     - --------------    -

gi|154146770|emb|CAM84072.1|: domain 1 of 1, from 1 to 439: score 477.7, E = 1.6e-140
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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gi|1541467     - ------------------------------------------------ -

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1541467     - ------------------------------------------------ -

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1541467     - ------------------------------------------------ -

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1541467     - ------------------------------------------------ -

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1541467     - ------------------------------------------------ -

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1541467     - ------------------------------------------------ -

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1541467     - ------------------------------------------------ -

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1541467     - ------------------------------------------------ -

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +tD +DAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLl +D+P tE
gi|1541467     1 --HTDAVDAITTHLGIGSYREWPEEKRQEWLLSELRGKRPLLSPDMPETE 48

                 EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                 Ev+Dvl++frvLAELP DsFG+YiismataPsDvLAvELLqREC+v+++L
gi|1541467    49 EVADVLGTFRVLAELPRDSFGPYIISMATAPSDVLAVELLQRECKVREPL 98

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                 +vvPLFE+LADL+AAPA+ve+LFs+DWYinri+GKq+vmvGYsDsGKDAG
gi|1541467    99 PVVPLFERLADLQAAPASVERLFSVDWYINRINGKQQVMVGYSDSGKDAG 148

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 RlsAAWqLY+AqEE+ KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1541467   149 RLSAAWQLYRAQEEMSKVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                 PPDtinGs+RvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PP +P
gi|1541467   199 PPDTINGSIRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPTAP 248

                 kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                 kPEWR Lm++mAvvA EEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
gi|1541467   249 KPEWRALMDDMAVVAAEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                 PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                 PaKRkP GGiesLRAiPWiF+WtqtRFHLPvWLGvGAAF+hA++KD+Kn+
gi|1541467   299 PAKRKPKGGIESLRAIPWIFSWTQTRFHLPVWLGVGAAFQHAMKKDSKNI 348

                 qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                 q+Lk mY+eWPFFRvtlDLlEmvFAKGDP iA+ yD+LLvaE+LkPFG++
gi|1541467   349 QMLKTMYNEWPFFRVTLDLLEMVFAKGDPAIAGYYDQLLVAEDLKPFGEQ 398

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                 LR kYv+t++lLL+iAGHk++LEGDPYLKqrlRLRd+Yit
gi|1541467   399 LRKKYVDTEQLLLQIAGHKEILEGDPYLKQRLRLRDPYITI--------- 439

                 KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

gi|1541467     - ------------------------------------------------ -

                 tmKGiAAGmqntG<-*
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  gi|1541467     - -------------    -

gi|154146812|emb|CAM84093.1|: domain 1 of 1, from 1 to 439: score 477.7, E = 1.7e-140
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDvlDA+ttHL+iGsYReW+EeKRqEWL +EL+GKRPLlg+DLP+tE
  gi|1541468     1 --HTDVLDAVTTHLGIGSYREWPEEKRQEWLPSELRGKRPLLGADLPQTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqRECgv+++L
  gi|1541468    49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECGVRHPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAa+++LFs+DWY+ ri G+qevm+GYsDsGKDAG
  gi|1541468    99 RVVPLFEKLADLEAAPAAMARLFSVDWYMGRIGGRQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+++vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYKAQEELVRVAKRHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDt+nGslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTVNGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR+Lm+emA vAtE YRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPEWRELMDEMAAVATEAYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+hA+ KDi+n+
  gi|1541468   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFQHAMRKDIRNI 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva++LkPFG++
  gi|1541468   349 QALREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADDLKPFGEQ 398
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                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR +Yv+t++lLL++AGHkD+LEGDPYLKqrlRLRd+Yitt
  gi|1541468   399 LRKNYVDTQQLLLQVAGHKDVLEGDPYLKQRLRLRDPYITT--------- 439

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146902|emb|CAM84138.1|: domain 1 of 1, from 1 to 439: score 477.1, E = 2.5e-140
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541469     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541469     - ------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541469     - ------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541469     - ------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541469     - ------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541469     - ------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541469     - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541469     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541469     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDvlDAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
  gi|1541469     1 --HTDVLDAITTHLGIGSYREWAEEKRQEWLLSELRGKRPLLGADLPQTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl++frvLAELP DsFGaY+ism+taPsDvLAvELLqRECgv+++L
  gi|1541469    49 EVADVLGTFRVLAELPADSFGAYVISMTTAPSDVLAVELLQRECGVRHPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLeAAPAav++LFs+DWY+ ri GKqevm+GYsDsGKDAG
  gi|1541469    99 RVVPLFEKLADLEAAPAAVARLFSVDWYMDRIGGKQEVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+++vA +yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541469   149 RLSAAWQLYKAQEELVQVAERYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541469   199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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                    kPEWR Lm++mAv  tEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541469   249 KPEWRALMDDMAVATTEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+n+
  gi|1541469   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVMKKDIRNI 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLva+eLkPFG++
  gi|1541469   349 HTLREMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDELLVADELKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y++t++ LL++AGHkD+LEGDPYLKqrlRLRd+Yitt
  gi|1541469   399 LRKNYEDTQQPLLQVAGHKDILEGDPYLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541469     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541469     - -------------    -

gi|154146876|emb|CAM84125.1|: domain 1 of 1, from 1 to 439: score 476.7, E = 3.3e-140
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDvlDA+ttHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
  gi|1541468     1 --HTDVLDAVTTHLGIGSYREWPEEKRQEWLLSELRGKRPLLGPDLPQTE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541468    49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECQVQHPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAav++LFs+D Y+ ri GKqevm+GYsDsGKDAG
  gi|1541468    99 RVVPLFEKLADLEAAPAAVARLFSVDRYMDRIGGKQEVMIGYSDSGKDAG 148
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                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYKAQEELVKVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDt+nGslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTVNGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+++AvvAtE YRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPEWRALMDKLAVVATEAYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+n+
  gi|1541468   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMNKDIRNI 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva++LkPFG+
  gi|1541468   349 QTLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADDLKPFGEL 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y +t++lLL++AGHk++LEGDPYLKqrlRLRd+Yitt
  gi|1541468   399 LRNNYADTQQLLLQVAGHKEILEGDPYLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146846|emb|CAM84110.1|: domain 1 of 1, from 1 to 439: score 476.5, E = 3.8e-140
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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                    +tDv+DAittH++iGsYR+W+EeKRqEWLl+EL+GKRPLl +D+P+tE
  gi|1541468     1 --HTDVIDAITTHIGIGSYRSWPEEKRQEWLLSELRGKRPLLAPDMPQTE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvl+ frvLAELP DsFG+YiismataPsDvLAvELLqREC+v  +L
  gi|1541468    49 EIADVLGCFRVLAELPRDSFGPYIISMATAPSDVLAVELLQRECHVTDPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFE+LADL+ APA++e+LFs+DWY  ri+GKq+vm+GYsDsGKDAG
  gi|1541468    99 PVVPLFERLADLQNAPASMERLFSVDWYLERINGKQQVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLY+AqEE+++vAK+y vKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541468   149 RLSAAWQLYRAQEELAQVAKRYSVKLTMFHGRGGTVGRGGGPSHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGs+RvtvqGEviE sFGE++LCFr+L RFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTINGSIRVTVQGEVIEHSFGEDHLCFRTLERFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWRkLm+emAvvAtEEYRsvv++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPEWRKLMDEMAVVATEEYRSVVFREPRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkP GGiesLRAiPWiF+WtqtRFHLPvWLGvGAAF+ A++KD+Kn+
  gi|1541468   299 PAKRKPKGGIESLRAIPWIFSWTQTRFHLPVWLGVGAAFQSAVKKDSKNI 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    qkLkEmYkeWPFFRvt+DLlEmvFAKGDP iA+LyD+LLva++LkPFG++
  gi|1541468   349 QKLKEMYKEWPFFRVTIDLLEMVFAKGDPSIAGLYDELLVADDLKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR+kY Et++lLL+iAGHk++LEGDPYLKq+lRLR++Yitt
  gi|1541468   399 LRNKYLETQQLLLQIAGHKEILEGDPYLKQGLRLRNPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146826|emb|CAM84100.1|: domain 1 of 1, from 1 to 439: score 476.0, E = 5.2e-140
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -
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                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tD lDAittHL+iGsYReW+Ee+RqEWLl+EL+GKRPLlgsD+P+ E
  gi|1541468     1 --HTDTLDAITTHLGIGSYREWPEERRQEWLLSELRGKRPLLGSDMPQSE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl++frvLAELP DsF aYiismataPsDvLAvELLqREC+v+++L
  gi|1541468    49 EVADVLGTFRVLAELPPDSFSAYIISMATAPSDVLAVELLQRECQVRHPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLeAAPA+v++LFs+DWY+ ri GKqevm+GYsDsGKDAG
  gi|1541468    99 RVVPLFEKLADLEAAPASVARLFSVDWYMDRIGGKQEVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYKAQEEMVKVAKHYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm PPvsP
  gi|1541468   199 PPDTINGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMRPPVSP 248

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                  kP WR Lm+emAvvAtE YRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPAWRALMDEMAVVATEAYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+n+
  gi|1541468   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMNKDIRNV 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q+L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva++LkPFG++
  gi|1541468   349 QMLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDQLLVADDLKPFGEQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y Et++lLL++ GHk +LEGDPYLKqrlRLRd+Yitt
  gi|1541468   399 LRNDYLETQQLLLQVTGHKNILEGDPYLKQRLRLRDPYITT--------- 439

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------ -

                  tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146908|emb|CAM84141.1|: domain 1 of 1, from 1 to 438: score 475.5, E = 7.5e-140
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541469     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541469     - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541469     - ------------------------------------------------ -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541469     - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|1541469     - ------------------------------------------------- -

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  gi|1541469     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541469     - ------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541469     - ------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541469     - ------------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDvlDAittHL+iGsYR+W+ e+RqEWLl+EL+GKRPLlgsDLP+ E
  gi|1541469     1 --HTDVLDAITTHLGIGSYRDWAGERRQEWLLSELRGKRPLLGSDLPQSE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v ++L
  gi|1541469    49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECQVCHPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPA+v++LFs+DWY+ ri GKqevm+GYsDsGKDAG
  gi|1541469    99 RVVPLFEKLADLEAAPASVARLFSVDWYMDRIGGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541469   149 RLSAAWQLYKAQEEMVKVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDt+nGslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541469   199 PPDTVNGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emAvvAtE YRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541469   249 KPEWRALMDEMAVVATEAYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+n+
  gi|1541469   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMNKDIRNV 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q+L+EmY+eWPFFRvtlDLlEmvFAKGDP iA+LyD+LLva++LkPFG++
  gi|1541469   349 QMLREMYNEWPFFRVTLDLLEMVFAKGDPRIAGLYDQLLVADDLKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y Et++lLL++ GHkD+LEGDPYLKqrlRLRd+Yit
  gi|1541469   399 LRNNYLETQQLLLQVTGHKDILEGDPYLKQRLRLRDPYIT---------- 438

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541469     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541469     - -------------    -

gi|154146732|emb|CAM84053.1|: domain 1 of 1, from 1 to 439: score 475.1, E = 1e-139
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------- -
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                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1541467    - ------------------------------------------------ -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1541467    - ------------------------------------------------ -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1541467    - ------------------------------------------------ -

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1541467    - ------------------------------------------------ -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1541467    - ------------------------------------------------ -

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1541467    - ------------------------------------------------ -

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1541467    - ------------------------------------------------ -

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  +tD lDAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
gi|1541467      1 --HTDALDAITTHLGIGSYREWAEEKRQEWLLSELRGKRPLLGPDLPQTE 48

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
gi|1541467     49 EVADVLGTFRVLAELPADSFGAYIISMATAPSDVLAVELLQRECQVRHPL 98

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                rvvPLFEkLADLeAAPAa+++LFs+DWY  ri GKqevm+GYsDsGKDAG
gi|1541467     99 RVVPLFEKLADLEAAPAAMARLFSVDWYTARIAGKQEVMIGYSDSGKDAG 148

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLYkAqEE+++vA+++GvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1541467    149 RLSAAWQLYKAQEELVRVAQRHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PPDt++GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm PPvsP
gi|1541467    199 PPDTVHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMRPPVSP 248

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                kPEWR Lm+++A  AtEEYRs+v++EPRFvEYFR AtPE+EYG+mniGsR
gi|1541467    249 KPEWRALMDDLAAAATEEYRSIVFREPRFVEYFRAATPETEYGRMNIGSR 298

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+n+
gi|1541467    299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMNKDIRNV 348

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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gi|1541467    349 QVLREMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDELLVADELKPFGEQ 398

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR++YvEt++lLL++AGHkD+LEGDPYL+qrlRLRd+Yitt
gi|1541467    399 LRNNYVETQQLLLQVAGHKDILEGDPYLRQRLRLRDPYITT--------- 439

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

gi|1541467    - ------------------------------------------------ -

                tmKGiAAGmqntG<-*
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  gi|1541467     - -------------    -

gi|154146744|emb|CAM84059.1|: domain 1 of 1, from 1 to 439: score 475.1, E = 1e-139
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  gi|1541467     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tD +DA+ttHL+iGsYReWsEeKRqEWLl+EL+GKRPLl  DLP  E
  gi|1541467     1 --HTDAIDAVTTHLGIGSYREWSEEKRQEWLLSELQGKRPLLVDDLPVSE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl+ frvLAELP DsFG+YiismataPsDvLAvELLqREC+++++L
  gi|1541467    49 EVADVLGCFRVLAELPADSFGPYIISMATAPSDVLAVELLQRECHIRNPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLFE+LADL+ APA+ve+LFsiDWY nri GKq++mvGYsDsGKDAG
  gi|1541467    99 PVVPLFERLADLQNAPASVERLFSIDWYLNRIGGKQQIMVGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLY+Aq E++KvAKky vKL+ FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYQAQAEVAKVAKKYDVKLTFFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvt+qGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541467   199 PPDTINGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEW kLm+emAvvAt+ YRsvvvKEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWSKLMDEMAVVATDAYRSVVVKEPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvG AFK AidKDiKn+
  gi|1541467   299 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGTAFKSAIDKDIKNF 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva++LkPFG++
  gi|1541467   349 QLLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVADDLKPFGEQ 398
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                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR kY Et++lLL+iAGHk++LEGDPYLKqrlRLRd+Yitt
  gi|1541467   399 LRSKYLETEQLLLQIAGHKEILEGDPYLKQRLRLRDPYITT--------- 439

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146924|emb|CAM84149.1|: domain 1 of 1, from 1 to 439: score 474.4, E = 1.6e-139
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541469     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541469     - ------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541469     - ------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541469     - ------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541469     - ------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541469     - ------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541469     - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541469     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541469     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tD +DAittHL+iGsYReWsEeKRqEWLl EL+GKRPLl +D+P+t+
  gi|1541469     1 --HTDAVDAITTHLGIGSYREWSEEKRQEWLLNELQGKRPLLVPDMPQTD 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+D l+ f+vLAELP DsFG+YiismataPsDvLAvELLqREC+v+q+L
  gi|1541469    49 EVADALGCFKVLAELPRDSFGPYIISMATAPSDVLAVELLQRECHVRQPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +vvPLFE+LADL+ APA+ve+LFs+DWY nri GKq++mvGYsDsGKDAG
  gi|1541469    99 PVVPLFERLADLQNAPASVERLFSVDWYLNRIGGKQQIMVGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLY+AqE ++KvAKky vK++ FHGRGGtvGRGGGPtHLAiLsq
  gi|1541469   149 RLSAAWQLYQAQEQVAKVAKKYDVKVTFFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP+tinGslRvt+qGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|1541469   199 PPETINGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPISP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWRkLm++mAvvAt+ YRsvvvKEPRFvEYFR+AtPE+EYG+mniGsR
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  gi|1541469   249 KPEWRKLMDDMAVVATDAYRSVVVKEPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvG AFK+AidKDiKn+
  gi|1541469   299 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGTAFKYAIDKDIKNF 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva++LkPFG++
  gi|1541469   349 QLLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVADDLKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR kY Et++lLLkiAGHkD+LEGDPYLKqrlRLRd+Yitt
  gi|1541469   399 LRGKYMETQELLLKIAGHKDILEGDPYLKQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541469     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541469     - -------------    -

gi|154146858|emb|CAM84116.1|: domain 1 of 1, from 1 to 439: score 473.6, E = 2.7e-139
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDv+DAittH+++GsYR+W+EeKRqEWLl+EL+GKRPLl +D+P+tE
  gi|1541468     1 --HTDVIDAITTHIGVGSYRSWPEEKRQEWLLSELRGKRPLLAPDMPQTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dvl+ frvLAELP DsFG+YiismataPs+vLAvELLqREC++k++L
  gi|1541468    49 EIADVLGCFRVLAELPRDSFGPYIISMATAPSEVLAVELLQRECHIKEPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLFE+LADL+ APA++e+LFs+DWY  ri+GKq+vm+GYsDsGKDAG
  gi|1541468    99 PVVPLFERLADLQNAPASMERLFSVDWYLQRINGKQQVMIGYSDSGKDAG 148
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                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLY+AqEE+++vAK+y vKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541468   149 RLSAAWQLYRAQEELAQVAKRYSVKLTMFHGRGGTVGRGGGPSHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGs+RvtvqGEviE sFGEE+LCFr+L RFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTINGSIRVTVQGEVIEHSFGEEHLCFRTLERFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWRkLm+emAvvAtEEYRs+vv+EPRFvEYFR+AtPE+EYGkmniGsR
  gi|1541468   249 KPEWRKLMDEMAVVATEEYRSIVVREPRFVEYFRSATPETEYGKMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkP GGi+sLRAiPWiF+WtqtRFHLPvWLGvGAAF+ A++KD+Kn+
  gi|1541468   299 PAKRKPQGGITSLRAIPWIFSWTQTRFHLPVWLGVGAAFQSAVKKDSKNI 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    qkLkEmYkeWPFFRvt+DLlEmvFAKGDP iA+LyD+LLva+eLkPFG++
  gi|1541468   349 QKLKEMYKEWPFFRVTIDLLEMVFAKGDPSIASLYDELLVADELKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR+kY Et++lLL+iAGHk++LEGDPYLKq+lRLR++Yitt
  gi|1541468   399 LRNKYLETQELLLQIAGHKEILEGDPYLKQGLRLRNPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146884|emb|CAM84129.1|: domain 1 of 1, from 1 to 439: score 472.7, E = 5.3e-139
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDvlDAittHL+iGsYReW+Ee+RqEWLl+EL+GKRPLlgsDLP tE
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  gi|1541468     1 --HTDVLDAITTHLGIGSYREWPEEQRQEWLLSELRGKRPLLGSDLPETE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl++frvLAELP DsFGaY+ismataPsDvLAvELLqREC+v+++L
  gi|1541468    49 EVADVLGTFRVLAELPADSFGAYVISMATAPSDVLAVELLQRECHVRRPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAav++LFs+DWY+ ri GKqevm+GYsDsGKDAG
  gi|1541468    99 RVVPLFEKLADLEAAPAAVARLFSVDWYVERIGGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+++vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYKAQEELVRVAKRHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTILGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+++AvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPEWRALMDDLAVVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA+ KDi+n+
  gi|1541468   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMSKDIRNI 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q L+EmY+eWPFFRvt+DLlEmvFAKGDPGiA+LyD+LLva++LkPFG++
  gi|1541468   349 QVLREMYNEWPFFRVTVDLLEMVFAKGDPGIAGLYDELLVADDLKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y +t+ lLL++AGH+++LEGDPYLKqrlRLRd+ itt
  gi|1541468   399 LRANYADTERLLLQVAGHREILEGDPYLKQRLRLRDPHITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146860|emb|CAM84117.1|: domain 1 of 1, from 1 to 439: score 472.5, E = 5.8e-139
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -
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                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDv+DAittH++iGsYR+W+EeKRqEWLl+EL+GKRPLl +D+P+tE
  gi|1541468     1 --HTDVIDAITTHIGIGSYRSWPEEKRQEWLLSELRGKRPLLAPDMPQTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++Dvl+ frvLAELP DsFG+YiismataPsDvLAvELLqREC+v+++L
  gi|1541468    49 EIADVLGCFRVLAELPRDSFGPYIISMATAPSDVLAVELLQRECHVREPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +vvPLFE+LADL+ APA++e+LFs+DWY  ri+GKq+vm+GYsDsGKDAG
  gi|1541468    99 PVVPLFERLADLQNAPASMERLFSVDWYLQRINGKQRVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLY+AqEE+++vAK+y vKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541468   149 RLSAAWQLYRAQEELAQVAKRYSVKLTMFHGRGGTVGRGGGPSHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGs+RvtvqGEviE sFGEE+LCFr+L RFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTINGSIRVTVQGEVIEHSFGEEHLCFRTLERFTAATLEHGMHPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWRkLm+emAvvAtEEYRsvvv+EPRFvEYFR+AtPE+EYGkmn GsR
  gi|1541468   249 KPEWRKLMDEMAVVATEEYRSVVVREPRFVEYFRSATPETEYGKMNTGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKRkP GGi+sLRAiPWiF+WtqtRFHLPvWLGvGAAF+ Ai+KD+Kn+
  gi|1541468   299 PAKRKPQGGITSLRAIPWIFSWTQTRFHLPVWLGVGAAFQSAIKKDSKNI 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  qkLkEmYkeWPFFRvt+DLlEmvFAKGDP iA+LyD+LLva++LkPFG++
  gi|1541468   349 QKLKEMYKEWPFFRVTIDLLEMVFAKGDPSIAGLYDELLVADDLKPFGEQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR+kY Et+++LL+iAGHk++LEGDP+LKq lRLR++Yitt
  gi|1541468   399 LRNKYLETQQFLLQIAGHKEILEGDPFLKQSLRLRNPYITT--------- 439

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------ -

                  tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146772|emb|CAM84073.1|: domain 1 of 1, from 1 to 439: score 472.5, E = 6.1e-139
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------ -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|1541467     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tD +DAittHL+iGsY+eW+EeKRqEWLl+EL+GKRPLl +D+P tE
  gi|1541467     1 --HTDAIDAITTHLGIGSYKEWPEEKRQEWLLSELQGKRPLLVPDMPVTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+ vl+ frvLAELP DsFG+YiismataPsDvLAvELLqRECgv+q+L
  gi|1541467    49 EVEAVLGCFRVLAELPRDSFGPYIISMATAPSDVLAVELLQRECGVRQPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLFE+LADL+ APA+ve+LFsiDWY nri GKq+vmvGYsDsGKDAG
  gi|1541467    99 PVVPLFERLADLQNAPASVERLFSIDWYLNRIGGKQQVMVGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLY+AqEE++KvAKky vK++ FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYQAQEEVAKVAKKYDVKVTFFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvt+qGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|1541467   199 PPDTINGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPISP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWRkLm+emAvvAt+ YRsvvvKEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWRKLMDEMAVVATDAYRSVVVKEPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK AidKDiKn+
  gi|1541467   299 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKSAIDKDIKNF 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q Lk+mY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva++LkPFG++
  gi|1541467   349 QLLKDMYREWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVADDLKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR kY Et+++LLkiAGHk++LE DPYLKqrlRLRd+Yitt
  gi|1541467   399 LRSKYLETQEFLLKIAGHKEILEADPYLKQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|156084500|ref|XP_001609733.1|: domain 1 of 1, from 5 to 954: score 472.1, E = 8e-139
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       + A L      +    +++     L+lD  L  L  +  + ++  v
  gi|1560845     5    DVLAALQERRKNRQE-GDHVDFQQPLVLDMTL--LEAILFQVVRKCV 48

                   qE.CYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    E+ YE   e    +D+  +     kL  Ld +    +A+++  +  + n
  gi|1560845    49 PEdVYEKISEIVQHEDSGDIKWARKKLHELDVSYWPHLARTLRIICAIGN 98
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                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                 A+  +   RRR    +     D     t   +   +     k+   Pe+
gi|1560845    99 TADKAQ-KKRRRDAYER-TNAEDSDFQGTTYTLRGSMEMFKQKG-MKPED 145

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                +++ + n  +D vltAHPt   R   L  + R+   L q   +  t+ +
gi|1560845   146 IYQHIANMHIDFVLTAHPTETHRLTSLMNHKRLCELLLQFDGQKCTPFEE 195

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  L   L   i   + tD iRR +Pt  DE+ a    i  t+++ vP
gi|1560845   196 ASLIKDLEMHIATMWHTDQIRRQKPTLFDEIVAVAHRIKSTIFDSVPNLY 245

                RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   D  L    +   lP d  L  FssW GGDRDG nP vtP++tR
gi|1560845   246 EYLDAFLEEQNLPP-LPLDTKLFTFSSWAGGDRDG-NPFVTPDITRQTVC 293

                LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyr........taa
                  ++ A  lY+  +E L  El +    dE +     l ++ +   ++  a
gi|1560845   294 FNKIHACDLYLHMMERLAEELPLKDATDEFKLYTSTLDKelgailgnMGA 343

                rdkvvKyYi.EFWKqvP...PtEPYRviLGdvRDKLYntRERaRHLLAtG
                 d +  y+ +EF   +P+ +P E YR +   +  +L  tR  aR  LA
gi|1560845   344 MDGIGAYFSdEFTCMMPdaqPDEVYRTLFRYIGTRLTITRYIARKDLANE 393

                iseisE...eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqv
                 s+++E+ +  vy  v e +EPL  CY sLCe G    A   L  ++R
gi|1560845   394 RSNVAEgirKCVYNSVAEIMEPLKRCYASLCEVGCSMFANSRLKGVIRCL 443

                stFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsE..eKRqEWLl
                 tFGL L +LDiRq+s ++t   D + + L++ s + +sE  e  +  Ll
gi|1560845   444 ETFGLYLLRLDIRQDSSKHTLAADYLFKKLGL-SNKRYSEmlECDKVALL 492

                aELkGKRPLlgsDLPktEE....vkDvldafrvLAELPiDsFGaYiisma
                +++  ++  +g    +  E +++v Dv+++f+v+ EL  +   aY+ism+
gi|1560845   493 SDIISQKGQFGITEDMLKEapdgVDDVVGTFKVVGELGTEVINAYVISMC 542

                taPsDvLAvELL.......qRECgvkqtLrvvPLFEkLADLeAAPAavek
                   sDvL v    ++  ++qR+ gv + +++vPL E +  L+    +++
gi|1560845   543 QEASDVLLVATFlekiagsQRD-GVSHRVKIVPLLETIGSLRSSSDTMKC 591

                LFsiDWYinri....dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiK
                LF    Y+  + + ++  qevm+GYsDsGKD GRl+A W LYkAq  + +
gi|1560845   592 LFGNPCYRDYLityhNSTQEVMIGYSDSGKDGGRLAASWELYKAQQMLYQ 641

                vAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEv
                vA +  vK+  FHGRGG + RGGGP H Ai+sqP  t+n  lR tvqGE
gi|1560845   642 VAEQSAVKIRYFHGRGGSISRGGGPLHHAIMSQPRGTLNNYLRLTVQGET 691

                iEfsFGEEnLCFrsLqRFtAAtLEHGmnP.PvsPkPEWRkLmeemAvvAt
                i ++F   + C r++  +    +   +n + +  kPEW +L +emA +
gi|1560845   692 IGYMFALPHDCLRTMEYYLTSCIQFNVNAdAIEVKPEWIELWDEMAEISY 741

                EEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAi
                  YR vv   P F EYF   tP  E   mniGsRPaKR   GGi+++RAi
gi|1560845   742 KAYRKVVRDIPGFPEYFTALTPVKEMKLMNIGSRPAKRTKDGGIDTIRAI 791

                PWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvt
                PW+F Wtq    +P+WLG+    +hAi      l  Lk+mY+ WPF
gi|1560845   792 PWVFGWTQVQLNMPIWLGLADGLQHAIS--TGRLELLKDMYRSWPFCSSF 839

                lDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiA
                l L+ mv  K    i   y+k Lv  +    G+ LR +     +l+ ++
gi|1560845   840 LHLVSMVLLKTNANITEEYEKALVPQDYIHIGEMLRTNLMRATNLIKQVT 889

                GHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhl
                  ++  + D  ++ + R     +     +q  tL R R
gi|1560845   890 CEREFCDHDIVVRRGFRCNARLLGPCAALQIETLVRYRN----------- 928

                sKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      E+          n   r+     D L++ mK iAA mq tG
gi|1560845   929 ----NPED----------N---RY----HDALVISMKAIAAIMQHTG    954
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gi|154146740|emb|CAM84057.1|: domain 1 of 1, from 1 to 438: score 471.8, E = 9.7e-139
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tD lDAit HL+iGsYReW+Ee+RqEWLl+EL+GKRPLlgsDLP+ E
  gi|1541467     1 --HTDALDAITMHLGIGSYREWPEERRQEWLLSELRGKRPLLGSDLPQSE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v ++L
  gi|1541467    49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECQVSHPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADL+AAPA+v++LFs+DWY+ ri GKqevm+GYsDsGKDAG
  gi|1541467    99 RVVPLFEKLADLQAAPASVARLFSVDWYMDRIGGKQEVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYKAQEEMVKVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm PPvsP
  gi|1541467   199 PPDTINGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMRPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+e+AvvAtE YRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWRALMDEIAVVATEAYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+n+
  gi|1541467   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMNKDIRNV 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q+LkEmY+eWPFFRvtlDLlEmvFAKGDP iA+LyD+LLva++LkPFG++
  gi|1541467   349 QMLKEMYNEWPFFRVTLDLLEMVFAKGDPRIAGLYDQLLVADDLKPFGEQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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                  LR+ Y Et++lLLk+ GHkD+LEGDPYLKqrlRLRd+Yit
  gi|1541467   399 LRNSYLETQQLLLKVTGHKDILEGDPYLKQRLRLRDPYIT---------- 438

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ---------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146794|emb|CAM84084.1|: domain 1 of 1, from 1 to 439: score 471.5, E = 1.2e-138
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ---------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ---------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ---------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ---------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDv+DAittHL+iGsYR+W+Ee+R+EWL++ELkGKRPLl++DLP+tE
  gi|1541467     1 --HTDVIDAITTHLGIGSYRSWPEEQRMEWLISELKGKRPLLPPDLPMTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++Dv++a++v+AELP+DsFG+YiismataPsDvLAvELLqRECgvkq+L
  gi|1541467    49 EIADVVGALKVIAELPVDSFGPYIISMATAPSDVLAVELLQRECGVKQPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +vvPLFE+LAD +  PA+ve+LFs DWY  ri+GKq+vmvGYsDsGKDAG
  gi|1541467    99 PVVPLFERLADRQNGPASVERLFSADWYLERIQGKQQVMVGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAW LY AqEE++KvAK++GvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWALYTAQEEMAKVAKRFGVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGs+RvtvqGEviEf FGEE+LCF++LqRFtAAtLEHG++PPvsP
  gi|1541467   199 PPDTINGSIRVTVQGEVIEFCFGEEHLCFQTLQRFTAATLEHGIHPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lmeem vvAtEEYRs+v+KEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWRALMEEMTVVATEEYRSIVFKEPRFVEYFRSATPETEYGRMNIGSR 298
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                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+P+GGi++LRA+PWiF+WtqtRFHLPvWLGvGAAF+ Ai+KD++n
  gi|1541467   299 PAKRRPGGGITTLRAVPWIFSWTQTRFHLPVWLGVGAAFQAAIKKDVRNN 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q Lk mY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva+eLkPFG++
  gi|1541467   349 QLLKQMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDQLLVADELKPFGEE 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR kYvEt++lLL+iAGHkD+LEGDPYLKq+lRLR++Yitt
  gi|1541467   399 LRKKYVETQKLLLEIAGHKDILEGDPYLKQGLRLRNPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|159900750|ref|YP_001546997.1|: domain 1 of 1, from 6 to 929: score 471.2, E = 1.5e-138
                    *->siDAqLRlLvP..GKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                            L +L+ + G v   + ++  D   +  F          +L E
  gi|1599007     6    TDRTPLSMLIHslGNVL-GDVIVAQDG--VSAF----------ELEE 39

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                     v             ++t+ L EL ++L     a  + + ka+ H   L
  gi|1599007    40 DVRQRTKQRRSDGTLQETQTLTELISQLPV---AQLMGLIKAFTHYFGLV 86

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    nLAE ve   R R+   +       ++A     +E  l+ L  ++  + +
  gi|1599007    87 NLAESVE---RLRVLAER---DRQNGDAPRSESVELALQELRDRG-ITAQ 129

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                     v + L    +  v+tAHPt + RR  L+K+ Ri     qL A
  gi|1599007   130 QVQDLLDHAEIRPVFTAHPTEAKRRTTLKKHHRIAGAARQLTADTTFQRQ 179

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    ++ L E +  E+   +  DE+R  +Pt  DE++  + Y+ E +++ +P+
  gi|1599007   180 RERLLESIREEVISLWQSDEVRIIKPTVIDEVKNNLYYFEESLFDMIPQL 229

                    LRRvDtALKni..GinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                     R  +  L+ i +    R+P     ++F sW+GGDRDG nP v P vt
  gi|1599007   230 YRDTEASLRQIypEHEWRVP---AFLRFGSWVGGDRDG-NPFVIPSVT-- 273

                    vCLLaRmmAanl..YisqvEDLmFElsmWRCndELRvRAEElyrtaardk
                    v  L  +m   l++ i  vE L   ls       + +  E  ++
  gi|1599007   274 VETLKLLMGRSLreHIHSVERLSHRLS--QSSRQVPISEELAQSLIHDAP 321

                    vvKyYiEFWKqvPPtEPYRviLGdvRDKLYnt...RERaRHLLAtGisei
                    +            P EPYR     +  KL  t    ER     A G
  gi|1599007   322 LFPELAQVLERRNPHEPYRQKCSYIHAKLHATlayVERYEPDWARGGHRP 371

                    sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                    +E   y +  ++L  L     sL   G   +ADG L D+      FGL
  gi|1599007   372 AEGTWYANANQYLADLATMEYSLRTNGAASVADGFLRDIQCSAKVFGLHT 421

                    vKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRP
                      LDiRq s R+t  l  i +  +i + Y + s   R   L  EL   RP
  gi|1599007   422 ATLDIRQHSSRHTNALSEIFEYAGICdDYASLSQAERTAVLERELANNRP 471

                    LlgsDLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLA
                    L++  L    E  +++++fr+ + vL +L  ++   Yiism+  PsD+LA
  gi|1599007   472 LIPTHLYYSPETVEIIETFRtiraVLSDLNAEAIETYIISMTEGPSDILA 521

                    vELLqRECgvkqt.....LrvvPLFEkLADLeAAPAavekLFsiDWYinr
                    v LL RE g+ q+++++ L +vPLFE  ADL AAP  +  L s + Y+ +
  gi|1599007   522 VLLLAREAGIYQPgehswLNIVPLFETGADLIAAPEIMHTLLSSEAYRQH 571

                    i...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
```

```
                    +  ++  qe+m+GYsDs KD G   A W LY Aq  ++    ++ v + l
  gi|1599007   572 LvlrNDVQEIMLGYSDSNKDGGFADAHWALYLAQVALAETCFRHRVAMRL 621

                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                    FHGRGG vGRGGGP   AiL qPP t+ G +++t qGEvi   + E +
  gi|1599007   622 FHGRGGAVGRGGGPANRAILGQPPGTVGGRIKITEQGEVISDRYAEPETA 671

                    FrsLqRFtAAtLEHGmnPPvs.PkPEWRkLmeemAvvAtEEYRsvvvKEP
                    +r       A L   +   +++   EW + m  +A v    YR +v+  P
  gi|1599007   672 YRHQEQIINAVLRSSLGVSIAhISQEWHDAMSSLAKVSRKVYRGLVYDHP 721

                    RFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRF
                     F EYFR AtP +E  ++niGsRPa Rk s  ie LRAiPW+F+W q R
  gi|1599007   722 HFLEYFRNATPITEISRLNIGSRPASRKASDRIEDLRAIPWVFSWMQSRH 771

                    HLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                     LP W G+G A  h i+ D   l  L+ mY++WPFFR  lD   m+  K
  gi|1599007   772 TLPGWYGLGSALEHLIQADANGLTTLQGMYNDWPFFRTMLDNAQMILSKA 821

                    DPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                    D  iAa y  L+    L +  FG  ++++Y  t +++ ++A   +lL+
  gi|1599007   822 DMDIAAQYALLVPDQALanEIFG-LIKAEYTRTVKWICEVAQINELLDTS 870

                    PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                    P L+  ++ R++Y+  L  +q   L+R+R
  gi|1599007   871 PILQHSIKQRNPYVDPLSFVQIELLRRLRT-------------------- 900

                    kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      +d+L +          LED ++L + GiAAG++ntG
  gi|1599007   901 -DPDGLEHSD--------LEDAILLSINGIAAGLKNTG    929

gi|154146720|emb|CAM84047.1|: domain 1 of 1, from 1 to 439: score 470.1, E = 3.1e-138
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tD +DAittHL+iGsYReWsEeKRqEWLl+EL+GKRPLl +D+P  +
  gi|1541467     1 --HTDAIDAITTHLGIGSYREWSEEKRQEWLLSELQGKRPLLVPDMPVSD 48
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                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl+ f+vLAELP DsFG+YiismataPsDvLAvELLqREC v+q+L
  gi|1541467     49 EVADVLGCFKVLAELPRDSFGPYIISMATAPSDVLAVELLQRECNVRQPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFE+LADL+ APA+ve+LFsiDWY nri GKq++mvGYsDsGKDAG
  gi|1541467     99 PVVPLFERLADLQNAPASVERLFSIDWYLNRIAGKQQIMVGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAW LY+AqE ++KvAKky v+++ FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467    149 RLSAAWSLYQAQEAVAKVAKKYNVQVTFFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGslRvt+qGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541467    199 PPDTINGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWRkLm+emAvvAt+ YRsvvv+EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467    249 KPEWRKLMDEMAVVATDMYRSVVVREPRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvG AFK AidKDiKn+
  gi|1541467    299 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGTAFKSAIDKDIKNF 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaE+LkPFG++
  gi|1541467    349 QMLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVAEDLKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR kY Et++lLL+iAGHkD+LEGDPYLKqrlRLR +Yitt
  gi|1541467    399 LRSKYLETQELLLQIAGHKDILEGDPYLKQRLRLRGPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146912|emb|CAM84143.1|: domain 1 of 1, from 1 to 438: score 469.1, E = 6.4e-138
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541469     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541469     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541469     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541469     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541469     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541469     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541469     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
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  gi|1541469     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541469     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tD lDAittHL+iGsY +W+EeKRq+WLl+EL+GKRPLl++D P+t+
  gi|1541469     1 --HTDALDAITTHLGIGSYCSWPEEKRQDWLLSELRGKRPLLPPDHPQTD 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl +frvL ELP+DsFGaYiismata sDvLAvELLqRECgv+++L
  gi|1541469    49 EVADVLSTFRVLSELPSDSFGAYIISMATAASDVLAVELLQRECGVRRPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeA PAav++LFs+DWY+ ri G+qevm+GYsDsGKDAG
  gi|1541469    99 RVVPLFEKLADLEATPAAVARLFSVDWYVGRIGGRQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541469   149 RLSAAWQLYKAQEEMVKVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541469   199 PPDTINGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWRkLm+emAvvAtE YRs+v+KEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541469   249 KPEWRKLMDEMAVVATEAYRSIVFKEPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+n+
  gi|1541469   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVMNKDIRNV 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q+L+EmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLva+eLkPFG++
  gi|1541469   349 QMLREMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDQLLVADELKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR +Y +tk+lLL++AGHkD+LEGDPYLKqrlRLRd+Yit
  gi|1541469   399 LRKNYLDTKQLLLQVAGHKDILEGDPYLKQRLRLRDPYIT---------- 438

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541469     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541469     - -------------    -

gi|154146816|emb|CAM84095.1|: domain 1 of 1, from 1 to 439: score 468.9, E = 7.4e-138
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------ -
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                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------ -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------ -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------ -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------ -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDv+DAittHL+iGsYReW+EeKRqEWLl+EL+GKRPL+g+DLP+ E
  gi|1541468     1 --HTDVIDAITTHLGIGSYREWPEEKRQEWLLSELRGKRPLVGADLPQIE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl++f vLAEL  DsFGaYiism+taPsDvLAvELLqREC+v+++L
  gi|1541468    49 EVADVLGTFGVLAELLLDSFGAYIISMTTAPSDVLAVELLQRECHVRHPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAav++LFs+DWY+ ri+GKqevm+GYsDsGKDAG
  gi|1541468    99 RVVPLFEKLADLEAAPAAVARLFSVDWYMDRINGKQEVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkA+EE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYKAKEELVQVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtv GEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTIHGSLRVTVPGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAvvAtE YRs+v++EPRFv YFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPEWRALMDEMAVVATEAYRSIVFREPRFVVYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+n+
  gi|1541468   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMKKDIRNI 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva++LkPFG++
  gi|1541468   349 QTLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADDLKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR+++ +t++lLL++AGHk++LEGDPYLKqrlRLRd+Yitt
  gi|1541468   399 LRNNFADTQQLLLQVAGHKEILEGDPYLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------ -

                    tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146774|emb|CAM84074.1|: domain 1 of 1, from 1 to 439: score 467.9, E = 1.5e-137
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------ -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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gi|1541467     - ------------------------------------------------- -

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1541467     - ------------------------------------------------- -

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1541467     - ------------------------------------------------- -

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1541467     - ------------------------------------------------- -

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1541467     - ------------------------------------------------- -

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1541467     - ------------------------------------------------- -

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1541467     - ------------------------------------------------- -

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +tD lDAit+HL+iGsYR W+EeKRqEWLl EL+GKRPL+g+DLP tE
gi|1541467     1 --HTDALDAITEHLGIGSYRGWPEEKRQEWLLFELRGKRPLFGPDLPTTE 48

                 EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                 Ev+Dvl++frvLAELP D+FGaYiismataPsDvLAvELLqREC+v q+L
gi|1541467    49 EVADVLGTFRVLAELPADCFGAYIISMATAPSDVLAVELLQRECKVEQPL 98

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                 rvvPLFEkLADLeAAPAav++LFsiDWY+ ri GKqevm+GYsDsGKDAG
gi|1541467    99 RVVPLFEKLADLEAAPAAVARLFSIDWYMDRIGGKQEVMIGYSDSGKDAG 148

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 RlsAAWqLYk qEE++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1541467   149 RLSAAWQLYKSQEELVKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                 PP+ti+GslRvtvqGEvi  sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
gi|1541467   199 PPETIHGSLRVTVQGEVIGHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                 kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                 kPEWR Lm++mAvvAt EYRs+v+KEPRFvEYFR+AtPE+EYG+mniGsR
gi|1541467   249 KPEWRALMDDMAVVATKEYRSMVFKEPRFVEYFRSATPETEYGRMNIGSR 298

                 PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                 P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA+d Di+n+
gi|1541467   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMDVDIRNI 348

                 qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                 q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLva++L+P G++
gi|1541467   349 QALREMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDELLVADDLRPLGER 398

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                 LR++Y++tk+lLL++AGHkD+LEGDPYLKqrlRLRd+Yitt
gi|1541467   399 LRNNYEDTKKLLLQVAGHKDVLEGDPYLKQRLRLRDPYITT--------- 439

                 KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

gi|1541467     - ------------------------------------------------- -

                 tmKGiAAGmqntG<-*

gi|1541467     - -------------    -
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gi|154146798|emb|CAM84086.1|: domain 1 of 1, from 1 to 439: score 467.7, E = 1.7e-137
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDv+DAittHL+iGsYR+W+EeKR+EWL +EL+GKRPLl +DLP+t+
  gi|1541467      1 --HTDVIDAITTHLGIGSYRSWPEEKRMEWLASELRGKRPLLAPDLPMTD 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++Dv++a+rv+AELP DsFG+YiismataPsDvLAvELLqREC +kq+L
  gi|1541467     49 EIADVVGALRVIAELPADSFGPYIISMATAPSDVLAVELLQRECRIKQPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADL+ AP +ve+LFs+DWY+ ri GKqe+mvGYsDsGKDAG
  gi|1541467     99 RVVPLFEKLADLQNAPVSVERLFSVDWYMDRIKGKQEIMVGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAW LYkAqEE++KvAK++Gv+L+ FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467    149 RLSAAWHLYKAQEEMAKVAKRFGVQLTFFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP+tinGslRvt+qGEviE+sFGEE+LCF++LqRFtAAtLEHGm+PPv+P
  gi|1541467    199 PPETINGSLRVTIQGEVIEYSFGEEHLCFQTLQRFTAATLEHGMHPPVAP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lmee+A +AtEEYRsvvvKEPRFvEYFR+AtPE+EYGk+niGsR
  gi|1541467    249 KPEWRTLMEELAAIATEEYRSVVVKEPRFVEYFRSATPETEYGKLNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKRkP+GGie+LRAiPWiF+WtqtRFHLPvWLG+G AFKhA++KD+Kn+
  gi|1541467    299 PAKRKPGGGIETLRAIPWIFSWTQTRFHLPVWLGFGGAFKHAMKKDSKNI 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q LkEmY+eWPFFRvtlDLlEmvFAKGDP iAaLyD+LLvaE+LkPFG++
  gi|1541467    349 QLLKEMYNEWPFFRVTLDLLEMVFAKGDPSIAALYDQLLVAEDLKPFGEN 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR +YvEt++lLL++AGHkD+LEGDPYLKqrlRLR++Yitt
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  gi|1541467   399 LRKNYVETQQLLLQVAGHKDILEGDPYLKQRLRLRNPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146750|emb|CAM84062.1|: domain 1 of 1, from 1 to 439: score 466.5, E = 3.8e-137
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tD lDAit HL+iGsYR+W+EeKRqEWLl+EL+G+RPL+g DLP+tE
  gi|1541467     1 --HTDALDAITAHLGIGSYRSWPEEKRQEWLLSELRGRRPLFGGDLPMTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl++frvLAELP D+FGaYiismataPsDvLAvELLqREC+v ++L
  gi|1541467    49 EVADVLGTFRVLAELPPDCFGAYIISMATAPSDVLAVELLQRECKVGHPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAav++LFsiDWY+ ri GKqevm+GYsDsGKDAG
  gi|1541467    99 RVVPLFEKLADLEAAPAAVARLFSIDWYMDRIGGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYKAQEELVKVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP+t+nGslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541467   199 PPETVNGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emAvvAtEEYR++v+KEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWRALMDEMAVVATEEYRAMVFKEPRFVEYFRSATPETEYGRMNIGSR 298
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                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGie+LRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+n+
  gi|1541467   299 PSKRKPSGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIMHKDIRNI 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLva+eLkP G++
  gi|1541467   349 QALREMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDELLVADELKPLGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR ++++tk+lL+++AGH+D+LE DPYLKqrlRLRd+Yitt
  gi|1541467   399 LRSNFEDTKKLLVQVAGHRDVLEDDPYLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146824|emb|CAM84099.1|: domain 1 of 1, from 1 to 439: score 464.8, E = 1.3e-136
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tD +DAittHL+iGsYReWsEeKRqEWLl+EL+GKRPLl +D+P+ +
  gi|1541468     1 --HTDAVDAITTHLGIGSYREWSEEKRQEWLLTELQGKRPLLVPDMPQSD 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl+ f+vLAELP DsFG+YiismataPsDvLAvELLqREC+v+q+L
  gi|1541468    49 EVADVLGCFKVLAELPRDSFGPYIISMATAPSDVLAVELLQRECQVRQPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFE+LADL+ APA+ve+LFs+DWY nri GKq++mvGYsDsGKDAG
  gi|1541468    99 PVVPLFERLADLQNAPASVERLFSVDWYLNRIGGKQQIMVGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLY+AqE ++KvAKky vK++ FHGRGGtvGRGGGPtHLAiLsq
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  gi|1541468   149 RLSAAWQLYQAQEAVAKVAKKYDVKVTFFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP+t+nGslRvt+qGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|1541468   199 PPETVNGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPISP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWRkLm++mAvvAt+ YR vvvKEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPEWRKLMDDMAVVATDAYRGVVVKEPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvG AFKhA+dKDiKn+
  gi|1541468   299 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGTAFKHAMDKDIKNF 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q Lk+mY+eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLva++LkPFG++
  gi|1541468   349 QVLKDMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDQLLVADDLKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR+kY Et++lLL+iAGHkD+LEGDPYLKqrlRLRd+Yitt
  gi|1541468   399 LRAKYMETQQLLLQIAGHKDILEGDPYLKQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - -------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146778|emb|CAM84076.1|: domain 1 of 1, from 1 to 441: score 464.7, E = 1.3e-136
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - -------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - -------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - -------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - -------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - -------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - -------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - -------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - -------------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlg..sDLPk
                     +tD lDA+ttHL+iGsYR W+EeKRqEWLl+EL+GKRPLlg+ +DLP+
  gi|1541467     1 --HTDALDAVTTHLGIGSYRGWPEEKRQEWLLSELRGKRPLLGgaADLPQ 48
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                   tEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                   t+Ev+Dvl++frvLAELP DsFGaY+ismataPsDvLAvELLqRECgv++
  gi|1541467    49 TDEVADVLGTFRVLAELPADSFGAYVISMATAPSDVLAVELLQRECGVRR 98

                   tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKD
                   +LrvvPLFEkLADLe APAav++LFs+DWY+ ri GKqevm+GYsDsGKD
  gi|1541467    99 PLRVVPLFEKLADLESAPAAVARLFSVDWYMDRIGGKQEVMIGYSDSGKD 148

                   AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                   AGRlsAAWqLYkAqEE+++vAK++GvKL++FHGRGGtvGRGGGPtHLAiL
  gi|1541467   149 AGRLSAAWQLYKAQEELVRVAKRHGVKLTMFHGRGGTVGRGGGPTHLAIL 198

                   sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                   sqPPDt++GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPv
  gi|1541467   199 SQPPDTVHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPV 248

                   sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                   sPkPEWR Lm+emAvvAt+EYRs+v++EPRFvEYFR+AtPE+EYG+mniG
  gi|1541467   249 SPKPEWRALMDEMAVVATDEYRSIVFREPRFVEYFRSATPETEYGRMNIG 298

                   sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                   sRP+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi+
  gi|1541467   299 SRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMKKDIR 348

                   nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                   n+ +L+EmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLva++LkPFG
  gi|1541467   349 NIHMLREMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDELLVADDLKPFG 398

                   ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                   ++LR++Y +t++lLL++AGHkD+LEGDPYLKqrlRLRd+Yitt
  gi|1541467   399 EQLRNEYLDTRQLLLQVAGHKDVLEGDPYLKQRLRLRDPYITT------- 441

                   tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL

  gi|1541467     - ------------------------------------------------- -

                   iLtmKGiAAGmqntG<-*

  gi|1541467     - ---------------    -

gi|154146734|emb|CAM84054.1|: domain 1 of 1, from 1 to 439: score 464.4, E = 1.6e-136
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
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  gi|1541467     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tD +DAittHL+iGsY+eW+EeKRqEWLl+EL+GKRPL+ +D+P  +
  gi|1541467     1 --HTDAIDAITTHLGIGSYKEWPEEKRQEWLLSELQGKRPLMVPDMPVSD 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl+ f+vLAELP+DsFG+YiismataPsDvLAvELLqREC+v+++L
  gi|1541467    49 EVADVLGCFKVLAELPSDSFGPYIISMATAPSDVLAVELLQRECKVRNPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLFE+LADL+ APA+ve+LFsiDWY  ri GKq++mvGYsDsGKDAG
  gi|1541467    99 PVVPLFERLADLQNAPASVERLFSIDWYLKRIAGKQQIMVGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLY+AqEE++KvAKky v+L+ FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYQAQEEVAKVAKKYNVQLTFFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvt+qGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|1541467   199 PPDTINGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPISP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWRkLm++mAvvAtE YRsvvvKEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWRKLMDDMAVVATEAYRSVVVKEPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvG AFK AidKDiKn+
  gi|1541467   299 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGTAFKSAIDKDIKNF 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q Lk+mY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG++
  gi|1541467   349 QVLKDMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVAEELKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR kY Et+dlLLkiAGH ++L GDPYLKqrlRLRd+Yitt
  gi|1541467   399 LRSKYLETEDLLLKIAGHSEILAGDPYLKQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146918|emb|CAM84146.1|: domain 1 of 1, from 1 to 439: score 464.0, E = 2.1e-136
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541469     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541469     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541469     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541469     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541469     - ------------------------------------------------ -
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                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541469     - ------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541469     - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541469     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541469     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tD +DAittHL+iGsYReWsEeKRqEWL++EL+GKRPLl +DLP+ E
  gi|1541469     1 --HTDAVDAITTHLGIGSYREWSEEKRQEWLISELRGKRPLLTPDLPQSE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl+ frvLAELP DsFG+Yiismat+PsDvLAvELLqRECgv++tL
  gi|1541469    49 EVADVLGCFRVLAELPRDSFGPYIISMATSPSDVLAVELLQRECGVRETL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +vvPLFEk ADLe APA+ve+LFs+DWY+ +i GKq+vm+GYsDsGKDAG
  gi|1541469    99 PVVPLFEKQADLEGAPATVERLFSVDWYKDHIGGKQQVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  Rl AAWqLYkAqEE++KvA+++GvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1541469   149 RLTAAWQLYKAQEELAKVAQRHGVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGs+RvtvqGEviEf FGEE+LCF++LqRFtAAtLEHGm+PPvsP
  gi|1541469   199 PPDTINGSIRVTVQGEVIEFFFGEEHLCFKTLQRFTAATLEHGMHPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+em  vAtE YRs v+KEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541469   249 KPEWRALMDEMSAVATEQYRSTVFKEPRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKRkP GGiesLRAiPWiF+WtqtRFHLPvWLGvGAAFKhAi+KD+Knl
  gi|1541469   299 PAKRKPKGGIESLRAIPWIFSWTQTRFHLPVWLGVGAAFKHAINKDSKNL 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+Ly +LLva+eLkPFG++
  gi|1541469   349 QLLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYNDLLVADELKPFGEQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR +Y Et++lLL++AGHk++LEGDPYLKqrlRLRd+Yitt
  gi|1541469   399 LRKNYIETQQLLLQVAGHKEILEGDPYLKQRLRLRDPYITT--------- 439

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541469     - ------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|1541469     - -------------    -

gi|154146906|emb|CAM84140.1|: domain 1 of 1, from 1 to 439: score 463.3, E = 3.6e-136
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541469     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541469     - ------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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  gi|1541469     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541469     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541469     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541469     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541469     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541469     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541469     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tD +DAittHL+iGsY+eW+EeKRqEWLl+EL+GKRPL+ +D+P tE
  gi|1541469      1 --HTDAIDAITTHLGIGSYKEWPEEKRQEWLLSELQGKRPLMVPDMPVTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+ vl+ f+vLAELP DsFG+YiismataPsDvLAvELLqRECgv+++L
  gi|1541469     49 EVEAVLGCFKVLAELPPDSFGPYIISMATAPSDVLAVELLQRECGVRNPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLFE+LADL+ APA+ve+LFsiDWY nri GKq++mvGYsDsGKDAG
  gi|1541469     99 PVVPLFERLADLQNAPASVERLFSIDWYLNRIGGKQQIMVGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLY+AqEE++KvAKky vK++ FHGRGGtvGRGGGPtHLAiLsq
  gi|1541469    149 RLSAAWQLYQAQEEVAKVAKKYNVKVTFFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvt+qGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|1541469    199 PPDTINGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPISP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWRkLm+emAv At+ YRsvvvKEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541469    249 KPEWRKLMDEMAVLATDAYRSVVVKEPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvG AFK AidKDiKn+
  gi|1541469    299 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGSAFKSAIDKDIKNF 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q Lk+mY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva+eLkPFG++
  gi|1541469    349 QLLKDMYREWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVADELKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR kY Et++lLL+iAGHk++LE DPYLKqrlRLRd+Yitt
  gi|1541469    399 LRSKYLETQQLLLQIAGHKEILEADPYLKQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541469     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541469     - -------------    -

gi|154146900|emb|CAM84137.1|: domain 1 of 1, from 1 to 439: score 463.2, E = 3.9e-136
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                *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

gi|1541469     -    ---------------------------------------------- -

                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|1541469     - ---------------------------------------------- -

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1541469     - ---------------------------------------------- -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1541469     - ---------------------------------------------- -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1541469     - ---------------------------------------------- -

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1541469     - ---------------------------------------------- -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1541469     - ---------------------------------------------- -

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1541469     - ---------------------------------------------- -

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1541469     - ---------------------------------------------- -

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  +tD lDAit  L+iGsYR W+EeKRqEWLl+EL+GKRPL+g DLP t+
gi|1541469     1 --HTDALDAITAYLGIGSYRHWPEEKRQEWLLSELRGKRPLFGDDLPVTD 48

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                Ev+Dvl++frvLAELP D+FGaYiismataPsDvLAvELLqREC+v  +L
gi|1541469    49 EVADVLGTFRVLAELPPDCFGAYIISMATAPSDVLAVELLQRECHVESPL 98

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                rvvPLFEkLADLeAAPAav++LFsiDWY+ ri GKqevm+GYsDsGKDAG
gi|1541469    99 RVVPLFEKLADLEAAPAAVARLFSIDWYMDRIGGKQEVMIGYSDSGKDAG 148

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLYkAqEE++ vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1541469   149 RLSAAWQLYKAQEELVEVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PP+ti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
gi|1541469   199 PPETIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                kPEWR Lm+emAvvAtEEYRs+v+KEPRFvEYFR+AtPE+EYG+mniGsR
gi|1541469   249 KPEWRALMDEMAVVATEEYRSMVFKEPRFVEYFRSATPETEYGRMNIGSR 298

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvW G+GAAFKhA++KDi+n+
gi|1541469   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWPGFGAAFKHAMHKDIRNI 348

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLva++Lk  G++
gi|1541469   349 QALREMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDELLVADDLKTLGEQ 398

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR++Y++tk+lL+++AGHkD+LEGDPYLKqrlRLRd+Yitt
gi|1541469   399 LRNNYEDTKKLLIQVAGHKDVLEGDPYLKQRLRLRDPYITT--------- 439
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                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541469     - ------------------------------------------------ -

                  tmKGiAAGmqntG<-*

  gi|1541469     - -------------    -

gi|154146828|emb|CAM84101.1|: domain 1 of 1, from 1 to 439: score 462.6, E = 5.9e-136
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------ -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------ -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tD +DAittHL+iGsY+eW+EeKRqEWLl+EL+GKRPLl +D+P tE
  gi|1541468     1 --HTDAIDAITTHLGIGSYKEWPEEKRQEWLLSELQGKRPLLVPDMPVTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+ vl+ frvLAELP DsFG+YiismataPsDvLAvELLqRECg++q+L
  gi|1541468    49 EVEAVLGCFRVLAELPRDSFGPYIISMATAPSDVLAVELLQRECGIRQPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +vvPLFE+LA L+ APA+ve+LFsiDWY nri GKq++mvGYsDsGKDAG
  gi|1541468    99 PVVPLFERLAGLQNAPASVERLFSIDWYLNRIGGKQQIMVGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLY+AqEE++KvAKky vK++ FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYQAQEEVAKVAKKYDVKVTFFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP+tinGslRvt+qGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPv+P
  gi|1541468   199 PPETINGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVAP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWRkLm+emAvvAtE YRsvvvKEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPEWRKLMDEMAVVATEAYRSVVVKEPRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
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                    PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK AidKDiKn+
  gi|1541468   299 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKSAIDKDIKNF 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q Lk+mY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva++LkPFG++
  gi|1541468   349 QLLKDMYREWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVADDLKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR kY Et++lLLkiAGHk++LE DPYLKqrlRLRd+Yitt
  gi|1541468   399 LRSKYLETQELLLKIAGHKEILEADPYLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146806|emb|CAM84090.1|: domain 1 of 1, from 1 to 439: score 461.6, E = 1.2e-135
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tD +DAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLl +D+P+ +
  gi|1541468     1 --HTDAVDAITTHLGIGSYREWPEEKRQEWLLSELQGKRPLLVPDMPQSD 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl+ f+vLAELP DsFG+YiismataPsDvLAvELLqREC v+q+L
  gi|1541468    49 EVADVLGCFKVLAELPRDSFGPYIISMATAPSDVLAVELLQRECLVRQPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFE+LADL+ APA+ve+LFs+DWY nri GKq++mvGYsDsGKDAG
  gi|1541468    99 PVVPLFERLADLQNAPASVERLFSVDWYLNRIGGKQQIMVGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLY+Aq E++KvAKkyGvKL+ FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYQAQAEVAKVAKKYGVKLTFFHGRGGTVGRGGGPTHLAILSQ 198
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                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP+tinGslRvt+qGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|1541468   199 PPETINGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPISP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEW kLm++mAvvAtE YR vvvKEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPEWSKLMDDMAVVATEAYRGVVVKEPRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvG AFK AidKDiKn+
  gi|1541468   299 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGTAFKSAIDKDIKNF 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q Lk+m + WPFFRvtlDLlEmvFAKGDPGiAaLyD+LLva++LkPFG++
  gi|1541468   349 QLLKDMHNAWPFFRVTLDLLEMVFAKGDPGIAALYDNLLVADDLKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR kY Et++lLLkiAGHkD+LEGDPYLKqrlRLRd+Yitt
  gi|1541468   399 LRSKYMETQELLLKIAGHKDILEGDPYLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146890|emb|CAM84132.1|: domain 1 of 1, from 1 to 439: score 461.4, E = 1.3e-135
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tD +DAittHL+iGsYReWsEeKRqEWLl+EL+GKRPLl +D+P+ +
  gi|1541468     1 --HTDAVDAITTHLGIGSYREWSEEKRQEWLLSELQGKRPLLVPDMPQSD 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
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                   Ev+Dvl+ frvLAELP DsFG+YiismataPsDvLAvELLqREC v+q+L
  gi|1541468    49 EVADVLGCFRVLAELPRDSFGPYIISMATAPSDVLAVELLQRECLVRQPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLFE+LADL+ APAave+LFs+DWY nri GKq++mvGYsDsGKDAG
  gi|1541468    99 PVVPLFERLADLQNAPAAVERLFSVDWYLNRIAGKQQIMVGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLY+Aq E++KvAKkyGvKL+ FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYQAQAEVAKVAKKYGVKLTFFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvt+qGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTINGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEW kLm+emAvvAtE YR vvvKEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPEWSKLMDEMAVVATEAYRGVVVKEPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvG AFK A+dKDiKn+
  gi|1541468   299 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGTAFKSAVDKDIKNF 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     LkEmY+eWPFFRvtlD+lEmvF KGDPGiAaLyDkLLv+++LkPFG++
  gi|1541468   349 RLLKEMYNEWPFFRVTLDMLEMVFTKGDPGIAALYDKLLVTDDLKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR kY Et++lLL+iAGHk++LEGDPYLKqrlRLRd+Yitt
  gi|1541468   399 LRSKYMETQELLLQIAGHKEILEGDPYLKQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|269925429|ref|YP_003322052.1|: domain 1 of 1, from 2 to 931: score 461.3, E = 1.4e-135
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         A  R+    K sed +      LL     ++L +  G  L E+v
  gi|2699254     2    ---AIERAGTGDKLSEDVR------LLGSIVGEVLIEQGGRRLFEIV 39

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         s     +   +   EL      LdPa a  v +a+     + nL
  gi|2699254    40 EKLRTTSIALRTRYSEELHRELVQITSELDPATAFDVIRAFNLFFLVVNL 89

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEE    +R R+ +++  + +   +   E  i E ++ L      s e
  gi|2699254    90 AEE---NHRVRVLRQR--EISSYPEP-LEGSIREAVRDLRNED-ISDEQL 132

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    e L       v+tAHPt s RR  L     i n +a L    +t+  ++
  gi|2699254   133 QELLNRLRARFVFTAHPTESRRRTTLMHLRHISNLIALLDDALLTPTQRE 182

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    + + L   + A + tD+ R ++PtP DE+   + ++ E v++  P   R
  gi|2699254   183 MVIDRLREVVTALWQTDDFRETRPTPLDEVYNSLYFFQESVFEILPSVYR 232

                   RvDtALKni..GinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                       ALK + +  n  +P   P+i+F  WmGGDRDG nP vtPEvt
  gi|2699254   233 EFSDALKSVykDWNFQIP---PVIQFGTWMGGDRDG-NPNVTPEVTIRTA 278

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    L + +    Yisq++ L   lsm        v  E +++  +  k+
  gi|2699254   279 RLQKGVLLRHYISQLDRLRRHLSM--SVRRAGVSDELMQSIEKERKILPE 326

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE.eAvy
                     E       +E YR  +G + +KL nt      L A    + + ++  y
  gi|2699254   327 ASERIEERNKNEMYRLKIGLMIEKLKNT------LSAMEARQRPQpDVAY 370
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                    tkvEeFLEPLELCYksL.CeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                      vE+F   +++   sL+ + GD+ +A G+  D+ R    FG  L K+D+
  gi|2699254   371 ESVEQFYTDIDMIVNSLkQNKGDR-LALGAAEDFRRLAEVFGFHLAKIDV 419

                    RqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgsD
                    Rq s R+   +  +   ++i  +Y e s e   E L   L+  RP++g
  gi|2699254   420 RQHSSRHSQAIAEVLSSVGICDrYLELSSEEQAELLRELLRDNRPIIGKV 469

                    L...PktEEvkDvldafrvLA.ELPiDsFGaYiismataPsDvLAvELLq
                     + +P tEE   v da+r + +E+  ++   Yiis a + +D L + LL
  gi|2699254   470 HhfsPSTEETIAVFDAIRTIQeEIGKEACDTYIISFAQSAADLLEIQLLA 519

                    RECgvkqt......LrvvPLFEkLADLeAAPAavekLFsiDWYinridG.
                    RE g+   +++ ++L++vPLFE + DL+     ++ L     Y+  +
  gi|2699254   520 RETGLLSIsegwsrLQIVPLFESIHDLNECGNIMANLLDDPIYRCNVKAw 569

                    ..KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    ++ qevm+GYsDs KD G +   W LYkAq  ++ v  + Gv L lFHGR
  gi|2699254   570 gdHQEVMIGYSDSNKDGGFFTSCWELYKAQRRLAAVCSERGVTLRLFHGR 619

                    GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                    GG +GRGGGPtH+AiL qPPDti+G l+ t qGEvi   +G   +  r L
  gi|2699254   620 GGAIGRGGGPTHMAILGQPPDTIHGELKLTEQGEVIFARYGNPAIAKRYL 669

                    qRFtAAtLEHGmnPPvsP.....kPEWRkLmeemAvvAtEEYRsvvvKEP
                         A L   + P v  ++++  PEW +  + +      EYR +v+  P
  gi|2699254   670 EQVLNALLRVSLSPTVIEnqsriEPEWQEAADTLSTYSYREYRNLVYETP 719

                    RFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRF
                     FvEYFR AtP  E   + i sRP +R+ +  ie LRAiPW+F+W q R
  gi|2699254   720 EFVEYFREATPIGEISLLPIASRPVRRQSGFDIEQLRAIPWVFSWMQSRH 769

                    HLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                     LP W G+G A    i  D   l+ L+EmY++W FFR tlD   m+  K
  gi|2699254   770 TLPGWYGLGTAIEKYIAGDDSKLKILQEMYQKWIFFRSTLDNAQMILSKA 819

                    DPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEGDP
                    D  +A++y  L+   +++ +   ++ ++Y+ t  +++k+ G   lL+  P
  gi|2699254   820 DIHVASMYAGLVSNPDVWNrVWPRIQQEYERTVYWVIKVTGLNRLLDNAP 869

                    YLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnsk
                     L+  + LR++Y+  +  +q   L+++R          +  K++  E
  gi|2699254   870 VLQRSIMLRNPYVDPISYIQVALLRKLR--------TIPDTKDHKKER-- 909

                    kadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       e +               + L + GiAAG+qntG
  gi|2699254   910 ---ESILQA------------VFLSINGIAAGLQNTG    931

gi|154146818|emb|CAM84096.1|: domain 1 of 1, from 1 to 439: score 460.9, E = 1.9e-135
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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  gi|1541468     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tD lDA+ttHL+iGsYReW+Ee+RqEWLl+EL+GKRPLlgsDLP+ E
  gi|1541468     1 --HTDALDAVTTHLGIGSYREWPEERRQEWLLSELRGKRPLLGSDLPQSE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl++frvL ELP DsFGaYiismataPsDvLAvELLqREC v+++L
  gi|1541468    49 EVADVLGTFRVLSELPPDSFGAYIISMATAPSDVLAVELLQRECRVRRPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPA+v++LFs+DWY+ ri GKqevm+GYsDsGKDAG
  gi|1541468    99 RVVPLFEKLADLEAAPASVARLFSVDWYMDRIGGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYKAQEEMVKVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvt+qGEviE sFGEE+LCFr+LqRFtAAtLEHGm PPvsP
  gi|1541468   199 PPDTINGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMRPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emA vAtE YRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPEWRALMDEMAAVATEAYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFK A++KD +n+
  gi|1541468   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKRAMNKDTRNV 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q+L+EmY+eWPFFRvtlDLlEmvFAKGDP iA+LyD+LLva++LkP G++
  gi|1541468   349 QMLREMYNEWPFFRVTLDLLEMVFAKGDPRIAGLYDQLLVADDLKPLGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR+ Y Et++lLLk+ GHkD+LEGDPYLKqrlRLRd+Yitt
  gi|1541468   399 LRNSYLETQQLLLKVTGHKDILEGDPYLKQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146914|emb|CAM84144.1|: domain 1 of 1, from 1 to 439: score 460.7, E = 2.2e-135
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541469     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541469     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541469     - ------------------------------------------------ -
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                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541469     - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541469     - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541469     - ------------------------------------------------ -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541469     - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541469     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541469     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tD +DAittHL+iGsYReWsEeKRqEWLl+EL+GKRPLl +D+P+ +
  gi|1541469     1 --HTDAIDAITTHLGIGSYREWSEEKRQEWLLSELQGKRPLLVADMPQSD 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  EvkDvl+ f+vLAELP DsFG+YiismataPsDvLAvELLqREC+v+++L
  gi|1541469    49 EVKDVLGCFKVLAELPKDSFGPYIISMATAPSDVLAVELLQRECQVRNPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +vvPLFE+LADL+ APA+ve+LFsiDWY nri GKq++mvGYsDsGKDAG
  gi|1541469    99 PVVPLFERLADLQNAPASVERLFSIDWYLNRIAGKQQIMVGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAW LY+AqE ++KvAKky vK++ FHGRGGtvGRGGGPtHLAiLsq
  gi|1541469   149 RLSAAWSLYQAQEAVVKVAKKYDVKVTFFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGslRvt+qGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541469   199 PPDTINGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWRkLm+em vvAt+ YRsvvvKEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541469   249 KPEWRKLMDEMSVVATDAYRSVVVKEPRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK AidKDiKn+
  gi|1541469   299 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKSAIDKDIKNF 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva+eLkPFG++
  gi|1541469   349 QVLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVADELKPFGEQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR kY Et++lLL+iAGHk++LE DPYLKqrl LRd+Yitt
  gi|1541469   399 LRSKYLETQQLLLQIAGHKEILESDPYLKQRLVLRDPYITT--------- 439

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541469     - ------------------------------------------------ -

                  tmKGiAAGmqntG<-*

  gi|1541469     - -------------    -

gi|154146760|emb|CAM84067.1|: domain 1 of 1, from 1 to 439: score 459.7, E = 4.4e-135
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
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gi|1541467     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|1541467     - ---------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1541467     - ---------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1541467     - ---------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1541467     - ---------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1541467     - ---------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1541467     - ---------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1541467     - ---------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1541467     - ---------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tD lDAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
gi|1541467      1 --HTDALDAITTHLGIGSYREWAEEKRQEWLLSELRGKRPLLGPDLPQTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   v+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
gi|1541467     49 GVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECHVRHPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLeAAPAav++LFs+DWY+ ri GKqevm+GYsDsGKDAG
gi|1541467     99 RVVPLFEKLADLEAAPAAVARLFSVDWYMDRIGGKQEVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqE +++vA+++GvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1541467    149 RLSAAWQLYKAQESLVRVAQRHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDt+ GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm PP  P
gi|1541467    199 PPDTVRGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMRPPAPP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  +PEWR Lm+e+A vAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
gi|1541467    249 RPEWRALMDELAAVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA+ KDi+n+
gi|1541467    299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMGKDIRNI 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q+L+EmY+eWPFFRvtlDLlEmvFAKGDP iA+LyD+LLva++LkPFG++
gi|1541467    349 QMLREMYNEWPFFRVTLDLLEMVFAKGDPSIAGLYDELLVADDLKPFGEQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Yv+t++lLL++AGHkD+LEGDPYL+qrlRLRd+Yitt
gi|1541467    399 LRNNYVDTQQLLLQVAGHKDILEGDPYLRQRLRLRDPYITT--------- 439
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                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146814|emb|CAM84094.1|: domain 1 of 1, from 1 to 439: score 459.6, E = 4.5e-135
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDvlDAittHL++GsYReW+EeKRqEWLl+EL+GKRPLlg+DLP+tE
  gi|1541468      1 --HTDVLDAITTHLGVGSYREWAEEKRQEWLLSELRGKRPLLGADLPQTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl++frvLAELP DsFGaY+ismataPsDvLAvELLqRECgvkq+L
  gi|1541468     49 EVADVLGTFRVLAELPPDSFGAYVISMATAPSDVLAVELLQRECGVKQPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkL DLeAAPA+v++LFs+DWY+ ri GKqevmvGYsDsGKDAG
  gi|1541468     99 RVVPLFEKLKDLEAAPASVARLFSVDWYMDRIGGKQEVMVGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  Rl AAWqLYkAqEE+++vA+++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468    149 RLTAAWQLYKAQEEMVRVAQRHGVKLTIFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm PP sP
  gi|1541468    199 PPDTIRGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMCPPASP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  +PEWR Lm++mA vAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468    249 RPEWRALMNDMAAVATEEYRSIVLREPRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiF+WtqtR HLPvWLGvGAAFKhA++KDi+n+
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  gi|1541468   299 PSKRKPSGGIESLRAIPWIFSWTQTRLHLPVWLGVGAAFKHAMNKDIRNI 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva++Lk FG++
  gi|1541468   349 HMLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVADDLKAFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR+kY +t++lLL++AGHkD+LEGDPYLKqrlRLRd+Yitt
  gi|1541468   399 LRNKYLDTQQLLLQVAGHKDILEGDPYLKQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146764|emb|CAM84069.1|: domain 1 of 1, from 1 to 439: score 458.5, E = 9.5e-135
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tD lDAittHL+iGsYReW+E++RqEWLl+EL+G+RPLlg+DLP+tE
  gi|1541467     1 --HTDALDAITTHLGIGSYREWPEQRRQEWLLSELRGRRPLLGPDLPQTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl++frvLAELP Ds GaYiismataPsDvLAvELLqREC v+q+L
  gi|1541467    49 EVADVLGTFRVLAELPPDSLGAYIISMATAPSDVLAVELLQRECRVRQPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAav++LFs+DWY+ ri GKqevm+GYsDsGKDAG
  gi|1541467    99 RVVPLFEKLADLEAAPAAVARLFSVDWYMDRIGGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+++vA+++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYKAQEELVRVAQRHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198
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                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541467   199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    +P WR Lm++mA vAtEEYRs+v++EPRFvEYFR+A PE+EYG+mniGsR
  gi|1541467   249 RPAWRALMDDMAAVATEEYRSIVFREPRFVEYFRSAAPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KR+PsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA+dKD++nl
  gi|1541467   299 PSKRRPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMDKDVRNL 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLva++LkPFG++
  gi|1541467   349 HTLREMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDELLVADDLKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y Et++lLL++AGHk++LEGDPYLKqrlRLRd+ itt
  gi|1541467   399 LRKNYLETQQLLLQVAGHKEVLEGDPYLKQRLRLRDPHITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|123966995|ref|YP_001012076.1|: domain 1 of 1, from 3 to 989: score 457.9, E = 1.5e-134
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s+  qL+      +s+++ L +   L+ D +  +L +   +d
  gi|1239669     3    SMK-QLKNHNVDLISNNDPLDKNRLLIEDLWESVLREECPNDQANRL 48

                    qECYElsAeYEGKkDtkKL..eELGakLtsLdPaDailvAkailHmLnLA
                        Els      +D ++  ++E+   + s+d a++i  A+a++    L
  gi|1239669    49 MKLKELSYCNQVEEDISRTfkNEIVDIVNSMDLAESISAARAFSLYFQLV 98

                    nLAEE.ve.....lAyRRRikkkkhGDFaDEasAttEsDiEEtlKkL...
                    n+ E +ve+++    +  ++ +k h      a A        t++ L  +
  gi|1239669    99 NILEQrVEedryiQSFTNKNNQKSHDNLDPFAPALARQNAPVTFRELfyr 148

                    vlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL
                      kln  P    e L+   + Lv+tAHPt  vR  +  K++R+ n L ++
  gi|1239669   149 LRKLNVPPGKLEELLQEMDIRLVFTAHPTEIVRHTIRHKQTRVANLLQKI 198

                    sA.KDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiH
                      +K +tveD k L   L  Ei   +RtDE+   +P   DE+ + + Y+
  gi|1239669   199 QVeKFLTVEDIKSLKIQLKEEIRLWWRTDELHQFKPSVIDEVDYALHYFQ 248

                    EtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPR
                      +++ +P+   R+  AL        +P +     F sW+G DRDG nP
  gi|1239669   249 QVLFNAMPQLRGRISSALTENYPDVQMPTES-FCTFGSWVGSDRDG-NPS 296

                    vtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyr
                    vtPE+t       R +    Yis    L   ls+    + +     E
  gi|1239669   297 VTPEITWRTACYQRKLMLERYISATSNLRDQLSVSMQWSQVSSSLLESLE 346

                    taardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtG.
                    t + +       E        EPYR  L  + +KL  t+ER   L   G
  gi|1239669   347 TDRVQ--FPEIYEARATRYRSEPYRLKLSYILEKLRLTKERNNLLAEAGw 394

                    .is.........eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGs
                    ++s ++++++++ e+ E   y  v+eF   LEL   sL +  D      s
  gi|1239669   395 kFSleresdnkniELVEKLHYRSVDEFTYDLELIKNSL-NSTDLTCEAVS 443

                    LLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEe
                       lL qv  FG sL  LDiRqEs R+ D +  +t  Le++  Y + +E
  gi|1239669   444 --KLLTQVHIFGFSLASLDIRQESTRHSDAIQELTNYLELpKKYDQMPEI 491

                    KRqEWLlaELkGKRPLlgsDLP...ktEEvkDvldafrvLA.ELPiDsFG
                     R EWL  EL  KRPL+++++  ++ tEE   v   ++ L +E  +
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  gi|1239669   492 ERIEWLKDELNTKRPLIPAEVSwtkSTEETFSVFKMVKRLQeEFGSRICH 541

                   aYiismataPsDvLAvELLqRECgv......kqtLrvvPLFEkLADLeAA
                   +Y+ism+ + sD L v LL +E g+ +++++k  L vvPLFE + DL+ A
  gi|1239669   542 SYVISMSHSASDLLEVLLLAKEMGLidqssqKSKLLVVPLFETVEDLKRA 591

                   PAavekLFsiDWYi.......nridGKqevmvGYsDsGKDAGRlsAAWqL
                   P  +e+LF +D+Y++  ++ + r    qe m+GYsDs KD G ls  W +
  gi|1239669   592 PEVMEQLFQLDFYRsllpkvgERFKPIQELMLGYSDSNKDSGFLSSNWEI 641

                   YkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGs
                    +Aq  +     k  + L lFHGRGG vGRGGGP   AiL+qP  t++G
  gi|1239669   642 HRAQIALQNLSSKNNILLRLFHGRGGSVGRGGGPAYQAILAQPSGTLKGR 691

                   lRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP.vsPkPEWRkL
                   +++t qGEv+   +   +L    L   t A +   +   ++   PEW +L
  gi|1239669   692 IKITEQGEVLASKYSLPELALYNLETVTTAVIQNSLVINrLDATPEWNDL 741

                   meemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs
                   m ++A      YR +v   P    +F   tP  E  k+ i sRPa+Rk +
  gi|1239669   742 MTRLAETSRIQYRKLVHENPNLLTFFQEVTPIEEISKLQISSRPARRKKG 791

                   G.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEm
                    + + sLRAiPW+F Wtq RF LP W GvG A    ++ D   +  L+ +
  gi|1239669   792 AkDLSSLRAIPWVFGWTQSRFLLPSWFGVGTALSVELKSDPEQIELLRVL 841

                   YkeWPFFRvtlDLlEmvFAKGDPGiAaLy.DkLLvaEeLkPFG...ksLR
                    + WPFFR+ +  +Em   K D  +A  y D L   E+ k FG+  + +
  gi|1239669   842 HQRWPFFRMLISKVEMTLSKVDLEVAKYYvDTLGSKENAKSFGdifDVIS 891

                   dkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKR
                    +Y  tk l+L+i G   lLE D  L+  + LR+  i  L  +q   L+R
  gi|1239669   892 KEYNLTKSLVLEITGKNKLLESDRDLRLSVNLRNKTIIPLGFLQVSLLRR 941

                   iRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtm
                   +RD     t +P++s E+ +E     +e  +    ++   G     +Lt+
  gi|1239669   942 LRDQ----TRQPPIS-EFLNER----NESERAYSRSELLRG----ALLTI 978

                   KGiAAGmqntG<-*
                    GiAAGm ntG
  gi|1239669   979 NGIAAGMRNTG    989

gi|154146864|emb|CAM84119.1|: domain 1 of 1, from 1 to 439: score 457.8, E = 1.6e-134
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ---------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ---------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ---------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ---------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ---------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ---------------------------------------------------- -
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                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDv+DAittH++iGsYR+W+EeKRqEWLl+EL+GKRPLl +D+P+tE
  gi|1541468     1 --HTDVIDAITTHIGIGSYRSWPEEKRQEWLLSELRGKRPLLAPDMPQTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++Dvl+ frvLAELP DsFG+YiismataPsDvLAvELLqREC+v  +L
  gi|1541468    49 EIADVLGCFRVLAELPRDSFGPYIISMATAPSDVLAVELLQRECHVSDPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +vvPLFE+LADL+ APA++e+LFs+DWY nri+GKq+vm+GYsDsGKDAG
  gi|1541468    99 PVVPLFERLADLQNAPASMERLFSVDWYLNRINGKQQVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLY+AqEE+++vAK+y vKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541468   149 RLSAAWQLYRAQEELAQVAKRYNVKLTMFHGRGGTVGRGGGPSHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGs+RvtvqGEviE sFGEE+LCFr+L RFtAAtLEHGm+PPv+P
  gi|1541468   199 PPDTINGSIRVTVQGEVIEHSFGEEHLCFRTLERFTAATLEHGMHPPVAP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWRkLm++mAvvAtEEYRsvvvKE RFvEYFR+AtPE+EYGkmniGsR
  gi|1541468   249 KPEWRKLMDDMAVVATEEYRSVVVKEQRFVEYFRSATPETEYGKMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKRkP GGi+sLRAiPWiF+WtqtRFHLPvWLGvGAAF +A++KD+Kn+
  gi|1541468   299 PAKRKPQGGITSLRAIPWIFSWTQTRFHLPVWLGVGAAFEWAVKKDSKNI 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q+Lk+mYkeWPFFRvt+DLlEmvFAKGDP iA LyD+LLv++eLk  G++
  gi|1541468   349 QMLKDMYKEWPFFRVTIDLLEMVFAKGDPSIAKLYDDLLVSDELKSLGEQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR+kY  t+++LL+iAGHk++LEGDP+LKq lRLR++Yitt
  gi|1541468   399 LRNKYLQTQQFLLQIAGHKEILEGDPFLKQSLRLRNPYITT--------- 439

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146738|emb|CAM84056.1|: domain 1 of 1, from 1 to 439: score 457.1, E = 2.6e-134
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|1541467     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tD +DAittHL+iGsY+eW+EeKRqEWLl+EL+GKRPLl +D+P tE
  gi|1541467     1 --HTDAVDAITTHLGIGSYKEWPEEKRQEWLLSELQGKRPLLVPDMPVTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+ vl+ f+vLAELP DsFG+YiismataPsDvLAvELLqRECgv+q+L
  gi|1541467    49 EVEAVLGCFKVLAELPRDSFGPYIISMATAPSDVLAVELLQRECGVRQPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLFE+LADL+ APA+ve+LFsiDWY nri GKq++mvGYsDsGKDAG
  gi|1541467    99 PVVPLFERLADLQNAPASVERLFSIDWYLNRIGGKQQIMVGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLY+AqE +++vAKky vK++ FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYQAQEQVAQVAKKYDVKVTFFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP+tinGslRvt+qGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|1541467   199 PPETINGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPISP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWRkLm+emAvvAt+ YRsvvvKEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWRKLMDEMAVVATDAYRSVVVKEPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKR+P+GGi +LRAiPWiF+WtqtRFHLPvWLGvG AFK AidKDiKn+
  gi|1541467   299 PAKRRPGGGISTLRAIPWIFSWTQTRFHLPVWLGVGSAFKSAIDKDIKNF 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q Lk+mY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva++LkPFG++
  gi|1541467   349 QLLKDMYREWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVADDLKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR kYvEt++lLL+iAGHk++LE DPYLKqrlRLRd+Yitt
  gi|1541467   399 LRSKYVETEQLLLQIAGHKEILEADPYLKQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|22299455|ref|NP_682702.1|: domain 1 of 1, from 6 to 1011: score 457.0, E = 2.8e-134
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       +    Rl+     +    L e   L+ +  +D+L    G++L +
  gi|2229945     6    DVTNRDRLIESESLA-ARTLQERLRLVEEVLVDVLAAESGQELVDLL 51

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        ls   EG       +EL  ++ sL+  +ai  A+a+     + n+
  gi|2229945    52 RRLGALSSP-EGHVLHAPEGELLKVIESLELNEAIRAARAFNLYFQIINI 100
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                AEE...........velAyRRRikkkk.hGDFaDE........asAt...
                 E + +++ ++++  +   RRR     +    + E+ + +++ a+At+ +
gi|2229945   101 VEQhyeqqynreraAQEGLRRRSVMSEpISGVSGEgfplphtaANATdvr 150

                ......tEsDiEEt.........lKkL...vlklnKsPeEvFeALKnqsv
                ++++++ E  + E  + +++ +++  L ++   ln  P  +   L    +
gi|2229945   151 sgpserLEHSLYEAipatqqygsFAWLfprLQMLNVPPRHIQKLLDQLDI 200

                DLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKD.....vtveDKkELDE
                 Lv+tAHPt  vR  +  K+ R+   L qL   ++ ++++t    + L
gi|2229945   201 KLVFTAHPTEIVRQTIRDKQRRVARLLEQLDVLEgasphLTDWNAQTLRA 250

                ALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLRRvDt
                 L  Ei   +RtDE+   +P   DE+ + + Y+ E ++  +PK  RR +
gi|2229945   251 QLMEEIRLWWRTDELHQFKPEVLDEVEYTLHYFKEVIFAVIPKLYRRLEQ 300

                ALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLLaRmm
                 L         P      +F sW+GGDRDG nP v PEvt       R +
gi|2229945   301 SLHET-FPALQPPRHRFCRFGSWVGGDRDG-NPYVKPEVTWQTACYQRNL 348

                AanlYisqvEDL..mFElsmWRCnd..ELRvRAEElyrtaardkvvKyYi
                    Yi  vE L ++  ls+  C   ++L    E  +r   +      Y
gi|2229945   349 VLEEYIKSVERLinLLSLSLHWCDVlpDLLDSLEQDQRQLPSI--YEQYA 396

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi.....seisEeA
                  ++q    EPYR  L  v  +L ntR+R R L    i++++  e+
gi|2229945   397 VRYRQ----EPYRLKLAYVLKRLQNTRDRNRALQTYCIrrneaEELNNGQ 442

                vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                 y + EeFL  L L  + L e G   +A   L Dl+ qv  FG  L  LD
gi|2229945   443 FYRHGEEFLAELLLIQRNLKETG---LACRELDDLICQVEVFGFNLAALD 489

                iRqEseRqtDvlDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLlg
                iRqEs  + + l  it  L+i +  Y e sE  R  WLl+EL+ +RPL++
gi|2229945   490 IRQESTCHAEALNEITAYLGIlpCPYTELSEAERTRWLLSELSTRRPLIP 539

                sDLPktEEvkDvldafrvL....AELPiDsFGaYiismataPsDvLAvEL
                 +LP  +   +++++fr++++ + E   D    Yiism+   sD L v L
gi|2229945   540 GELPFSDRTNEIIETFRMVrqlqQEFGTDLCNTYIISMSHEVSDLLEVLL 589

                LqRECgv......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYi....
                  +E g+ ++ ++  tL+ +PLFE + DL+ APA + +LFs+ + ++  +
gi|2229945   590 FAKEAGLfdpatgASTLQAIPLFETVEDLKHAPAVLTQLFSLPFCRsylg 639

                .nridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                +n     qevm+GYsDs KD G ls  W +YkAq  + K+A  +G +L +
gi|2229945   640 sNSTPFLQEVMLGYSDSNKDSGFLSSNWEIYKAQQQLQKIAESFGFQLRI 689

                FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                FHGRGG vGRGGGP   AiL+qP  ti+G +++t qGEv+   +   +L
gi|2229945   690 FHGRGGSVGRGGGPAYAAILAQPAQTIKGRIKITEQGEVLASKYSLPELA 739

                FrsLqRFtAAtLEHG.mnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEP
                   L   + A +    +   +     W ++mee+A      YR +++  P
gi|2229945   740 LFNLETVATAVIQASllRSSIDEIEPWHEIMEELATRSRQCYRHLIYEQP 789

                RFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRF
                 F+E+F   tP  E  ++ i sRP++R     +esLRAiPW+F+WtqtRF
gi|2229945   790 EFIEFFNEVTPIQEISQLQISSRPTRRGGKKTLESLRAIPWVFSWTQTRF 839

                HLPvWLGvGAAFKhAi.dKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAK
                 LP W GvG A K  +++K    l  L+  Y +WPFFR+ +  +Em  AK
gi|2229945   840 LLPAWYGVGTALKEFLeEKPAEHLSLLRYFYYKWPFFRMVISKVEMTLAK 889

                GDPGiAaLyDkLLva....EeLkPFGksLRdkYvEtkdlLLkiAGHkDlL
                 D  iA  y + L  ++++E      +++ ++Y  t +l+L i GH  lL
gi|2229945   890 VDLEIARYYVQELSQpqnrEAFCRLYDQIAQEYRLTTELVLTITGHERLL 939

                EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                +GDP L+  + LR+  i  L  +q   LKR+R  + + t    l   y
gi|2229945   940 DGDPALQRSVQLRNRTIVPLGFLQVSLLKRLRQHNSQTTSGAILRSRYGR 989
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                  EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   +      L++               +Lt+ GiAAGm ntG
  gi|2229945   990 GE------LLRGA-------------LLTINGIAAGMRNTG    1011

gi|154146840|emb|CAM84107.1|: domain 1 of 1, from 1 to 439: score 456.7, E = 3.5e-134
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDvlDA+ttHL+iGsYReW+EeKRqEWLl+E +GKRPLlg+DLP+tE
  gi|1541468     1 --HTDVLDAVTTHLGIGSYREWPEEKRQEWLLSEPRGKRPLLGPDLPQTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v+++L
  gi|1541468    49 EVADVLGTFRVLAELPPDSFGAYIISMATAPSDVLAVELLQRECQVRHPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLeAA Aav++LFs+DWY+ ri GKqevm+GYsDsGKDAG
  gi|1541468    99 RVVPLFEKLADLEAALAAVARLFSVDWYMDRIGGKQEVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYKAQEELVKVAKRYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDt+nGslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTVNGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+e+AvvAtE YRs+v++E RFvEYFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPEWRALMDELAVVATEAYRSIVFREQRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPv LG+GAA KhA++KDi+n+
  gi|1541468   299 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVRLGFGAAIKHAMNKDIRNI 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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                    q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLva++LkPFG++
  gi|1541468   349 QTLREMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVADDLKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y +t++lLL++AGHk++LEGD YLKqrlRLRd+Yitt
  gi|1541468   399 LRNNYADTQQLLLQVAGHKEILEGDLYLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------ -

                    tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|147839189|emb|CAN72376.1|: domain 1 of 1, from 1 to 434: score 456.6, E = 3.6e-134
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1478391     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1478391     - ------------------------------------------------ -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1478391     - ------------------------------------------------ -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1478391     - ------------------------------------------------ -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1478391     - ------------------------------------------------ -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1478391     - ------------------------------------------------ -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1478391     - ------------------------------------------------ -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1478391     - ------------------------------------------------ -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1478391     - ------------------------------------------------ -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1478391     - ------------------------------------------------ -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                                          mataPsDvLAvELLqREC+vkq+L
  gi|1478391     1 --------------------------MATAPSDVLAVELLQRECHVKQPL 24

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAav++LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|1478391    25 RVVPLFEKLADLEAAPAAVARLFSIDWYKNRINGKQEVMIGYSDSGKDAG 74

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAW LYkAqEE+iKvAK+yG+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1478391    75 RLSAAWALYKAQEELIKVAKQYGIKLTMFHGRGGTVGRGGGPTHLAILSQ 124

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|1478391   125 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 174
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                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|1478391   175 KPEWRALMDEMAVVATENYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 224

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFK+Ai+KDi+nl
  gi|1478391   225 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKYAIEKDIRNL 274

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+ +L+ FG++
  gi|1478391   275 HLLQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSKDLWSFGER 324

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+ tk lLL+iAGHkDlLEGDPYLKqrlRLRdsYittLnv+qA tL
  gi|1478391   325 LRSNYEQTKSLLLQIAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQACTL 374

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPsy v +rPh+ K+  +     a+eLv Lnpt+ + PGLEDtLiL
  gi|1478391   375 KRIRDPSYDVKVRPHICKDIMESA---AQELVNLNPTSDYGPGLEDTLIL 421

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|1478391   422 TMKGIAAGMQNTG    434

gi|154146780|emb|CAM84077.1|: domain 1 of 1, from 1 to 442: score 456.1, E = 5.2e-134
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlg...sDLP
                      +tD lDAittHL+iGsYR W+EeKRqEWLl+EL+GKRPLlg++  D P
  gi|1541467     1 --HTDALDAITTHLGIGSYRGWPEEKRQEWLLSELRGKRPLLGggaGDPP 48

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                    +tEEv+Dvl++frvLAELP DsFGaY+ismat+PsDvLAvELLqREC v+
  gi|1541467    49 QTEEVADVLGTFRVLAELPADSFGAYVISMATSPSDVLAVELLQRECRVR 98

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
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                    ++LrvvPLFEkLADLe APAav++LFs+DWY+ ri GKqevm+GYsDsGK
  gi|1541467     99 RPLRVVPLFEKLADLESAPAAVARLFSVDWYMDRIGGKQEVMIGYSDSGK 148

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAGRlsAAWqLYkAqEE+++vAK++GvKL++FHGRGGtvGRGGGPtHLAi
  gi|1541467    149 DAGRLSAAWQLYKAQEELVRVAKRHGVKLTMFHGRGGTVGRGGGPTHLAI 198

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    LsqPPDt++GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PP
  gi|1541467    199 LSQPPDTVHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPP 248

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                    vsPkPEWRkLm+emAvvAt+EYRs+v++EPRFvEYFR+AtPE+EYG+mni
  gi|1541467    249 VSPKPEWRKLMDEMAVVATDEYRSIVFREPRFVEYFRSATPETEYGRMNI 298

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    GsRP+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++KDi
  gi|1541467    299 GSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMKKDI 348

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                    +n+  L+Em +eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLva++LkPF
  gi|1541467    349 RNIHVLREMHNEWPFFRVTLDLLEMVFAKGDPGIAALYDELLVADDLKPF 398

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    G++LR++Y +t++lLL++AGHkD+LEGDPYLKqrlRLRd+Yitt
  gi|1541467    399 GEQLRNEYLDTRQLLLQVAGHKDVLEGDPYLKQRLRLRDPYITT------ 442

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt

  gi|1541467     - ------------------------------------------------- -

                    LiLtmKGiAAGmqntG<-*

  gi|1541467     - ----------------    -

gi|220907631|ref|YP_002482942.1|: domain 1 of 1, from 47 to 1018: score 455.9, E = 5.8e-134
                    *->siDAqLRlLvP..GKvsedekLieYDALLlDkFLDiLqDLHGe.dLk
                        +  qLR+L  ++G+v    + ++ + L l   LD    +   ++
  gi|2209076     47    DLLRQLRALCSpeGQVR---RALDEEVLRLIEKLDFNEAIRAArSFA 90

                    EavqECYElsAeYEGKkDtkK........LeELGakLtsLdPaDailvAk
                     + q    +   YE ++   +++++++++L +L + + +    D     +
  gi|2209076     91 LYFQLINIVEQHYEQQESLYRthpesghpLPDLISHISGESFPDKSFSGQ 140

                    ailHmLnLAn....LAEEvelAyRRRikkkkh.GDFaDEasAttEsDiEE
                     ++   n    +++L E ve       ++ +h+G Fa
  gi|2209076    141 NFSAHNNTVDvrggLTERVEHSLYEATSLERHqGTFA------------W 178

                    tlKkLvlklnKsPeEvFeALKnqs.vDLvltAHPtqsvRRsLLqKnaRiR
                     + +L  +    P    + L  q ++ Lv+tAHPt  vR  +  K+ Ri
  gi|2209076    179 LFPHLWQQN--VPPRYLQNLIDQLdIKLVFTAHPTEIVRQTIRDKQRRIA 226

                    nCLaqLsAKDvtve.....DKkELDEALHREiqAAFRtDEiRRaqPtPqD
                      L qL   + t  ++++ + + L E L  Ei   +RtDE+   +P   D
  gi|2209076    227 RILEQLDRVEATLGsrsgvEMQNLHEQLIEEIRLWWRTDELHQFKPQVLD 276

                    EmRaGmsYiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWm
                    E+ + + Y+ E v++ +P+  RR+   L+    n R P      kF sW+
  gi|2209076    277 EVEYSLHYFKEVVFEIIPQLYRRITQSLQQSFPNLRPPRHN-FCKFGSWV 325

                    GGDRDGknPRvtPEvtRDvCLLaRmmAanlYisqvEDLm..FElsmWRCn
                    G DRDG nP vtPEvt +     R +    Y   vE L++   ls+  C
  gi|2209076    326 GADRDG-NPSVTPEVTWETACYQRDLVLEKYTKSVEKLInvLSLSLHWCD 374

                    dELRvRAEElyrtaardkvvKyYiEFWKqvPP...tEPYRviLGdvRDKL
                        v  + l +  + +   + + E + q+  + + EPYR  L  v  +L
  gi|2209076    375 ----VLPDLLDSLEQDQ---QQFPELYEQLSArfrHEPYRFKLSYVLRRL 417

                    YntRERaRHL......LAtGiseisEeAvytkvEeFLEPLELCYksLCeC
                     ntR+R R L+++  +  t  s   +  +y k EeFL  L L  + L
  gi|2209076    418 ENTRDRNRQLqngyypFSTDSSGYGDLQIYRKGEEFLAELLLIQRNLQA- 466
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                    GDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei.
                        +    L Dl+ qv  FG  L +LDiRqEs  + + l  i t L+i
  gi|2209076   467 --TNLSCRQLEDLICQVEIFGFNLAQLDIRQESSCHSEALNEIITYLQIl 514

                    .GsYReWsEeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAEL
                    +  Y e sE  R EWL+ EL+ +RPL++++LP  E  +++++++r++  L
  gi|2209076   515 pRPYNELSEGERTEWLVKELQTRRPLIPAELPFSERTREIIETLRMVRRL 564

                    PiDsFGa.....YiismataPsDvLAvELLqRECgvkqt......LrvvP
                      + FG++  ++Y+ism+   sD L v LL +E g+  + +++++L+vvP
  gi|2209076   565 QQE-FGPdicktYVISMSHEASDLLEVLLLAKEAGLYDPvtgtgnLQVVP 613

                    LFEkLADLeAAPAavekLFsiDWYinridGK.........qevmvGYsDs
                    LFE + DL+ AP  + +L  + +Y+  +d   ++ + ++ qevm+GYsDs
  gi|2209076   614 LFETVEDLKKAPTVLTQLLELPFYRAYLDSDcpsadvpplQEVMLGYSDS 663

                    GKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHL
                     KD G ls  W +YkAq  +   A +yGv L +FHGRGG vGRGGGP
  gi|2209076   664 NKDSGFLSSNWEIYKAQQSLQHTAERYGVALRIFHGRGGSVGRGGGPAYA 713

                    AiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHG.m
                    AiL+qP  ti+G +++t qGEv+   +   +L    L   t A +    +
  gi|2209076   714 AILAQPGRTIDGRIKITEQGEVLASKYSLPELALYNLETITTAVIQASlL 763

                    nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGk
                       +     W ++mee+A      YR +++  P Fv++F   tP  E  +
  gi|2209076   764 RTSIDEIQPWHEIMEELALRSRQHYRQLIYEQPDFVDFFHQVTPIEEISQ 813

                    mniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFK.hAi
                    + i sRP++R     ++sLRAiPW+F+Wtq RF LP W GvG A +++
  gi|2209076   814 LEISSRPSRRGGKRTLTSLRAIPWVFSWTQSRFLLPAWYGVGTAIQdFLA 863

                    dKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva..
                    +K +  l  L+  Y +WPFFR+ +   Em  AK D  iA  y + L  ++
  gi|2209076   864 EKPVEHLSLLQYFYFKWPFFRMVISKAEMTLAKVDLQIAQHYVRELTHpe 913

                    ..EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYi
                    ++E   P  +++ ++Y  t +l+L i GHk lL+GDP L+  + LR+  i
  gi|2209076   914 drERFAPLYDQIAQEYYRTCELILTITGHKRLLDGDPDLQRSVQLRNGNI 963

                    ttLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpter
                      L  +q   LKR+R  + +      l   y   +
  gi|2209076   964 VPLGFLQVLLLKRLRQHQSQTSSGALLRSRYSKGE--------------- 998

                    vaPGLEDtLiLtmKGiAAGmqntG<-*
                        L    +Lt+ GiAAGm ntG
  gi|2209076   999 ----LRRGALLTINGIAAGMRNTG    1018

gi|154146766|emb|CAM84070.1|: domain 1 of 1, from 1 to 439: score 455.4, E = 8.5e-134
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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  gi|1541467     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tD lDAittHL+iGsYReW+E++RqEWLl+EL+G+RPLlg+DLP+tE
  gi|1541467     1 --HTDALDAITTHLGIGSYREWPEQRRQEWLLSELRGRRPLLGPDLPQTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl++frvLAELP Ds GaYiismataPsDvLAvE LqREC v+q+L
  gi|1541467    49 EVADVLGTFRVLAELPPDSLGAYIISMATAPSDVLAVEFLQRECRVRQPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADLeAAPAav++LFs+DWY+ ri GKqevm+GYsDsGKDAG
  gi|1541467    99 RVVPLFEKLADLEAAPAAVARLFSVDWYMDRIGGKQEVMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYk qEE+++vA+++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYKVQEELVRVAQRHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541467   199 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   +PEWR Lm++mA vAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 RPEWRALMDDMAAVATEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KR+PsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA+dKD++nl
  gi|1541467   299 PSKRQPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMDKDVRNL 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+EmY eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLva++LkPFG++
  gi|1541467   349 HTLREMYSEWPFFRVTLDLLEMVFAKGDPGIAALYDELLVADDLKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR +Y Et++lLL++AGHk++LEGDPYLKqrlRLRd+ itt
  gi|1541467   399 LRKNYLETQQLLLQVAGHKEVLEGDPYLKQRLRLRDPHITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146748|emb|CAM84061.1|: domain 1 of 1, from 1 to 439: score 455.1, E = 1.1e-133
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------ -
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                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------ -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tD lDAit  L+iGsYR+W+EeKRqEWLl+ELkGKRPL+g DLP+ E
  gi|1541467     1 --HTDALDAITAYLGIGSYRSWPEEKRQEWLLSELKGKRPLFGDDLPMNE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dv+++frvLAELP D+FGaY+ismataPsDvLAvELLqREC+v ++L
  gi|1541467    49 EVADVIGTFRVLAELPPDCFGAYVISMATAPSDVLAVELLQRECHVEHPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLeAAPAav++LFsiDWY+ ri GKqevm+GYsDsGKDAG
  gi|1541467    99 RVVPLFEKLADLEAAPAAVARLFSIDWYMDRIGGKQEVMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqE ++ vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYKAQEQLVEVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP+t++GslRvtvqGEviE sFGEE+LCFr+LqRFtAA  EHGm+PPvsP
  gi|1541467   199 PPETVHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAAAQEHGMHPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+emAvvAtEEYR++v+KEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWRALMDEMAVVATEEYRAMVFKEPRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkP+GGie+LRAiPWiFaWtqtRFHLPvWLG+GAAFKhA+++Di+n+
  gi|1541467   299 PSKRKPGGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMQRDIRNI 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLva++LkP G++
  gi|1541467   349 QALREMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDELLVADDLKPLGEQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR +Y+Et++lL+++AGHkD+LE DPYLKqrlRLR +Yitt
  gi|1541467   399 LRSNYEETRKLLVQVAGHKDVLEDDPYLKQRLRLRHPYITT--------- 439

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------ -

                  tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|157414180|ref|YP_001485046.1|: domain 1 of 1, from 5 to 989: score 454.6, E = 1.5e-133
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
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                    q++      +s+++ L +   L+ D +  +L +   +d  E
gi|1574141     5    ---RQIKNNNVDLISNNDPLDKNRLLIEDLWESVLREECPDDQAERL 48

                  qECYElsAeYEGKkDtkKL..eELGakLtsLdPaDailvAkailHmLnLA
                      Els       D++K  ++E+   + s+d a++i  A+a++    L
gi|1574141    49 IQLKELSYSKQMNGDSSKTfkNEIVDIVNSMDLAESIAAARAFSLYFQLV 98

                  nLAEE.ve.....lAyRRRikkkkhGDFaDEasAttEsDiEEtlKkL...
                  n+ E +ve+++    +  +  +k h      a A        t++ L  +
gi|1574141    99 NILEQrVEedryiQSFTNKDVQKSHDNLDPFAPALARQNAPVTFRELfyr 148

                  vlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL
                    kln  P    e L+   + Lv+tAHPt  vR  +  K++R+ n L ++
gi|1574141   149 LRKLNVPPGKLEELLQEMDIRLVFTAHPTEIVRHTIRHKQTRVANLLKKI 198

                  sAKD.vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiH
                       +t e+K  L   L  E+   +RtDE+   +P   DE+ + + Y+
gi|1574141   199 QIEQfLTKEEKNSLKNQLKEEVRLWWRTDELHQFKPSVLDEVDYALHYFQ 248

                  EtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPR
                    +++ +P+   R+  AL        lP +     F sW+G DRDG nP
gi|1574141   249 QVLFNAMPQLRGRIAEALTENYPDVQLPSQS-FCNFGSWVGSDRDG-NPS 296

                  vtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyr
                  vtPE+t       R +    Yi     L   ls+    + +     E
gi|1574141   297 VTPEITWRTACYQRQLMLERYIIATSNLRDQLSVSMQWSQVSSSLLESLE 346

                  taardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi
                  t + +       E        EPYR  L  + +KL  t ER   L   G
gi|1574141   347 TDRVK--FPEIYEARATRYRSEPYRLKLSYILEKLRLTQERNNLLSDNGW 394

                  .....sei.......sEeAvytkvEeFLEPLELCYksLCeCGDkviADGs
                  + + + ei++++ ++ E+  y  v eF   LEL   sL   G   +   s
gi|1574141   395 kfdleGEIdnknldkVENLYYKSVNEFTYDLELIKNSLISTG---LTCES 441

                  LLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEe
                  +  lL qv  FG sL  LDiRqEs R+ D +  +t  L++  +Y + sEe
gi|1574141   442 VNTLLTQVHIFGFSLASLDIRQESTRHSDAIQELTNYLDLTMkYDQMSEE 491

                  KRqEWLlaELkGKRPLlgsDLP...ktEEvkDvldafrvL.AELPiDsFG
                   +  WL+ EL  KRPL++sD+  ++ tEE   v   ++ L+ E  +
gi|1574141   492 EKIKWLIDELNTKRPLIPSDVNwtkTTEETFSVFKMVKRLqQEFGSRICH 541

                  aYiismataPsDvLAvELLqRECgv......kqtLrvvPLFEkLADLeAA
                  +Y+ism+ + sD L v LL +E g+ +++++k  L vvPLFE + DL+ A
gi|1574141   542 SYVISMSHSASDLLEVLLLAKEMGLldqnsqKSKLLVVPLFETVEDLKRA 591

                  PAavekLFsiDWYinri.......dGKqevmvGYsDsGKDAGRlsAAWqL
                  P  +e+LF +D+Y+  +++ +++    qe m+GYsDs KD G +s  W +
gi|1574141   592 PEVMERLFKLDFYRSLLpkvgesfKPLQELMLGYSDSNKDSGFVSSNWEI 641

                  YkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGs
                   +Aq  +     +  + L lFHGRGG vGRGGGP   AiL+qP  t++G
gi|1574141   642 HRAQIALQNLSSRNNILLRLFHGRGGSVGRGGGPAYQAILAQPSGTLKGR 691

                  lRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsPkPEWRkL
                  +++t qGEv+   +   +L    L   t A +   + n  +   PEW +L
gi|1574141   692 IKITEQGEVLASKYSLPELALYNLETVTTAVIQNSLvNNRLDATPEWNQL 741

                  meemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs
                  m ++A      YR +v   P    +F   tP  E  k+ i sRPa+Rk +
gi|1574141   742 MSRLAETSRSHYRKLVHENPDLLNFFQEVTPIEEISKLQISSRPARRKKG 791

                  G.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEm
                   + + sLRAiPW+F Wtq RF LP W GvG A    ++ D + +  L+ +
gi|1574141   792 AkDLSSLRAIPWVFGWTQSRFLLPSWFGVGTALSSELNSDPRQIELLRVL 841

                  YkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk....PFGksLR
                   + WPFFR+ +  +Em   K D  +A  y + L + e k++ +   + +
gi|1574141   842 HQRWPFFRMLISKVEMTLSKVDLEVARYYVDTLGSRENKdsfdDIFEVIS 891
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                  dkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKR
                   +Y  tk l+L+i G   lLE D  LK  + LR+  i  L  +q   L+R
  gi|1574141   892 KEYNLTKSLILEITGKNKLLESDRDLKLSVSLRNKTIIPLGFLQVSLLRR 941

                  iRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtm
                  +RD     t +P++s E+  +     de  +    ++   G     +Lt+
  gi|1574141   942 LRDQ----TRQPPIS-EFIIDK----DESRRAYSRSELLRG----ALLTI 978

                  KGiAAGmqntG<-*
                   GiAAGm ntG
  gi|1574141   979 NGIAAGMRNTG    989

gi|154146894|emb|CAM84134.1|: domain 1 of 1, from 1 to 439: score 451.6, E = 1.1e-132
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tD +DAittHL+iGsYReWsEeKRqEWLl EL GKRPL+ +DLP  E
  gi|1541468     1 --HTDAVDAITTHLGIGSYREWSEEKRQEWLLNELAGKRPLMVPDLPHSE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev Dvl+ f+vLAELP DsFG+YiismataPsDvLAvELLqREC++kq+L
  gi|1541468    49 EVGDVLGCFKVLAELPRDSFGPYIISMATAPSDVLAVELLQRECQIKQPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +vvPLFE+LADL+ APA+ve+LFs+DWY nri GKq++mvGYsDsGKDAG
  gi|1541468    99 PVVPLFERLADLQNAPASVERLFSVDWYLNRIGGKQQIMVGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLY+Aq  ++KvAKky vK++lFHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWQLYQAQAAVAKVAKKYNVKVTLFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP+tinGslRvt+qGEviE sFGEE+LCFr+LqRFtAAtLEHGmnPP+sP
  gi|1541468   199 PPETINGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMNPPISP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEW kLm++mAvvAt+ YRsvvvKEPRFvEYFR+AtPE+EYG+mniGsR
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  gi|1541468   249 KPEWSKLMDDMAVVATDAYRSVVVKEPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKRkP+GGi++LRAiPWiF+WtqtRFHLPvWLGvG AFK AidKDiKn+
  gi|1541468   299 PAKRKPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGTAFKSAIDKDIKNF 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q Lk+mY+eWPFFRvtlDLlEmvFAKGDP iAaLyDkLLva++LkPFG++
  gi|1541468   349 QLLKDMYNEWPFFRVTLDLLEMVFAKGDPSIAALYDKLLVADDLKPFGEN 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR kY Et++lLLkiAGHk++LEGDPYLKqrlRLRd+Yitt
  gi|1541468   399 LRSKYLETQELLLKIAGHKEILEGDPYLKQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|159904236|ref|YP_001551580.1|: domain 1 of 1, from 18 to 1007: score 451.5, E = 1.3e-132
                   *->siDAqLR..lLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                       +    R++     K s    L +  AL+ D +  +L      d
  gi|1599042    18    DLHSSFRnnQASTTKNS-GSLLQQRLALVEDLWETVLCSECPSDQIN 63

                   avqECYEls..AeYEGKkDtkK.LeELGakLtsLdPaDailvAkailHmL
                    v     ls++ ++ G ++ k + +E+   +  +d a++i  A+a++
  gi|1599042    64 RVLRLKKLSnpNNFAGEEEQKNpFNEIVLLIEEMDLAESIAAARAFSLYF 113

                   nLAnLA.....EEvelAyRRRikkkkhGDF.......aDEasAttEsDiE
                    L n+ +++ +E+  l    Ri+      F++  ++ a  +   t s +
  gi|1599042   114 QLVNILeqrieEDTYLETIGRIEEDASNQFdpfapplASQTAPATFSQLF 163

                   EtlKkLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiR
                   E lK+L    n  P      ++   + Lv+tAHPt  vR  +  K+ R+
  gi|1599042   164 ERLKRL----NVPPGQLEALMQEIDIRLVFTAHPTEIVRHTVRHKQRRVA 209

                   nCLaqL.sAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRa
                   n L q +s   +    K+ L   L  Ei   +RtDE+   +Pt  DE+ +
  gi|1599042   210 NLLQQFhSEAAISFSQKESLRQQLEEEIRLWWRTDELHQFKPTVLDEVDY 259

                   GmsYiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDR
                    + Y+   +++ +P+  RR+  AL        +P +     F sW+G DR
  gi|1599042   260 ALHYFQQVLFDAMPQLRRRINAALVKSYPDVEVPRES-FCTFGSWVGSDR 308

                   DGknPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvR
                   DG nP vtPE+t       R +    Yi+ v DL   ls+    + +
  gi|1599042   309 DG-NPSVTPEITWRAACYQRQLMLERYINSVQDLRDQLSISMQWSQVGSQ 357

                   AEElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRH
                     E     + +     Y E        EPYR  +  +  +L  t  R
  gi|1599042   358 LLESLEMDRVQ-FPEVYEERAARY-RLEPYRLKISYILQRLKLTHQRNQE 405

                   LLAtGiseis.............EeAvytkvEeFLEPLELCYksLCeCGD
                   L A G   +++  ++  +++++ E+  y  + eF   LEL   sL
  gi|1599042   406 LAAAGWKIVPeamnslitsgkpfEDLYYCSIAEFRSDLELIRNSLVATD- 454

                   kviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei.Gs
                     +   sL  lL qv  FG sL  LDiRqEs+R+ D +D +t+ ++++
  gi|1599042   455 --LSCESLDTLLTQVHIFGFSLASLDIRQESNRHSDAIDEVTRFIDLpVI 502

                   YReWsEeKRqEWLlaELkGKRPLlgsDL...PktEEvkDvldafrvLA.E
                   Y e  E  +  WL+ EL+ +RPL++s ++ +P t E   v + ++ L +E
  gi|1599042   503 YSEMDEKEKVQWLMQELETRRPLIPSSVdwsPSTQETISVFQMLHRLQeE 552

                   LPiDsFGaYiismataPsDvLAvELLqRECgvkqt......LrvvPLFEk
                     +    +Y+ism+ + sD L v LL +E g+   ++++ +L vvPLFE
  gi|1599042   553 FGSRICRSYVISMSHSVSDLLEVLLLAKEAGLVDIssgsadLLVVPLFET 602
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                    LADLeAAPAavekLFsiDWYin.......ridGKqevmvGYsDsGKDAGR
                    + DL+ AP  +e LFs  +Y n  ++ +++++  qe m+GYsDs KD G
  gi|1599042   603 VEDLQRAPSVMEELFSSSFYLNllprvgeKLQPLQELMLGYSDSNKDSGF 652

                    lsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqP
                    ls  W + +Aq  +   A  +Gv L lFHGRGG vGRGGGP   AiL+qP
  gi|1599042   653 LSSNWEIHQAQIALQNLASSHGVALRLFHGRGGSVGRGGGPAYQAILAQP 702

                    PDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsP
                      t++G +++t qGEv+   +   +L    L   t A L   +    +
  gi|1599042   703 SGTLKGRIKITEQGEVLASKYSLPELAMYNLETVTTAVLQNSLvTNQLDA 752

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                     P W +Lm ++A      YRs+v   P  v +F   tP  E  k+ i sR
  gi|1599042   753 TPSWNELMTRLAARSRRHYRSLVHDNPDLVPFFQEVTPIEEISKLQISSR 802

                    PaKRkPsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    P++Rk + + + sLRAiPW+F Wtq RF LP W GvG A    ++ D
  gi|1599042   803 PTRRKSGSkDLSSLRAIPWVFGWTQSRFLLPSWFGVGHALFIELEEDPAQ 852

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva....EeLk
                    +  Lk + + WPFFR+ +  +Em   K D  +A  y   L +++++E
  gi|1599042   853 IELLKMLHQRWPFFRMLISKVEMTLSKVDLEVANHYVTSLGSrqnkEAFN 902

                    PFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvf
                       + + d+Y  tk l+L+i G   lL  DP L+  + LR+  i  L  +
  gi|1599042   903 KIFEVISDEYHLTKRLVLRITGKSKLLSADPALQASVELRNRTIVPLGFL 952

                    qAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLE
                    q   L+R+RD       +P++s E  +E      +L +    ++   G
  gi|1599042   953 QVALLRRLRDQK----RQPPVSEELFNER-----DLARTYSRSELLRG-- 991

                    DtLiLtmKGiAAGmqntG<-*
                       +Lt+ GiAAGm ntG
  gi|1599042   992 --ALLTINGIAAGMRNTG    1007

gi|154146804|emb|CAM84089.1|: domain 1 of 1, from 1 to 442: score 451.2, E = 1.6e-132
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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  gi|1541468     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlg..sDLP.
                     +tD lDAit HL+iGsYR+W+EeKRqEWLl+EL+GKRPLlg + DLP+
  gi|1541468     1 --HTDALDAITAHLGIGSYRSWPEEKRQEWLLSELRGKRPLLGlrGDLPd 48

                   ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                    t+Ev+Dvl++frvLAELP D+FGaY+ismataPsDvLAvELLqREC+v
  gi|1541468    49 TTDEVADVLGTFRVLAELPADCFGAYVISMATAPSDVLAVELLQRECHVA 98

                   qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                   ++LrvvPLFEkLADLe APAav++LFsiDWY+ ri GKqevm+GYsDsGK
  gi|1541468    99 RPLRVVPLFEKLADLESAPAAVARLFSIDWYMERIGGKQEVMIGYSDSGK 148

                   DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                   DAGRlsAAWqLYkAqEE++ vAK+yGvKL++FHGRGGtvGRGGGPtHLAi
  gi|1541468   149 DAGRLSAAWQLYKAQEELVEVAKRYGVKLTMFHGRGGTVGRGGGPTHLAI 198

                   LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                   LsqPPDt++ slRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PP
  gi|1541468   199 LSQPPDTVHWSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPP 248

                   vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                   vsPkP WR Lm+emAvvAtEEYRs+v+KEPRFvEYFR+AtPE+EYG+mni
  gi|1541468   249 VSPKPKWRALMDEMAVVATEEYRSMVFKEPRFVEYFRSATPETEYGRMNI 298

                   GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                   GsRP+KRkP+GGie+LRAiPWiFaWtqtRFHLPvWLG+GAAFKhA+ KDi
  gi|1541468   299 GSRPSKRKPGGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMRKDI 348

                   KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                   +n+q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLva++LkP
  gi|1541468   349 RNIQALREMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDELLVADDLKPL 398

                   GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                   G++LR +Y++tk+lL+++AGHkD+LEGDPYLKqrlRLRd+Yitt
  gi|1541468   399 GEQLRSNYEDTKKLLIQVAGHKDVLEGDPYLKQRLRLRDPYITT------ 442

                   YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt

  gi|1541468     - ------------------------------------------------ -

                   LiLtmKGiAAGmqntG<-*

  gi|1541468     - ----------------    -

gi|154146742|emb|CAM84058.1|: domain 1 of 1, from 1 to 439: score 450.6, E = 2.4e-132
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------ -
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                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tD +DAittHL+iGsYReW+Ee RqEWLl+EL+GKRPLl  DLP  E
  gi|1541467     1 --HTDAIDAITTHLGIGSYREWAEEERQEWLLSELRGKRPLLVFDLPVSE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl+ frvLAELP DsFG+YiismataPsDvLAvELLqRECgv+++L
  gi|1541467    49 EVADVLGCFRVLAELPPDSFGPYIISMATAPSDVLAVELLQRECGVRNPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +vvPLFE+LADL+ APA+ve+LFsiDWY nri GKq+vmvGYsDsGKDAG
  gi|1541467    99 PVVPLFERLADLQNAPASVERLFSIDWYLNRIGGKQQVMVGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLY+Aq E++KvAKkyGvKL+ FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYQAQAEVAKVAKKYGVKLTFFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGslRvt+qGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541467   199 PPDTINGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEW +Lm++mAvvAt+ YR+vvv+EPRFvE FR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWSRLMDDMAVVATDAYRAVVVREPRFVEHFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvG AFK Aid+Di n+
  gi|1541467   299 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGTAFKSAIDRDINNF 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q Lk+mY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva++LkPFG++
  gi|1541467   349 QLLKDMYREWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVADDLKPFGEQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR kY Et++lLL+iAGHk++LEGDPYLKqrlRLRd+Yitt
  gi|1541467   399 LRSKYLETQELLLQIAGHKEILEGDPYLKQRLRLRDPYITT--------- 439

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146790|emb|CAM84082.1|: domain 1 of 1, from 1 to 438: score 450.0, E = 3.7e-132
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|1541467     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDv+DAittHL+iGsYR+W+EeKRqEWLl+EL+GKRPLl +D+P+ +
  gi|1541467     1 --HTDVIDAITTHLGIGSYRSWPEEKRQEWLLSELRGKRPLLAPDMPQSD 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+D +++frvLAELP DsFG+YiismataPsDvLAvELLqREC+v+++L
  gi|1541467    49 EVADAIGTFRVLAELPADSFGPYIISMATAPSDVLAVELLQRECQVRNPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLFEkLADL+ APA+ve+LFs+DWY+nri GKq vmvGYsDsGKDAG
  gi|1541467    99 PVVPLFEKLADLQSAPASVERLFSVDWYKNRIAGKQMVMVGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAq+E+ +vAK++Gv L+ FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYKAQDEMQQVAKRHGVDLTFFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP+ti+GslRvt+qGEviE sFGE+nLCFr+LqRFtAAtLEHGmnPPvsP
  gi|1541467   199 PPETIHGSLRVTIQGEVIEHSFGEDNLCFRTLQRFTAATLEHGMNPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm++mAvvAtEEYRs+v+KEPRFvEYFR+AtPE+E+G+mniGsR
  gi|1541467   249 KPEWRALMDDMAVVATEEYRSIVMKEPRFVEYFRSATPETEFGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkP+GGie+LRAiPWiF+WtqtRFHLPvWLG+GAAFKh + KD Kn+
  gi|1541467   299 PSKRKPGGGIETLRAIPWIFSWTQTRFHLPVWLGIGAAFKH-VMKDTKNF 347

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+EmY+eWPFFRvtlDL+EmvFAKGDPGiAaLyD+LLva+ LkPFG++
  gi|1541467   348 NTLREMYNEWPFFRVTLDLVEMVFAKGDPGIAALYDQLLVADTLKPFGEQ 397

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR kY+Et++lLL++AGHk++LEGDPYLKqrlRLRd+Yitt
  gi|1541467   398 LRKKYEETQQLLLQVAGHKEILEGDPYLKQRLRLRDPYITT--------- 438

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146784|emb|CAM84079.1|: domain 1 of 1, from 1 to 439: score 449.2, E = 6.2e-132
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ------------------------------------------- -
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|1541467    - ------------------------------------------------- -

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1541467    - ------------------------------------------------- -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1541467    - ------------------------------------------------- -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1541467    - ------------------------------------------------- -

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1541467    - ------------------------------------------------- -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1541467    - ------------------------------------------------- -

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1541467    - ------------------------------------------------- -

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1541467    - ------------------------------------------------- -

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  + D lDAit  L+iGsYR+W+EeKRqEWLl+EL+GKRPL+g DLP+ E
gi|1541467      1 --HNDALDAITAYLGIGSYRSWPEEKRQEWLLSELRGKRPLFGGDLPMNE 48

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                Ev+Dvl++frvLAELP D+FGaY+ismataPsDvLAvELLqREC v ++L
gi|1541467     49 EVADVLGTFRVLAELPPDCFGAYVISMATAPSDVLAVELLQRECDVEHPL 98

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                rvvPLFEkLADL  APAav++LFsiDWY+ ri GKqevm+GYsDsGKDAG
gi|1541467     99 RVVPLFEKLADLVNAPAAVARLFSIDWYMDRIGGKQEVMIGYSDSGKDAG 148

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLYkAqEE++ vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1541467    149 RLSAAWQLYKAQEELVEVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PP t++GslRvtvqGEviE sFGE++LCFr+LqR tAAtLEHGm+PPvsP
gi|1541467    199 PPGTVHGSLRVTVQGEVIEHSFGEDHLCFRTLQRSTAATLEHGMHPPVSP 248

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                kPEWR Lm+emAvvAtEEYR++v+KEPRFvEYFR+AtPE+EYG+mniGsR
gi|1541467    249 KPEWRALMDEMAVVATEEYRAMVFKEPRFVEYFRSATPETEYGRMNIGSR 298

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+KRkP+GGie+LRAiPWiFaWtqtRFHLPvWLG+GAAFKhAi+KDi+n+
gi|1541467    299 PSKRKPGGGIETLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAIQKDIRNI 348

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                q L+EmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLva++LkP G++
gi|1541467    349 QALREMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDELLVADDLKPLGEQ 398

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR +Y+Et++lL+++AGHkD+LE DPYLKqrlRLRd+Yitt
gi|1541467    399 LRSNYEETRKLLVQVAGHKDVLEDDPYLKQRLRLRDPYITT--------- 439

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

gi|1541467    - ------------------------------------------------- -
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                  tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|254526567|ref|ZP_05138619.1|: domain 1 of 1, from 5 to 989: score 449.0, E = 7e-132
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         q++      +s+++ L +   L+ D +  +L +   +d  E
  gi|2545265     5    ---RQIKNNNVDLISNNDPLDKNRLLIEDLWESVLREECPDDQAERL 48

                  qECYElsAeYEGKkDtkKL..eELGakLtsLdPaDailvAkailHmLnLA
                      Els       D++K  ++E+   + s+d a++i  A+a++    L
  gi|2545265    49 IQLKELSYSKQMNGDSSKTfkNEIVDIVNSMDLAESIAAARAFSLYFQLV 98

                  nLAEE.ve.....lAyRRRikkkkhGDFaDEasAttEsDiEEtlKkL...
                  n+ E +ve+++    +  +  +k h      a A        t++ L  +
  gi|2545265    99 NILEQrVEedryiQSFTNKDVQKSHDNLDPFAPALARQNAPVTFRELfyr 148

                  vlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL
                    kln  P    e L+   + Lv+tAHPt  vR  +  K++R+ n L ++
  gi|2545265   149 LRKLNVPPGKLEELLQEMDIRLVFTAHPTEIVRHTIRHKQTRVANLLKKI 198

                  sAKDv.tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiH
                       +t e+K  L   L  E+   +RtDE+   +P   DE+ + + Y+
  gi|2545265   199 QIEQFpTKEEKNSLKNQLKEEVRLWWRTDELHQFKPSVLDEVDYALHYFQ 248

                  EtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPR
                    +++ +P+   R+  AL        lP +     F sW+G DRDG nP
  gi|2545265   249 QVLFNAMPQLRGRIAEALTENYPDVQLPSQS-FCNFGSWVGSDRDG-NPS 296

                  vtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyr
                  vtPE+t       R +    Yi  +  L   ls+    + +     E
  gi|2545265   297 VTPEITWRTACYQRQLMLERYIIAISNLRDQLSVSMQWSQVSSSLLESLE 346

                  taardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi
                  t + +       E        EPYR  L  + +KL  t ER   L   G
  gi|2545265   347 TDRVK--FPEIYEARATRYRSEPYRLKLSYILEKLRLTQERNNLLSDNGW 394

                  .....sei.......sEeAvytkvEeFLEPLELCYksLCeCGDkviADGs
                  + + + ei++++ ++ E+  y  v eF   LEL   sL   G   +   s
  gi|2545265   395 kfdleGEIdnknldkVENLYYKSVNEFTYDLELIKNSLISTG---LTCES 441

                  LLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEe
                  +  lL qv  FG sL  LDiRqEs R+ D +  +   L++  +Y + sEe
  gi|2545265   442 VNTLLTQVHIFGFSLASLDIRQESTRHSDAIQELSNYLDLTMkYDQMSEE 491

                  KRqEWLlaELkGKRPLlgsDLP...ktEEvkDvldafrvL.AELPiDsFG
                   +  WL+ EL  KRPL++sD+  ++ tEE   v   ++ L+ E  +
  gi|2545265   492 EKIKWLIDELNTKRPLIPSDVNwtkTTEETFSVFKMVKRLqQEFGSRICH 541

                  aYiismataPsDvLAvELLqRECgv......kqtLrvvPLFEkLADLeAA
                  +Y+ism+ + sD L v LL +E g+ +++++k  L vvPLFE + DL+ A
  gi|2545265   542 SYVISMSHSASDLLEVLLLAKEMGLldqhsqKSKLLVVPLFETVEDLKRA 591

                  PAavekLFsiDWYinri.......dGKqevmvGYsDsGKDAGRlsAAWqL
                  P  +e+LF +D+Y+  +++ +++    qe m+GYsDs KD G +s  W +
  gi|2545265   592 PEVMERLFKLDFYRSLLpkvgesfKPLQELMLGYSDSNKDSGFVSSNWEI 641

                  YkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGs
                   +Aq  +     +  + L lFHGRGG vGRGGGP   AiL+qP  t++G
  gi|2545265   642 HRAQIALQNLSSRNNILLRLFHGRGGSVGRGGGPAYQAILAQPSGTLKGR 691

                  lRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsPkPEWRkL
                  +++t qGEv+   +   +L    L   t A +   + n  +   PEW +L
  gi|2545265   692 IKITEQGEVLASKYSLPELALYNLETVTTAVIQNSLvNNRLDATPEWNQL 741

                  meemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs
                  m ++A      YR +v   P    +F   tP  E  k+ i sRPa+Rk +
  gi|2545265   742 MSRLAETSRSHYRKLVHENPDLLNFFQEVTPIEEISKLQISSRPARRKKG 791

                  G.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEm
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                    + + sLRAiPW+F Wtq RF LP W GvG A    ++ D + +  L+ +
  gi|2545265   792 AkDLSSLRAIPWVFGWTQSRFLLPSWFGVGTALSSELNSDPRQIELLRVL 841

                    YkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk....PFGksLR
                     + WPFFR+ +  +Em   K D  +A  y + L + e k++ +   + +
  gi|2545265   842 HQRWPFFRMLISKVEMTLSKVDLEVARYYVDTLGSRENKdsfdDIFEVIS 891

                    dkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKR
                     +Y  tk l+L+i     lLE D  LK  + LR+  i  L  +q   L+R
  gi|2545265   892 KEYNLTKSLILEITRKNKLLESDRDLKLSVSLRNKTIIPLGFLQVSLLRR 941

                    iRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtm
                    +RD     t +P++s E+  +     de  +    ++   G     +Lt+
  gi|2545265   942 LRDQ----TRQPPIS-EFIIDK----DESRRAYSRSELLRG----ALLTI 978

                    KGiAAGmqntG<-*
                     GiAAGm ntG
  gi|2545265   979 NGIAAGMRNTG    989

gi|78780052|ref|YP_398164.1|: domain 1 of 1, from 5 to 989: score 448.6, E = 9.1e-132
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           q++      +s ++ L +   L+ D +  +L +   +d  E
  gi|7878005     5    ---QQIKNNKVDLISTNDPLDKNRLLIEDLWESVLREECPDDQAERL 48

                    qECYElsAeYEGKkDtkKL..eELGakLtsLdPaDailvAkailHmLnLA
                        Els       D++K  + E+   + s+d a++i  A+a++    L
  gi|7878005    49 IQLKELSYSKQIEGDSSKTfkKEIVDIVNSMDLAESIAAARAFSLYFQLV 98

                    nLAEE.ve.....lAyRRRikkkkhGDFaDEasAttEsDiEEtlKkL...
                    n+ E +ve+++    +  ++ +k        a A        t++ L  +
  gi|7878005    99 NILEQrVEedryiQSFTNKNVQKSPDNLDPFAPALARQNAPVTFRELfyr 148

                    vlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL
                      kln  P    e L+   + Lv+tAHPt  vR  +  K++R+ n L ++
  gi|7878005   149 LRKLNVPPGKLEELLQEMDIRLVFTAHPTEIVRHTIRHKQTRVANLLKKI 198

                    sAKD.vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiH
                         +t e+K  L   L  E+   +RtDE+   +P   DE+ + + Y+
  gi|7878005   199 QVEQfLTKEEKNFLKIQLKEEVRLWWRTDELHQFKPSVLDEVDYALHYFQ 248

                    EtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPR
                      +++ +P+   R+  AL        lP +     F sW+G DRDG nP
  gi|7878005   249 QVLFNAMPQLRGRIAEALTENYPDVQLPSQS-FCNFGSWVGSDRDG-NPS 296

                    vtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyr
                    vtPE+t       R +    Yi     L   ls+    + +     E
  gi|7878005   297 VTPEITWRTACYQRQLMLERYITATSHLRDQLSVSMQWSQVSSSLLESLE 346

                    taardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi
                    t + +       E        EPYR  L  + +KL  t ER   L   G
  gi|7878005   347 TDRVK--FPAIYEARATRYRSEPYRLKLSYILEKLRLTQERNNLLADNGW 394

                    ............seisEeAvytkvEeFLEPLELCYksLCeCGDkviADGs
                    + + +++ ++++ +  E+  y  v eF   LEL   sL        A
  gi|7878005   395 kfdlegelntknIDKVENLYYKSVNEFTYDLELIKNSLISTDLTCEAVNT 444

                    LLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEe
                    L   L qv  FG sL  LDiRqEs R+ D +  +t+ L++  +Y + sE+
  gi|7878005   445 L---LTQVHIFGFSLASLDIRQESTRHSDAIQELTKYLDLSVqYDQMSED 491

                    KRqEWLlaELkGKRPLlgsDL...PktEEvkDvldafrvL.AELPiDsFG
                     +  WL+ EL  KRPL++sD++ +  tEE   v   ++ L+ E  +
  gi|7878005   492 EKIKWLVDELNTKRPLIPSDVkwtNTTEETFSVFKMVKRLqQEFGSRICH 541

                    aYiismataPsDvLAvELLqRECgvkqt......LrvvPLFEkLADLeAA
                    aY+ism+ + sD L v LL +E g+   ++++++L vvPLFE + DL+ A
  gi|7878005   542 AYVISMSHSASDLLEVLLLAKEMGLLDQnsknsnLLVVPLFETVEDLKRA 591

                    PAavekLFsiDWYinri.......dGKqevmvGYsDsGKDAGRlsAAWqL
                    P  +ekLF +D+Y+  +++ +++    qe m+GYsDs KD G +s  W +
  gi|7878005   592 PEVMEKLFKLDFYKSLLpkvgesfKPLQELMLGYSDSNKDSGFVSSNWEI 641
```

```
                    YkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGs
                     +Aq  +   A +  + L lFHGRGG vGRGGGP   AiL+qP  t++G
  gi|7878005   642 HRAQIALQNLASRNNILLRLFHGRGGSVGRGGGPAYQAILAQPSGTLKGR 691

                    lRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsPkPEWRkL
                    +++t qGEv+   +   +L    L   t A +   + n  +   PEW +L
  gi|7878005   692 IKITEQGEVLASKYSLPELALYNLETVTTAVIQNSLvNNRLDATPEWNQL 741

                    meemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs
                    m ++A      YR +v+  P    +F   tP  E  k+ i sRPa+Rk +
  gi|7878005   742 MSRLAETSRSHYRKLVYENPDLLNFFQEVTPIEEISKLQISSRPARRKKG 791

                    G.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEm
                     + + sLRAiPW+F Wtq RF LP W GvG A    ++ D + +  L+ +
  gi|7878005   792 AkDLSSLRAIPWVFGWTQSRFLLPSWFGVGTALSSELNSDPQQIELLRVL 841

                    YkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk....PFGksLR
                     + WPFFR+ +  +Em   K D  +A  y + L +Ee k++ +   + +
  gi|7878005   842 HQRWPFFRMLISKVEMTLSKVDLEVAKYYVDTLGSEENKdsfdDIFEVIS 891

                    dkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKR
                     +Y  tk l+L+i G   lLE D  LK  + LR+  i  L  +q   L+R
  gi|7878005   892 KEYSLTKSLVLEITGKNKLLESDRDLKSSVSLRNKTIIPLGFLQVSLLRR 941

                    iRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtm
                    +RD     t +P++s E+  +     de  +    ++   G     +Lt+
  gi|7878005   942 LRDQ----TRQPPIS-EFLIDK----DESRRAYSRSELLRG----ALLTI 978

                    KGiAAGmqntG<-*
                     GiAAGm ntG
  gi|7878005   979 NGIAAGMRNTG    989

gi|154146822|emb|CAM84098.1|: domain 1 of 1, from 1 to 440: score 448.5, E = 1e-131
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLl.gsDLPkt
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                     +tD lDAittHL+iGsYR W+EeKRqEWLl+EL+GKRPLl+g DLP+t
  gi|1541468     1 --HTDALDAITTHLGIGSYRGWPEEKRQEWLLSELRGKRPLLgGGDLPQT 48

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    EEv+Dvl++frvLAELP DsF aY+ismataPsDvLAvELLqREC v+++
  gi|1541468    49 EEVADVLGTFRVLAELPADSFSAYVISMATAPSDVLAVELLQRECRVRRP 98

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    LrvvPLFEkLADLe APAav++LFs+DWY+ ri GKqevm+GYsDsGKDA
  gi|1541468    99 LRVVPLFEKLADLESAPAAVARLFSVDWYMDRIGGKQEVMIGYSDSGKDA 148

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                    GRlsAAWqLYkAqEE+++vAK++GvKL +FHGRGGtvGRGGGPtHLAiLs
  gi|1541468   149 GRLSAAWQLYKAQEELVRVAKRHGVKLAMFHGRGGTVGRGGGPTHLAILS 198

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPPDt++GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvs
  gi|1541468   199 QPPDTVHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVS 248

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    PkPEWR Lm+emA vAt+EYRs+vv+EPRFvEYFR+AtPE+EYG+mniGs
  gi|1541468   249 PKPEWRALMDEMATVATDEYRSIVVREPRFVEYFRSATPETEYGRMNIGS 298

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RP+KRkPsGGiesLRAiPWiFaWtqtR HLPvWLG+GAAFKhA++KDi+n
  gi|1541468   299 RPSKRKPSGGIESLRAIPWIFAWTQTRSHLPVWLGFGAAFKHAMKKDIRN 348

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    + +L+EmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyD+LLva++LkPFG+
  gi|1541468   349 IHMLREMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDELLVADDLKPFGE 398

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR++Y +t++lLL++AGHkD+LEGDP LKqrlRLRd+Yitt
  gi|1541468   399 QLRNEYLDTRQLLLQVAGHKDVLEGDPHLKQRLRLRDPYITT-------- 440

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi

  gi|1541468     - ------------------------------------------------- -

                    LtmKGiAAGmqntG<-*

  gi|1541468     - --------------    -

gi|154146898|emb|CAM84136.1|: domain 1 of 1, from 1 to 439: score 448.5, E = 1e-131
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -
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                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDv+DAittHL+iGsYReWsEeKRqEWL++EL+GKRPLl +D+P+tE
  gi|1541468     1 --HTDVIDAITTHLGIGSYREWSEEKRQEWLISELQGKRPLLSPDMPQTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++Dvl+ f+vLAELP DsFG+YiismataPsDv AvELLqREC+vkq+L
  gi|1541468    49 EIADVLGCFQVLAELPRDSFGPYIISMATAPSDVFAVELLQRECHVKQPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +vvPLFEkLADL+ APA+ve+LFs+DWY nri GKq+vmvGYsDsGKDAG
  gi|1541468    99 PVVPLFEKLADLQSAPASVERLFSVDWYFNRIGGKQQVMVGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAW LYkAqEE++KvAK+yGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWHLYKAQEEMAKVAKRYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP+tinGslRvtvqGEviE+sFGEE+LCF++LqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPETINGSLRVTVQGEVIEYSFGEEHLCFQTLQRFTAATLEHGMHPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+e+A v tEEYRsvv+KEPRFvEYFR+AtPE+EYG++niGsR
  gi|1541468   249 KPEWRALMDELAAVSTEEYRSVVMKEPRFVEYFRSATPETEYGRLNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKRkP GGiesLRAiPWiF+WtqtRFHLPvWLGvG AFKhA++KD+Kn+
  gi|1541468   299 PAKRKPKGGIESLRAIPWIFSWTQTRFHLPVWLGVGGAFKHAMNKDMKNF 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +Lk mYkeWPFFRvtlDLlEmvFAKGDP iA+Ly +LLva+eLkPFG++
  gi|1541468   349 EMLKAMYKEWPFFRVTLDLLEMVFAKGDPSIAGLYNELLVADELKPFGEQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y Et++lLL++AGHk++LE DP LKq+lRLRd+Yit
  gi|1541468   399 LRNNYIETEKLLLQVAGHKEILESDPGLKQQLRLRDPYITI--------- 439

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------ -

                  tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|226326777|ref|ZP_03802295.1|: domain 1 of 1, from 1 to 691: score 448.5, E = 1e-131
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2263267     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2263267     - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                             +k+ k
  gi|2263267     1 -----------MKLEK--------------------------------- 5

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2263267     - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
```

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                                  iR   PtP DE + G + +   +W+GvP FLR
  gi|2263267     6 ------------------IR---PTPIDEAKWGFAVVENSLWEGVPAFLR 34

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         LK   i   lP ++  i+F+sWmGGDRDG nP vt E+tR   LL
  gi|2263267    35 EFNEQLKE-SIDYNLPVEASPIRFTSWMGGDRDG-NPNVTAEITRHALLL 82

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    +R  Aa l+++ +  L+ Elsm     ELR    El   a
  gi|2263267    83 SRWKAADLFLNDIQVLVSELSMTESTPELR----ELAGGADVA------- 121

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             EPYR i  + R +L  tR+     + +G   ++ e    +
  gi|2263267   122 ---------EPYREIAKQLRTRLQVTRDYLEQRI-KGQQSLPPEGLLIDN 161

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                     e  EPL  CY+sL +CG ++iA G LLD LR +  FGL LvKLDiRqEs
  gi|2263267   162 AELWEPLYACYQSLTQCGMRIIANGQLLDTLRRIRCFGLQLVKLDIRQES 211

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +t+ l  +t+ Le+G Y +WsEe++q +Ll EL  KRPL++
  gi|2263267   212 TNHTEALSELTQYLELGDYANWSEEQKQTFLLEELNSKRPLIPTNWQPSA 261

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                      ++v ++ rv+A  P Ds  +Y+isma  PsDvLAv LL +E g    L
  gi|2263267   262 PTQEVFETCRVIAQSPKDSIASYVISMAKVPSDVLAVKLLLKEAGADIRL 311

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +v PLFE L DL+ A   + +LF i WY+  id Kq vm+GYsDs KDAG
  gi|2263267   312 PVAPLFETLEDLNNAESVMTRLFDIPWYRDLIDDKQMVMIGYSDSAKDAG 361

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     ++A W  Y+Aq+ +iK   k Gv L+lFHGRGGt+GRGG P H A+Lsq
  gi|2263267   362 VMAASWAQYRAQDALIKLCEKSGVTLTLFHGRGGTIGRGGAPAHAALLSQ 411

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  ++G lRvt qGE+i f FG  ++   sL  ++ A LE  + PP  P
  gi|2263267   412 PPGSLKGGLRVTEQGEMIRFKFGLPQVTISSLAHYAGAILEANLLPPPEP 461

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    k  W ++m+ +  v    YR  v  E  Fv YFR AtPE E Gk+ +GsR
  gi|2263267   462 KAPWIEVMDSLSDVSCAMYRDYVRGEEDFVPYFRAATPEGELGKLPLGSR 511

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR+P GG+e+LRAiPWiFaWtq R  LP WLG GAA +h i  D+
  gi|2263267   512 PAKRRPTGGVETLRAIPWIFAWTQNRLMLPAWLGAGAALQHEI--DSGKQ 559

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L +m ++WPFF   + +lEmv+AK D  +A  yD+ Lv E L+P G +
  gi|2263267   560 AVLDDMCENWPFFNTRIAMLEMVYAKADLWLAEYYDQRLVDERLWPLGTK 609

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++  +  + +L i     l+   P++   + LR+ Y   Lnv+qA  L
  gi|2263267   610 LRQQLSDDIKSVLAISKDEHLMADLPWVAESIALRNVYTDPLNVLQAELL 659

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    +R R                                  ++  P +E  L++
  gi|2263267   660 QRSR------------------------------THSESDPRIEQALMV 678

                    tmKGiAAGmqntG<-*
                    t+ GiAAGm ntG
  gi|2263267   679 TIAGIAAGMRNTG    691

gi|123969314|ref|YP_001010172.1|: domain 1 of 1, from 5 to 989: score 447.4, E = 2.1e-131
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           q++      +s+++ L +   L+ D +  +L +   +d  E
  gi|1239693     5    ---RQVKNNNVDLISNNDPLDKNRLLIEDLWESVLREECPDDQAERL 48

                    qECYElsAeYEGKkDtkKL..eELGakLtsLdPaDailvAkailHmLnLA
                        Els       D++K  ++E+   + s+d a++i  A+a++    L
  gi|1239693    49 IQLKELSYSKQIDGDSSKTfkNEIVDIVNSMDLAESIAAARAFSLYFQLV 98
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                nLAEE.ve....lAyRRRikkkkhGDFaD.EasAttEsDiEEtlKkL...
                n+ E +ve+++ +        +k  D  D+ a A        t++ L  +
gi|1239693    99 NILEQrVEedryIQSFTNKDVQKSPDNLDpFAPALARQNAPVTFRELfyr 148

                vlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL
                  kln  P    e L+   + Lv+tAHPt  vR  +  K++R+ n L ++
gi|1239693   149 LRKLNVPPGKLEELLQEMDIRLVFTAHPTEIVRHTIRHKQTRVANLLKKI 198

                sAKD.vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiH
                     +t e+K  L   L  E+   +RtDE+   +P   DE+ + + Y+
gi|1239693   199 QIEQfLTKEEKNSLKTQLKEEVRLWWRTDELHQFKPSVLDEVDYALHYFQ 248

                EtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPR
                  +++ +P+   R+  AL        lP +     F sW+G DRDG nP
gi|1239693   249 QVLFNAMPQLRGRIAEALTDNYPDVQLPSES-FCNFGSWVGSDRDG-NPS 296

                vtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyr
                vtPE+t       R +    Yi     L   ls+    + +     E
gi|1239693   297 VTPEITWRTACYQRQLMLERYIIATSNLRDQLSVSMQWSQVSSSLLESLE 346

                taardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi
                t + +       E        EPYR  L  + +KL  t ER   L   G
gi|1239693   347 TDRVK--FPEIYEARATRYRSEPYRLKLSYILEKLRLTQERNNLLADSGW 394

                s............eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGs
                  + ++++++++ +  E   y  v eF   LEL   sL       +   s
gi|1239693   395 KfdlegetdnknlDKVESLYYKSVKEFTYDLELIKNSLISTD---LNCES 441

                LLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEe
                +  lL qv  FG sL  LDiRqEs R+ D +  +t  L++  +Y + sEe
gi|1239693   442 VNTLLTQVHIFGFSLASLDIRQESTRHSDAIQELTNYLDLSVqYDQMSEE 491

                KRqEWLlaELkGKRPLlgsDLP...ktEEvkDvldafrvL.AELPiDsFG
                 +  WL+ EL  KRPL++sD+  ++ tEE   v   ++ L+ E  +
gi|1239693   492 EKIKWLIDELNTKRPLIPSDVHwtkTTEETFSVFKMVKRLqQEFGSRICH 541

                aYiismataPsDvLAvELLqRECgv......kqtLrvvPLFEkLADLeAA
                +Y+ism+ + sD L v LL +E g+ +++++k  L vvPLFE + DL+ A
gi|1239693   542 SYVISMSHSASDLLEVLLLAKEMGLldqnsqKSKLLVVPLFETVEDLKRA 591

                PAavekLFsiDWYinri.......dGKqevmvGYsDsGKDAGRlsAAWqL
                P  +ekLF +D+Y+  +++ +++    qe m+GYsDs KD G +s  W +
gi|1239693   592 PEVMEKLFKLDFYRSLLpkvgesfKPLQELMLGYSDSNKDSGFVSSNWEI 641

                YkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGs
                 +Aq  +     +  + L lFHGRGG vGRGGGP   AiL+qP  t++G
gi|1239693   642 HRAQIALQNLSSRNNILLRLFHGRGGSVGRGGGPAYQAILAQPSGTLKGR 691

                lRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsPkPEWRkL
                +++t qGEv+   +   +L    L   t A +   + n  +   PEW +L
gi|1239693   692 IKITEQGEVLASKYSLPELALYNLETVTTAVIQNSLvNNRLDATPEWNQL 741

                meemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs
                m ++A      YR +v   P    +F   tP  E  k+ i sRPa+Rk +
gi|1239693   742 MSRLAETSRSHYRKLVHENPDLLNFFQEVTPIEEISKLQISSRPARRKKG 791

                G.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEm
                 + + sLRAiPW+F Wtq RF LP W GvG A    ++ D + +  L+ +
gi|1239693   792 AkDLSSLRAIPWVFGWTQSRFLLPSWFGVGTALSSELNLDPQQIELLRVL 841

                YkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP....FGksLR
                 + WPFFR+ +  +Em   K D  +A  y + L + e k + ++  + +
gi|1239693   842 HQRWPFFRMLISKVEMTLSKVDLEVARYYVDTLGSKENKDsfdnIFEVIS 891

                dkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKR
                 +Y  tk l+L+i G   lLE D  LK  + LR+  i  L  +q   L+R
gi|1239693   892 KEYNLTKSLILEITGKNKLLESDRDLKSSVSLRNKTIIPLGFLQVSLLRR 941

                iRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtm
                +RD     t +P++s  + d +     e  +    ++   G     +Lt+
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  gi|1239693   942 LRDQ----TRQPPISEFFLDKD-----ESTRAYSRSELLRG----ALLTI 978

                   KGiAAGmqntG<-*
                    GiAAGm ntG
  gi|1239693   979 NGIAAGMRNTG    989

gi|91070220|gb|ABE11140.1|: domain 1 of 1, from 5 to 989: score 447.2, E = 2.5e-131
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          q++      +s+++ L +   L+ D +  +L +   +d  E
  gi|9107022     5    ---RQIKNNNVDLISNNDPLDKNRLLIEDLWESVLREECPDDQAERL 48

                   qECYElsAeYEGKkDtkKL..eELGakLtsLdPaDailvAkailHmLnLA
                       Els       D++K  ++E+   + s+d a++i  A+a++    L
  gi|9107022    49 IQLKELSYSKQIDGDSSKTfkNEIVDIVNSMDLAESIAAARAFSLYFQLV 98

                   nLAEE.ve....lAyRRRikkkkhGDFaD.EasAttEsDiEEtlKkL...
                   n+ E +ve+++ +        +k  D  D+ a A        t++ L  +
  gi|9107022    99 NILEQrVEedryIQSFTNKDVQKSPDNLDpFAPALARQNAPVTFRELfyr 148

                   vlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL
                     kln  P    e L+   + Lv+tAHPt  vR  +  K++R+ n L ++
  gi|9107022   149 LRKLNVPPGKLEELLQEMDIRLVFTAHPTEIVRHTIRHKQTRVANLLKKI 198

                   sAKD.vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiH
                        +t e+K  L   L  E+   +RtDE+   +P   DE+ + + Y+
  gi|9107022   199 QIEQfLTKEEKISLKTQLKEEVRLWWRTDELHQFKPSVLDEVDYALHYFQ 248

                   EtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPR
                     +++ +P+   Rv  AL        lP +     F sW+G DRDG nP
  gi|9107022   249 QVLFNAMPQLRGRVAEALTENYPDVQLPPES-FCNFGSWVGSDRDG-NPS 296

                   vtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyr
                   vtPE+t       R +    Y+     L   ls+    + +     E
  gi|9107022   297 VTPEITWRTACYQRQLMLERYVIATSNLRDQLSVSMQWSQVSSSLLESLE 346

                   taardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi
                   t + +       E        EPYR  L  + +KL  t ER   L   G
  gi|9107022   347 TDRVK--FPEIYEARATRYRSEPYRLKLSYILEKLRLTQERNNLLADSGW 394

                   .....sei.......sEeAvytkvEeFLEPLELCYksLCeCGDkviADGs
                   + + + ei++++ ++ E+  y  + eF   LEL   sL       +   s
  gi|9107022   395 kfdleGEIdnknidkVENLYYKSINEFTYDLELIKNSLISTD---LTCES 441

                   LLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEe
                   +  lL qv  FG sL  LDiRqEs R+ D +  +t  L++  +Y + sEe
  gi|9107022   442 VNNLLTQVHIFGFSLASLDIRQESTRHSDAIQELTNYLDLSVqYDQMSEE 491

                   KRqEWLlaELkGKRPLlgsDLP...ktEEvkDvldafrvL.AELPiDsFG
                    +  WL+ EL  KRPL++sD+  ++ tEE   v   ++ L+ E  +
  gi|9107022   492 EKIKWLIDELNTKRPLIPSDVNwtkTTEETFSVFKMVKRLqQEFGSRICH 541

                   aYiismataPsDvLAvELLqRECgv......kqtLrvvPLFEkLADLeAA
                   +Y+ism+ + sD L v LL +E g+ +++++k  L vvPLFE + DL+ A
  gi|9107022   542 SYVISMSHSASDLLEVLLLAKEMGLldqnsqKSKLLVVPLFETVEDLKRA 591

                   PAavekLFsiDWYinri.......dGKqevmvGYsDsGKDAGRlsAAWqL
                   PA +e+LF +D+Y+  +++ +++    qe m+GYsDs KD G +s  W +
  gi|9107022   592 PAVMEQLFKLDFYKSLLpkvgesfKPLQELMLGYSDSNKDSGFVSSNWEI 641

                   YkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGs
                    +Aq  +     +  + L lFHGRGG vGRGGGP   AiL+qP  t++G
  gi|9107022   642 HRAQIALQNLSSRNDILLRLFHGRGGSVGRGGGPAYQAILAQPSGTLKGR 691

                   lRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsPkPEWRkL
                   +++t qGEv+   +   +L    L   t A +   + n  +   PEW +L
  gi|9107022   692 IKITEQGEVLASKYSLPELALYNLETVTTAVIQNSLvNNRLDATPEWNQL 741

                   meemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs
                   m ++A      YR +v   P    +F   tP  E  k+ i sRPa+Rk +
  gi|9107022   742 MSRLAETSRSHYRKLVHENPDLLNFFQEVTPIEEISKLQISSRPARRKKG 791
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                    G.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEm
                     + + sLRAiPW+F Wtq RF LP W GvG A    ++ D + +  L+ +
  gi|9107022   792 AkDLSSLRAIPWVFGWTQSRFLLPSWFGVGTALSSELNSDPQQIELLRVL 841

                    YkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP....FGksLR
                     + WPFFR+ +  +Em   K D  +A  y + L + e k + ++  + +
  gi|9107022   842 HQRWPFFRMLISKVEMTLSKVDLEVARYYVDTLGSKENKDsfdnIFEVIS 891

                    dkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKR
                     +Y  tk l+L+i G   lLE D  LK  + LR+  i  L  +q   L+R
  gi|9107022   892 KEYNLTKSLILEITGKNKLLESDRDLKSSVSLRNKTIIPLGFLQVSLLRR 941

                    iRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtm
                    +RD     t +P++s E+  +     de  +    ++   G     +Lt+
  gi|9107022   942 LRDQ----TRQPPIS-EFIIDK----DESRRAYSRSELLRG----ALLTI 978

                    KGiAAGmqntG<-*
                     GiAAGm ntG
  gi|9107022   979 NGIAAGMRNTG    989

gi|154146836|emb|CAM84105.1|: domain 1 of 1, from 1 to 439: score 446.1, E = 5.4e-131
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tD lDAit  L+iGsYReWsEeKRqEWLl+EL+GKRPL+g+DLP+ E
  gi|1541468     1 --HTDALDAITAYLGIGSYREWSEEKRQEWLLSELRGKRPLFGPDLPQSE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl++frvLAELP DsFGaYiismataPsDvLAvELLqREC+v q+L
  gi|1541468    49 EVADVLGTFRVLAELPADSFGAYIISMATAPSDVLAVELLQRECHVGQPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAav++LFsiDWY+ ri GKqevm+GYsDsGKDAG
  gi|1541468    99 RVVPLFEKLADLEAAPAAVARLFSIDWYVDRIGGKQEVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAW LY+AqE ++ vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
```

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  gi|1541468   149 RLSAAWALYRAQEQLVEVAKRHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP+ti+GslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPETIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emA vAt EYR+vv+KEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468   249 KPEWRALMDEMAAVATQEYRAVVFKEPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRF LPvWLG+GAAFKh ++KDi+n+
  gi|1541468   299 PSKRKPSGGIESLRAIPWIFAWTQTRFNLPVWLGFGAAFKHVMQKDIRNI 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q L+EmY+eWPFFRvtlDLlEmvFAKGDP iAaLyD+LLva++LkP G++
  gi|1541468   349 QALREMYNEWPFFRVTLDLLEMVFAKGDPCIAALYDELLVADDLKPLGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR +Y++tk+lLL++AGHkD+LEGDPYLKqrlRLRd+Yitt
  gi|1541468   399 LRKDYEDTKELLLQVAGHKDVLEGDPYLKQRLRLRDPYITT--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - -------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146726|emb|CAM84050.1|: domain 1 of 1, from 1 to 439: score 445.1, E = 1.1e-130
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - -------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - -------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - -------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - -------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - -------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - -------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - -------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - -------------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +t+v+DA+ttHL+iGsYR+WsEe RqEWL++EL+GKRPLl +D+P+ E
  gi|1541467     1 --HTEVIDAVTTHLGIGSYRSWSEEERQEWLISELRGKRPLLAPDMPMSE 48
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                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+D +++f+vLAELP DsFG+Yiism+ta sDvLAv LLqREC++k++L
  gi|1541467     49 EVADAIGTFKVLAELPDDSFGPYIISMCTAASDVLAVYLLQRECHIKNPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFE+LADL+AAPA++e LFs+DWY   i+GKq+vm+GYsDsGKDAG
  gi|1541467     99 PVVPLFERLADLQAAPASMELLFSVDWYAETINGKQQVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLY+AqE+++K+AKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467    149 RLSAAWQLYRAQEDLAKIAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGs+Rvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541467    199 PPDTINGSIRVTIQGEVIEYSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAvvAtEEYRsvv++EPRFvEYFR+AtPE+EYGkmniGsR
  gi|1541467    249 KPEWRALMDEMAVVATEEYRSVVFREPRFVEYFRSATPETEYGKMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkP GGiesLRAiPWiF+WtqtRFH+PvWLGvG AF+ Ai+KD Knl
  gi|1541467    299 PAKRKPKGGIESLRAIPWIFSWTQTRFHVPVWLGVGSAFQSAIKKDAKNL 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      Lk mY+eWPFFRvtlDLlEmvFAKG P iAa+yD+LLvaEeLkP G+
  gi|1541467    349 DLLKGMYDEWPFFRVTLDLLEMVFAKGNPNIAAVYDDLLVAEELKPLGET 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR kYvEt++lLL+iAGHkD+LEGDPYLKqrlRLRd+Yitt
  gi|1541467    399 LRSKYVETQELLLQIAGHKDILEGDPYLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467      - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541467      - -------------    -

gi|33862131|ref|NP_893692.1|: domain 1 of 1, from 3 to 989: score 444.8, E = 1.3e-130
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s+  q +      +s+++ L +  AL+ D +  +L +   +d
  gi|3386213      3    SMK-QFKNNNVDLISNNDPLDKNRALIEDLWESVLREECPDDQANRL 48

                    qECYElsAeYEGKkDtkK..LeELGakLtsLdPaDailvAkailHmLnLA
                        Els      + + K+   E+   + s+d a++i  A+a++    L
  gi|3386213     49 IQLKELSYSNKVEEYSPKnfKTEIVDIVNSMDLAESISAARAFSLYFQLV 98

                    nLAEE.ve.....lAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlk
                    n+ E +ve+++    +   + kk h      a A        t+K L  +
  gi|3386213     99 NILEQrVEedryiQSFTNQNVKKSHDNLDPFAPALARQNAPVTFKELFFR 148

                    l...nKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL
                    l++ n  P    e L+   + Lv+tAHPt  vR  +  K++R+ n L ++
  gi|3386213    149 LrrlNVPPGKLEELLQEMDIRLVFTAHPTEIVRHTIRHKQTRVANLLQKI 198

                    sA.KDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiH
                      +K +t+eD k L   L  Ei   +RtDE+   +P   DE+ + + Y+
  gi|3386213    199 QVeKFLTIEDIKSLKIQLKEEIRLWWRTDELHQFKPSVIDEVDYALHYFQ 248

                    EtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPR
                      +++ +P+   R+  AL        +P +     F sW+G DRDG nP
  gi|3386213    249 QVLFDAMPQLRGRISSALTENYPDVQMPTES-FCTFGSWVGSDRDG-NPS 296

                    vtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyr
                    vtPE+t       R +    Yi     L   ls+    + +     E
  gi|3386213    297 VTPEITWRTACYQRQLMLERYIKATSNLRDQLSVSMQWSQVSSSLLESLE 346

                    taardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi
                    t + +       E        EPYR  L  + +KL  t ER   L   G
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  gi|3386213   347 TDRVK--FPEIYEARATRYRSEPYRLKLSYILEKLRLTHERNNLLSEGGW 394

                   s............eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGs
                     + ++++++++ e+ E   y  v+eF   LEL   sL        A
  gi|3386213   395 KlsleresdnknlELVEKLHYKSVDEFTYDLELIKNSLNSTDLTCEA--- 441

                   LLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEe
                   +  lL qv  FG sL  LDiRqEs R+ D +  +t  Le++  Y + sE
  gi|3386213   442 VNKLLTQVHIFGFSLASLDIRQESTRHSDAIQELTNYLELpKQYDQMSEK 491

                   KRqEWLlaELkGKRPLlgsDLP...ktEEvkDvldafrvLA.ELPiDsFG
                    R  WL  EL  KRPL++s++  ++ tEE   v   ++ L +E  +
  gi|3386213   492 DRIQWLNEELNTKRPLIPSEVNwnkSTEETFSVFKMVKRLQeEFGSRICH 541

                   aYiismataPsDvLAvELLqRECgv......kqtLrvvPLFEkLADLeAA
                   +Y+ism+ + sD L v LL +E g+ +++++k tL vvPLFE + DL+ A
  gi|3386213   542 SYVISMSHSASDLLEVLLLAKEMGLidqgsqKSTLLVVPLFETVEDLQRA 591

                   PAavekLFsiDWYinri.......dGKqevmvGYsDsGKDAGRlsAAWqL
                   P  +e+LF +D+Y+  +++ +++    qe m+GYsDs KD G ls  W +
  gi|3386213   592 PDVMEQLFQLDFYKSLLpkvgesfKPLQELMLGYSDSNKDSGFLSSNWEI 641

                   YkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGs
                    +Aq  +     +  + L lFHGRGG vGRGGGP   AiL+qP  t++G
  gi|3386213   642 HRAQIALQNLSSRNNILLRLFHGRGGSVGRGGGPAYQAILAQPSGTLKGR 691

                   lRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsPkPEWRkL
                   +++t qGEv+   +   +L    L   t A +   + n  +   PEW +L
  gi|3386213   692 IKITEQGEVLASKYSLPELALYNLETVTTAVIQNSLvNNRLDATPEWNDL 741

                   meemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs
                   m ++A      YR +v   P    +F   tP  E  k+ i sRPa+Rk +
  gi|3386213   742 MTRLAETSRIQYRKLVHENPNLLTFFQEVTPIEEISKLQISSRPARRKKG 791

                   G.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEm
                    + + sLRAiPW+F Wtq RF LP W GvG A    ++ D   +  L+ +
  gi|3386213   792 AkDLSSLRAIPWVFGWTQSRFLLPSWFGVGTALSVELKSDPEQIELLRVL 841

                   YkeWPFFRvtlDLlEmvFAKGDPGiAaLy.DkLLvaEeLkPFGk...sLR
                    + WPFFR+ +  +Em   K D  +A  y D L   E+ k F +  + +
  gi|3386213   842 HQRWPFFRMLISKVEMTLSKVDLEVAKYYvDTLGSKENSKSFEEifdVIS 891

                   dkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKR
                    +Y  tk l+L+i G   lLE D  L+  + LR+  i  L  +q   L+R
  gi|3386213   892 KEYNLTKSLVLEITGKNKLLESDRDLRSSVNLRNKTIIPLGFLQVSLLRR 941

                   iRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtm
                   +RD     t +P++s E+ ++        ++          L    +Lt+
  gi|3386213   942 LRDQ----TRQPPIS-EFIEDR-------IESK-RAYSRSELLRGALLTI 978

                   KGiAAGmqntG<-*
                    GiAAGm ntG
  gi|3386213   979 NGIAAGMRNTG    989

gi|154146802|emb|CAM84088.1|: domain 1 of 1, from 1 to 439: score 444.7, E = 1.4e-130
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ---------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ---------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ---------------------------------------------------- -
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                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +t+v+DAittHL+iGsYR+WsEeKRqEWLl+EL+GKRPLl +DLP+ E
  gi|1541468      1 --HTEVIDAITTHLGIGSYRSWSEEKRQEWLLSELQGKRPLLSPDLPQSE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+D l++frvLAELP DsFG+YiismataPsDvLAvELLqREC+v  +L
  gi|1541468     49 EVADALGTFRVLAELPRDSFGPYIISMATAPSDVLAVELLQRECKVADPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +vvPLFE+LADL+AAPA++e+LFs+DWY  ri+GKq+vmvGYsDsGKDAG
  gi|1541468     99 PVVPLFERLADLQAAPATMERLFSVDWYEKRINGKQQVMVGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAW LY AqEE+ KvA  +GvK++lFHGRGGtvGRGGGPtHLAiLsq
  gi|1541468    149 RLSAAWALYTAQEEVLKVANSHGVKITLFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP tinGs+RvtvqGEviE sFGEE+LCFr+L RFtAAtLEHGm+PPv P
  gi|1541468    199 PPKTINGSIRVTVQGEVIEHSFGEEHLCFRTLERFTAATLEHGMHPPVFP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+e+AvvAtE YRsvv+KEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541468    249 KPEWRALMDELAVVATEAYRSVVFKEPRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKRkP GGiesLRAiPWiF+WtqtRFHLPvWLGvGAAFK+A++KDiKn+
  gi|1541468    299 PAKRKPKGGIESLRAIPWIFSWTQTRFHLPVWLGVGAAFKYAMKKDIKNF 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q+LkEmY+eWPFFRvtlDLlEmvFAKGDPGi +Ly +LLva+eLkPFG++
  gi|1541468    349 QMLKEMYNEWPFFRVTLDLLEMVFAKGDPGIVGLYNDLLVADELKPFGEQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y +t++lLL++AGHk++LEG PYLKqrlRLRd+Yitt
  gi|1541468    399 LRNDYLDTQQLLLQVAGHKEILEGSPYLKQRLRLRDPYITT--------- 439

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146886|emb|CAM84130.1|: domain 1 of 1, from 1 to 439: score 442.0, E = 9.2e-130
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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gi|1541468     - ------------------------------------------------ -

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1541468     - ------------------------------------------------ -

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1541468     - ------------------------------------------------ -

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1541468     - ------------------------------------------------ -

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1541468     - ------------------------------------------------ -

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1541468     - ------------------------------------------------ -

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1541468     - ------------------------------------------------ -

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1541468     - ------------------------------------------------ -

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +tDv+DAittHL+iGsYR+W+EeKRqEWLl+EL+GKRPLl sDLP+tE
gi|1541468      1 --HTDVIDAITTHLGIGSYRSWPEEKRQEWLLSELSGKRPLLSSDLPQTE 48

                 EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                 E++Dvl+ f+vLAELP DsFG+YiismataPsDvLAvELLqREC++k++L
gi|1541468     49 EIADVLGCFHVLAELPRDSFGPYIISMATAPSDVLAVELLQRECHIKEPL 98

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                 +vvPLFEkLADL+ AP ++e+LFs DWYinri GKq+vmvGYsDsGKDAG
gi|1541468     99 PVVPLFEKLADLQSAPESIERLFSFDWYINRIGGKQQVMVGYSDSGKDAG 148

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 RlsAAW LYkAqE +++vAKky vKL+lFHGRGGtvGRGGGPtHLAiLsq
gi|1541468    149 RLSAAWHLYKAQEAMAQVAKKYNVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                 PP+tinGslRvtvqGEviE+sFGEE+LCF++LqRFtAAtLEHGm+PPvsP
gi|1541468    199 PPETINGSLRVTVQGEVIEYSFGEEHLCFQTLQRFTAATLEHGMHPPVSP 248

                 kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                 kPEWR L++e+A v tEEYRsvv+KEPRFvEYFR+AtPE+EYGk+niGsR
gi|1541468    249 KPEWRALLDEIAAVSTEEYRSVVMKEPRFVEYFRSATPETEYGKLNIGSR 298

                 PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                 PaKRkP GGiesLRAiPWiF+WtqtRFHLPvWLG+GAAFKhA++KDiKn+
gi|1541468    299 PAKRKPKGGIESLRAIPWIFSWTQTRFHLPVWLGFGAAFKHAMKKDIKNF 348

                 qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                 q+LkEmY+eWPFFRvtlDLlEmv AKGDP iA+LyD+LLvaEeLkPFG +
gi|1541468    349 QMLKEMYNEWPFFRVTLDLLEMVLAKGDPTIAGLYDELLVAEELKPFGAQ 398

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                 LR++YvE ++l+L++ GHk++LE DP LKq+lRLRd+Yit
gi|1541468    399 LRENYVESEKLILQVIGHKEILESDPALKQQLRLRDPYITI--------- 439

                 KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

gi|1541468     - ------------------------------------------------ -

                 tmKGiAAGmqntG<-*
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  gi|1541468     - -------------    -

gi|126697104|ref|YP_001091990.1|: domain 1 of 1, from 5 to 989: score 441.1, E = 1.7e-129
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          q++      +s+++ L +   L+ D +  +L +   +d  E
  gi|1266971     5    ---RQIKNNNVDLISNNDPLDKNRLLIEDLWESVLREECPDDQAERL 48

                   qECYEl..sAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                       El+ s + +G       +E+   + s+d a++i  A+a++    L
  gi|1266971    49 IQLKELsySKQIDGNSSKTFKNEIVDIVNSMDLAESIAAARAFSLYFQLV 98

                   nLAEE.ve....lAyRRRikkkkhGDFaD.EasAttEsDiEEtlKkL...
                   n+ E +ve+++ +        +k  D  D+ a A        t++ L  +
  gi|1266971    99 NILEQrVEedryIQSFTNKDVQKSPDNLDpFAPALARQNAPVTFRELfyr 148

                   vlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL
                     kln  P    e L+   + Lv+tAHPt  vR  +  K++R+ n L ++
  gi|1266971   149 LRKLNVPPGKLEELLQEMDIRLVFTAHPTEIVRHTIRHKQTRVANLLKKI 198

                   sAKD.vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiH
                        +t ++K  L   L  E+   +RtDE+   +P   DE+ + + Y+
  gi|1266971   199 QIEQfLTKDEKISLKTQLKEEVRLWWRTDELHQFKPSVLDEVDYSLHYFQ 248

                   EtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPR
                     +++ +P+   R+  AL        lP +     F sW+G DRDG nP
  gi|1266971   249 QVLFNAMPQLRGRITEALTENYPDVQLPPES-FCNFGSWVGSDRDG-NPS 296

                   vtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyr
                   vtP++t       R +    Yi     L   ls+    + +     E
  gi|1266971   297 VTPDITWRTACYQRQLMLDRYIVATSNLRDQLSVSMQWSQVSSSLLESLE 346

                   taardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi
                   t + +       E        EPYR  L  + +KL  t ER   L   G
  gi|1266971   347 TDRVK--FPEIYEARATRYRSEPYRLKLSYILEKLRLTQERNNLLADSGW 394

                   .....sei.......sEeAvytkvEeFLEPLELCYksLCeCGDkviADGs
                   + + + ei++++ ++ E+  y  v eF   LEL   sL       +   s
  gi|1266971   395 kfdfeGEIdnknidkVENLYYKSVNEFTYDLELIKNSLISTD---LTCDS 441

                   LLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEe
                   +  lL qv  FG sL  LDiRqEs R+ D +  +t  L++  +Y + sEe
  gi|1266971   442 VNNLLTQVHIFGFSLASLDIRQESTRHSDAIQELTNYLDLSVqYDQMSEE 491

                   KRqEWLlaELkGKRPLlgsDLP...ktEEvkDvldafrvL.AELPiDsFG
                    +  WL+ EL  KRPL++sD+  ++ tEE   v   ++ L+ E  +
  gi|1266971   492 EKIKWLIDELNTKRPLIPSDVNwtkTTEETFSVFKMVKRLqQEFGSRICH 541

                   aYiismataPsDvLAvELLqRECgv......kqtLrvvPLFEkLADLeAA
                   +Y+ism+ + sD L v LL +E g+ +++++k  L vvPLFE + DL+ A
  gi|1266971   542 SYVISMSHSASDLLEVLLLAKEMGLldqdsqKSKLLVVPLFETVEDLQRA 591

                   PAavekLFsiDWYinri.......dGKqevmvGYsDsGKDAGRlsAAWqL
                   P  +ekLF +D+Y+  +++ +++    qe m+GYsDs KD G +s  W +
  gi|1266971   592 PEVMEKLFKLDFYKSLLpkvgesfKPLQELMLGYSDSNKDSGFVSSNWEI 641

                   YkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGs
                    +Aq  +     +  + L lFHGRGG vGRGGGP   AiL+qP  t++G
  gi|1266971   642 HRAQIALQNLSSRNNILLRLFHGRGGSVGRGGGPAYQAILAQPSGTLKGR 691

                   lRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsPkPEWRkL
                   +++t qGEv+   +   +L    L   t A +   + n  +   PEW +L
  gi|1266971   692 IKITEQGEVLASKYSLPELALYNLETVTTAVIQNSLvNSRLDATPEWNQL 741

                   meemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs
                   m ++A      YR +v   P    +F   tP  E  k+ i sRPa+Rk +
  gi|1266971   742 MSRLAETSRSHYRKLVHENPDLLNFFQEVTPIEEISKLQISSRPARRKKG 791

                   G.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEm
                    + + sLRAiPW+F Wtq RF LP W GvG A    ++ D + +  L+ +
  gi|1266971   792 AkDLSSLRAIPWVFGWTQSRFLLPSWFGVGTALSAELNSDPQQIELLRVL 841
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                    YkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP....FGksLR
                     + WPFFR+ +  +Em   K D  +A  y + L + e k + ++  + +
  gi|1266971   842 HQRWPFFRMLISKVEMTLSKVDLEVARYYVDTLGSKENKDsfdnIFEVIS 891

                    dkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKR
                     +Y  tk l+L+i G   lLE D  LK  + LR+  i  L  +q   L+R
  gi|1266971   892 KEYNLTKSLILEITGKNKLLESDRDLKSSVSLRNKTIIPLGFLQVSLLRR 941

                    iRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtm
                    +RD     t +P++s E+  +     de  +    ++   G     +Lt+
  gi|1266971   942 LRDQ----TRQPPIS-EFLIDK----DESRRAYSRSELLRG----ALLTI 978

                    KGiAAGmqntG<-*
                     GiAAGm ntG
  gi|1266971   979 NGIAAGMRNTG    989

gi|154146728|emb|CAM84051.1|: domain 1 of 1, from 1 to 439: score 440.7, E = 2.3e-129
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +t+v+DAittHL+iGsYR+WsEe Rq WL+ EL+GKRPLl +D+P+ E
  gi|1541467     1 --HTEVVDAITTHLGIGSYRSWSEEERQKWLINELRGKRPLLAPDMPMSE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+D +++f+vLAELP DsFG+Yiism+ta sDvLAv LLqRECg+k++L
  gi|1541467    49 EVADAIGTFKVLAELPDDSFGPYIISMCTAASDVLAVYLLQRECGIKNPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFE+LADL+AAPA++e LFs+DWY   i+GKq+vm+GYsDsGKDAG
  gi|1541467    99 PVVPLFERLADLQAAPASMELLFSVDWYAQTINGKQQVMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLY+AqE+++K+AKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWQLYRAQEDLAKIAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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                    P DtinGs+Rvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541467   199 PSDTINGSIRVTIQGEVIEYSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAvvAtEEYRsvv++EPRFvEYFR+AtPE+EYGkmniGsR
  gi|1541467   249 KPEWRALMDEMAVVATEEYRSVVFREPRFVEYFRSATPETEYGKMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkP GGiesLRAiPWiF+WtqtRFH+PvWLGvG AF+ Ai+KD Knl
  gi|1541467   299 PAKRKPKGGIESLRAIPWIFSWTQTRFHVPVWLGVGSAFQSAIKKDPKNL 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      LkEmY+eWPFFRvtlDLlEmvFAKG P iAa+yD+LLvaEeLkP G+
  gi|1541467   349 DLLKEMYNEWPFFRVTLDLLEMVFAKGNPNIAAIYDELLVAEELKPLGET 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR kYvEt++lLL+iAGHkD+LEGDPYLKqrlRLRd+Yitt
  gi|1541467   399 LRSKYVETQELLLQIAGHKDILEGDPYLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146792|emb|CAM84083.1|: domain 1 of 1, from 1 to 438: score 437.3, E = 2.4e-128
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDv+DAittHL+iGsYR+WsEeKRqEWLl+EL+GKRPLl +D+P+ +
  gi|1541467     1 --HTDVIDAITTHLGIGSYRSWSEEKRQEWLLSELSGKRPLLAPDMPQSD 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+D +++frvLAELP DsFG+YiismataPsDvLAvELLqREC+++++L
  gi|1541467    49 EVADAIGTFRVLAELPADSFGPYIISMATAPSDVLAVELLQRECQIRKPL 98
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                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFEkLADL+ APA+ve+LFs+DWY+nri GKq vmvGYsDsGKDAG
  gi|1541467     99 PVVPLFEKLADLQSAPASVERLFSVDWYKNRIAGKQMVMVGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAq+E+ +vAK++Gv L+ FHGRGGtvGRGGGPtHLAiLsq
  gi|1541467    149 RLSAAWQLYKAQDEMQQVAKRHGVDLTFFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP+ti+GslRvt+qGEviE sFGE+nLCFr+LqRFtAAtLEHGmnPPvsP
  gi|1541467    199 PPETIHGSLRVTIQGEVIEHSFGEDNLCFRTLQRFTAATLEHGMNPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm++m vvAtEEYRs+v+KEPRFvEYFR+AtPE+E+G+mniGsR
  gi|1541467    249 KPEWRALMDDMDVVATEEYRSIVMKEPRFVEYFRSATPETEFGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkP+GGie+LRAiPWiF+WtqtRFHLPvWLG+GAAFK  + KD+Kn+
  gi|1541467    299 PSKRKPGGGIETLRAIPWIFSWTQTRFHLPVWLGIGAAFK-NVMKDSKNF 347

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvtlDL+EmvFAKG PGiAaLyD+LLva+ LkPFG++
  gi|1541467    348 NTLREMYNEWPFFRVTLDLVEMVFAKGGPGIAALYDELLVADALKPFGQQ 397

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR kY+Et++lLL++AGHk++LE DPYLKqrlRLRd+Yitt
  gi|1541467    398 LRKKYEETQQLLLQVAGHKEILESDPYLKQRLRLRDPYITT--------- 438

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146856|emb|CAM84115.1|: domain 1 of 1, from 1 to 439: score 437.0, E = 2.9e-128
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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  gi|1541468     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDv+DAittHL+iGsYReWsEeKRqEWL++ELkGKRPLl  DLP+tE
  gi|1541468     1 --HTDVIDAITTHLGIGSYREWSEEKRQEWLISELKGKRPLLSKDLPQTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dvl+ f+vLAELP DsFG+YiismataPsDvLAvELLqREC++k +L
  gi|1541468    49 EIADVLGCFHVLAELPRDSFGPYIISMATAPSDVLAVELLQRECHIKDPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLFEkLADL+ APA+ve+LFs+DWYinri GKq+vmvGYsDsGKDAG
  gi|1541468    99 PVVPLFEKLADLQSAPASVERLFSLDWYINRIGGKQQVMVGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAW LYkAqEE++KvAK+y vKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWHLYKAQEEMAKVAKRYDVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvt+qGEviE+sFGEE+LCF++LqR tAAtLEHGm+PPvsP
  gi|1541468   199 PPDTINGSLRVTIQGEVIEYSFGEEHLCFQTLQRHTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L++e+A vAtEEYRsvv+KEPRFvEYFR+AtPE+EYG++niGsR
  gi|1541468   249 KPEWRALLDEIAAVATEEYRSVVMKEPRFVEYFRSATPETEYGRLNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKRkP GGiesLRAiPWiF+Wtq RF LPvWLG+GAAFKhA++KDiKn+
  gi|1541468   299 PAKRKPKGGIESLRAIPWIFSWTQNRFNLPVWLGFGAAFKHAMKKDIKNF 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +LkEmYkeWPFFRvtlDLlEmv AKGDP iA+LyD+LLvaEeLkPFG++
  gi|1541468   349 EMLKEMYKEWPFFRVTLDLLEMVLAKGDPTIAGLYDQLLVAEELKPFGEQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++YvEt++l+L++ GHk++LE DP LKq+lRLRd+Yit
  gi|1541468   399 LRNNYVETEKLILEVLGHKEVLEDDPTLKQQLRLRDPYITI--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146868|emb|CAM84121.1|: domain 1 of 1, from 1 to 439: score 434.7, E = 1.4e-127
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------ -
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                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------ -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------ -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------ -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDvlDAittHL+iGsYReW+EeKR EWLl+EL+GKRPLl +D+P+tE
  gi|1541468     1 --HTDVLDAITTHLGIGSYREWPEEKRIEWLLSELSGKRPLLAPDMPQTE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvl+afrv+AELP DsFG+Yiismata sDvLAvELLqREC+v+q+L
  gi|1541468    49 EIADVLGAFRVIAELPRDSFGPYIISMATATSDVLAVELLQRECHVRQPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                     vvPLFE+LADL+AAPA+ve+LF ++WY+nri GKq vmvGYsDsGKDAG
  gi|1541468    99 HVVPLFERLADLQAAPASVERLFKMEWYMNRIGGKQMVMVGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAW LYkAq + + vAKkyGvKL+ FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWELYKAQVDTAAVAKKYGVKLTFFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGslRvt+qGEviE  FGEE+LCF +LqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTINGSLRVTIQGEVIEHQFGEEHLCFLTLQRFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm++mAvvAtEEYRs+v+KEPRFvEYFR+AtPE+E  +mniGsR
  gi|1541468   249 KPEWRALMDDMAVVATEEYRSIVFKEPRFVEYFRSATPETELPRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkP+GG+++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+A+ KD+Kn+
  gi|1541468   299 PAKRKPGGGVTTLRAIPWIFSWTQTRFHLPVWLGVGAAFKWAMTKDSKNI 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+L++mY+eWPFFRvt+DLlEmvFAKGDP iA+LyD+LLva+eLkPFG++
  gi|1541468   349 QMLRDMYNEWPFFRVTVDLLEMVFAKGDPSIASLYDDLLVADELKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR kYv+t +lLL++AGHkD+LEGDP L+q+lRLR++Yitt
  gi|1541468   399 LRSKYVDTLQLLLQVAGHKDILEGDPILRQQLRLRNPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------ -

                    tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146872|emb|CAM84123.1|: domain 1 of 1, from 1 to 439: score 432.2, E = 8.1e-127
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ------------------------------------------------ -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ------------------------------------------------ -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|1541468     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tDv+DAittHL+iGsYR+W+E +RqEWLl+EL+GKRPLl +DLP+tE
  gi|1541468     1 --HTDVIDAITTHLGIGSYRSWPEKQRQEWLLSELSGKRPLLSPDLPQTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dvl+ f+vLAELP DsFG+YiismataPsDvLAvELLqREC+vk++L
  gi|1541468    49 EIADVLGCFHVLAELPRDSFGPYIISMATAPSDVLAVELLQRECKVKEPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLFEkLADL+ AP +ve LFs+DWY nri GKq+vmvGYsDsGKDAG
  gi|1541468    99 PVVPLFEKLADLQSAPVSVETLFSMDWYLNRIGGKQQVMVGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAW LYkAqEE+ KvAK++GvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWHLYKAQEEMGKVAKRFGVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvt+qGEviE sFGEE+LCF++LqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTINGSLRVTIQGEVIEHSFGEEHLCFQTLQRFTAATLEHGMHPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L++e+A vAtEE+Rsvv+KEPRFvEYFR+AtPE+EYGk+niGsR
  gi|1541468   249 KPEWRVLLDEIAAVATEEFRSVVMKEPRFVEYFRSATPETEYGKLNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKRkP+GGie+LRAiPWiF+Wtq RF LPvWLG+G AFKhA++KDiKn+
  gi|1541468   299 PAKRKPGGGIETLRAIPWIFSWTQNRFNLPVWLGFGSAFKHAMKKDIKNF 348

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q+LkEmY+eWPFFRvtlDLlEmv AKGDP iA+LyD+LLvaEeLkPFGk+
  gi|1541468   349 QMLKEMYNEWPFFRVTLDLLEMVLAKGDPTIAGLYDELLVAEELKPFGKQ 398

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++YvEt++l+L++ GHk++LE DP LKq+lRLRd+Yit
  gi|1541468   399 LRENYVETEKLILQVVGHKEVLESDPGLKQQLRLRDPYITI--------- 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|86605542|ref|YP_474305.1|: domain 1 of 1, from 28 to 978: score 430.7, E = 2.3e-126
                   *->siDAqLRlLvPGKvse.dekLieYDALLlDkFLD..iLqDLHGedLk
                        D   R+L+     ++ ++L++    +++   +  iLq+  G+ L
  gi|8660554    28    ERDPLARALAVDEALDgRNNLLNRRLQMVEELWEavILQEC-GQPLV 73
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                EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                +  q    +    EG+     + E+   +  L    ai  A+a+     L
gi|8660554    74 DLLQRLRSMCSP-EGQALEYPIPEVLQIVEHLSLDAAIQTARAFALFFQL 122

                AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                 n+ E  +   R   +  +  D +           E  +  L l++   P
gi|8660554   123 INIVE--QHYERAEDSDMRMVD-SQQRTVRENEKFERLFPYLRLQG-VPP 168

                eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL.sAKDvtv
                      L    + Lv+tAHPt  vR  +  K+      L+qL+ A    +
gi|8660554   169 GLLRRLLERLHIRLVFTAHPTEIVRHTIREKQRAFSHLLSQLdWAEQSHP 218

                eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                   + L E L  E+   +RtDE+  ++Pt   E+ + + Y+ E +++ +P
gi|8660554   219 LQAQMLREQLAEEVLLWWRTDELHQSKPTVLNEVDYTLHYFEEVLFQAIP 268

                KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                          LK        P  +    F sW+GGDRDG nP vt  vt
gi|8660554   269 LLHEYLSRSLKK-SFPSVEPPPAGFCNFGSWVGGDRDG-NPSVTANVTWQ 316

                vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                     R +    Yi+ v  L   ls+     ++     ++    +r  +
gi|8660554   317 TARYQRNLILGKYIESVKALTKTLSVSLHWGDVDSQLLDVLEQDRRR-MP 365

                KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei..sEe
                  Y  F  q   +EPYR  L  +  +L  tRER R L       ++++ +
gi|8660554   366 EVYESFSLQY-RQEPYRLKLSYIQRRLELTRERNRNLADSACLPVppPLD 414

                AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                  y + EeFL  L L   sL + G   +    L  l+ qv  FG  L  L
gi|8660554   415 NAYANAEEFLADLQLIQSSLKNSG---LSCRQLDHLICQVQVFGFHLAHL 461

                DiRqEseRqtDvlDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLl
                DiRq+s  +   l  i + L i +  Y e  Ee +  +Ll EL+ +RPL+
gi|8660554   462 DIRQDSSYHEAALTEIFEYLRIlpRPYSEMTEEEKTAFLLRELQTRRPLI 511

                gsDLPktEEvkDvldafrvL....AELPiDsFGaYiismataPsDvLAvE
                + + P  +  ++ + +fr L++ + E  +     Y+ism+   sD L v
gi|8660554   512 PLEAPFSDKAAELIATFRTLrrlqQEFGMAMCQTYVISMSRQLSDLLEVL 561

                LLqRECgv......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                LL +E g+ ++ +++ +L vvPLFE + DL+ AP  + +L  i +Y+  +
gi|8660554   562 LLAKEVGLydpisgRGSLAVVPLFETVEDLKGAPEVLRQLLEIPFYRQYL 611

                dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                  +++ qevm+GYsDs KDAG ls  W +YkAq  +  vA  yGvKL +F
gi|8660554   612 AQQenlQEVMLGYSDSNKDAGFLSSNWEIYKAQQRLQAVAESYGVKLQIF 661

                HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                HGRGG vGRGGGP   AiL+qP   + G +++t qGEv+   +   +L
gi|8660554   662 HGRGGSVGRGGGPAYEAILAQPGRSVGGRIKITEQGEVLASKYSLQDLAI 711

                rsLqRFtAAtLEHGmnPPv.sPkPEWRkLmeemAvvAtEEYRsvvvKEPR
                  L   t A +   +    +    EW +Lme +A      YR +v+
gi|8660554   712 FNLETVTSAVIQASLLRTYpNDLHEWSRLMESLAERSRQVYRNLVYEQEG 761

                FvEYFRlAtPElEYGkmniGsRPaKRk.PsGGiesLRAiPWiFaWtqtRF
                FvE+F   tP  E  ++ i sRPa+R + s  i sLRAiPW+F+Wtq RF
gi|8660554   762 FVEFFHEVTPIEEISQLQISSRPARRSgNSKDIGSLRAIPWVFSWTQSRF 811

                HLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                 LP W GvG A      K   nl  L+ +Y+eWPFFR+ +  +Em  AK
gi|8660554   812 LLPAWYGVGTALEEYAAKGEHNLNHLQHLYREWPFFRMVISKVEMTLAKA 861

                DPGiAaLyDkLLva....EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE
                D  iA  y + + ++++ E      + + ++   t++++Lki GHk+lLE
gi|8660554   862 DLQIARHYVREMSSperlERAMELFELIAQEMYRTREMVLKITGHKELLE 911

                GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                 DPYLK  + LR+  i  L  +q   LKR+R  +          K +
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  gi|8660554   912 NDPYLKRSVQLRNRSIVPLGFIQVSLLKRLRGKQ----------KSHFHN 951

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                         +eL++               +Lt+ GiAAGm ntG
  gi|8660554   952 TQYNRAELLRGA-------------LLTINGIAAGMRNTG    978

gi|72382985|ref|YP_292340.1|: domain 1 of 1, from 9 to 994: score 430.4, E = 2.9e-126
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        i     + v  +      L +   L+ D +  +L+    +d  E
  gi|7238298     9    NISNHSTVCVEDQDP-GSLLQQRLELVEDLWKTVLKSECPPDQTERL 54

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls      +D +    +   +t +d a+ai  A+a++    L n+
  gi|7238298    55 LRLKQLSDPSKSNQDNSS-KAIVQLITKMDLAEAISAARAFSLYFQLVNI 103

                    AEEv..elAyRRRikkkkhGDFaDE.........asAttEsDiEEtlKkL
                     E   +e  y   i+k k  D +  + ++  +  as t  +     + +L
  gi|7238298   104 LEQRieEDSYLESIEKGK-LDTSNYkidpfapalASQTAPATFTQLFERL 152

                    vlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL
                      +ln  P+     ++   + Lv+tAHPt  vR  +  K+ R+   L qL
  gi|7238298   153 -RRLNVPPAQLDGLMREMDIRLVFTAHPTEIVRHTVRHKQRRVATLLQQL 201

                    sAKDvtveDKkELDEA.LHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiH
                        +  e  kE+   +L  Ei   +RtDE+   +Pt  DE+ + + Y+
  gi|7238298   202 QSNSLISESEKEIFRLqLEEEIRLWWRTDELHQFKPTVLDEVDYALHYFQ 251

                    EtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPR
                      +++ +P+  RR  tAL        +P ++    F sW+G DRDG nP
  gi|7238298   252 QVLFDAMPQLRRRLTTALASSYPDVEIPNEA-FCTFGSWVGSDRDG-NPS 299

                    vtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyr
                    vtPE+t       R +    Yi  v DL   ls+    + +     E
  gi|7238298   300 VTPEITWRTACYQRQLMLDRYIASVQDLRDQLSISMQWSQVSSPLLESLE 349

                    taardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtG.
                      +       Y E        EPYR  L    ++L  t  R + L   G
  gi|7238298   350 MDRVR-FPEVYEERAARY-RLEPYRLKLSYTLERLRLTQLRNKQLADAGw 397

                    .........is...eisEeAvytkvEeFLEPLELCYksLCeCGDkviADG
                    + ++++++ is+++   E   y  vEe    LEL   sL       +
  gi|7238298   398 qfspdgkplIStnnSFDEVLHYKSVEELKNELELIRNSLVSTD---LTCE 444

                    sLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsE
                     L  lL qv  FG sL  LDiRqEs R+ D lD +t+ L+++ sY   sE
  gi|7238298   445 PLDTLLNQVHIFGFSLASLDIRQESTRHSDALDELTRYLDLpESYGVMSE 494

                    eKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGa..
                    e R  WL+ EL+ +RPL+++        ++ +  f++L  L  + FG +
  gi|7238298   495 ESRVQWLMKELRTRRPLIPPSFEWSKSTQETISVFHMLHRLQKE-FGTri 543

                    ...YiismataPsDvLAvELLqRECgvkqt......LrvvPLFEkLADLe
                     ++Y+ism+ + sD L v LL +E g+  ++ + ++L vvPLFE + DL+
  gi|7238298   544 crsYVISMSHTASDLLEVLLLAKESGLIDPtlgasdLLVVPLFETVEDLQ 593

                    AAPAavekLFsiDWYin...ridGK....qevmvGYsDsGKDAGRlsAAW
                     AP  +e L  +D Y+   +r+  K+++ qe m+GYsDs KD G ls  W
  gi|7238298   594 HAPSVMESLLQTDVYRE llpRVGEKkqplQELMLGYSDSNKDSGFLSSNW 643

                    qLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtin
                     + kAq  +   A + G+ L +FHGRGG vGRGGGP   AiL+qP  t++
  gi|7238298   644 EIHKAQIALQDLASRQGIALRIFHGRGGSVGRGGGPAYQAILAQPSGTLQ 693

                    GslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP.vsPkPEWR
                    G +++t qGEv+   +   +L    L   t A +   +   ++   P W
  gi|7238298   694 GRIKITEQGEVLASKYSLPELALYNLETVTTAVIQNSLVTNkLDATPSWN 743

                    kLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRk
                    +Lm ++A    E YR++v   P  v +F + tP  E  k+ i sRPa+Rk
  gi|7238298   744 ELMTRLAARSREHYRALVHDNPDLVQFFQVVTPIEEISKLQISSRPARRK 793
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                    PsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLk
                     + + + sLRAiPW+F Wtq RF LP W GvG A    ++ D   + +L+
  gi|7238298   794 SGAkDLSSLRAIPWVFGWTQSRFLLPSWFGVGTALATELKADPDQMEMLR 843

                    EmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL.vaEeLkPFGk...s
                     + + WPFFR+ +  +Em   K D  +A  y   L+ +++   F +  +
  gi|7238298   844 MLNQRWPFFRMLISKVEMTLSKVDLDVAHHYVVSLgGSDDRDAFARifdI 893

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    +  +Y  tk+l+L+i G   lL  DP L+  + LR+  i  L  +q   L
  gi|7238298   894 ISSEYSLTKKLILEITGKSKLLSADPALQLSVNLRNRTIVPLGFLQVALL 943

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KR+RD +     +P++s +   + ++ +    +          L    +L
  gi|7238298   944 KRLRDQN----RQPPISEDVSIDSTQSSRTYSRSE--------LLRGALL 981

                    tmKGiAAGmqntG<-*
                    t+ GiAAGm ntG
  gi|7238298   982 TINGIAAGMRNTG    994

gi|124026726|ref|YP_001015841.1|: domain 1 of 1, from 9 to 994: score 430.2, E = 3.3e-126
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        i     + v  +      L +   L+ D +  +L+    +d  E
  gi|1240267     9    NISNHSTVCVEDQDP-GSLLQQRLELVEDLWKTVLKSECPPDQTERL 54

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls      +D +    +   +t +d a+ai  A+a++    L n+
  gi|1240267    55 LRLKQLSDPSKSNQDNSS-KAIVQLITKMDLAEAISAARAFSLYFQLVNI 103

                    AEEv..elAyRRRikkkkhGDFaDE.........asAttEsDiEEtlKkL
                     E   +e  y   i+k k  D +  + ++  +  as t  +     + +L
  gi|1240267   104 LEQRieEDSYLESIEKGK-LDTSNYkidpfapalASQTAPATFTQLFERL 152

                    vlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL
                      +ln  P+     ++   + Lv+tAHPt  vR  +  K+ R+   L qL
  gi|1240267   153 -RRLNVPPAQLDGLMREMDIRLVFTAHPTEIVRHTVRHKQRRVATLLQQL 201

                    sAKDvtveDKkELDEA.LHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiH
                        +  e  kE+   +L  Ei   +RtDE+   +Pt  DE+ + + Y+
  gi|1240267   202 QSNSLISESEKEIFRLqLEEEIRLWWRTDELHQFKPTVLDEVDYALHYFQ 251

                    EtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPR
                      +++ +P+  RR  tAL        +P ++    F sW+G DRDG nP
  gi|1240267   252 QVLFDAMPQLRRRLTTALASSYPDVEIPNEA-FCTFGSWVGSDRDG-NPS 299

                    vtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyr
                    vtPE+t       R +    Yi  v DL   ls+    + +     E
  gi|1240267   300 VTPEITWRTACYQRQLMLDRYIASVQDLRDQLSISMQWSQVSSPLLESLE 349

                    taardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtG.
                      +       Y E        EPYR  L    ++L  t  R + L   G
  gi|1240267   350 MDRVR-FPEVYEERAARY-RLEPYRLKLSYTLERLRLTQLRNKQLADAGw 397

                    .is.....eis......EeAvytkvEeFLEPLELCYksLCeCGDkviADG
                    ++s++++++is++++ +E   y  vEe    LEL   sL       +
  gi|1240267   398 qFSpdgkpQIStnnsfdEVLHYKSVEELKNELELIRNSLVSTD---LTCE 444

                    sLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsE
                     L  lL qv  FG sL  LDiRqEs R+ D lD +t+ L+++ sY   sE
  gi|1240267   445 PLDTLLNQVHIFGFSLASLDIRQESTRHSDALDELTRYLDLpESYGVMSE 494

                    eKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGa..
                    e R  WL+ EL+ +RPL+++        ++ +  f++L  L  + FG +
  gi|1240267   495 ESRVQWLMKELRTRRPLIPPSFEWSKSTQETISVFHMLHRLQKE-FGTri 543

                    ...YiismataPsDvLAvELLqRECgvkqt......LrvvPLFEkLADLe
                     ++Y+ism+ + sD L v LL +E g+  ++ + ++L vvPLFE + DL+
  gi|1240267   544 crsYVISMSHTASDLLEVLLLAKESGLIDPtlgasdLLVVPLFETVEDLQ 593

                    AAPAavekLFsiDWYin...ridGK....qevmvGYsDsGKDAGRlsAAW
                     AP  +e L   D Y+   +r+  K+++ qe m+GYsDs KD G ls  W
```

```
  gi|1240267   594 HAPSVMESLLQSDVYREllpRVGEKkqplQELMLGYSDSNKDSGFLSSNW 643

                   qLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtin
                    + kAq  +   A + G+ L +FHGRGG vGRGGGP   AiL+qP  t++
  gi|1240267   644 EIHKAQIALQDLASRQGIALRIFHGRGGSVGRGGGPAYQAILAQPSGTLQ 693

                   GslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP.vsPkPEWR
                   G +++t qGEv+   +   +L    L   t A +   +   ++   P W
  gi|1240267   694 GRIKITEQGEVLASKYSLPELALYNLETVTTAVIQNSLVTNkLDATPSWN 743

                   kLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRk
                   +Lm ++A    E YR++v   P  v +F + tP  E  k+ i sRPa+Rk
  gi|1240267   744 ELMTRLAARSREHYRALVHDNPDLVQFFQVVTPIEEISKLQISSRPARRK 793

                   PsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLk
                    + + + sLRAiPW+F Wtq RF LP W GvG A    ++ D   + +L+
  gi|1240267   794 SGAkDLSSLRAIPWVFGWTQSRFLLPSWFGVGTALATELKADPDQMEMLR 843

                   EmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL.vaEeLkPFG...ks
                    + + WPFFR+ +  +Em   K D  +A  y   L+ +++   F +  +
  gi|1240267   844 MLNQRWPFFRMLISKVEMTLSKVDLDVAHHYVVSLgGSDDRDAFAsifDI 893

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   +  +Y  tk+l+L+i G   lL  DP L+  + LR+  i  L  +q   L
  gi|1240267   894 ISSEYSLTKKLILEITGKSKLLSADPALQLSVNLRNRTIVPLGFLQVALL 943

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KR+RD +     +P++s +   + ++ +    +          L    +L
  gi|1240267   944 KRLRDQN----RQPPISEDVSIDSTQSSRTYSRSE--------LLRGALL 981

                   tmKGiAAGmqntG<-*
                   t+ GiAAGm ntG
  gi|1240267   982 TINGIAAGMRNTG    994

gi|154146888|emb|CAM84131.1|: domain 1 of 1, from 1 to 439: score 430.0, E = 3.9e-126
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ---------------------------------------------- -
```

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                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDv+DAittHL+iGsYR+W+EeKRqEWLl+EL+GKRPLl +DLP+tE
  gi|1541468     1 --HTDVIDAITTHLGIGSYRSWPEEKRQEWLLSELSGKRPLLSPDLPQTE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvl+ f+vLAELP DsFG+YiismataPsDvLAvELLqREC++k++L
  gi|1541468    49 EIADVLGCFHVLAELPRDSFGPYIISMATAPSDVLAVELLQRECHIKEPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFEkLADL+ AP ++e+LFs+DWYinri GKq+vmvGYsDsGKDAG
  gi|1541468    99 PVVPLFEKLADLQSAPESIERLFSMDWYINRIGGKQQVMVGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAW LYkAqE +++vAKky vKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWALYKAQEAMAQVAKKYNVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP+tinGslRvtvqGEviE+sFGEE+LCF++LqRFtAA LEHGm+PP sP
  gi|1541468   199 PPETINGSLRVTVQGEVIEYSFGEEHLCFQALQRFTAASLEHGMHPPTSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++e+A v tEEYRsvv+KEPRFvEYFR+AtPE+EYGk+niGsR
  gi|1541468   249 KPEWRALLDEIAAVSTEEYRSVVMKEPRFVEYFRSATPETEYGKLNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkP GGiesLRAiPWiF+WtqtRFHLPvWLG+GAAF hA++KDiKn+
  gi|1541468   299 PAKRKPKGGIESLRAIPWIFSWTQTRFHLPVWLGFGAAFEHAMKKDIKNF 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+LkEmY+eWPFFRvtlDLlEmv AKGDP iA+LyD+LLvaEeLkPFG +
  gi|1541468   349 QMLKEMYNEWPFFRVTLDLLEMVLAKGDPTIAGLYDELLVAEELKPFGAQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++YvE ++l+L++ GHk++LE DP LKq+lRLRd+Yit
  gi|1541468   399 LRENYVESEKLILQVIGHKEILESDPGLKQQLRLRDPYITI--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|119487042|ref|ZP_01620914.1|: domain 1 of 1, from 3 to 1038: score 428.1, E = 1.4e-125
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLk.Ea
                       s+      +    vs +  L e D LL  + L i+ DL    L++E
  gi|1194870     3    SLLHPSDQVSNKIVSSNGTLTESDLLLRNR-LKIVEDLWESVLRqEC 48

                    vqECYElsAeY......EGKkDtkKLeELGakLtsLdPaDailvAkailH
                     qE  +l  + ++ +++EG+    +   +   +  Ld  ++i  A+a+
  gi|1194870    49 GQELVDLLNQMrsmtspEGQASHFQESNVLQLVEQLDINESIRAARAFAL 98

                    mLnLAnLAE......EvelAyRRRikkkkhGDF.aDEasAttE.......
                       L n+ E++ +++E + Ay +  +  k   F+aD  +   E+++++ +
  gi|1194870    99 YFQLINIVEqhyeqrEQQQAYTKGLSTEKQPLFpADQKNSVFEtrnqrfs 148

                    .........sDiE.........EtlKkL..vlklnKsPeEvFeAL.Knqs
                    ++++ + + sDi  +++++++  t+  L ++l+    P    + L  n
  gi|1194870   149 dereyplnlSDISaksqteqelATFHYLfpMLRSLNVPSQLIQRLiDNLD 198

                    vDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv....eDK.....
                    v Lv+tAHPt  vR  +  K+ Ri   L qL   D   ++ +e K+++++
  gi|1194870   199 VRLVFTAHPTEIVRHTIRTKQRRIAKVLQQLDNVDQNTsslsENKthdqt 248

                    .......kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvW
                    ++ ++ + EL E L  Ei   +RtDE+   +Pt  DE+ + + Y+ E ++
  gi|1194870   249 stlsswtDELYEQLTEEIRLWWRTDELHQFKPTVLDEVDYTLHYFQEVLF 298

                    kGvPKFLRRvDtALKniGinERlPYdvP....LikFssWmGGDRDGknPR
                    + +P+   R+  AL         PY  P++ +  kF sW+G DRDG nP
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  gi|1194870   299 DAIPQLYQRIKHALHA-----SFPYLKPprydFCKFGSWVGADRDG-NPS 342

                   vtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyr
                   vtPEvt       R +    Yi  vE L   ls+    +++     El
  gi|1194870   343 VTPEVTWRTACYQRHLVLEKYIGAVEYLNGLLSLSLHWSDV---LPELLE 389

                   taardkvvKyYiEFWKqvP.PtEPYRviLGdvRDKLYntRERaRHLLAtG
                      rd+v    i     +   +EPYR  L  v  +L ntR+R   L
  gi|1194870   390 ALDRDRVQLPEIYDKLAIRyRQEPYRLKLAYVQKRLENTRDRNWRLYNSD 439

                   iseisEe.........AvytkvEeFLEPLELCYksLCeCGDkviADGsL
                      +  e+  +++++ +  y    eFL+ L L  + L e G   i    L
  gi|1194870   440 DVTLEREklvspdksmgSFYQSGSEFLDELTLIQRNLHETG---IECRDL 486

                   LDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei..GsYReWsEe
                    DlL qv  +G sL +LD+RqEs  +   l  i   Lei + sY e sE
  gi|1194870   487 EDLLCQVQIYGFSLARLDMRQESSVHSNALSEIADYLEIlpKSYNELSEA 536

                   KRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGa...
                    R  WL +EL+ +RPL++s+LP  E   + +++fr++ +L  + FG++
  gi|1194870   537 ERSLWLSTELQTRRPLIPSELPFSEKTCETIQTFRMMRDLQRE-FGPeic 585

                   ..YiismataPsDvLAvELLqRECgvkqt......LrvvPLFEkLADLeA
                   ++Yiism+   sD L v LL +E g+  + ++ ++L+vvPLFE + DL+
  gi|1194870   586 qtYIISMSHEVSDLLEVLLLAKEAGLYDSatgipnLQVVPLFETVEDLKR 635

                   APAavekLFsiDWYinridG.................KqevmvGYsDsGKD
                   AP  ++ LF +  Y+  + G+ ++ +++++++ +++ qe+m+GYsDs KD
  gi|1194870   636 APIVMKNLFDLPLYRAMLGGgyehyqsnntpeldrsLQEIMLGYSDSNKD 685

                   AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                    G ls  W + kAq  + KvA  y v L +FHGRGG vGRGGGP   AiL
  gi|1194870   686 SGFLSSNWEIHKAQKALQKVAESYNVSLRIFHGRGGSVGRGGGPAYKAIL 735

                   sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHG.mnPP
                   +qP   i G +++t qGEv+   +   +L    L     A +    ++
  gi|1194870   736 AQPGKSISGRIKITEQGEVLASKYSLPQLALYNLESVSTAVIQASlLHTG 785

                   vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                         W ++mee+ v     YR++++  P  vE+F   tP  E  ++ i
  gi|1194870   786 FDEIETWNQIMEELSVKSRSHYRALIYEQPDLVEFFDQVTPIQEISQLQI 835

                   GsRPaKRkPs..GGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidK
                    sRP++R   ++  i  LRAiPW+F+Wtq RF LP W GvGAA +  ++K
  gi|1194870   836 SSRPSRRSGDkkKDISGLRAIPWVFSWTQSRFLLPSWYGVGAALQEFVQK 885

                   D.iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva.Ee
                   ++   ++ L+  Y +WPFFR t+  +Em  AK D  iA  y + L a+E+
  gi|1194870   886 EpEEHIKLLRYFYYKWPFFRTTISKVEMTLAKVDMQIAHHYVRELSArED 935

                   LkPFG...ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYit
                   L  F    +++ ++++ t++l+L+i  H  lL+GDP L+  + LR+  i
  gi|1194870   936 LARFEvlyEQISQEFQLTRQLVLEITEHERLLDGDPTLQRSVQLRNGTII 985

                   tLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpterv
                    L  +q   LKR+R  ++ v   P +             eL++
  gi|1194870   986 PLGFLQVALLKRLR--QHGVASAPGVIHSRYSKG-----ELLRGA----- 1023

                   aPGLEDtLiLtmKGiAAGmqntG<-*
                           +Lt+ GiAAGm ntG
  gi|1194870  1024 --------LLTINGIAAGMRNTG    1038

gi|75908353|ref|YP_322649.1|: domain 1 of 1, from 47 to 1023: score 428.0, E = 1.5e-125
                   *->siDAqLRlLvP..GKvsedekLieYDALLlDkFLDiLqDLHGe.dLk
                       +  qLR L  ++G+  +d+ +    A+ l   L i   +   +
  gi|7590835    47    DLLRQLRDLCSpeGQATKDQAV---SAVKLIEQLNINEAIRAArAFA 90

                   EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailH...m
                    + q    +  eYE ++   +  +L a    L+ ++ i   +    ++ +
  gi|7590835    91 LYFQLINIIEQEYEQRQQLTRYSDLEAETAPLNGSENITSSSNHNEddvI 140
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                LnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkln
                 n     +     +  R + k++G Fa              l  L +kln
gi|7590835   141 FNRGLGTDFLGKNWTNRGQGKQKGTFA-------------ALFPLLSKLN 177

                KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL.....
                  P+ +   +    v Lv+tAHPt  vR  +  K+  +   L qL++ ++
gi|7590835   178 VPPQQIQRLISQLDVRLVFTAHPTEIVRHTIRDKQRQVVDLLQQLdeven 227

                sAKDvt..veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYi
                 AK+  + + +  E+ E L  Ei   +RtDE+   +Pt  DE+ + + Y+
gi|7590835   228 RAKEGGgyPWEAGEIREKLLEEIRLWWRTDELHQFKPTVLDEVDYALHYF 277

                HEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknP
                 E +++G+P+  +R   AL n       P       F sW+G DRDG nP
gi|7590835   278 QEVLFDGIPQLYKRFKYAL-NQTFSWLEPPSKDFCSFGSWVGSDRDG-NP 325

                RvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndEL...RvRAE
                 vtPE+t       R m    Yi  v  L+  ls+    +++ ++
gi|7590835   326 SVTPEITWQTACYQRKMVLERYIKSVKQLIELLSISMHWSDVlpdLLESL 375

                ElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLL
                El +   ++ v       ++q    EPYR  L  v  +L ntR+R   L
gi|7590835   376 ELDQSQLSE-VYDALALRYRQ----EPYRLKLAYVLKRLENTRDRNLALY 420

                AtGiseisEeA.vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                 +G     E+ ++y    eFL  L L  + L e G   +    L  l+ q
gi|7590835   421 -KGETPTNEDSpMYRSGAEFLAELRLIQHNLTETG---LSCRELDNLICQ 466

                vstFGLsLvKLDiRqEseRqtDvlDAittHLei..GsYReWsEeKRqEWL
                v  F   L KLDiRqEs R+ D l  i   L++ +  Y + sEe+R  WL
gi|7590835   467 VEIFDFNLTKLDIRQESTRHSDALNEILDYLQLlpQPYNDLSEEQRVAWL 516

                laELkGKRPLlgsDLPktEEvkDvldafrvL....AELPiDsFGaYiism
                 +EL+ +RPL+ s+LP  +   Dv+ +frv+++ + E  i     Yiism
gi|7590835   517 TTELQTRRPLISSELPFSDKTNDVIKTFRVVrslqQEFGINICQTYIISM 566

                ataPsDvLAvELLqRECgvkq......tLrvvPLFEkLADLeAAPAavek
                +   sDvL v LL +E  +  +    +t++vvPLFE + DL+     + +
gi|7590835   567 CRQVSDVLEVLLLAKEARLFDpaiavgTIQVVPLFETVEDLQRSRSVMRQ 616

                LFsiDWYinridG..........................KqevmvGYsD
                LF +  Y+  + G+ ++++ + +++++++ +++++  +++ qevm+GYsD
gi|7590835   617 LFELPLYRALLAGgykstevkvpspestplptphsvltpdLQEVMLGYSD 666

                sGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtH
                s KD G ls  W + kAq  + K+A +yGv L +FHGRGG vGRGGGP H
gi|7590835   667 SNKDSGFLSSNWEIHKAQKSLQKIAEEYGVNLRIFHGRGGSVGRGGGPAH 716

                LAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm
                 AiL+qP   inG +++t qGEv+   +   +L    L   t A +   +
gi|7590835   717 EAILAQPGHSINGRIKITEQGEVLASKYSLLDLALYNLETITTAVIQASL 766

                nPPvsPkPE.WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYG
                        E+W ++mee+A      YR +++  P F+++F   tP  E
gi|7590835   767 LRTGFDDIEpWNEIMEELAARSRQHYRGLIYEQPDFIDFFHQVTPIEEIS 816

                kmniGsRPaKRkPsG..GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKh
                ++ i sRPa R+PsG++ + sLRAiPW+F+WtqtRF LP W GvG A +
gi|7590835   817 QLQISSRPA-RRPSGkkDLSSLRAIPWVFSWTQTRFLLPSWYGVGTALQE 865

                AidKD.iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLy.DkLL
                  + ++   l+ ++  Y +WPFF++ +  +Em  AK D  +A+ y  +L
gi|7590835   866 FFNEEpEEHLKLMRYFYVKWPFFKMVISKVEMTLAKVDMQMAGHYvQELS 915

                vaEeLkPFG...ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRd
                  E+   F +  +++ ++Y  t+dl+Lki  H  lL+GDP L+  + LR+
gi|7590835   916 DPEDKSRFEkvfEQIANEYYLTRDLVLKITDHSRLLDGDPVLQRSVQLRN 965

                sYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnp
                  i  L  +q   LKR+R            sK   +       ++++
gi|7590835   966 GTIVPLGFIQVSLLKRLRQ-----------SKNNNATS-----GVIH--- 996
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                    tervaPG.LEDtLiLtmKGiAAGmqntG<-*
                     +r++ G+L    +Lt+ GiAAGm ntG
  gi|7590835   997 -SRYSKGeLLRGALLTINGIAAGMRNTG    1023

gi|161353735|ref|NP_488901.2|: domain 1 of 1, from 47 to 1026: score 425.8, E = 6.6e-125
                    *->siDAqLRlLvP..GKvsedekLieYDALLlDkFLDiLqDLHGe.dLk
                        +  qLR L  ++G+  +d+ +    A+ l   L i   +   +
  gi|1613537    47    DLLRQLRDLCSpeGQATKDQAV---SAVKLIEQLNINEAIRAArAFA 90

                    EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailH...m
                     + q    +  eYE ++   +  +L a    L+ ++ i   +    ++ +
  gi|1613537    91 LYFQLINIIEQEYEQRQQLTRYSDLEAETAPLNGSENITSSSNHNEddvI 140

                    LnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkln
                     n     +     +  R + k++G Fa              l  L +kln
  gi|1613537   141 FNRGLGTDFLGKNWTNRGQGKQKGTFA-------------ALFPLLSKLN 177

                    KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL.....
                      P+ +   +    v Lv+tAHPt  vR  +  K+  +   L qL++ ++
  gi|1613537   178 VPPQQIQRLISQLDVRLVFTAHPTEIVRHTIRDKQRQVVDLLQQLdeven 227

                    sAKDvt..veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYi
                     AKD  + + +  E+ E L  Ei   +RtDE+   +Pt  DE+ + + Y+
  gi|1613537   228 RAKDGGgyPWEAGEIREKLLEEIRLWWRTDELHQFKPTVLDEVDYALHYF 277

                    HEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknP
                     E +++G+P+  +R   AL n       P       F sW+G DRDG nP
  gi|1613537   278 QEVLFDGIPQLYKRFKYAL-NQTFSWLEPPSKDFCSFGSWVGSDRDG-NP 325

                    RvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndEL...RvRAE
                     vtPE+t       R m    Yi  v  L+  ls+    +++ ++
  gi|1613537   326 SVTPEITWQTACYQRKMVLERYIKSVTQLIELLSISMHWSDVlpdLLESL 375

                    Elyrtaardkvv KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLL
                    El +   ++ v       ++q    EPYR  L  v  +L ntR+R   L
  gi|1613537   376 ELDQSQLSE-VYDALALRYRQ----EPYRLKLAYVLKRLENTRDRNLALY 420

                    AtGiseisEeA.vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                     +G     E+ ++y    eFL  L L  + L e G   +    L  l+ q
  gi|1613537   421 -KGETPTNEDSpMYRSGSEFLAELRLIQHNLTETG---LSCRELDNLICQ 466

                    vstFGLsLvKLDiRqEseRqtDvlDAittHLei..GsYReWsEeKRqEWL
                    v  F   L KLDiRqEs R+ D l  i   L++ +  Y + sEe+R  WL
  gi|1613537   467 VEIFDFNLTKLDIRQESTRHSDALNEILDYLQLlpQPYNDLSEEQRVAWL 516

                    laELkGKRPLlgsDLPktEEvkDvldafrvL....AELPiDsFGaYiism
                     +EL+ +RPL+ s+LP  +   Dv+ +frv+++ + E  i     Yiism
  gi|1613537   517 TTELQTRRPLISSELPFSDKTNDVIKTFRVVrslqQEFGINICQTYIISM 566

                    ataPsDvLAvELLqRECgvkq......tLrvvPLFEkLADLeAAPAavek
                    +   sDvL v LL +E  +  +    +t++vvPLFE + DL+     + +
  gi|1613537   567 CRQVSDVLEVLLLAKEARLFDpaiavgTIQVVPLFETVEDLQRSRSVMRQ 616

                    LFsiDWYinridG.............................KqevmvG
                    LF +  Y+  + G+ ++++ + ++++ +++++ +++++  +++ qevm+G
  gi|1613537   617 LFELPLYRALLAGgykntevkvpnteltpqspapspqsvltpdLQEVMLG 666

                    YsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGG
                    YsDs KD G ls  W + kAq  + ++A +yGv L +FHGRGG vGRGGG
  gi|1613537   667 YSDSNKDSGFLSSNWEIHKAQKSLQQIAEEYGVNLRIFHGRGGSVGRGGG 716

                    PtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLE
                    P H AiL+qP   inG +++t qGEv+   +   +L    L   t A +
  gi|1613537   717 PAHEAILAQPGHSINGRIKITEQGEVLASKYSLLDLALYNLETITTAVIQ 766

                    HGmnPPvsPkPE.WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPEl
                      +        E+W ++mee+A      YR +++  P F+++F   tP
  gi|1613537   767 ASLLRTGFDDIEpWNEIMEELAARSRQHYRGLIYEQPDFIDFFHQVTPIE 816

                    EYGkmniGsRPaKRkPsG..GiesLRAiPWiFaWtqtRFHLPvWLGvGAA
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                    E  ++ i sRPa R+PsG++ + sLRAiPW+F+WtqtRF LP W GvG A
  gi|1613537   817 EISQLQISSRPA-RRPSGkkDLSSLRAIPWVFSWTQTRFLLPSWYGVGTA 865

                    FKhAidKD.iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDk
                     +   + ++   l+ ++  Y +WPFF++ +  +Em  AK D  +A+ y +
  gi|1613537   866 LQEFFNEEpEEHLKLMRYFYVKWPFFKMVISKVEMTLAKVDMQMAGHYVQ 915

                    LLvaEeLkP....FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                     L   e kP+ ++  +++ ++Y  t+dl+Lki  H  lL+GDP L+  +
  gi|1613537   916 ELSDPEDKPrfekVFEQIANEYYLTRDLVLKITDHGRLLDGDPVLQRSVQ 965

                    LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                    LR+  i  L  +q   LKR+R            sK   +       ++++
  gi|1613537   966 LRNGTIVPLGFIQVSLLKRLRQ-----------SKNNTATS-----GVIH 999

                    LnptervaPG.LEDtLiLtmKGiAAGmqntG<-*
                        +r++ G+L    +Lt+ GiAAGm ntG
  gi|1613537  1000 ----SRYSKGeLLRGALLTINGIAAGMRNTG    1026

gi|142080|gb|AAA22023.1|: domain 1 of 1, from 3 to 982: score 425.8, E = 6.6e-125
                    *->siDAqLRlLvP..GKvsedekLieYDALLlDkFLDiLqDLHGe.dLk
                        +  qLR L  ++G+  +d+ +    A+ l   L i   +   +
  gi|142080|     3    DLLRQLRDLCSpeGQATKDQAV---SAVKLIEQLNINEAIRAArAFA 46

                    EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailH...m
                     + q    +  eYE ++   +  +L a    L+ ++ i   +    ++ +
  gi|142080|    47 LYFQLINIIEQEYEQRQQLTRYSDLEAETAPLNGSENITSSSNHNEddvI 96

                    LnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkln
                     n     +     +  R + k++G Fa              l  L +kln
  gi|142080|    97 FNRGLGTDFLGKNWTNRGQGKQKGTFA-------------ALFPLLSKLN 133

                    KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL.....
                      P+ +   +    v Lv+tAHPt  vR  +  K+  +   L qL++ ++
  gi|142080|   134 VPPQQIQRLISQLDVRLVFTAHPTEIVRHTIRDKQRQVVDLLQQLdeven 183

                    sAKDvt..veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYi
                     AKD  + + +  E+ E L  Ei   +RtDE+   +Pt  DE+ + + Y+
  gi|142080|   184 RAKDGGgyPWEAGEIREKLLEEIRLWWRTDELHQFKPTVLDEVDYALHYF 233

                    HEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknP
                     E +++G+P+  +R   AL n       P       F sW+G DRDG nP
  gi|142080|   234 QEVLFDGIPQLYKRFKYAL-NQTFSWLEPPSKDFCSFGSWVGSDRDG-NP 281

                    RvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndEL...RvRAE
                     vtPE+t       R m    Yi  v  L+  ls+    +++ ++
  gi|142080|   282 SVTPEITWQTACYQRKMVLERYIKSVTQLIELLSISMHWSDVlpdLLESL 331

                    Elyrtaardkvv KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLL
                    El +   ++ v       ++q    EPYR  L  v  +L ntR+R   L
  gi|142080|   332 ELDQSQLSE-VYDALALRYRQ----EPYRLKLAYVLKRLENTRDRNLALY 376

                    AtGiseisEeA.vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                     +G     E+ ++y    eFL  L L  + L e G   +    L  l+ q
  gi|142080|   377 -KGETPTNEDSpMYRSGSEFLAELRLIQHNLTETG---LSCRELDNLICQ 422

                    vstFGLsLvKLDiRqEseRqtDvlDAittHLei..GsYReWsEeKRqEWL
                    v  F   L KLDiRqEs R+ D l  i   L++ +  Y + sEe+R  WL
  gi|142080|   423 VEIFDFNLTKLDIRQESTRHSDALNEILDYLQLlpQPYNDLSEEQRVAWL 472

                    laELkGKRPLlgsDLPktEEvkDvldafrvL....AELPiDsFGaYiism
                     +EL+ +RPL+ s+LP  +   Dv+ +frv+++ + E  i     Yiism
  gi|142080|   473 TTELQTRRPLISSELPFSDKTNDVIKTFRVVrslqQEFGINICQTYIISM 522

                    ataPsDvLAvELLqRECgvkq......tLrvvPLFEkLADLeAAPAavek
                    +   sDvL v LL +E  +  +    +t++vvPLFE + DL+     + +
  gi|142080|   523 CRQVSDVLEVLLLAKEARLFDpaiavgTIQVVPLFETVEDLQRSRSVMRQ 572

                    LFsiDWYinridG.............................KqevmvG
                    LF +  Y+  + G+ ++++ + ++++ +++++ +++++  +++ qevm+G
  gi|142080|   573 LFELPLYRALLAGgykntevkvpnteltpqspapspqsvltpdLQEVMLG 622
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                    YsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGG
                    YsDs KD G ls  W + kAq  + ++A +yGv L +FHGRGG vGRGGG
  gi|142080|   623 YSDSNKDSGFLSSNWEIHKAQKSLQQIAEEYGVNLRIFHGRGGSVGRGGG 672

                    PtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLE
                    P H AiL+qP   inG +++t qGEv+   +   +L    L   t A +
  gi|142080|   673 PAHEAILAQPGHSINGRIKITEQGEVLASKYSLLDLALYNLETITTAVIQ 722

                    HGmnPPvsPkPE.WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPEl
                      +        E+W ++mee+A      YR +++  P F+++F   tP
  gi|142080|   723 ASLLRTGFDDIEpWNEIMEELAARSRQHYRGLIYEQPDFIDFFHQVTPIE 772

                    EYGkmniGsRPaKRkPsG..GiesLRAiPWiFaWtqtRFHLPvWLGvGAA
                    E  ++ i sRPa R+PsG++ + sLRAiPW+F+WtqtRF LP W GvG A
  gi|142080|   773 EISQLQISSRPA-RRPSGkkDLSSLRAIPWVFSWTQTRFLLPSWYGVGTA 821

                    FKhAidKD.iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDk
                     +   + ++   l+ ++  Y +WPFF++ +  +Em  AK D  +A+ y +
  gi|142080|   822 LQEFFNEEpEEHLKLMRYFYVKWPFFKMVISKVEMTLAKVDMQMAGHYVQ 871

                    LLvaEeLkP....FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                     L   e kP+ ++  +++ ++Y  t+dl+Lki  H  lL+GDP L+  +
  gi|142080|   872 ELSDPEDKPrfekVFEQIANEYYLTRDLVLKITDHGRLLDGDPVLQRSVQ 921

                    LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                    LR+  i  L  +q   LKR+R            sK   +       ++++
  gi|142080|   922 LRNGTIVPLGFIQVSLLKRLRQ-----------SKNNTATS-----GVIH 955

                    LnptervaPG.LEDtLiLtmKGiAAGmqntG<-*
                        +r++ G+L    +Lt+ GiAAGm ntG
  gi|142080|   956 ----SRYSKGeLLRGALLTINGIAAGMRNTG    982

gi|124023967|ref|YP_001018274.1|: domain 1 of 1, from 22 to 1002: score 425.7, E = 7.1e-125
                    *->siDAqLRlLvPGKvsedekLieYDALLl.DkFLDiLqDLHGedLkEa
                           q R++  G+ +   +L++    L++D +  +L     +d  E
  gi|1240239    22    ---DQPRAIGEGQQA--GRLLQNRLELVeDLWQTVLRSECPPDQAER 63

                    vqECYEls..AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                          ls++   EG  + +    +   +  +d a+ai  A+a++    L
  gi|1240239    64 LLRLKQLSepLALEGADENSASTAIVLLIKEMDLAEAITAARAFSLYFQL 113

                    AnLAEE.ve....lAyRRRikkkkhGD.....FaDEasAttE.sDiEEtl
                     n+ E ++e+++ lA     k     D++ ++Fa      t+++   E +
  gi|1240239   114 VNILEQrIEedsyLASMSSGKENNRQDkpydpFAPPLATQTDpATFSELF 163

                    KkLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL
                     +L l+    P+     L+   + Lv+tAHPt  vR  +  K+ ++ n L
  gi|1240239   164 ERLRLLN-VPPAQLETLLQEMDIRLVFTAHPTEIVRHTVRHKQRKVANLL 212

                    aqLsAKDvtveDKkE.LDEALHREiqAAFRtDEiRRaqPtPqDEmRaGms
                     qL          kE+L   L  Ei   +RtDE+   +P   DE+ + +
  gi|1240239   213 QQLQSDPTKSSSEKEsLRLQLEEEIRLWWRTDELHQFKPSVLDEVDYALH 262

                    YiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGk
                    Y+   +++ +P+  RR  tA+        +P ++    F sW+G DRDG
  gi|1240239   263 YFQQVLFDAMPQLRRRLITAMAESYPDVHIP-QAAFCTFGSWVGSDRDG- 310

                    nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEE
                    nP vtPE+t       R +    Y++ v  L   ls+    + +     E
  gi|1240239   311 NPSVTPEITWRTACYQRQLMLERYVNAVQKLRDQLSISMQWSQVSTPLLE 360

                    lyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLA
                         +       Y E        EPYR  L    ++L  t ER   L
  gi|1240239   361 SLEMDRLR-FPEVYEERAARY-RLEPYRLKLSYTLERLKLTQERNQQLAE 408

                    tGiseisE............eAv.ytkvEeFLEPLELCYksLCeCGDkvi
                     G    +E+ +++ +  + +eA +y  v eF   LEL   sL       +
  gi|1240239   409 AGWQTPPEglnpslnlinagEALhYKSVAEFRSDLELIRNSLVSTD---L 455

                    ADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYRe
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                       L  lL qv  F  sL  LDiRqEs R+ D lD +t+ L+++ +Y +
  gi|1240239   456 SCEPLDTLLNQVHIFAFSLASLDIRQESTRHSDALDELTRYLNLpKAYGD 505

                   WsEeKRqEWLlaELkGKRPLlgsDL...PktEEvkDvldafrvLA.ELPi
                    +E+ R  WL+ EL+ +RPL++s +  +P t E   v   ++ L +E  +
  gi|1240239   506 MAENERVQWLIEELQTRRPLIPSAViwsPSTAETVAVFRMLHRLQeEFGS 555

                   DsFGaYiismataPsDvLAvELLqRECgvkqt......LrvvPLFEkLAD
                        Y+ism+ + sD L v LL +E g+  +  ++ +L vvPLFE + D
  gi|1240239   556 RICRTYVISMSHTVSDLLEVLLLAKEAGLVDPaaghaeLLVVPLFETVED 605

                   LeAAPAavekLFsiDWYin.......ridGKqevmvGYsDsGKDAGRlsA
                   L+ APA +e L s   Y+n  ++ +++++  qe m+GYsDs KD G ls
  gi|1240239   606 LQRAPAVMEALLSSPVYRNllprvseQVQPLQELMLGYSDSNKDSGFLSS 655

                   AWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDt
                    W + +Aq  +   A + Gv L lFHGRGG vGRGGGP   AiL+qP  t
  gi|1240239   656 NWEIHQAQIALQDLANRQGVALRLFHGRGGSVGRGGGPAYQAILAQPSGT 705

                   inGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsPkPE
                   + G +++t qGEv+   +   +L    L  Ft A L   +    +   P
  gi|1240239   706 VRGRIKITEQGEVLASKYSLPELALYNLETFTTAVLQNSLvTNQLDATPS 755

                   WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaK
                   W +Lm ++A    E YR++v   P  v +F   tP  E  k+ i sRPa+
  gi|1240239   756 WNQLMTRLAGRSREHYRALVHNNPDLVAFFQQVTPIEEISKLQISSRPAR 805

                   RkPsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqk
                   Rk + + + sLRAiPW+F Wtq RF LP W GvG A    ++ D   l
  gi|1240239   806 RKSGAkDLSSLRAIPWVFGWTQSRFLLPSWFGVGTALAAEVESDADQLDL 855

                   LkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP....FG
                   L+ + + WPFFR+ +  +Em   K D  +A  y   L +E+ +   ++
  gi|1240239   856 LRRLHQRWPFFRMLISKVEMTLSKVDLDLAHHYMTSLGSEDYREafnrIF 905

                   ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                   + +  +Y  t+ l+L i G   lL  DP L+q + LR+  i  L  +q
  gi|1240239   906 EIIETEYSLTRRLVLNITGQPRLLGADPALQQSVDLRNRTIVPLGFLQVA 955

                   tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    L+++RD +     +P++  E  d  +    eL++
  gi|1240239   956 LLRKLRDQN----RQPPM-NEAGDGRTYSRSELLRGA------------- 987

                   iLtmKGiAAGmqntG<-*
                   +Lt+ GiAAGm ntG
  gi|1240239   988 LLTINGIAAGMRNTG    1002

gi|154146892|emb|CAM84133.1|: domain 1 of 1, from 1 to 439: score 425.6, E = 7.7e-125
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ---------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ---------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ---------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ---------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ---------------------------------------------------- -
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                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------ -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------ -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------ -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDv+DAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLl  D+P+tE
  gi|1541468     1 --HTDVIDAITTHLGIGSYREWPEEKRQEWLLSELRGKRPLLSKDMPQTE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvl+ f+vLAEL  DsFG+YiismataPsDvLAvELLqREC vkq+L
  gi|1541468    49 EIADVLGCFHVLAELLRDSFGPYIISMATAPSDVLAVELLQRECNVKQPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFEkLADL+ APA+ve+LFs+DWY nri GKq+vmvGYsDsGKDAG
  gi|1541468    99 PVVPLFEKLADLQSAPASVERLFSLDWYLNRIGGKQQVMVGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAW LY AqE ++KvAK+yGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWALYTAQEAMAKVAKRYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGslRvt+qGEviE+sFGEE+LCF++LqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTINGSLRVTIQGEVIEYSFGEEHLCFQTLQRFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+e+  vAt+EYRsvv++EPRFvEYFR+AtPE+EYG++niGsR
  gi|1541468   249 KPEWRALMDEITAVATDEYRSVVMREPRFVEYFRSATPETEYGRLNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkP GGiesLRAiPWiF+Wtq RF LPvWLG+GAAFKhA++KDiKn+
  gi|1541468   299 PAKRKPKGGIESLRAIPWIFSWTQNRFNLPVWLGFGAAFKHAMNKDIKNF 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q LkEmY+eWPFFRvtlDL+Emv AKGDP iA+LyD+LLva+e+kPFG++
  gi|1541468   349 QILKEMYNEWPFFRVTLDLIEMVLAKGDPTIAGLYDQLLVADEIKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++YvEt++l+L++ GHk++LEGDP LKq+lRLRd+Yit
  gi|1541468   399 LRNNYVETEKLILQVLGHKEILEGDPGLKQQLRLRDPYITI--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------ -

                    tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|261409477|ref|YP_003245718.1|: domain 1 of 1, from 1 to 928: score 425.2, E = 1e-124
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                            +  L     s+ ++L++ D   l   L+++L    G++L ++
  gi|2614094     1    -----MTELTVTAKSNSNNLLRRDVRFLGNILgEVLVHQGGNELLDI 42

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v    E s        ++   +    +  L+P     v +a+     L n
  gi|2614094    43 VEKIRETSKSLRSVFLPELFADFKRIISTLEPDIRHQVIRAFAIYFQLVN 92

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R+R   +  G+    +s      iE  ++ L  +   + eE
  gi|2614094    93 IAEQNHRIRRKRDYERSAGESVQPGS------IESAVQDLKERN-ITFEE 135

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
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                    v e L   s +Lv+tAHPt + RR++L  + Ri   + qL    +t  ++
  gi|2614094   136 VQEILESLSLELVMTAHPTEAMRRAILDIHKRIADDVMQLDNPTLTFRER 185

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + L E L  E+   + tDE+R  +Pt  DE+R Gm Y+HEt+++  P
  gi|2614094   186 EQLREKLLNEVITLWQTDELRDRKPTVLDEVRNGMYYFHETLFHILPEVY 235

                    RRvDtALKni..GinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                       +  L    +G    +P     ++F sW+GGDRDG nP vt +vt
  gi|2614094   236 QELERCLTKYypGHHWHVP---TYLRFGSWIGGDRDG-NPSVTADVTWRT 281

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaa.rdkvv
                      + R +A   Y   + + m  ls     + + v  E l++  ++r++v+
  gi|2614094   282 LEMQRKLAIREYQRILREFMKYLSF--SSSIVNVSDELLQSIEKdREHVT 329

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                       +E W      EPYRv       KL     +  H+L     ++
  gi|2614094   330 LKKMEIWHN--EKEPYRV-------KLVYMLAKMSHILDE---NMTGGER 367

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y   EeF+E L +  +sL       +AD  +  l+Rq   FG     LDi
  gi|2614094   368 YQTPEEFIEDLKIIDRSLRFHFADYVADTYIQKLIRQAELFGFHTATLDI 417

                    RqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgsD
                    Rq s+ +   +  i + +++  +Y + sE+ + E L   L   RPL  +
  gi|2614094   418 RQHSQEHENAMAEILRKMNVTQdYAQLSEDEKIELLNNLLNDPRPLTTPY 467

                    LPk...tEEvkDvlda.frvLAELPiDsFGaYiismataPsDvLAvELLq
                       +++tEE  +v  + fr   E  + +  +Y+isma   sD+L v +
  gi|2614094   468 QEYsdsTEECLEVYRTvFRAQQEFGVKCISSYLISMAEGASDILEVMVFA 517

                    RECg.........vkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                    +E g  +++++++v  tL+  PLFE + DL+AAP  + kLFs+  Y+  +
  gi|2614094   518 KEVGlfrkdndgsVIATLQAAPLFETIDDLHAAPDIMRKLFSLPIYREAV 567

                    ...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                    +  +  qe+m+GYsDs KD G + A W L +A  Ei  vA ++G+K+  F
  gi|2614094   568 samNELQEIMLGYSDSNKDGGAITANWELQVALKEITAVANEFGIKVKYF 617

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGG  GRGG P    iL+qP  ti G +++t qGEvi   +    + +
  gi|2614094   618 HGRGGSLGRGGMPLNRSILAQPASTIAGGIKITEQGEVISSRYSLKGIAY 667

                    rsLqRFtAAtLEHGmnPPv....sPkPEWRkLmeemAvvAtEEYRsvvvK
                    rsL   t A +   +n   ++++s   EW  +   +  v    Y  ++++
  gi|2614094   668 RSLDQATSALITASLNARYpekeSTEKEWEVISSSISAVSQKKYQDLIFR 717

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                    +P F  +F+  tP  E G +niGsRP+KRk s   e LRAiPW+FaWtq
  gi|2614094   718 DPDFLTFFKESTPLPEVGELNIGSRPSKRKNSDRFEDLRAIPWVFAWTQS 767

                    RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                    R+ LP W   G   +   +    n++ L+ mY  +PFF   +D l m  A
  gi|2614094   768 RYLLPAWYAAGTGLQSFYQGKEENMKVLQQMYTSYPFFTSLIDTLQMALA 817

                    KGDPGiAaLyDkLLvaEeL...kPFGksLRdkYvEtkdlLLkiAGHkDlL
                    K D  iA  y  L+  ++  +++ FG  + ++++ tk+l+Lki G +D+L
  gi|2614094   818 KADLIIAKEY-SLMTKDDQareRIFG-LIQEEFKLTKELVLKITGQQDIL 865

                    EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                    +  P L+  +RLR++Y+  L  +q   L
  gi|2614094   866 DNQPVLQESIRLRNPYVDPLSYLQVQLL---------------------- 893

                    EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     n     eL +L   e+  P L   ++Lt+ GiAAG+ ntG
  gi|2614094   894 -N-----ELRELREQEQDDPDLLREVLLTINGIAAGLRNTG    928

gi|56751855|ref|YP_172556.1|: domain 1 of 1, from 53 to 1053: score 425.0, E = 1.2e-124
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLk.Ea
                       s D   R +       d +L       l + L ++ +L    L++E
  gi|5675185    53    SSDDAFRTVSSPLAT-DLDLSSPLEFFLRHRLTVVEELWEVVLRqEC 98
```

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                vqECYElsAeY......EGKkDtkKLeELGakLtsLdPaDailvAkailH
                 qE  ++  + ++ +++EG+      e L  ++  L+ +Dai  A+a+
gi|5675185    99 GQELVDILTQLrdltspEGQAPEVGGEALVQVIETLELSDAIRAARAFAL 148

                mLnLAnLAE......EvelAyRR.RikkkkhGDFaDEasAttEsDiEE..
                   L n+ E++ +++  +lAy R+R + +   D + E+  t E      +
gi|5675185   149 YFQLINIVEqhyeqtQYQLAYERsRLEPLPGPDESPEGLHTIEIPQHQld 198

                .............tlKkL...vlklnKsPeEvFeALKnqsvDLvltAHPt
                +     + ++++ t++ L ++  +ln  P+ + e      + Lv+tAHPt
gi|5675185   199 pfaaviplnqdpaTFQTLfprLRQLNVPPQMIQELTDRLDIRLVFTAHPT 248

                qsvRRsLLqKnaRiRnCLaqLsAKDvtve......DKkELDEALHREiqA
                  vR  +  K+ Ri   L qL   +   +++ ++ + + +   L  Ei
gi|5675185   249 EIVRHTIRDKQRRIAYLLRQLDELETGKNrgfrelEAQNIRQQLTEEIRL 298

                AFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLRRvDtALKniGin
                 +RtDE+   +Pt  DE+ + + Y+ E +++ +P    R   AL+
gi|5675185   299 WWRTDELHQFKPTVLDEVDYALHYFQEVLFEAIPLLYQRFRLALQGT-FP 347

                ERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLLaRmmAanlYisq
                +  P      +F sW+G DRDG nP vt  vt       R +    Yi
gi|5675185   348 DLQPPRYNFCQFGSWVGSDRDG-NPSVTSAVTWQTACYQRSLVLDRYITA 396

                vEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYiEFWKqvPP...t
                vE L   ls+    +E+     El +   ++     + E + q+  + ++
gi|5675185   397 VEHLRNVLSLSMHWSEV---LPELLSSLEQE--SMLFPETYEQLAVryrQ 441

                EPYRviLGdvRDKLYntRERaRHLL.......AtGiseisEeAvytkvEe
                EPYR  L  + ++L ntR+R   L +++++++ t + e  +   y
gi|5675185   442 EPYRLKLSYILERLHNTRDRNTRLQqqqekdpTTPLPEYRDGTLYQAGTA 491

                FLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseR
                FLE L L  + L + G   +    L  l+ qv  FG  Lv LDiRqEs R
gi|5675185   492 FLEDLKLIQHNLKQTG---LSCYELEKLICQVEIFGFNLVHLDIRQESSR 538

                qtDvlDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                + D +  i + L+i +  Y e sE  R  WL+ ELk +RPL+++ +P  E
gi|5675185   539 HSDAINEICEYLQIlpQPYNELSEAERTAWLVQELKTRRPLVPARMPFSE 588

                EvkDvldafrvLAELPiDsFG.....aYiismataPsDvLAvELLqRECg
                  +++++++r++  L  + FG+   + Yiism+   sD L v LL +E g
gi|5675185   589 STREIIETLRMVKQL-QEEFGeaacqTYIISMSRELSDLLEVLLLAKEVG 637

                v......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYin....ridGK
                + ++ ++k +L+v+PLFE + DL+ AP  +  LF + +Y   ++++ +
gi|5675185   638 LydpvtgKSSLQVIPLFETVEDLQNAPRVMTALFELPFYTQlnptQSEPL 687

                qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                qevm+GYsDs KD G ls  W + kAq  +  vA+++ vKL +FHGRGG
gi|5675185   688 QEVMLGYSDSNKDSGFLSSNWEIHKAQKALGTVARDHRVKLRIFHGRGGS 737

                vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                vGRGGGP   AiL+qP  t +G +++t qGEv+   +   +L    L
gi|5675185   738 VGRGGGPAYEAILAQPGRTTDGRIKITEQGEVLASKYALPELALYNLETI 787

                tAAtLEHGmnPPvsPkPE.WRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                t A +   +        E+W ++mee+A      YR++v+  P  v++F
gi|5675185   788 TTAVIQSSLLGSGFDDIEpWNQIMEELAARSRRHYRALVYEQPDLVDFFN 837

                lAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWL
                  tP  E  k+ i sRPa+Rk ++  + sLRAiPW+F+Wtq RF LP W
gi|5675185   838 QVTPIEEISKLQISSRPARRKTGkRDLGSLRAIPWVFSWTQSRFLLPSWY 887

                GvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiA
                GvG A +++  ++  +nl  L+  Y++WPFFR+ +  +Em  AK D  iA
gi|5675185   888 GVGTALQeFLQERPEQNLNLLRYFYEKWPFFRMVISKVEMTLAKVDLQIA 937

                aLy.DkLLvaEeLkPFGk...sLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                  y  +L   E+   F +  +++ ++++ t  l+L i  H  lL+GDP L
```

```
  gi|5675185   938 HHYvHELANPEDQERFERvfsQIAAEFQLTCHLVLTITNHGRLLDGDPEL 987

                   KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                   +  + LR+  i  L  +q   LKR+R              y +    +
  gi|5675185   988 QRSVQLRNGTIVPLGFLQVALLKRLR-------------QYRQQT--ET 1021

                   deLvkLnptervaPG.LEDtLiLtmKGiAAGmqntG<-*
                    +L++    +r++ G+L    +Lt+ GiAAGm ntG
  gi|5675185  1022 TGLMR----SRYSKGeLLRGALLTINGIAAGMRNTG    1053

gi|81301061|ref|YP_401269.1|: domain 1 of 1, from 17 to 1017: score 425.0, E = 1.2e-124
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLk.Ea
                      s D   R +       d +L       l + L ++ +L    L++E
  gi|8130106    17    SSDDAFRTVSSPLAT-DLDLSSPLEFFLRHRLTVVEELWEVVLRqEC 62

                   vqECYElsAeY......EGKkDtkKLeELGakLtsLdPaDailvAkailH
                    qE  ++  + ++ +++EG+      e L  ++  L+ +Dai  A+a+
  gi|8130106    63 GQELVDILTQLrdltspEGQAPEVGGEALVQVIETLELSDAIRAARAFAL 112

                   mLnLAnLAE......EvelAyRR.RikkkkhGDFaDEasAttEsDiEE..
                      L n+ E++ +++  +lAy R+R + +   D + E+  t E      +
  gi|8130106   113 YFQLINIVEqhyeqtQYQLAYERsRLEPLPGPDESPEGLHTIEIPQHQld 162

                   .............tlKkL...vlklnKsPeEvFeALKnqsvDLvltAHPt
                   +     + ++++ t++ L ++  +ln  P+ + e      + Lv+tAHPt
  gi|8130106   163 pfaaviplnqdpaTFQTLfprLRQLNVPPQMIQELTDRLDIRLVFTAHPT 212

                   qsvRRsLLqKnaRiRnCLaqLsAKDvtve......DKkELDEALHREiqA
                     vR  +  K+ Ri   L qL   +   +++ ++ + + +   L  Ei
  gi|8130106   213 EIVRHTIRDKQRRIAYLLRQLDELETGKNrgfrelEAQNIRQQLTEEIRL 262

                   AFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLRRvDtALKniGin
                    +RtDE+   +Pt  DE+ + + Y+ E +++ +P    R   AL+
  gi|8130106   263 WWRTDELHQFKPTVLDEVDYALHYFQEVLFEAIPLLYQRFRLALQGT-FP 311

                   ERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLLaRmmAanlYisq
                   +  P      +F sW+G DRDG nP vt  vt       R +    Yi
  gi|8130106   312 DLQPPRYNFCQFGSWVGSDRDG-NPSVTSAVTWQTACYQRSLVLDRYITA 360

                   vEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYiEFWKqvPP...t
                   vE L   ls+    +E+     El +   ++     + E + q+  + ++
  gi|8130106   361 VEHLRNVLSLSMHWSEV---LPELLSSLEQE--SMLFPETYEQLAVryrQ 405

                   EPYRviLGdvRDKLYntRERaRHLL.......AtGiseisEeAvytkvEe
                   EPYR  L  + ++L ntR+R   L +++++++ t + e  +   y
  gi|8130106   406 EPYRLKLSYILERLHNTRDRNTRLQqqqekdpTTPLPEYRDGTLYQAGTA 455

                   FLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseR
                   FLE L L  + L + G   +    L  l+ qv  FG  Lv LDiRqEs R
  gi|8130106   456 FLEDLKLIQHNLKQTG---LSCYELEKLICQVEIFGFNLVHLDIRQESSR 502

                   qtDvlDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   + D +  i + L+i +  Y e sE  R  WL+ ELk +RPL+++ +P  E
  gi|8130106   503 HSDAINEICEYLQIlpQPYNELSEAERTAWLVQELKTRRPLVPARMPFSE 552

                   EvkDvldafrvLAELPiDsFG.....aYiismataPsDvLAvELLqRECg
                     +++++++r++  L  + FG+   + Yiism+   sD L v LL +E g
  gi|8130106   553 STREIIETLRMVKQL-QEEFGeaacqTYIISMSRELSDLLEVLLLAKEVG 601

                   v......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYin....ridGK
                   + ++ ++k +L+v+PLFE + DL+ AP  +  LF + +Y   ++++ +
  gi|8130106   602 LydpvtgKSSLQVIPLFETVEDLQNAPRVMTALFELPFYTQlnptQSEPL 651

                   qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                   qevm+GYsDs KD G ls  W + kAq  +  vA+++ vKL +FHGRGG
  gi|8130106   652 QEVMLGYSDSNKDSGFLSSNWEIHKAQKALGTVARDHRVKLRIFHGRGGS 701

                   vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                   vGRGGGP   AiL+qP  t +G +++t qGEv+   +   +L    L
  gi|8130106   702 VGRGGGPAYEAILAQPGRTTDGRIKITEQGEVLASKYALPELALYNLETI 751
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                    tAAtLEHGmnPPvsPkPE.WRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                    t A +   +        E+W ++mee+A      YR++v+  P  v++F
  gi|8130106   752 TTAVIQSSLLGSGFDDIEpWNQIMEELAARSRRHYRALVYEQPDLVDFFN 801

                    lAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWL
                      tP  E  k+ i sRPa+Rk ++  + sLRAiPW+F+Wtq RF LP W
  gi|8130106   802 QVTPIEEISKLQISSRPARRKTGkRDLGSLRAIPWVFSWTQSRFLLPSWY 851

                    GvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiA
                    GvG A +++  ++  +nl  L+  Y++WPFFR+ +  +Em  AK D  iA
  gi|8130106   852 GVGTALQeFLQERPEQNLNLLRYFYEKWPFFRMVISKVEMTLAKVDLQIA 901

                    aLy.DkLLvaEeLkPFGk...sLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                      y  +L   E+   F +  +++ ++++ t  l+L i  H  lL+GDP L
  gi|8130106   902 HHYvHELANPEDQERFERvfsQIAAEFQLTCHLVLTITNHGRLLDGDPEL 951

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                    +  + LR+  i  L  +q   LKR+R               y +    +
  gi|8130106   952 QRSVQLRNGTIVPLGFLQVALLKRLR--------------QYRQQT--ET 985

                    deLvkLnptervaPG.LEDtLiLtmKGiAAGmqntG<-*
                     +L++    +r++ G+L    +Lt+ GiAAGm ntG
  gi|8130106   986 TGLMR----SRYSKGeLLRGALLTINGIAAGMRNTG    1017

gi|251799599|ref|YP_003014330.1|: domain 1 of 1, from 8 to 936: score 424.4, E = 1.9e-124
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        + Aq R  +       ++L++ D   l   L+++L    G +L ++
  gi|2517995     8    TLSAQHRPQA-------NNLLRRDVRFLGNILgEVLVHQGGRELLDI 47

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v    E s        ++  e   + + sL P     v +a+     L n
  gi|2517995    48 VEQIRETSKALRAEFVPELFEQFKTTIASLSPEIRHQVIRAFAIYFQLVN 97

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R+R   +  G+    +s   Es i + lK          e
  gi|2517995    98 IAEQNHRIRRKRDYERSAGESVQRGS--IESAISD-LKERNIDI----EG 140

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v e L n s +Lv+tAHPt + RR++L  + Ri   +  L    +t  ++
  gi|2517995   141 VQEILSNISLELVMTAHPTEATRRAVLDIHKRIAEDVMELDNPTLTYRER 190

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + L + L  E+   + tDE+R  +Pt  DE+R G+ Y+ Et+++  P
  gi|2517995   191 EILRDKLLNEVLILWQTDELRDRKPTVIDEVRNGLYYFDETLFEVLPNVY 240

                    RRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDvC
                       +  L      E   + vP+ ++F sW+GGDRDG nP vt  vt +
  gi|2517995   241 EELERNLTKYYPGE--SWHVPsYLRFGSWIGGDRDG-NPSVTAKVTWETL 287

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk..vv
                     L R +A   Y +++ +L+  ls       L    EEl    ++d+++v
  gi|2517995   288 TLNRQLAIKKYEEKLHELVSILSF---STNLVEVSEELINSIKKDRehVE 334

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                       i+ W+     EPYR+ LG + +KL ntR+ +    A
  gi|2517995   335 LKCIDLWRNA--KEPYRIKLGFMLEKLANTRDESLKGSAMR--------- 373

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y    e LE L +  +sL       +AD  +  l+Rqv  FG  +  LDi
  gi|2517995   374 YNSAGELLEDLYIIDRSLRGHFADYVADTHIGKLVRQVELFGFHMLTLDI 423

                    RqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgsD
                    Rq s+ +   +  i   ++i s+Y + sEe + E L   L+  RPL  s
  gi|2517995   424 RQHSQEHENAMAEILAKMNIVSnYGSLSEEEKIELLSNLLEDPRPLTSSH 473

                    L...PktEEvkDvldaf.rvLAELPiDsFGaYiismataPsDvLAvELLq
                    L+ +  t E  Dv  ++ r   E   ++   Y+ism+   sD+L v +
  gi|2517995   474 LdysASTRECLDVYHTVyRAQQEFGPECISTYLISMTQGASDMLEVMVFA 523

                    RECg.........vkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                    +E g  +++ +++v+ tL+ vPLFE + DL+AAP  ++ LF +  Y+  +
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  gi|2517995   524 KEVGlfrkeadgsVRCTLQSVPLFETIDDLHAAPGIMKLLFELPIYRQAV 573

                   dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                     +++  e+m+GYsDs KD G + A W L +A  +i   A ++GvKL  F
  gi|2517995   574 AARgdlHEIMLGYSDSNKDGGAVTANWELRVALNDITATAGEHGVKLKFF 623

                   HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                   HGRGG  GRGG P    iL+qPP t+ G +++t qGEv+   +    + +
  gi|2517995   624 HGRGGALGRGGMPLNRSILAQPPHTVGGGIKITEQGEVLSSRYSMQGIAY 673

                   rsLqR.....FtAAtL.EHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvv
                   rsL   +    tAA L         +   EW ++   +   A   Y  ++
  gi|2517995   674 RSLEQatwalVTAARLaKYPQAQDDAVLKEWEEISRSISETALNKYQDLI 723

                   vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWt
                   +++P F  YF+  tP  E G +niGsRP+KRk s   e LRAiPW+FaWt
  gi|2517995   724 FRDPDFLTYFKESTPLPEVGELNIGSRPSKRKNSDRFEDLRAIPWVFAWT 773

                   qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                   q R+ LP W   G A K     D + l  Lk mY+++PFFR  +D l m
  gi|2517995   774 QSRYLLPAWYAAGTALKQYTGDDAQRLETLKTMYEKFPFFRSLIDNLQMA 823

                   FAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlL
                    AK D  iA  y +++    ++ +   ++ ++Y  t d++L i G  ++L
  gi|2517995   824 LAKADLTIAKEYADMIADSTIRDrIFTQIENEYTLTSDMILSITGQDEIL 873

                   EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                   +  P ++  +RLR++Y+  L  +q   L  +R+
  gi|2517995   874 DNVPVIQESIRLRNPYVDPLSYMQVQLLTELRE----------------- 906

                   EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                             L   e+  P L   ++Lt+ GiAAG+ ntG
  gi|2517995   907 -----------LRAKEEDDPELLREVLLTINGIAAGLRNTG    936

gi|154146810|emb|CAM84092.1|: domain 1 of 1, from 1 to 439: score 423.8, E = 2.7e-124
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ---------------------------------------------- -
```

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                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDv+DAi tHL+iGsYR+W+EeKRqEWLl+EL+GKRPLl +DLP+t
  gi|1541468     1 --HTDVIDAIITHLGIGSYRSWPEEKRQEWLLSELRGKRPLLSPDLPQTQ 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvl+ f+vLAELP DsFG+YiismataPsDvLAvELLqREC+vk++L
  gi|1541468    49 EIADVLGCFHVLAELPRDSFGPYIISMATAPSDVLAVELLQRECHVKEPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFEkLADL+ APA+ve+LFs+DWY nri GKq++mvGYsDsGKDAG
  gi|1541468    99 PVVPLFEKLADLQSAPASVERLFSMDWYLNRIAGKQQIMVGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAW LYkAqE ++KvAK++ vKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWHLYKAQEAMAKVAKRFNVKLTLFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP+tinGslRvt+qGEviE+sFGEE+LCF++LqRFtAAtLEHGm+PP sP
  gi|1541468   199 PPETINGSLRVTIQGEVIEYSFGEEHLCFQTLQRFTAATLEHGMHPPASP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++e+A vAtEEYRsvv+KEPRFvEYFR+AtPE+EYGk+niGsR
  gi|1541468   249 KPEWRALLDEIAAVATEEYRSVVMKEPRFVEYFRSATPETEYGKLNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkP+GGie+LRAiPWiF+Wtq R  LPvWLG+GAAFKhA++KDiKn+
  gi|1541468   299 PAKRKPGGGIETLRAIPWIFSWTQNRLNLPVWLGFGAAFKHAMKKDIKNF 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+Lk+mY++WPFFRvtlDLlEmv AK DP iA+LyD+LLvaEeLkPFGk+
  gi|1541468   349 QMLKDMYNDWPFFRVTLDLLEMVLAKADPIIAGLYDELLVAEELKPFGKQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LRd+YvEt++l+L++ GHk++LEGDP LKq+lRLRd+Yit
  gi|1541468   399 LRDNYVETEKLILQVLGHKEVLEGDPGLKQQLRLRDPYITI--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|253577082|ref|ZP_04854404.1|: domain 1 of 1, from 2 to 933: score 422.9, E = 5.2e-124
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                            L + +    s  ++L++ D   l   L+++L    G++L ++
  gi|2535770     2    ---TELTVTAGKGNS--NNLLRRDIRFLGNILgEVLVHQGGNELLDI 43

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v    E s        ++  eE    + sL+P+    v +a+     L n
  gi|2535770    44 VEKIREASKSLRAVFLPELHEEFKGMINSLEPGIRHQVIRAFAIYFQLVN 93

                    LAEEvelAyRRRikkkkhGDFaDEasAttEs.DiEEtlKkLvlklnKsPe
                    +AE        Ri++k+  D+   a     s+ iE  ++ L  ++  s
  gi|2535770    94 IAEQ-----NHRIRRKR--DYERSAGEEVQSgTIEAAVRDLKEQG-FSYS 135

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    E  e L   s +Lv+tAHPt + RR++L  + Ri   + qL    +t  +
  gi|2535770   136 EAQELLSGMSLELVMTAHPTEAMRRAILDIHKRIADDVMQLDNPTLTFRE 185

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    ++ L E L  E+   + tDE+R  +Pt  DE+R Gm Y+HEt+++  P
  gi|2535770   186 REQLREKLLNEVITLWQTDELRDRKPTVLDEVRNGMYYFHETLFHVLPEV 235

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                        +  L      E        ++F sW+GGDRDG nP vt +vt +
  gi|2535770   236 YQELERCLTKY-YPEHYWHVPTYLRFGSWIGGDRDG-NPSVTSDVTWETL 283

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk..vv
                     + R +A   Y   + DL   ls       +    +El    +rd+ +v+
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  gi|2535770   284 RMQRKLAVREYQRILSDLFKHLSF---STTIVDVTDELMASIQRDRlqVT 330

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                          W      EPYR+ L  + +KL n       +L     + +E
  gi|2535770   331 LRKTQQWNN--EKEPYRIKLTYMTEKLHN-------VLDDSTKDTPER-- 369

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y +vE F+  L +  +sL       +AD  +  l+Rq   FG     LDi
  gi|2535770   370 YPNVEAFIQDLKIIDRSLRHHYADYVADTHIKKLIRQAELFGFHTATLDI 419

                    RqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaELkGKRPLlgsD
                    Rq s  +   +  i   ++i   Y e  E+ +   L   L   RPL  +
  gi|2535770   420 RQHSKEHENAMTEILAKMNIvENYAELEEQEKIQLLERLLNDPRPLTSPY 469

                    LPktEEvkDvldafrvL....AELPiDsFGaYiismataPsDvLAvELLq
                        E  ++ ld +r + + + E    +  +Y+ism+ a sD+L v +
  gi|2535770   470 QDYSESTRECLDVYRTVyqaqKEYGTQCITSYLISMTEAASDILEVMVFS 519

                    RECg.........vkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                    +E g  +++ +++v  tL+ vPLFE + DL+AAP  + +LFs+  Y+  +
  gi|2535770   520 KEVGlfrkeadgtVVCTLQSVPLFETIDDLHAAPGIMRQLFSMPIYRESV 569

                    ...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                       +  qe+m+GYsDs KD G + A W L +A   i   A ++G+KL  F
  gi|2535770   570 aamNDLQEIMLGYSDSNKDGGVVTANWELRVALKQITATANEFGIKLKFF 619

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGG  GRGG P    iL qPP+ti G +++t qGEvi   +    + +
  gi|2535770   620 HGRGGALGRGGMPLNRSILVQPPETIGGGIKITEQGEVISSRYSLRGIAY 669

                    rsLqRFtAAtLE.......HGmnPPvsPkPEWRkLmeemAvvAtEEYRsv
                    rsL   t A +    + + H  + P +    W ++m  +       Y  +
  gi|2535770   670 RSLEQATSALITaaiqaklHQDQGPSAEEQRWEEIMSGISETSLQKYQDL 719

                    vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaW
                    v++EP F  +FR  tP +E G +niGsRP+KRk s   e LRAiPW+FaW
  gi|2535770   720 VFREPDFLKFFRESTPLVEVGELNIGSRPSKRKNSDRFEDLRAIPWVFAW 769

                    tqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEm
                    tq R+  P W   G       +    nl+ L++mY+++ FFR  +D l
  gi|2535770   770 TQSRYLFPAWYAAGTGLYNFYQNNEENLKVLQDMYQNFSFFRTVIDTLQF 819

                    vFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDl
                       K D  iA  y k+   +e++ +   ++ +++  t++++Lki G  ++
  gi|2535770   820 ALSKADLVIAKEYAKMCKDDEVRErILGQIEEEFHLTREMVLKICGISEI 869

                    LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                     +  P L+  +RLR++Y+  L  +q   L  +R               A
  gi|2535770   870 FDNLPGLQESIRLRNPYVDPLSYLQVQLLTELRS---------------A 904

                    dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     E  +  +eL++               +Lt+ GiAAG+ ntG
  gi|2535770   905 REKGQDDAELLREV-------------LLTINGIAAGLRNTG    933

gi|254431278|ref|ZP_05044981.1|: domain 1 of 1, from 6 to 1000: score 422.6, E = 6.3e-124
                    *->siD..AqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLk.
                       s D++A +R LvP  v           Ll   L+++ DL    L++
  gi|2544312     6    SDDrpASMRQLVPSVVE----PSPRATRLLGERLELVEDLWQTVLRs 48

                    .......EavqECYElsAeYEGKkDtkKLeELGakLt.sLdPaDailvAk
                    + ++++ E       ls   EG   +   +    +L + +d a+ai  A+
  gi|2544312    49 ecpphhaERLLRLKRLSDPSEGDTASIDTGAAIVQLIrEMDLAEAIAAAR 98

                    ailHmLnLAnLAEEv..elAyRRRikkkkhGDFaDEasAttEsDiE.Etl
                    a++    L n+ E   +e  y    k +     +D       s  E+ t+
  gi|2544312    99 AFSLYFQLVNILEQHieEDSYLDSLKTLPEPVASDPFLPPLASQTEpATF 148

                    KkLvlkl...nKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiR
                    ++L  +l++ n  P+ + + L+     Lv+tAHPt  vR  +  K+ R+
  gi|2544312   149 RQLFERLrnlNVPPAQIENLLRDLDLRLVFTAHPTEIVRHTVRHKQRRVA 198
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                    nCLaqL.sAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRa
                      + +L+    +   +++ L   L  Ei   +RtDE+   +Pt  DE+ +
  gi|2544312   199 TLIQKLeQGSGLNRVERQSLRLQLEEEIRLWWRTDELHQFKPTVLDEVDY 248

                    GmsYiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDR
                     + ++ E +++ +P    Rv  AL         P d+    F sW+G DR
  gi|2544312   249 ALHFFQEVLFEAMPLLRQRVSAALTESYPDVEPPSDA-FCTFGSWVGADR 297

                    DGknPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvR
                    DG nP vtP++t       R +    Yi  v +L   ls+    + +
  gi|2544312   298 DG-NPSVTPDITWRTACFQRQLMLERYIRAVGELRDQLSISMQWSQVSPA 346

                    AEElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRH
                      E     +       Y E        EPYR  L   v ++L  t ER
  gi|2544312   347 LLESLEMDRLR-FPEIYEERAARY-RLEPYRLKLSYVLERLRLTQERNQL 394

                    LLAtGi........seis...........EeAvytkvEeFLEPLELCYks
                    L   G +++ ++  s  ++ ++ +++ +  +  y  v+eF   LEL  +s
  gi|2544312   395 LADAGWespcdglaSTAPplgslgggaglQDLHYAAVDEFRNDLELVLQS 444

                    LCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittH
                    L   G   +   sL  l+ qv  F   L  LDiRqEs R+ D lD + +
  gi|2544312   445 LEGTG---LSCESLQHLISQVQIFAFCLASLDIRQESTRHSDALDELSRY 491

                    LeiGs.YReWsEeKRqEWLlaELkGKRPLlgsDL...PktEEvkDvldaf
                    L++  +Y e  Ee+R  WLl EL+ +RPL+++  + +P t E   vl  +
  gi|2544312   492 LQLPVpYGEMEEEQRVAWLLGELQTRRPLFPPTAswsPATTETFAVLRMV 541

                    rvL.AELPiDsFGaYiismataPsDvLAvELLqRECgvkqt......Lrv
                    + L+ E        Y+ism+ + sD L v LL +E g+  +  ++++L v
  gi|2544312   542 QRLqQEFGTRICSTYVISMSHTVSDLLEVLLLAKEAGLVDPvaqsssLLV 591

                    vPLFEkLADLeAAPAavekLFsiDWYinridGK......qevmvGYsDsG
                    vPLFE + DL+ APA + +LFs  +Y+  + G + +++ qevm+GYsDs
  gi|2544312   592 VPLFETVEDLQGAPAVMGHLFSQPFYRRLLTGSdaspplQEVMLGYSDSN 641

                    KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                    KD G ls  W + kAq  + + A ++ v L +FHGRGG v RGGGP   A
  gi|2544312   642 KDSGFLSSNWEIHKAQIALQQLATQHDVALRIFHGRGGSVSRGGGPAYQA 691

                    iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.n
                    +L+qP  t+ G +++t qGEv+   +   +L    L   t A L   +
  gi|2544312   692 VLAQPSGTLSGRIKITEQGEVLASKYSLPELALYNLETLTTAVLQNSLvS 741

                    PPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkm
                     Pv   P W +Lm ++A    + YR++v   P  v +F   tP  E  k+
  gi|2544312   742 TPVDNTPVWNELMGRLAARSRDFYRALVHDNPDLVAFFQQCTPIEEISKL 791

                    niGsRPaKRkPsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid
                     i sRPa+Rk + + + sLRAiPW+F Wtq RF LP W GvGAA +  +d
  gi|2544312   792 QISSRPARRKSGAkDLSSLRAIPWVFGWTQSRFLLPSWFGVGAALREELD 841

                    KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL....v
                     D   l  L+ +Y+ WPFFR+ +  +Em   K D  +A  y + L++++
  gi|2544312   842 HDPEQLELLRLLYQRWPFFRMLISKVEMTLSKVDIDLAHHYVQALgrpeR 891

                    aEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYit
                     E      + + +++  t+dl+L i GH+ lL+GDP L+  + LR+  i
  gi|2544312   892 REAFEQIFQTIAAEFDLTRDLVLAITGHQRLLDGDPALQLSVDLRNRTIV 941

                    tLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpterv
                     L  +q   L+R+RD +     +P++     +      d+       ++
  gi|2544312   942 PLGFLQVALLRRLRDQN----RQPPMREATGAGS----DGRTYSR--SEL 981

                    aPGLEDtLiLtmKGiAAGmqntG<-*
                      G     +Lt+ GiAAGm ntG
  gi|2544312   982 LRG----ALLTINGIAAGMRNTG    1000

gi|154146730|emb|CAM84052.1|: domain 1 of 1, from 1 to 439: score 421.0, E = 1.9e-123
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
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gi|1541467     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|1541467     - ---------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1541467     - ---------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1541467     - ---------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1541467     - ---------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1541467     - ---------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1541467     - ---------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1541467     - ---------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1541467     - ---------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tD +DAittHL+iGsY++W+EeKRqEWLl+EL+GKRPLl +DLP  +
gi|1541467     1 --HTDAIDAITTHLGIGSYKSWPEEKRQEWLLSELQGKRPLLTPDLPTSD 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl+ frvLAELP DsFG+YiismataPsDvLAvELLqREC++k +L
gi|1541467    49 EVADVLGCFRVLAELPRDSFGPYIISMATAPSDVLAVELLQRECQIKDPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  +vvPLFE+LADL+A PA+ve+LFs+DWY  ri+GKq+vmvGYsDsGKDAG
gi|1541467    99 PVVPLFERLADLQAGPASVERLFSTDWYLKRINGKQQVMVGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAW LY+AqE ++ vAKkyGv+++ FHGRGGtvGRGGGPtHLAiLsq
gi|1541467   149 RLSAAWALYRAQEGMAEVAKKYGVQITFFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP tinGslRvt+qGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PP sP
gi|1541467   199 PPNTINGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPASP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+e+  vAtEEYRs v+KEPRFvEYFR+AtPE+EYG++niG R
gi|1541467   249 KPEWRALMDEITAVATEEYRSYVFKEPRFVEYFRSATPETEYGRLNIGGR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   aKRkP+GGiesLRAiPWiF+WtqtRFHLPvWLG+GAAF +Ai+KD++n+
gi|1541467   299 TAKRKPGGGIESLRAIPWIFSWTQTRFHLPVWLGFGAAFNYAIKKDVRNI 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q LkEmY+eWPFFRvtlDL+EmvFAKGDPGi + y +LLva+eLkPFG++
gi|1541467   349 QTLKEMYNEWPFFRVTLDLVEMVFAKGDPGIVGFYNDLLVADELKPFGEQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR +Y +t +lLL++AGHk++LEGDPYLKqrlRLRd+Yitt
gi|1541467   399 LRKNYIDTVQLLLQVAGHKEILEGDPYLKQRLRLRDPYITT--------- 439

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
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  gi|1541467     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|159027003|emb|CAO86722.1|: domain 1 of 1, from 1 to 1018: score 420.5, E = 2.7e-123
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedL.kEa
                           + +LvP     ++++     L l + L ++ DL  e L  E
  gi|1590270     1    -----MSVLVPSTET-EQDIFPTSNLFLQQRLKLIEDLWKEVLiSEC 41

                   vqECYEl......sAeYEGK.kDtkKLeELGakLtsLdPaDailvAkail
                    qE  +l +  ++    EG+  D +    +   +  L+ ++ai v +a+
  gi|1590270    42 GQELVDLlellrhLCSEEGQvTDDSAEATIAKMIEDLELGEAIKVTRAFA 91

                   HmLnLAnLAEEvelAyRRRikkkkhGDFaDE.............asAtt
                       L n+ E  +    R  ++++     +E++++++++++  a
  gi|1590270    92 LYFQLINIIE--QHYEQRDQQLLRRTVIGEEnespktdppqksllATIVG 139

                   EsDiEEtlKk.................LvlklnKsPeEvFeALKnqsvDLv
                      +E tl  +++++++++  +   +   + n  P+E+   L    + Lv
  gi|1590270   140 ADWLEKTLNEsdhsgpksglfhwlfpYLKQVNVPPQEIQRLLDQLDIRLV 189

                   ltAHPtqsvRRsLLqKnaRiRnCLaqL.sAKDv.......tveDKkELDE
                   +tAHPt  vR  +  K+ Ri   L +L+ A ++ ++ + +   + + +
  gi|1590270   190 FTAHPTEIVRHTIRIKQRRISGILEKLdQAEEIfrsmgltNSREAQTVTK 239

                   ALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLRRvDt
                    L  Ei   +RtDE+   +Pt  DE+ + + Y+ E +++  P+   R
  gi|1590270   240 QLKEEIRFWWRTDELHQFKPTVVDEVDYALHYFDEVLFDSLPQLTLRLQQ 289

                   ALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLLaRmm
                    L+        P +    +F sW+GGDRDG nP vtPEvt   C   R +
  gi|1590270   290 SLQSSFPRLQAPKNN-FCRFGSWVGGDRDG-NPSVTPEVTWKTCCYQRNL 337

                   AanlYisqvEDL..mFElsmWRCndELRvRAEElyrtaardkvvKyYiEF
                       Y++ + DL+++   s+  C     v  E l +  + +   +   E
  gi|1590270   338 VIKKYLDAIRDLtsILSASLHWC----HVLPELLDSLDRDK---QQMPEI 380

                   WKqvPP...tEPYRviLGdvRDKLYntRERaRHL....LAtGiseisEeA
                   + q+  + ++EPYR  L  +  +L ntR+R   L++++  + +  + E
  gi|1590270   381 YSQLAIryrQEPYRLKLAFIQKRLENTRDRNNRLndpeERQLLTKLNETN 430

                   vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                   +y    eFL  L L  +sL + G   +    L  l+ qv  FG  L +LD
  gi|1590270   431 IYRSGSEFLAELKLLQRSLLQTG---LSCQELDQLIAQVEIFGFVLTQLD 477

                   iRqEseRqtDvlDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLlg
                    RqEs R+ + ++ i   L++ +  Y + sE  +  WL+aELk +RPL++
  gi|1590270   478 FRQESTRHAECIEEIAAYLGVlpKPYGQLSESEKIAWLVAELKTRRPLIP 527

                   sDLPktEEvkDvldafrvL....AELPiDsFGaYiismataPsDvLAvEL
                    ++P  E   + ++++rvL++ + E   +    Yiism+   sDvL v L
  gi|1590270   528 REMPFSERTCETIETLRVLrslqGEFGLEICQTYIISMTNEASDVLEVLL 577

                   LqRECgv......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                   L  E g+ ++ +++ +Lr+vPLFE + DL+ AP  ++ LF +  Y+  +
  gi|1590270   578 LAQEAGLydpatsRSSLRIVPLFETVDDLKHAPGIMQTLFELPLYRAALA 627

                   G.......................KqevmvGYsDsGKDAGRlsAAWqLY
                   G+ ++ +  ++++ ++++   ++++ qe+mvGYsDs KD G ls  W +
  gi|1590270   628 GgydhlgalngedvtpepailepsnLQEIMVGYSDSNKDSGFLSSNWEIH 677

                   kAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGsl
                   kAq  + K AK+yGv L lFHGRGG vGRGGGP   AiL+qP  tinG +
  gi|1590270   678 KAQKALQKTAKQYGVDLRLFHGRGGSVGRGGGPAYAAILAQPRGTINGRI 727

                   RvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE.WRkLm
                   ++t qGEv+   +   +L    L     A +   +        E+W ++m
  gi|1590270   728 KITEQGEVLASKYSLPELALYNLETAVTAVIQASLLGSGFDDLEpWNRIM 777
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                    eemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs.
                    e++A      YRs+++ EP F ++F + tP  E   + i sRPa+Rk ++
  gi|1590270   778 EDLATCSRQTYRSLIYEEPDFLDFFLSVTPIPEISLLQISSRPARRKSGq 827

                    GGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD.iKnlqkLkEm
                      + +LRAiPW+F+WtqtRF LP W G+G A +  +d  + +nl  L+
  gi|1590270   828 QDLSTLRAIPWVFSWTQTRFLLPAWYGLGTALQMFLDDSpNRNLELLRHF 877

                    YkeWPFFRvtlDLlEmvFAKGDPGiAaLy.DkLLvaEeLkPFG...ksLR
                    Y++WPFF + +   Em   K D  +A  y  +L   E+   F +  ++++
  gi|1590270   878 YHKWPFFQMVISKAEMTLSKVDLQMAYHYvSELSKQEDRERFQrlfERIK 927

                    dkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKR
                    ++Y  t +++L+i G k lL+ DP L+  + LR+  i  L  +q   LKR
  gi|1590270   928 EEYNRTSEIVLQITGEKHLLDNDPSLQRSVQLRNGSIVPLGFLQVSLLKR 977

                    iRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtm
                    +R  + +      +   y  E+      L++               ++t+
  gi|1590270   978 LRQYNSQ-AQSGVIHFRYSKEE------LLRGA-------------LMTI 1007

                    KGiAAGmqntG<-*
                     GiAAGm ntG
  gi|1590270  1008 NGIAAGMRNTG    1018

gi|260436235|ref|ZP_05790205.1|: domain 1 of 1, from 19 to 1009: score 420.5, E = 2.8e-123
                    *->siDAqLRlLvPGKvsedekLieYDALLl.DkFLDiLqDLHGedLkEa
                        +  q  +   G  s   +L++    L++D +  +L     ++  E
  gi|2604362    19    PVSEQETARLSGGGSGAGQLLQNRLDLIeDLWKSVLRSECPPEQSER 65

                    vqECYEls..AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                          ls++   EG+   +  e +   + ++d ++ai  A+a++    L
  gi|2604362    66 LLRLKQLSdpVSLEGRDGDSTSEAIVELIKAMDLSEAISAARAFSLYFQL 115

                    AnLAEEvelAyRRRikkkkhGDFaDE.............asAttEsDiEE
                     n+ E  ++        ++    aDE +++  ++  ++ a+ t  +   E
  gi|2604362   116 INILEQ-RIEEDSYLDSLRPNSSADEaqrdafdpfapplANQTDPATFGE 164

                    tlKkLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRn
                     + +L       P+ v + L+   + Lv+tAHPt  vR  +  K+ R+ n
  gi|2604362   165 VFERLRRMN-VPPAQVEQLLRELDIRLVFTAHPTEIVRHTVRHKQRRVAN 213

                    CLaqLsAKD.vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaG
                     L qL    ++  + ++E  + L  Ei   +RtDE+   +Pt  DE+
  gi|2604362   214 LLQQLQSDApLAHQLREECRDQLEEEIRLWWRTDELHQFKPTVIDEVDST 263

                    msYiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRD
                    + Y+   +++ +P+  RR    L        +P ++    F sW+G DRD
  gi|2604362   264 LHYFQQVLFDAMPQLRRRLISSLHRHYPDVQVP-QASFCTFGSWVGSDRD 312

                    GknPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRA
                    G nP vtPE+t       R +   lYis v  L   ls+    + +
  gi|2604362   313 G-NPSVTPEITWRTACYQRQLMLELYISSVQSLRQQLSISMQWSQVAPSL 361

                    EElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL
                     E     +         E        EPYR  L  v +KL  t  R   L
  gi|2604362   362 LESLEMDRLR--FPEIYERRAARYRLEPYRLKLCYVLEKLERTLARNNQL 409

                    LAtGiseisEeAv.............ytkvEeFLEPLELCYksLCeCGD
                       G  +++ eA ++++ + ++ +  +yt v++F   LEL   sL
  gi|2604362   410 SEAGW-QMPCEALtdpqvglsgaevlhYTSVDQFRSDLELVRNSLVS--- 455

                    kviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei.Gs
                      +    L  lL qv  FG sL  LDiRqEs R+ D +D +t+ Le++ +
  gi|2604362   456 TELSCEQLDTLLHQVHIFGFSLASLDIRQESTRHSDAIDELTRSLELpQA 505

                    YReWsEeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiD
                    Y +  E  R+ WLl EL+ +RPL+++        ++ l  fr+L  L  +
  gi|2604362   506 YGDMNETERMAWLLQELQTRRPLIPPAASWSAATAETLAVFRMLQRL-QE 554

                    sFGa.....YiismataPsDvLAvELLqRECgv......kqtLrvvPLFE
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                     FG++  ++Y+ism+ + sD L v LL +E g+ ++++++ +L vvPLFE
  gi|2604362   555 EFGPricnsYVISMSHTASDLLEVLLLAKEAGLvdppkkRASLLVVPLFE 604

                     kLADLeAAPAavekLFsiDWYinri.......dGKqevmvGYsDsGKDAG
                      + DL+ AP  +e LF +  Y+  ++  +++++  qe m+GYsDs KD G
  gi|2604362   605 TVEDLQRAPEVMEGLFKTPLYRELLpvvgqqkQPLQELMLGYSDSNKDSG 654

                     RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                      ls  W + +Aq  +   A +  v L lFHGRGG v RGGGP   AiL+q
  gi|2604362   655 FLSSNWEIHQAQIALQELASRQDVALRLFHGRGGSVSRGGGPAYQAILAQ 704

                     PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvs
                     P  t++G +++t qGEv+   +   +L    L   t A +   +    +
  gi|2604362   705 PSGTLQGRIKITEQGEVLASKYSLPELALYNLETVTTAVVQNSLvTNQLD 754

                     PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                       P W +Lm ++A    E YR++v   P  v +F   tP  E  k+ i s
  gi|2604362   755 ATPSWNQLMSRLATRSREHYRALVHDNPDLVAFFQQVTPIEEISKLQISS 804

                     RPaKRkPsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                     RPa+Rk + + + sLRAiPW+F Wtq RF LP W G+G A    +  D+
  gi|2604362   805 RPARRKTGAkDLSSLRAIPWVFGWTQSRFLLPSWFGFGTALSEEVGGDSE 854

                     nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL....vaEeL
                      l  L+ + + WPFFR+ +  +Em   K D  +A  y + L++++  E
  gi|2604362   855 QLDLLRRLHQRWPFFRMLISKVEMTLSKVDLDLAHHYMNSLghpeQREAF 904

                     kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnv
                         + +  +Y+ t++l+L+i G   lL  D  L+  + LR+  i  L
  gi|2604362   905 EAIFQVIAKEYELTRQLVLEITGQNRLLGADQGLQLSVDLRNRTIVPLGF 954

                     fqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGL
                     +q   L+R+RD +     +P++s E A  +     e  +    ++   G
  gi|2604362   955 LQVALLRRLRDQN----RQPPMS-ETAGAP-----EDTRTYSRSELLRG- 993

                     EDtLiLtmKGiAAGmqntG<-*
                         +Lt+ GiAAGm ntG
  gi|2604362   994 ---ALLTLNGIAAGMRNTG    1009

gi|154146920|emb|CAM84147.1|: domain 1 of 1, from 1 to 439: score 417.2, E = 2.7e-122
                     *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541469     -    ------------------------------------------------ -

                     qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541469     - ------------------------------------------------ -

                     AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541469     - ------------------------------------------------ -

                     FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541469     - ------------------------------------------------ -

                     ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541469     - ------------------------------------------------ -

                     RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541469     - ------------------------------------------------ -

                     aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541469     - ------------------------------------------------ -

                     EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541469     - ------------------------------------------------ -
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                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541469     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +t+v+D ittHL+iGsYR+W+EeKRqEWLl+EL+GKRPLl +DLP+ E
  gi|1541469     1 --HTEVIDTITTHLGIGSYRSWPEEKRQEWLLSELQGKRPLLSPDLPQSE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+D l++frvLAELP DsFG+YiismataPsDvLAvELLqREC+v  +L
  gi|1541469    49 EVADALGTFRVLAELPRDSFGPYIISMATAPSDVLAVELLQRECKVADPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFE+LADL+AAPA++e LFs+DWY+ ri+GKq+vmvGYsDsGKDAG
  gi|1541469    99 PVVPLFERLADLQAAPATMETLFSMDWYKKRINGKQQVMVGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAW LY AqEE+ KvA ++GvK++lFHGRGGt+GRGGGPtHLA+Lsq
  gi|1541469   149 RLSAAWALYTAQEEVWKVANNHGVKITLFHGRGGTIGRGGGPTHLALLSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP tinGs+RvtvqGEviE sFGEE+LCFr+L RFtAAtLEHGm+PPvsP
  gi|1541469   199 PPKTINGSIRVTVQGEVIEHSFGEEHLCFRTLERFTAATLEHGMHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+e+ vv tE YRsvv+KEPRFvEYFR+AtPE+ YG+mniGsR
  gi|1541469   249 KPEWRALMDELTVVSTEVYRSVVFKEPRFVEYFRSATPETGYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkP GGiesLRAiPWiF+WtqtRFHLPvWLGvGAAFK+A++KDiKn+
  gi|1541469   299 PAKRKPKGGIESLRAIPWIFSWTQTRFHLPVWLGVGAAFKYAMKKDIKNF 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+Lk+mY+eWPFFRvtlDLlEmvFAKGDPGi +Ly +LLva+eLkPFG++
  gi|1541469   349 QMLKDMYNEWPFFRVTLDLLEMVFAKGDPGIVGLYNELLVADELKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y +t+++LL+iAGHk++LE  P LKqrlRLRd+Yitt
  gi|1541469   399 LRNDYLDTQQILLQIAGHKEILEASPRLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541469     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541469     - -------------    -

gi|87300934|ref|ZP_01083776.1|: domain 1 of 1, from 13 to 1002: score 417.0, E = 3.1e-122
                    *->siDAqLRlLvPG.KvsedekLieYDALLlDkFLDiLqDLHGedLkEa
                       + D q    +P ++v     L e   L+ D +  +L     +d  E
  gi|8730093    13    AQDPQGVPTAPApRVT--RLLGERLELVEDLWQTVLLSECPPDQAER 57

                    vqECYElsAeYEGKkDtkKLeELGakLt.sLdPaDailvAkailHmLnLA
                          ls   E    t        +L + +d ++ai  A+a++    L
  gi|8730093    58 LLRLKRLSDPLEAADGTVDTTAAIVQLIrEMDLSEAIAAARAFSLYFQLV 107

                    nLAEE.ve....lAyRRRikkkkhGD.Fa.DEasAttEsDiEEtlKkLvl
                    n+ E ++e+++ lA     +     D+Fa+  as t  +   E + +L
  gi|8730093   108 NILEQhIEedsyLASLQEASTPTSPDpFApPLASQTDPATFRELFTRLRG 157

                    klnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsA
                    +    P+ + + L+   + Lv+tAHPt  vR  +  K+ R+   +  L
  gi|8730093   158 LN-VPPAQIENLLRELDIRLVFTAHPTEIVRHTVRHKQRRVAALIHRLQQ 206

                    KDvt.veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEt
                       t+ +D + L   L  Ei   +RtDE+   +P   DE+ + + Y+
  gi|8730093   207 DNPTeLQDERSLRLQLEEEIRLWWRTDELHQFKPSVLDEVDYALHYFQQV 256

                    vWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvt
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                  +++ +P    R+  AL         P d+    F sW+G DRDG nP vt
  gi|8730093   257 LFDAMPLLRQRIINALAGSYPDVEAPRDA-FCTFGSWVGSDRDG-NPSVT 304

                  PEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrta
                  P++t       R +    Yi  v  L   ls+    + + +   E
  gi|8730093   305 PDITWRTACYQRQLMIERYITAVQGLRDQLSISMQWSQVSAPLLESLEMD 354

                  ardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.......
                  +       Y E        EPYR  L  + ++L  t  R   L + + ++
  gi|8730093   355 RLR-FPEIYEERAARY-RLEPYRLKLSYIVERLRLTHQRNQQLaeagwes 402

                  .........LAtG...iseisEeAvytkvEeFLEPLELCYksLCeCGDkv
                  + ++ ++  L tG+++++  + e  y  v e    LEL   sL   G
  gi|8730093   403 pcenagpavLSTGtgpMAAAPPELHYGSVNELRQDLELLRDSLETTG--- 449

                  iADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YR
                  +    L  lL qv  F   L  LDiRqEs R+ D lD +t+ L++  +Y
  gi|8730093   450 LSCEPLQTLLSQVHIFAFCLASLDIRQESTRHSDALDELTRYLQLPIpYG 499

                  eWsEeKRqEWLlaELkGKRPLlgsDL...PktEEvkDvldafrvL.AELP
                  e  Ee+R EWLl EL+ +RP+l++  + +P tEE   v   ++ L+ E
  gi|8730093   500 EMEEEQRVEWLLQELQTRRPMLPPAArwsPATEETFAVFRMLQRLqQEFG 549

                  iDsFGaYiismataPsDvLAvELLqRECg......vkqtLrvvPLFEkLA
                       +Yiisma + sD L v LL +E g  +++ v+  L vvPLFE +
  gi|8730093   550 PRICRSYIISMAHTVSDLLEVLLLAKEAGlvdpkaVQTQLLVVPLFETVE 599

                  DLeAAPAavekLFsiDWYinridGK.......qevmvGYsDsGKDAGRls
                  DL+ APA +++LFs  +Y+  +    + +++ qevm+GYsDs KD G ls
  gi|8730093   600 DLQRAPAVMQRLFSEPFYRTLLASSaeadkplQEVMLGYSDSNKDSGFLS 649

                  AAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPD
                    W + kAq  + + A ++ v L +FHGRGG vGRGGGP   AiL+qP
  gi|8730093   650 SNWEIHKAQIALQRLACEHDVALCIFHGRGGSVGRGGGPAYQAILAQPSG 699

                  tinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP.vsPkP
                  t+nG +++t qGEv+   +   +L    L   t A L   +   +v   P
  gi|8730093   700 TLNGRIKITEQGEVLASKYSLPELALYNLETVTTAVLQNSLVSTnVDDTP 749

                  EWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPa
                   W +Lm ++A      YR +v   P  v +F   tP  E  k+ i sRPa
  gi|8730093   750 TWNDLMGRLAARSRVHYRRLVHENPDLVAFFQQVTPIEEISKLQISSRPA 799

                  KRkPsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlq
                  +Rk + + + sLRAiPW+F Wtq RF LP W GvGAA +  +d D   l
  gi|8730093   800 RRKSGAkDLSSLRAIPWVFGWTQSRFLLPSWFGVGAALQEELDDDPGQLE 849

                  kLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL....vaEeLkPF
                   L+ +Y+ WPFFR+ +  +Em   K D  +A  y + L+++  E
  gi|8730093   850 LLRLLYQRWPFFRMLISKVEMTLSKVDLDLAHHYVQALgrpsHREAFEEI 899

                  GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                   + + ++++ t+dl+Lki GH  lL+GDP L+  + LR+  i  L  +q
  gi|8730093   900 FQVIAAEFELTRDLVLKISGHARLLDGDPALQLSVDLRNQTIVPLGYLQV 949

                  YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                    L+R+RD +     +P++s     +     d+       ++   G
  gi|8730093   950 ALLRRLRDQN----RQPPMSEASSGDG---QDGRTYSR--SELLRG---- 986

                  LiLtmKGiAAGmqntG<-*
                   +Lt+ GiAAGm ntG
  gi|8730093   987 ALLTINGIAAGMRNTG    1002

gi|166366623|ref|YP_001658896.1|: domain 1 of 1, from 7 to 1018: score 416.6, E = 4.1e-122
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                     s +    +           L +   L+ D + ++L    G++L +
  gi|1663666     7    STETEQDIFSTSNLF----LQQRLKLIEDLWKEVLVSECGQELVDLL 49

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       l  e     D +    +   +  L+ ++ai v +a+     L n+
  gi|1663666    50 ELLRHLCSEEGQVTDDSPEATIAKMIEDLELGEAIKVTRAFALYFQLINI 99
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                AE......EvelAyRRRikkkkhGDFaDEasAttEsDi......EEtlKk
                 E++ ++++ +l  R  i        aD ++    + i + +  E tl
gi|1663666   100 IEqhyeqrDQQLLRRTVIGEENESPKADPTQKSLLATIvgadwlEKTLNE 149

                .................LvlklnKsPeEvFeALKnqsvDLvltAHPtqsvR
                +++++++++  +   +   + n  P+E+   L    + Lv+tAHPt  vR
gi|1663666   150 sdhsgpksglfhwlfpYLKQVNVPPQEIQRLLDQLDIRLVFTAHPTEIVR 199

                RsLLqKnaRiRnCLaqL.sAKDv.......tveDKkELDEALHREiqAAF
                  +  K+ Ri   L +L+ A ++ ++ + +   + + +   L  Ei   +
gi|1663666   200 HTIRIKQRRISGILEKLdQAEEIfrsmgltNSREAQTVTKQLKEEIRFWW 249

                RtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLRRvDtALKniGinER
                RtDE+   +Pt  DE+ + + Y+ E +++  P+   R    L+
gi|1663666   250 RTDELHQFKPTVVDEVDYALHYFDEVLFDSLPQLTLRLQQSLQSSFPRLQ 299

                lPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLLaRmmAanlYisqvE
                 P +    +F sW+GGDRDG nP vtPEvt   C   R +    Y++ +
gi|1663666   300 APKNN-FCRFGSWVGGDRDG-NPSVTPEVTWKTCCYQRNLVIKKYLDAIR 347

                DL..mFElsmWRCndELRvRAEElyrtaardkvvKyYiEFWKqvPP...t
                DL+++   s+  C     v  E l +  + +   +   E + q+  + ++
gi|1663666   348 DLtsILSASLHWC----HVLPELLDSLDRDK---QQMPEIYSQLAIryrQ 390

                EPYRviLGdvRDKLYntRERaRHL....LAtGiseisEeAvytkvEeFLE
                EPYR  L  +  +L ntR+R   L++++  + +  + E  +y    eFL
gi|1663666   391 EPYRLKLAFIQKRLENTRDRNDRLndpeERQLLTKLNETNIYRSGSEFLA 440

                PLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtD
                 L L  +sL + G   +    L  l+ qv  FG  L +LD RqEs R+ +
gi|1663666   441 ELQLLKRSLFQTG---LSCQELDRLIAQVEIFGFVLTQLDFRQESTRHAE 487

                vlDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLlgsDLPktEEvk
                 ++ i + L++ +  Y +  E  +  WL+aELk +RPL++ ++P  E
gi|1663666   488 CIEEIAQYLGVlpKPYGKLTESEKIAWLVAELKTRRPLIPREMPFSERTC 537

                DvldafrvL....AELPiDsFGaYiismataPsDvLAvELLqRECgv...
                + ++++rvL++ + E   +    Yiism+   sDvL v LL  E g+ ++
gi|1663666   538 ETIETLRVLrslqGEFGLEICQTYIISMTNEASDVLEVLLLAQEAGLydp 587

                ...kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG.........
                 +++ +Lr+vPLFE + DL+ AP  ++ LF +  Y+  + G+ ++    +
gi|1663666   588 atsRSSLRIVPLFETVDDLKHAPGIMQTLFELPLYRATLAGgydhlaaln 637

                ...............KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvA
                +++ ++++   ++++ qe+mvGYsDs KD G ls  W + kAq  + K A
gi|1663666   638 gedvtpepailepsnLQEIMVGYSDSNKDSGFLSSNWEIHKAQKALQKTA 687

                KkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviE
                K+yGv L lFHGRGG vGRGGGP   AiL+qP  tinG +++t qGEv+
gi|1663666   688 KQYGVNLRLFHGRGGSVGRGGGPAYAAILAQPRGTINGRIKITEQGEVLA 737

                fsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE.WRkLmeemAvvAtEE
                  +   +L    L     A +   +        E+W ++mee+A
gi|1663666   738 SKYSLPELALYNLETAVTAVIQASLLGSGFDDLEpWNRIMEELATRSRQT 787

                YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs.GGiesLRAiP
                YRs+++ EP F ++F + tP  E   + i sRPa+Rk ++  + +LRAiP
gi|1663666   788 YRSLIYEEPDFLDFFLSVTPIPEISLLQISSRPARRKSGqQDLSTLRAIP 837

                WiFaWtqtRFHLPvWLGvGAAFKhAidKD.iKnlqkLkEmYkeWPFFRvt
                W+F+WtqtRF LP W G+G A +  +d  +++nl  L+  Y++WPFF +
gi|1663666   838 WVFSWTQTRFLLPAWYGLGTALQMFLDDSpSRNLELLRHFYHKWPFFQMV 887

                lDLlEmvFAKGDPGiAaLy.DkLLvaEeLkPFG...ksLRdkYvEtkdlL
                +   +m   K D  +A  y  +L   E+   F +  ++++++Y  t +++
gi|1663666   888 ISKADMTLSKVDLQMAYHYvSELSKQEDRERFQrlfERIKEEYNRTSEIV 937

                LkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtl
                L+i G k lL+ DP L+  + LR+  i  L  +q   LKR+R  + +
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  gi|1663666   938 LQITGEKHLLDNDPNLQRSVQLRNGSIVPLGFLQVSLLKRLRQYNSQ-AQ 986

                   rPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqnt
                      +   y  E+      L++              ++t+ GiAAGm nt
  gi|1663666   987 SGVIHFRYSKEE------LLRGA-------------LMTINGIAAGMRNT 1017

                   G<-*
                   G
  gi|1663666  1018 G    1018

gi|154146776|emb|CAM84075.1|: domain 1 of 1, from 1 to 439: score 416.4, E = 4.6e-122
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ---------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ---------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ---------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ---------------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +t+v+D ittHL+iGsYR+W+EeKR EWL++EL+GKRPLl +D P+ E
  gi|1541467     1 --HTEVIDTITTHLGIGSYRSWPEEKRVEWLVSELQGKRPLLSPDPPQSE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+D l++fr LAELP DsFG+YiismataPsDvLAvELLqREC++  +L
  gi|1541467    49 EVADALGTFRALAELPRDSFGPYIISMATAPSDVLAVELLQRECKIADPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLFE+LADL+ APA++e LFs+DWY+ ri+GKq+vm+GYsDsGKDA
  gi|1541467    99 PVVPLFERLADLQNAPATMETLFSLDWYKKRINGKQQVMIGYSDSGKDAE 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAW LY AqE + KvA k+GvK++lFHGRGGt+GRGGGPtHLAiLsq
  gi|1541467   149 RLSAAWALYTAQEAVLKVANKHGVKITLFHGRGGTIGRGGGPTHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDt+nGs+RvtvqGEviE sFGEE+LCFr+L RFtAAtLEHGm+PP+sP
  gi|1541467   199 PPDTVNGSIRVTVQGEVIEHSFGEEHLCFRTLERFTAATLEHGMHPPISP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+e+ vvAtE YRs+v+KEPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWRALMDELTVVATEGYRSIVFKEPRFVEYFRSATPETEYGRMNIGSR 298
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                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkP GGiesLRAiPWiF+WtqtRFHLPvWLGvG AFK+Ai+KDiKn+
  gi|1541467   299 PAKRKPKGGIESLRAIPWIFSWTQTRFHLPVWLGVGTAFKYAIEKDIKNF 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+Lk mY+eWPFFRvtlDLlEmvFAKGDPGi +Ly +LLvaEeLkPFG++
  gi|1541467   349 QMLKQMYNEWPFFRVTLDLLEMVFAKGDPGIVSLYNDLLVAEELKPFGEK 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y Et++lLL++AGHk++LEG PYLKqrlRLRd+Yitt
  gi|1541467   399 LRNEYLETQKLLLQVAGHKEILEGSPYLKQRLRLRDPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|116075789|ref|ZP_01473048.1|: domain 1 of 1, from 15 to 1003: score 416.0, E = 6.3e-122
                    *->siDAqL......RlLvPGKvsedekLieYDALLlDkFLDiLqDLHGe
                       s  Aq ++++++ +  P +    + L +  AL+ D +  +L     +
  gi|1160757    15    STHAQTpesdrsGIAEPFQAG-GQLLKQRLALVEDLWETVLRSECPP 60

                    dLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHm
                    d  E       ls        +   + +   +  +d  +ai  A+a++
  gi|1160757    61 DQAERLLRMKQLSDPVASDGAAVSSDAVAQLIREMDLVEAIAAARAFSLY 110

                    LnLAnLAEEvelAyRRRikkkkhGDFaDE........asAttEsDiEEtl
                      L n+ E          +  +  D a+  ++  ++ as t  +   E +
  gi|1160757   111 FQLVNILEQRIEEDSYLESISRSHDHAEAvdpfapplASQTEPATFRELF 160

                    KkLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL
                     +L  +    P+     L+n  + Lv+tAHPt  vR  +  K+ R+   L
  gi|1160757   161 ERLRHLN-VPPAQLEALLQNLDIRLVFTAHPTEIVRHTVRHKQRRVATLL 209

                    aqLsAK.DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGms
                     qL A + v   +   L   L  Ei   +RtDE+   +Pt  DE+ + +
  gi|1160757   210 QQLQATpAVSSSESSSLRQQLEEEIRLWWRTDELHQFKPTVLDEVDYALH 259

                    YiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGk
                    Y+   +++ +P+  RR+  AL       RlP  +    F sW+G DRDG
  gi|1160757   260 YFQQVLFDAMPQLRRRISSALASSYPDVRLPPSA-FCTFGSWVGSDRDG- 307

                    nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEE
                    nP vtPE+t       R +    Yi  v  L   ls+    + + +   E
  gi|1160757   308 NPSVTPEITWRTSCYQRQLMLERYIAAVQALRDQLSISMQWSQVSAPLLE 357

                    lyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLA
                         +       Y E        EPYR  L  + ++L  t  R + L
  gi|1160757   358 SLEMDRLR-FPDVYEERAARY-RLEPYRLKLSYMLERLRLTQLRNKQLAE 405

                    tGiseisEeAv.............ytkvEeFLEPLELCYksLCeCGDkvi
                     G     E  v ++++++++++ +y  v eF   LEL   sL       +
  gi|1160757   406 AGWQTPTEGLVansttpggqeelhYGSVAEFRSDLELIRNSLVS---TEL 452

                    ADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYRe
                        L  lL qv  FG sL  LDiRqEs R+ D lD +t+ L ++ sY +
  gi|1160757   453 SCEPLDTLLTQVHIFGFSLASLDIRQESTRHSDALDELTRYLRLpKSYED 502

                    WsEeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFG
                      E  R  WLl EL+ +RPL+++ +      ++ +  fr+L  L  + FG
  gi|1160757   503 MDESERVTWLLEELQTRRPLIPPAVQWSPGTAETIAVFRMLHRL-QEEFG 551

                    .....aYiismataPsDvLAvELLqRECgvkqt......LrvvPLFEkLA
                    ++  + Y+ism+ + sD L v LL +E g+  +  ++ +L vvPLFE +
  gi|1160757   552 sricrTYVISMSNSASDLLEVLLLAKEAGLVDPaaehadLLVVPLFETVE 601

                    DLeAAPAavekLFsiDWYi.......nridGKqevmvGYsDsGKDAGRls
                    DL+ APA +e+LF    Y++  ++ + +++  qe m+GYsDs KD G ls
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  gi|1160757   602 DLQRAPAVMEQLFENPLYRkllpqvgEHVQPLQELMLGYSDSNKDSGFLS 651

                   AAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPD
                     W + +Aq  +   A ++Gv L lFHGRGG vGRGGGP   AiL+qP
  gi|1160757   652 SNWEIHQAQIALQDLASRHGVALRLFHGRGGSVGRGGGPAYQAILAQPSG 701

                   tinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsPkP
                   t++G +++t qGEv+   +   +L    L     A +   +    +   P
  gi|1160757   702 TLQGRIKITEQGEVLASKYSLPELALYNLETVSTAVVQNSLvTNQLDATP 751

                   EWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPa
                    W +Lm ++A      YR++v   P  v +F   tP  E  k+ i sRPa
  gi|1160757   752 SWNELMARLAARSRSHYRALVHDNPDLVAFFQQVTPIEEISKLQISSRPA 801

                   KRkPsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlq
                   +Rk + + + sLRAiPW+F Wtq RF LP W GvG A    +  D   l
  gi|1160757   802 RRKTGAkDLSSLRAIPWVFGWTQSRFLLPSWFGVGTALAEEVASDPEQLD 851

                   kLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL.vaEeLkPFGk.
                    L+ + + WPFFR+ +  +Em   K D  +A  y   L+ +E    F +
  gi|1160757   852 VLRRLHQRWPFFRMLISKVEMTLSKVDLELARHYVTSLgRSEHRDAFERi 901

                   ..sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    + +  +   t +l+L i G   lL+GDP L+  + LR+  i  L  +q
  gi|1160757   902 ysTIAREHALTLQLVLDITGQERLLDGDPGLQLSVDLRNRTIVPLGFLQV 951

                   YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                     L+R+RD + +  +r   s +  d  +    eL++
  gi|1160757   952 ALLRRLRDQNRQPPMREATSGD-SDGRTYSRSELLRGA------------ 988

                   LiLtmKGiAAGmqntG<-*
                    +Lt+ GiAAGm ntG
  gi|1160757   989 -LLTINGIAAGMRNTG    1003

gi|78211948|ref|YP_380727.1|: domain 1 of 1, from 7 to 997: score 415.6, E = 8.2e-122
                   *->siDAqLRlLvPGKvsedekLieYDALLl.DkFLDiLqDLHGedLkEa
                       +  q  +   G  s   +L++    L++D +  +L     ++  E
  gi|7821194     7    PVSEQETARMSGGGSGAGQLLQHRLDLIeDLWKSVLRSECPPEQSER 53

                   vqECYEls..AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                         ls++   EG+   +  e +   + ++d ++ai  A+a++    L
  gi|7821194    54 LLRLKQLSdpVSLEGRDGNSTSEAIVELIKAMDLSEAISAARAFSLYFQL 103

                   AnLAEE.ve....lAyRRRi..kkkkhGDFaD.....EasAttEsDiEEt
                    n+ E ++e+++ l   R +++    h D  D+  ++ a+ t  +   E
  gi|7821194   104 INILEQrIEedsyLDSLRPNpsADAAHRDAFDpfappLANQTDPATFGEV 153

                   lKkLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnC
                   + +L       P+ v   L+   + Lv+tAHPt  vR  +  K  R+ n
  gi|7821194   154 FERLRRMN-VPPAQVEHLLRELDIRLVFTAHPTEIVRHTVRHKIRRVANL 202

                   LaqLsAKD.vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGm
                   L qL    ++  + ++E    L  Ei   +RtDE+   +Pt  DE+   +
  gi|7821194   203 LQQLQSDApLAHQMREECRGQLEEEIRLWWRTDELHQFKPTVIDEVDSTL 252

                   sYiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDG
                    Y+   +++ +P   RR  tAL        +P ++    F sW+G DRDG
  gi|7821194   253 HYFQQVLFDAMPTLRRRLITALHRHYPDVQVP-QASFCTFGSWVGSDRDG 301

                   knPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE
                    nP vtPE+t       R +   lYis v  L   ls+    + +
  gi|7821194   302 -NPSVTPEITWRTACYQRQLMLELYISSVQSLRQQLSISMQWSQVAPSLL 350

                   Elyrtaardkvv KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.
                   E     +         E        EPYR  L  v +KL  t  R   L+
  gi|7821194   351 ESLEMDRLR--FPEIYERRAARYRLEPYRLKLCYVLEKLERTLARNNQLs 398

                   ..........LAtGiseisEeAv..ytkvEeFLEPLELCYksLCeCGDkv
                   + + + + + LA   + +s   v +yt v++F   LEL   sL
  gi|7821194   399 eagwqmpceaLADPQAGLSGAEVlhYTSVDQFRSDLELVRNSLVS---TE 445
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                    iADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYR
                    +    L  lL qv  FG sL  LDiRqEs R+ D +D +t+ L+++ +Y
  gi|7821194   446 LSCEQLDTLLHQVHIFGFSLASLDIRQESTRHSDAIDELTRNLDLpQAYG 495

                    eWsEeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsF
                    +  E  R+ WLl EL+ +RPL+++        ++ l  fr+L  L  + F
  gi|7821194   496 DMDEAERMAWLLQELQTRRPLIPPAASWSAATAETLAVFRMLQRL-QEEF 544

                    Ga.....YiismataPsDvLAvELLqRECgv......kqtLrvvPLFEkL
                    G++  ++Y+ism+ + sD L v LL +E g+ ++++++ +L vvPLFE +
  gi|7821194   545 GPricnsYVISMSHTASDLLEVLLLAKEAGLvdppnkRASLLVVPLFETV 594

                    ADLeAAPAavekLFsiDWYinri.......dGKqevmvGYsDsGKDAGRl
                     DL+ AP  +e LF +  Y+  ++  +++++  qe m+GYsDs KD G l
  gi|7821194   595 EDLQRAPEVMEGLFKTPLYRELLpvvgqqkQPLQELMLGYSDSNKDSGFL 644

                    sAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPP
                    s  W + +Aq  +   A +  v L lFHGRGG v RGGGP   AiL+qP
  gi|7821194   645 SSNWEIHQAQIALQELASRQDVALRLFHGRGGSVSRGGGPAYQAILAQPS 694

                    DtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsPk
                     t++G +++t qGEv+   +   +L    L   t A +   +    +
  gi|7821194   695 GTLQGRIKITEQGEVLASKYSLPELALYNLETVTTAVVQNSLvTNQLDAT 744

                    PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRP
                    P W +Lm ++A    + YR++v   P  v +F   tP  E  k+ i sRP
  gi|7821194   745 PSWNQLMSRLATRSRDHYRALVHDNPDLVAFFQQVTPIEEISKLQISSRP 794

                    aKRkPsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    a+Rk + + + sLRAiPW+F Wtq RF LP W G+G A    +  D+  l
  gi|7821194   795 ARRKTGAkDLSSLRAIPWVFGWTQSRFLLPSWFGFGTALTEEVGGDSEQL 844

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL....vaEeLkP
                      L+ + + WPFFR+ +  +Em   K D  +A  y + L++++  E
  gi|7821194   845 DLLRRLHQRWPFFRMLISKVEMTLSKVDLDLAHHYMNSLghpeQREAFEA 894

                    FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfq
                      + +  +Y+ t++l+L+i G   lL  D  L+  + LR+  i  L  +q
  gi|7821194   895 IFQVIAKEYELTRKLVLEITGQNRLLGADQGLQLSVDLRNRTIVPLGFLQ 944

                    AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                       LKR+RD +     +P++s     E    +++       ++   G
  gi|7821194   945 VALLKRLRDQN----RQPPMS-----ETPGAPEDTRTYS-RSELLRG--- 981

                    tLiLtmKGiAAGmqntG<-*
                      +Lt+ GiAAGm ntG
  gi|7821194   982 -ALLTLNGIAAGMRNTG    997

gi|282900199|ref|ZP_06308155.1|: domain 1 of 1, from 2 to 985: score 413.3, E = 4e-121
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            L l     v   e+L e           +L    G+ + +
  gi|2829001     2    ---SELFLRHRLHVV--EELWE----------SVLRQECGQKMVDLL 33

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        +l    EG+    +     a +  L+  +ai  A+a+     L n+
  gi|2829001    34 RQLRDLCSP-EGQTTHDQASSAVALIEQLNINEAIRAARAFALYFQLINI 82

                    AEEvelAyRRRikkkkhGDFaDEas........AttEsDi...EEt....
                     E  e   +    +    D  D  s ++   ++   E D++ + Et++++
  gi|2829001    83 IEQ-EYEQKQQLTRYSVPDPMDQESwpniiystNQRENDLpinKETgndk 131

                    ...........lKkLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRs
                     ++ ++++   l  L  +ln  P+ +   +    v Lv+tAHPt  vR
  gi|2829001   132 itpyqkgtfavLFPLLFRLNVPPQQIQRLISQLDVRLVFTAHPTEIVRHT 181

                    LLqKnaRiRnCLaqLsAKD....vtveDKkELDEALHREiqAAFRtDEiR
                    +  K+  +   L qL    ++++  + +  E+ E L  Ei   +RtDE+
  gi|2829001   182 IRDKQRQVVHLLQQLDTLQthtgAHPWELAEIKERLLEEIRLWWRTDELH 231

                    RaqPtPqDEmRaGmsYiHEtvWkGvPKFLRRvDtALKniGinERlPYdvP
                      +Pt  DE+ + + Y+ E +++G+P+  +R   ALK        P+  P
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  gi|2829001   232 QFKPTVLDEVDYALHYFQEVLFDGIPQLYKRFAYALK-----QTFPWLEP 276

                    ....LikFssWmGGDRDGknPRvtPEvtRDvCLLaRmmAanlYisqvEDL
                    ++++   F sW+G DRDG nP vtPEvt       R m    Yi+ v  L
  gi|2829001   277 pgknFCSFGSWVGSDRDG-NPSVTPEVTWKTACYQRKMVLERYIQSVKKL 325

                    mFElsmWRCndEL...RvRAEElyrtaardkvvKyYiEFWKqvPPtEPYR
                    +  ls+    +++ ++     El +    d v       ++q    EPYR
  gi|2829001   326 IELLSISMHWSDVlpdLLESLELDQSVLGD-VYDALALRYRQ----EPYR 370

                    viLGdvRDKLYntRERaRHLLAtGiseisEeAvytkvEeFLEPLELCYks
                      L  v  +L ntR+R   L         +   y   EeFL  L L  +
  gi|2829001   371 LKLSYVLRRLENTRDRNLSLYRGETPTNEDSDKYASGEEFLAELRLIQRN 420

                    LCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittH
                    L e G   +  G L  l+ qv  F   L +LDiRqEs R+ D +  i +
  gi|2829001   421 LTETG---LSCGELDNLICQVEIFDFHLAQLDIRQESSRHSDAINEILEY 467

                    Lei..GsYReWsEeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrv
                    L+i +G Y e sE  R  WL aEL+ +RPL++++LP  E   Dv+++frv
  gi|2829001   468 LQIlpGTYNELSESERVSWLTAELQTRRPLIPAELPFSEKTNDVIETFRV 517

                    L....AELPiDsFGaYiismataPsDvLAvELLqRECgvkqt......Lr
                    +++ + E  i     Yiism+   sDvL v LL +E ++  + +  +++r
  gi|2829001   518 VrslqQEFRIRICQTYIISMCRQVSDVLEVLLLAKEAQLFDPatavgsIR 567

                    vvPLFEkLADLeAAPAavekLFsiDWYinridG.................
                    vvPLFE + DL+     +  LF +  Y+  + G+ ++++++++ ++++ +
  gi|2829001   568 VVPLFETVEDLQRSRSVMRELFELPLYRAFLAGgykpdhtennlshsdlk 617

                    ..KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    ++ qevm+GYsDs KD G ls  W + kAq  +  +A +yG  L +FHGR
  gi|2829001   618 pnLQEVMLGYSDSNKDSGFLSSNWEIHKAQKSLQEIAEEYGLNLRIFHGR 667

                    GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                    GG vGRGGGP   AiL+qP   inG +++t qGEv+   +   +L    +
  gi|2829001   668 GGSVGRGGGPAYEAILAQPGHSINGRIKITEQGEVLASKYSLLDLALYHI 717

                    qRFtAAtLEHG.mnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvE
                       t A +    +         W ++mee+ v     YR++++ +P F++
  gi|2829001   718 ETITSAVVQASlLRTGFDDIEAWNEIMEELSVRSRQHYRALIYEDPDFID 767

                    YFRlAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLP
                    +F   tP  E  ++ i sRPa+R  ++  + sLRAiPW+F+WtqtRF LP
  gi|2829001   768 FFHQVTPIEEISQLQISSRPARRSSGkKDLGSLRAIPWVFSWTQTRFLLP 817

                    vWLGvGAAF.KhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                     W GvG A + +  +K    l+ ++  Y +WPFF++ +  +Em  AK D
  gi|2829001   818 SWYGVGTALdEFLQEKPEEHLKLMRYFYIKWPFFKMVISKVEMTLAKVDI 867

                    GiAaLyDkLLva.EeLkPFGk...sLRdkYvEtkdlLLkiAGHkDlLEGD
                     +A  y + L ++E+   F k   ++  +Y  t+dl+Lki G + lL+ D
  gi|2829001   868 EMARHYVQELSSpEDRSRFEKvffQIAREYYLTRDLVLKITGNQRLLDED 917

                    PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                    P L+  + LR+s i  L  +q   LKR+R  +yk    P +
  gi|2829001   918 PTLQRSVQLRNSTILPLGFIQVSLLKRLR--QYKTSSTPGVIHSRYSKG- 964

                    kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        eL++               +Lt+ GiAAGm ntG
  gi|2829001   965 ----ELLRGA-------------LLTINGIAAGMRNTG    985

gi|33241179|ref|NP_876121.1|: domain 1 of 1, from 3 to 1001: score 413.2, E = 4.2e-121
                    *->siDAqLRlLvPGKvsedek..LieYDAL...LlDkFLDiLqDLHGed
                        +D    l +  +v +  +++ i  D ++++Ll k L+++ DL
  gi|3324117     3    ELDNFSMLEASKQVPDRKEssQILADHMsgrLLQKRLELVEDLWETV 49

                    Lk.....EavqECYEl.....sAeYEGKkDtkKLeELGakLtsLdPaDai
                    ++++ + E v     l++ ++s    G + t +++E+   +  +d a+ai
  gi|3324117    50 VRsecplEQVERLLRLkqlsnSSGIVGEEQTNQINEIVELIKEMDLAEAI 99
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                lvAkailHmLnLAnLAEE.ve.......lAyRRRikkkkhGD.Fa.DEas
                  A+a++    L n+ E ++e+++  +++      k     D+Fa+  as
gi|3324117   100 SAARAFSLYFQLVNILEQrIEedsylesISRGQEEKINTSIDpFApPLAS 149

                AttEsDiEEtlKkLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsL
                 t  +   E + +L  +ln  P    e L+   + Lv+tAHPt  vR  +
gi|3324117   150 QTAPATFSELFDRL-RRLNVPPGQLEELLREMDIRLVFTAHPTEIVRHTV 198

                LqKnaRiRnCLaqLsAKDv.tveDKkELDEALHREiqAAFRtDEiRRaqP
                  K+ R+   L qL   +v    ++  L   L  Ei   +RtDE+   +P
gi|3324117   199 RHKQRRVASLLQQLQSDEVfSLSERDNLRLQLEEEIRLWWRTDELHQFKP 248

                tPqDEmRaGmsYiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikF
                t  DE+ + + Y+   +++ +P+  RR+  AL        +P ++    F
gi|3324117   249 TVLDEVDYALHYFQQVLFDAMPQLRRRICSALSQSYPDIDVPQEA-FCTF 297

                ssWmGGDRDGknPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWR
                 sW+G DRDG nP vtPE+t       R +    Y+  v +L   ls+
gi|3324117   298 GSWVGSDRDG-NPSVTPEITWRTACYQRKLMLDRYMHSVQELRNQLSISM 346

                CndELRvRAEElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLY
                  + +     E     +      +  E        EPYR  L    ++L
gi|3324117   347 QWSQVSTQLLESLEMDRVR--FPHIYEERAARYRLEPYRLKLSYTLERLK 394

                ntRERaRHLLAtGis......eis....EeAvytkvEeFLEPLELCYksL
                 t  R   L   G +++ +++++s++++E+  y  ++eF   LEL   sL
gi|3324117   395 FTQQRNQELSEAGWAttiertNVSnnpdEDLHYCSIDEFRRDLELIRNSL 444

                CeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHL
                       +    L  lL qv  F  sL  LDiRqEs R+ + +D +t+ L
gi|3324117   445 VA---TNLSCEQLDTLLTQVHIFAFSLASLDIRQESTRHSEAIDELTRYL 491

                ei.GsYReWsEeKRqEWLlaELkGKRPLlgsDLP...ktEEvkDvldafr
                +++ sY e  E+ +  WL+ EL+  RPL++s +  ++ tEE   v   +
gi|3324117   492 NLpKSYIEMTEDEKVIWLMDELQTLRPLIPSAVQwskSTEETFAVFRMLD 541

                vLA.ELPiDsFGaYiismataPsDvLAvELLqRECgvkqt......Lrvv
                 L +E  +    +Y+ism+ + sD L v LL +E g+   ++++++L v+
gi|3324117   542 RLQkEFGSRICRSYVISMSHTVSDLLEVLLLAKEYGLVDIssessdLLVI 591

                PLFEkLADLeAAPAavekLFsiDWYin...ridGK....qevmvGYsDsG
                PLFE + DL+ AP  +e LF  + Y    +r+  K+++ qe m+GYsDs
gi|3324117   592 PLFETVEDLQHAPSVMEELFQSEIYLKllpRVGEKsqplQELMLGYSDSN 641

                KDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLA
                KD G ls  W + +Aq  +   A  +Gv L lFHGRGG vGRGGGP   A
gi|3324117   642 KDSGFLSSNWEIHQAQIALQNLASSHGVALRLFHGRGGSVGRGGGPAYQA 691

                iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.n
                iL+qP  t++G +++t qGEv+   +   +L    L   t A L   +
gi|3324117   692 ILAQPSGTLKGRIKITEQGEVLASKYSLPELALYNLETVTTAVLQNSLvT 741

                PPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkm
                      P W +Lm ++Av     YR++v   P  v +F   tP  E  k+
gi|3324117   742 NQWDATPSWNELMTRLAVRSRQHYRALVHDNPDLVAFFQEVTPIEEISKL 791

                niGsRPaKRkPsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid
                 i sRPa+Rk + + + sLRAiPW+F Wtq RF LP W GvG A    ++
gi|3324117   792 QISSRPARRKTGAkDLSSLRAIPWVFGWTQSRFLLPSWFGVGTALEEELK 841

                KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva...
                 D   +  L+ + + WPFFR+ +  +Em   K D  +A  y   L ++++
gi|3324117   842 SDPDHIELLRMLNQRWPFFRMLISKVEMTLSKVDLEVAYHYMTSLGShen 891

                .EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYit
                +E      + + ++Y+ t+ l+L+i G   lL  DP L+  + LR+  i
gi|3324117   892 rEAFNCIFEIISNEYKLTRRLVLEITGKPKLLSADPALQLSVDLRNRTIV 941

                tLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpterv
                 L  +q   L R+RD +     +P++s     E      ++ +    ++
gi|3324117   942 PLGFLQVALLCRLRDQN----RQPPMSETLLTEG-----DIGRTYSRSEL 982
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                  aPGLEDtLiLtmKGiAAGmqntG<-*
                    G     +Lt+ GiAAGm ntG
  gi|3324117   983 LRG----ALLTINGIAAGMRNTG    1001

gi|282897196|ref|ZP_06305198.1|: domain 1 of 1, from 31 to 984: score 413.2, E = 4.4e-121
                  *->siDAqLRlLvP..GKvsedekLieYDALLlDkFLDiLqDLHGe.dLk
                      +  qLR L  ++G+   d+  +   A+ l   L i   +   +
  gi|2828971    31    DLLRQLRDLCSpeGQTTHDQASL---AVALIEQLNINEAIRAArAFA 74

                  EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                   + q    +  eYE K+          +Lt     D  +v ++   ++
  gi|2828971    75 LYFQLINIIEQEYEQKQ----------QLTRYSVPDP-VVQESWPNIIYS 113

                  AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                   n  E  +l   +  +        D a A         +  L  +ln  P
  gi|2828971   114 TNQREN-DLPINKELSTDT-PTGNDKATAHQKGTFGVLF-PLLFRLNVPP 160

                  eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                  + +   +    + Lv+tAHPt  vR  +  K+  +   L qL
  gi|2828971   161 QQIQRLISQLDIRLVFTAHPTEIVRHTIRDKQRQVVHLLQQLDTLQTHAG 210

                  ....DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWk
                  +++ +  E+ E L  Ei   +RtDE+   +Pt  DE+ + + Y+ E +++
  gi|2828971   211 ghtwELAEIKERLLEEIRLWWRTDELHQFKPTVLDEVDYALHYFQEVLFD 260

                  GvPKFLRRvDtALKniGinERlPYdvP....LikFssWmGGDRDGknPRv
                  G+P+  +R   ALK        P+  P++++   F sW+G DRDG nP v
  gi|2828971   261 GIPQLYKRFAYALK-----QTFPWLEPpgknFCSFGSWVGSDRDG-NPSV 304

                  tPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndEL...RvRAEEl
                  tPEvt       R m    Yi+ v  L+  ls+    +++ ++     El
  gi|2828971   305 TPEVTWKTACYQRKMVLERYIQSVKKLIELLSISMHWSDVlpdLLESLEL 354

                  yrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAt
                   +    d v       ++q    EPYR  L  v  +L ntR+R   L
  gi|2828971   355 DQSVLGD-VYDALALRYRQ----EPYRLKLSYVLRRLENTRDRNLSLYRG 399

                  GiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvst
                        +   y   EeFL  L L  + L e G   +  G L  l+ qv
  gi|2828971   400 ETPSNEDGDKYASGEEFLAELRLIQRNLTETG---LSCGELDNLICQVEI 446

                  FGLsLvKLDiRqEseRqtDvlDAittHLei..GsYReWsEeKRqEWLlaE
                  F   L +LDiRqEs R+ D +  i + L+i +  Y e sE  R  WL  E
  gi|2828971   447 FDFHLAQLDIRQESSRHSDAINEILEYLQIlpRTYNELSESERVSWLTGE 496

                  LkGKRPLlgsDLPktEEvkDvldafrvL....AELPiDsFGaYiismata
                  L+ +RPL++++LP  E   Dv+++frv+++ + E  i     Yiism+
  gi|2828971   497 LQTRRPLIPAELPFSEKTNDVIETFRVVrslqQEFRISICQTYIISMCRQ 546

                  PsDvLAvELLqRECgvkqt......LrvvPLFEkLADLeAAPAavekLFs
                   sDvL v LL +E  +  + +  +++rvvPLFE + DL+     +  LF
  gi|2828971   547 VSDVLEVLLLAKESRLFDPatavgsIRVVPLFETVEDLQRSRSVMRELFE 596

                  iDWYinridG.............KqevmvGYsDsGKDAGRlsAAWqLYkAq
                  +  Y+  + G+ ++++++ +++ qevm+GYsDs KD G ls  W + kAq
  gi|2828971   597 LPLYRAFLAGgykpdhsdlrpdLQEVMLGYSDSNKDSGFLSSNWEIHKAQ 646

                  EEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvt
                    + ++A kyG  L +FHGRGG vGRGGGP   AiL+qP   inG +++t
  gi|2828971   647 KSLQRIAEKYGLNLRIFHGRGGSVGRGGGPAYEAILAQPGHSINGRIKIT 696

                  vqGEviEfsFGEEnLCFrsLqRFtAAtLEHG.mnPPvsPkPEWRkLmeem
                   qGEv+   +   +L    +   t A +    ++        W ++mee+
  gi|2828971   697 EQGEVLASKYSLLDLALYHIETITSAVVQASlLKTGFDDIEAWNEIMEEL 746

                  AvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs.GGi
                   v     YR++++ +P F+++F   tP  E  ++ i sRPa+R  ++  +
  gi|2828971   747 SVRSRQHYRALIYDDPDFIDFFHQVTPIEEISQLQISSRPARRSSGkKDL 796

                  esLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD.iKnlqkLkEmYke
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                    LRAiPW+F+WtqtRF LP W GvG A    ++  +   l+ ++  Y +
  gi|2828971   797 GGLRAIPWVFSWTQTRFLLPSWYGVGTALNEFLQEQpEEHLKLMRYFYIK 846

                    WPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP.FGk...sLRdkY
                    WPFF++ +  +Em  AK D  +A  y + L + e +P+F k  +++  +Y
  gi|2828971   847 WPFFKMVISKVEMTLAKVDIEMARHYVQELSSPEDRPrFEKvftQIAREY 896

                    vEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRD
                      t++l Lki G + lL+ DP L+  + LR+s i  L  +q   LKR+R
  gi|2828971   897 YLTRELALKITGNQRLLDEDPTLQRSVQLRNSTILPLGFIQVSLLKRLR- 945

                    PsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGi
                     +yk    P +             eL++              +Lt+ Gi
  gi|2828971   946 -QYKTSSTPGVIHSRYSKG-----ELLRGA-------------LLTINGI 976

                    AAGmqntG<-*
                    AAGm ntG
  gi|2828971   977 AAGMRNTG    984

gi|86609298|ref|YP_478060.1|: domain 1 of 1, from 28 to 978: score 412.7, E = 6.2e-121
                    *->siDAqLRlL.vPGKvsedekLieYDALLlDkFLD..iLqDLHGedLk
                         D     L+v       ++L++    L++   ++ iLq+  G++L
  gi|8660929    28    ERDPLAHSLqVNEAFNRRNNLLNRRLQLVEELWEsvILQEC-GQSLV 73

                    EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    +  q    +    EG+     + E+   +  L    +i  A+a+     L
  gi|8660929    74 DLLQRLRSMCSP-EGQALEYPIPEVLQIIEYLSLDATIQTARAFALFFQL 122

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                     n+ E  +   R   +  +  D +           E  +  L  ++   P
  gi|8660929   123 INIVE--QHYERAEDSDMRMVD-SQQRTVRENEKFERLFPYLRAQG-VPP 168

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL.sAKDvtv
                          L    + +v+tAHPt  vR  +  K+      L+qL+ A    +
  gi|8660929   169 GLLRRLLEQLHIRMVFTAHPTEIVRHTIREKQRAFSRLLSQLdWAEQTQP 218

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                       + + E +  E+   +RtDE+  ++Pt   E+ + + Y+ E +++ +P
  gi|8660929   219 LQAQMIKEQMAEEVLLWWRTDELHQSKPTVLNEVDYTLHYFEEVLFQAIP 268

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                             LK        P  +    F sW+GGDRDG nP vt +vt
  gi|8660929   269 LLHEYLSRSLKK-AFPSVEPPPAGFCNFGSWVGGDRDG-NPSVTADVTWQ 316

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                         R +    Yi+ v  L   ls+     ++     +      r  +
  gi|8660929   317 TARYQRNLILGKYIESVKALTKTLSISLHWGDVDSQLLDALEQDHRL-MP 365

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei..sEe
                      Y  F  q   +EPYR  L  +  +L  tRER R L        +++ +
  gi|8660929   366 EVYESFSLQY-RQEPYRLKLSYIQRRLELTRERNRNLADSACLPTppPVD 414

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y + EeFL  L L  ksL + G   +    L  l+ qv  FG  L  L
  gi|8660929   415 NAYANAEEFLADLQLIQKSLKNSG---LSCRQLDHLIQQVQVFGFHLAHL 461

                    DiRqEseRqtDvlDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLl
                    DiRq+s  +   l  i + L i +  Y e  Ee +  +Ll EL+ +RPL+
  gi|8660929   462 DIRQDSSYHEAALTEIFEYLRIlpRPYNEMTEEEKTAFLLQELQTRRPLI 511

                    gsDLPktEEvkDvldafrvLAELPiDsFG.....aYiismataPsDvLAv
                    + ++   E  ++ + +fr L  L  + FG    + Y+ism+   sD L v
  gi|8660929   512 PLEIAFSEKTAELIATFRTLRRLQQE-FGlaicqTYVISMSRQLSDLLEV 560

                    ELLqRECgv......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                     L+ +E g+ ++ +++ +L vvPLFE + DL+ AP  + +L  i +Y+
  gi|8660929   561 LLMAKEVGLydpisgRGSLAVVPLFETVEDLKRAPEVLRQLLEIPFYRQY 610

                    idGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                    +  +++ qevm+GYsDs KD G ls  W +YkAq  +  vA  yGvKL +
  gi|8660929   611 LAQQgnlQEVMLGYSDSNKDSGFLSSNWEIYKAQQRLQTVAESYGVKLQI 660
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                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                    FHGRGG vGRGGGP   AiL+qP   + G +++t qGEv+   +   +L
  gi|8660929   661 FHGRGGSVGRGGGPAYEAILAQPGRSVGGRIKITEQGEVLASKYSLQDLA 710

                    FrsLqRFtAAtLEHGmnPPv.sPkPEWRkLmeemAvvAtEEYRsvvvKEP
                       L   t A +   +    +    EW +Lme +A      YR +v+
  gi|8660929   711 IFNLETVTSAVIQASLLRTYpNDLHEWSRLMESLAERSRQVYRNLVYEQE 760

                    RFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqtR
                     FvE+F   tP  E  ++ i sRPa+R  s + i sLRAiPW+F+Wtq R
  gi|8660929   761 GFVEFFHEVTPIEEISQLQISSRPARRSGSQkDIGSLRAIPWVFSWTQSR 810

                    FHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAK
                    F LP W GvG A +  + +   nl  L+ +Y+eWPFFR+ +  +Em  AK
  gi|8660929   811 FLLPAWYGVGTALQEYVARGEHNLNHLQHLYREWPFFRMVISKVEMTLAK 860

                    GDPGiAaLyDkLLva....EeLkPFGksLRdkYvEtkdlLLkiAGHkDlL
                     D  iA  y + + ++++ E      + + ++   t+ ++L+i GH++lL
  gi|8660929   861 VDLQIARHYVREMSSperlERAMELFECIAQEMHRTRTIVLQITGHRELL 910

                    EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                    E DPYLK  + LR+  i  L  +q   LKR+R+ +   t r    +
  gi|8660929   911 ENDPYLKRSVQLRNRSIVPLGFIQVSLLKRLRERQGSRTGRTRYDR---- 956

                    EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                          +eL++               +Lt+ GiAAGm ntG
  gi|8660929   957 ------AELLRGA-------------LLTINGIAAGMRNTG    978

gi|87124941|ref|ZP_01080788.1|: domain 1 of 1, from 1 to 979: score 408.8, E = 9e-120
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                              +       d++L++    L++   +++L     ++  E
  gi|8712494     1    --------MSRCPNG-DDQLLQQRLELVEELWEtVLRSECPPEQAER 38

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                          ls    G  D++  + +   +  +d  +ai  A+a++    L n
  gi|8712494    39 LLRMKQLSEPLAGDGDSSSSDAVVQLIREMDLVEAIAAARAFSLYFQLVN 88

                    LAEE.ve....lAyRRRikkkkhGDFaDEasAttEsDiE.EtlKkL...v
                    + E ++e+++ lA   R +     +  D       s  E+ t++ L ++
  gi|8712494    89 ILEQrIEedsyLASMSRCQESSEAEGVDPFAPPLASQTEpATFRDLferL 138

                    lklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLs
                     +ln  P+     L+n  + Lv+tAHPt  vR  +  K+ R+   L qL
  gi|8712494   139 RRLNVPPAQLEALLQNLDIRLVFTAHPTEIVRHTVRHKQRRVASLLQQLQ 188

                    .AKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHE
                    +  D+   D+  L   L  Ei   +RtDE+   +P   DE+ + + Y+
  gi|8712494   189 gTVDMASSDQASLRRQLEEEIRLWWRTDELHQFKPSVLDEVDYALHYFQQ 238

                    tvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRv
                     +++ +P+  RR+  AL       RlP  +    F sW+G DRDG nP v
  gi|8712494   239 VLFDAMPQLRRRIQAALSQNYPDVRLP-PAAFCTFGSWVGSDRDG-NPSV 286

                    tPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrt
                    tPE+t       R +    Y+s v DL   ls+    + + +   E
  gi|8712494   287 TPEITWRTACYQRQLMLDRYVSAVQDLRDQLSISMQWSQVSAPLLESLEM 336

                    aardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGis
                     +       Y E        EPYR  L    ++L  t  R   L   G
  gi|8712494   337 DRLR-FPEVYEERAARY-RLEPYRLKLSYTLERLRLTQQRNQQLSEAGWR 384

                    eisEeAv.............ytkvEeFLEPLELCYksLCeCGDkviADG
                      +E  v+ ++++ + ++  +y  v eF   LEL   sL       +
  gi|8712494   385 TPPEGLVpcqptgasagealhYGSVAEFRSDLELIRNSLVS---TELTCD 431

                    sLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsE
                     L  lL qv  FG sL  LDiRqEs R+ D lD +t+ L ++ +Y    E
  gi|8712494   432 PLDTLLTQVHIFGFSLASLDIRQESTRHSDALDELTRYLKLpTAYGAMDE 481

                    eKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFG...
```

```
                     R EWLl E++ +RPL+++ +      ++ +  fr+L  L  + FG++
  gi|8712494   482 SARVEWLLEEMQTRRPLIPPAVEWSAATAETIAVFRMLHRL-QEEFGsri 530

                    ..aYiismataPsDvLAvELLqRECgvkqt......LrvvPLFEkLADLe
                     + Y+ism+ + sD L v LL +E g+  +  ++ +L vvPLFE + DL+
  gi|8712494   531 crTYVISMSHSVSDLLEVLLLAKEAGLVDPaahhadLLVVPLFETVEDLQ 580

                    AAPAavekLFsiDWYi.......nridGKqevmvGYsDsGKDAGRlsAAW
                     AP  + +LF    Y++  ++ + + +  qe m+GYsDs KD G ls  W
  gi|8712494   581 RAPEVMGQLFEHPLYRqllpragEQAQPLQELMLGYSDSNKDSGFLSSNW 630

                    qLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtin
                     + +Aq  +   A ++ + L lFHGRGG vGRGGGP   AiL+qP  t++
  gi|8712494   631 EIHQAQIALQDLASRHDIGLRLFHGRGGSVGRGGGPAYQAILAQPSGTLQ 680

                    GslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsPkPEWR
                    G +++t qGEv+   +   +L    L     A +   +    +   P W
  gi|8712494   681 GRIKITEQGEVLASKYSLPELALYNLETMSTAVVQNSLvTSQLDATPSWN 730

                    kLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRk
                    +Lm ++A      YR++v   P  v +F   tP  E  k+ i sRPa+Rk
  gi|8712494   731 DLMSRLASRSRSHYRALVHDNPDLVAFFQQVTPIEEISKLQISSRPARRK 780

                    PsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLk
                     + + + sLRAiPW+F Wtq RF LP W GvG A    +  D   l  L+
  gi|8712494   781 SGAkDLSSLRAIPWVFGWTQSRFLLPSWFGVGTALADEVANDQEQLELLR 830

                    EmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva....EeLkPFGks
                     + + WPFFR+ +  +Em   K D  +A  y   L + +++E
  gi|8712494   831 RLHQRWPFFRMLISKVEMTLSKVDLELARHYVTSLGSadhrEAFERIYAT 880

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    + d+Y  t+ l+L i G   lL+ DP L+  + LR+  i  L  +q   L
  gi|8712494   881 IADEYSLTRRLVLAITGQERLLDADPALQLSVDLRNRTIVPLGFLQVALL 930

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    +R+RD +     +P++s     ++    d+       ++   G     +L
  gi|8712494   931 RRLRDQN----RQPPMSEAPNTDP----DGRTYSR--SELLRG----ALL 966

                    tmKGiAAGmqntG<-*
                    t+ GiAAGm ntG
  gi|8712494   967 TINGIAAGMRNTG    979

gi|170078023|ref|YP_001734661.1|: domain 1 of 1, from 9 to 995: score 407.0, E = 3.1e-119
                    *->siDAqLRlLvPGKvsedekLieYDALLl.DkFLDiLqDLHGedLkEa
                       s +A L        s  + L++    L++D +  +Lq   G+ L E
  gi|1700780     9    SAEAEL-------LSTSQSLLRQRLTLVeDIWQAVLQKECGQKLVER 48

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                               +G+        +   +  Ld  Dai  A+a+     L n
  gi|1700780    49 LNH-LRATRTADGQSLNFSPSSISELIETLDLEDAIRAARAFALYFQLIN 97

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEE.......tlKkLv..
                      E  +   R   + ++    a  ++A   s   E  +++ +t+  L ++
  gi|1700780    98 SVEQ-HYEQREQQQFRRNLASANASEANGNSVHTEiaptqagTFDWLFph 146

                    lklnKsPeEvFeALKnqs.vDLvltAHPtqsvRRsLLqKnaRiRnCLaqL
                    lk +  P    + L nq ++ Lv+tAHPt  vR  +  K+ Ri   L qL
  gi|1700780   147 LKHQNMPPQTIQRLLNQLdIRLVFTAHPTEIVRHTIRNKQRRIAGILRQL 196

                    s.....AKDvtveDKkELDEA...LHREiqAAFRtDEiRRaqPtPqDEmR
                     +++++ K +   D  E++  +++L  Ei   +RtDE+   +P   DE+
  gi|1700780   197 DqteegLKSLGTSDSWEIENIqqqLTEEIRLWWRTDELHQFKPQVLDEVD 246

                    aGmsYiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGD
                    + + Y+ E +++  P    R   ALK      ++P       F sW+GGD
  gi|1700780   247 YALHYFEEVLFDTLPELSVRLQQALKASFPTLKVP-TTNFCNFGSWVGGD 295

                    RDGknPRvtPEvtRDvCLLaRmmAanlYisqvEDL..mFElsmWRCndEL
                    RDG nP vtP+vt       R +    Yi  vE L+++  ls+   n
  gi|1700780   296 RDG-NPSVTPDVTWKTACYQRGLVLERYIASVESLsdVLSLSLHWSN--- 341
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                    RvRAEElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRER
                     v  + l +  + + +     E       +EPYR  L  ++ +L nt ER
  gi|1700780   342 -VLPDLLDSLEQDQNIFPDIYETLAIRYRQEPYRLKLAYIKRRLENTLER 390

                    aRHLLAtGi....seisEeAvytkvEeFLEPLELCYksLCeCGDkviADG
                     R L      +++ e +++ vy    eFL  L L   sL +     i
  gi|1700780   391 NRRLANMPAwenkVEAADDKVYICGQEFLADLKLIRESLVQ---TEINCA 437

                    sLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei..GsYReWs
                    +L  l+ qv  F   L +LD RqEs R+ D +  i   L++ + sY + s
  gi|1700780   438 ALDKLICQVEIFSFVLTRLDFRQESTRHSDAIAEIVDYLGVlpKSYNDLS 487

                    EeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvL....AELPiDs
                    +  +  WL+ ELk +RPL++ ++   E   + +++++vL++ + E  i
  gi|1700780   488 DAEKTTWLVQELKTRRPLIPKEMHFSERTVETIQTLQVLrrlqQEFGIGI 537

                    FGaYiismataPsDvLAvELLqRECgvkqtL......rvvPLFEkLADLe
                       Yiism+   sDvL v LL  E g+  +L++ ++ r+ PLFE + DL+
  gi|1700780   538 CQTYIISMTNEVSDVLEVLLLAQEAGLYDPLtgmttiRIAPLFETVDDLR 587

                    AAPAavekLFsiDWYinridG.....................KqevmvGY
                     AP  ++ LF i  Y+  + G+ +++ +++ +++ +++  ++ qe+m+GY
  gi|1700780   588 NAPEIMQALFEIPLYRACLAGgyeppadgrcdetfgdrlvpnLQEIMLGY 637

                    sDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGP
                    sDs KD G ls  W + kAq  + +vA  yG+ L +FHGRGG vGRGGGP
  gi|1700780   638 SDSNKDSGFLSSNWEIHKAQKNLQQVADPYGIDLRIFHGRGGSVGRGGGP 687

                    tHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEH
                       AiL+qPP tinG +++t qGEv+   +   +L    L     A +
  gi|1700780   688 AYAAILAQPPNTINGRIKITEQGEVLASKYSLPDLALYHLESVSTAVIQS 737

                    GmnPP.vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElE
                     +   +      W ++me++       YR++++ EP F ++F + tP  E
  gi|1700780   738 SLLASgFDDIQPWNRIMEDLSQRSRAAYRALIYEEPDFLDFFMSVTPIPE 787

                    YGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFK
                      ++ i sRPa+Rk + + + sLRAiPW+F+Wtq RF +P W GvG A +
  gi|1700780   788 ISQLQISSRPARRKKGNkDLSSLRAIPWVFSWTQSRFLVPAWYGVGTALQ 837

                    hAidKD.iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLy.DkL
                       + D++ nl+ ++  Y +WPFFR+ +  +Em   K D  +A+ y  +L
  gi|1700780   838 GFFEEDpVENLKLMRYFYSKWPFFRMVISKVEMTLSKVDLQMASHYvHEL 887

                    LvaEeLkPFG...ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLR
                       E++  F +  +++ ++Y  tk l+L+i     lL+GD  L+  + LR
  gi|1700780   888 AEKEDIPRFEkllEQISQEYNLTKRLILEITENEALLDGDRPLQRSVQLR 937

                    dsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLn
                    +  i  L  +q   LKR+R              y  E     + +v+
  gi|1700780   938 NGTIVPLGFLQVSLLKRLR--------------QYTRET---QASIVHFR 970

                    ptervaPGLEDtLiLtmKGiAAGmqntG<-*
                            L    +Lt+ GiAAGm ntG
  gi|1700780   971 ---YSKEELLRGALLTINGIAAGMRNTG    995

gi|119512252|ref|ZP_01631340.1|: domain 1 of 1, from 57 to 1034: score 405.8, E = 7e-119
                    *->siDAqLRl.LvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEa
                       s + q R + +   v   e+L   +A+   +   +   L     +E+
  gi|1195122    57    SPEGQARNdQAASAVKLIEQLNINEAIRAARAFALYFQLINIIEQEY 103

                    vqECYElsAeYEGKkDtkKLeELGakLt..sLdPaDailvAkailHmLnL
                     q    l    EG  +t   eE  +  t +s +  D  +v k i
  gi|1195122   104 EQR-QQLTRYSEGEAETVIQEETLSNATysSNQNEDDAIVNKGIETCTEA 152

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                     n        +  +   k++G Fa             tl     kln  P
  gi|1195122   153 IN--HSTTTSWVTKSTGKQKGTFA-------------TLFPHLFKLNVPP 187

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
```

```
                + +   +    v Lv+tAHPt  vR  +  K+  + n L +L   +   e
gi|1195122   188 QQIQRLISHLDVRLVFTAHPTEIVRHTIRDKQRQVVNLLQKLDVAENRTE 237

                ........DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHE
                ++ ++ + +  +L E L  Ei   +RtDE+   +Pt  DE+ + + Y+ E
gi|1195122   238 stlggypwEAADLREQLLEEIRLWWRTDELHQFKPTVLDEVDYALHYFQE 287

                tvWkGvPKFLRRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPR
                 +++G+P+  +R   AL+K     E  P       F sW+G DRDG nP
gi|1195122   288 VLFDGIPQLYKRLKYALgKTFTWLE--PPHKNFCSFGSWVGSDRDG-NPS 334

                vtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyr
                vtPE+t       R m    Yi  v  L+  ls+    +++     E
gi|1195122   335 VTPEITWQTACYQRKMVLERYIKSVKQLIELLSVSMHWSDVLPELLESLE 384

                taardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi
                  +++       +       +EPYR  L  v  +L ntR+R   L
gi|1195122   385 MDQSQ--LGDVYDALALRYRQEPYRLKLAYVLRRLENTRDRNVALYNREK 432

                seisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFG
                s   +  +y    eFL  L L  + L e G   +    L  l+ qv  F
gi|1195122   433 SPKEDSPMYRSGSEFLAELRLIERNLTETG---LSCRELETLICQVEIFD 479

                LsLvKLDiRqEseRqtDvlDAittHLei..GsYReWsEeKRqEWLlaELk
                  L +LDiRqEs R+ D l  i + L++ + sY e sEe+R  WL  EL+
gi|1195122   480 FNLTQLDIRQESTRHSDALNEILEYLQVlpQSYNELSEEQRVAWLTGELQ 529

                GKRPLlgsDLPktEEvkDvldafrvL....AELPiDsFGaYiismataPs
                 +RPL++++LP  E   Dv+++fr+L++ + E  +     Yiism+   s
gi|1195122   530 TRRPLIPAELPFSEKTNDVIETFRILrslqQEFGVNICQTYIISMCREVS 579

                DvLAvELLqRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiD
                DvL v LL +E  +  +    +t++vvPLFE + DL+     + +LF +
gi|1195122   580 DVLEVLLLAKESRLFDpvvavgTIQVVPLFETVEDLQRSRSVMRQLFELP 629

                WYinridG.........................KqevmvGYsDsGKD
                 Y+  + G+ +  +  ++++++ +  +++ ++ +++ qevm+GYsDs KD
gi|1195122   630 LYRALLAGgyealkaiqqegsslpivpttaspltpnLQEVMLGYSDSNKD 679

                AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                 G ls  W + kAq  +  +A  yG  L +FHGRGG vGRGGGP   AiL
gi|1195122   680 SGFLSSNWEIHKAQKSLQTIAEGYGLSLRIFHGRGGSVGRGGGPAYEAIL 729

                sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                +qP   inG +++t qGEv+   +   +L    L   t A +   +
gi|1195122   730 AQPGHSINGRIKITEQGEVLASKYSLLDLALYNLETITTAVIQASLLRTG 779

                sPkPE.WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                    E+W ++mee+Av     YR +++  P F+++F   tP  E  ++ i
gi|1195122   780 FDDIEpWNEIMEELAVRSRQHYRNLIYEQPDFIDFFHQVTPIEEISQLQI 829

                GsRPaKRkPsG..GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidK
                 sRPa R+PsG++ + sLRAiPW+F+WtqtRF LP W G+G A +  +d
gi|1195122   830 SSRPA-RRPSGkkDLSSLRAIPWVFSWTQTRFLLPSWYGIGTALQGFLDE 878

                D...iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLy.DkLLva
                ++++   l+ L+  Y +WPFF++ +   Em  AK D  +A  y  +L
gi|1195122   879 EeesEEHLKLLRYFYLKWPFFKMVISKAEMTLAKVDMQMAHHYvQELGNP 928

                Ee...LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsY
                E++ +L    +++ d++  t+dl+Lki G   lL+GDP L+  + LR+
gi|1195122   929 EDqarLEKVFQQIADEFYLTRDLVLKITGNTRLLDGDPVLQRSVQLRNGT 978

                ittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpte
                i  L  +q   LKR+R            s+   +       ++++    +
gi|1195122   979 IVPLGFIQVSLLKRLRQ-----------SRNITATS-----GVIH----S 1008

                rvaPG.LEDtLiLtmKGiAAGmqntG<-*
                r++ G+L    +Lt+ GiAAGm ntG
gi|1195122  1009 RYSKGeLLRGALLTINGIAAGMRNTG    1034
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gi|148254376|ref|YP_001238961.1|: domain 1 of 1, from 8 to 928: score 405.8, E = 7.4e-119
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                     s D      +  +  e++  ++ D  Ll + L+D + D  G d+ +
  gi|1482543     8    SEDIRPSRAADAQAMEEDARLRDDIRLLGRILgDTVRDQEGADVFDL 54

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v      s  +   +D +   EL   L ++  a+++ + +a++    LAn
  gi|1482543    55 VERIRQTSVRFHRDEDRQARRELEQILDGMTIAETVRIVRAFSYFSHLAN 104

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  +AE+ +   R R +          + A     +  tl +  + +    ++
  gi|1482543   105 IAEDQNNIRRMRARSDA------NGGAGM---LAATLAHAKSAG-FEAAD 144

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                           v  vltAHPt   R+s + ++  +   L       +t++++
  gi|1482543   145 LRKFFSTALVSPVLTAHPTEVRRKSTMDREMEVAMLLDRRERMQLTPDER 194

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  +  DEAL R +   + t  +RR++ t  DE+  G+s++  t  + vP+ L
  gi|1482543   195 EANDEALRRAVLTLWQTNLLRRTKLTVLDEVTNGLSFYDYTFLREVPRLL 244

                  RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                     +  L n G  E     +  ++  sW+GGDRDG nP vt Ev R
  gi|1482543   245 CTLEDRL-NDG-AEVAGDLASFLRMGSWIGGDRDG-NPFVTAEVMRGTLK 291

                  LaRmmAanlYisqvEDLmFElsmWR....CndELRvRAEElyrtaardkv
                  L   +A   Y++ +  L  Els+  +  +  +ELR+ AE    t+
  gi|1482543   292 LQSSLALHYYLEELHLLGGELSIAAhladVSEELRALAERSPDTSPHR-- 339

                  vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseis..E
                               EPYR  +  +  +L  t  +    L   is ++ +
  gi|1482543   340 ------------SGEPYRLAVSGIYARLAATAKK----LGIQISRLPvgV 373

                  eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                   A y  v +F + L++  +sL      viA G L  l R v  FG  L +
  gi|1482543   374 GAPYDSVKQFQDDLDVLHRSLIANNAEVIARGRLRLLRRAVDCFGFHLAR 423

                  LDiRqEseRqt.DvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLl
                  LDiRq s  + + v + i t +   sY   sE+ R   L++EL+  RPL+
  gi|1482543   424 LDIRQNSTVHErTVAELIDTAMPGMSYMALSEDARVGLLVSELRNTRPLV 473

                  gsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAvE
                     +   +E    l+ fr  AE + +   D     iism+   sD+L v
  gi|1482543   474 SQFVKYSDETVGELELFRAAAEahatFGADVISQCIISMCKGMSDMLEVA 523

                  LLqRECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                  LL +E g+ +++++ ++ +vPLFE + DL+A    ++++ ++  Y+  +d
  gi|1482543   524 LLLKEVGLidpsgRCAVNIVPLFETIEDLQASSGIMDRMLALHDYRRLVD 573

                  GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                   ++  qevm+GYsDs KD G +   W LYkA   ++ +  ++G++L lFH
  gi|1482543   574 SRgavQEVMLGYSDSNKDGGFVTSGWELYKAEIGLVEIFERHGIRLRLFH 623

                  GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                  GRGG vGRGGGP   Ai++qP   +nG +R+t qGE+i   +   ++
  gi|1482543   624 GRGGSVGRGGGPSYDAIIAQPGGAVNGQIRITEQGEIISSKYSNAEVGRN 673

                  sLqRFtAAtLEHGmnPPvsPkP..EWRkLmeemAvvAtEEYRsvvvKEPR
                   L   +AAtLE  +  P  P P++E+   m+++   A   YR +v+
  gi|1482543   674 NLEILAAATLEASLLHPRQPAPkrEYLTAMDRLSELAFKAYRGLVYETDG 723

                  FvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFH
                  Fv+YF   t   E   +niGsRPa Rk    ie LRAiPW+F+W q R
  gi|1482543   724 FVDYFWASTVINEIATLNIGSRPASRKKTRAIEDLRAIPWVFSWAQCRLM 773

                  LPvWLGvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                  LP W G+G A  ++  +   + +  L+E+Y+eWPFFR+ l  ++mv AK
  gi|1482543   774 LPGWYGFGSAVEtWIAENPEQGMPFLRELYQEWPFFRMLLSNMDMVLAKS 823

                  DPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                     iA+ y +L+  E L++k FG+ +R ++    + LL i G   lL G
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  gi|1482543   824 SIAIASRYAELVPDEALreKIFGR-IRREWHLAIETLLDIMGQERLLQGN 872

                   PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                   P L   +R R +Y+  Ln +q                  +l KE+ + n
  gi|1482543   873 PLLERSVRNRFPYLDPLNHVQV----------------ELLKEHRAQN- 904

                   kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                             p e+v  G+     Lt+ Gi AG+ ntG
  gi|1482543   905 ----------PDEQVLRGIQ----LTINGISAGLRNTG    928

gi|116072588|ref|ZP_01469854.1|: domain 1 of 1, from 4 to 995: score 404.4, E = 1.9e-118
                   *->siDAqLRlLvP...GKvsedekLieYDALLl.DkFLDiLqDLHGedL
                      s    L    P+++G      +L++   +L++D +  +L     ++
  gi|1160725     4    STAHALQGEQPkesGVTPGAGRLLQNRLVLVeDLWQTVLRSECPPEQ 50

                   kEavqECYEls..AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHm
                    +       ls++   EG+   +  e +   + ++d ++ai  A+a++
  gi|1160725    51 SDRLLRLKQLSdpVALEGRDGKSTSEAIVELIRAMDLSEAIAAARAFSLY 100

                   LnLAnLAEEv..elAyRRRikkkkhGD.........Fa.DEasAttEsDi
                     L n+ E   +e  y    + +k  D+++++  ++Fa+  as t  +
  gi|1160725   101 FQLINILEQRieEDSYLDSLSPRKSEDggrreafdpFApPLASQTDPATF 150

                   EEtlKkLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRi
                    E + +L       P+ v   L+   + Lv+tAHPt  vR  +  K+ R+
  gi|1160725   151 GEVFERLRRMN-VPPAQVEALLQELDIRLVFTAHPTEIVRHTVRHKQRRV 199

                   RnCLaqLsAKD.vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmR
                    n L qL    ++  + K +L   L  Ei   +RtDE+   +Pt  DE+
  gi|1160725   200 ANLLQQLQSDSpMALQVKDDLRQQLEEEIRLWWRTDELHQFKPTVLDEVD 249

                   aGmsYiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGD
                     + Y+   +++ +P+  RR    L        +P ++    F sW+G D
  gi|1160725   250 STLHYFQQVLFEAMPQLRRRLTSSLHRHYPDVQVP-QASFCTFGSWVGSD 298

                   RDGknPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRv
                   RDG nP vt E+t       R +   lYis v  L   ls+    + +
  gi|1160725   299 RDG-NPSVTTEITWRTACYQRQLMLELYISSVQALRNQLSISMQWSQVAP 347

                   RAEElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaR
                      E     +         E        EPYR  L  + ++L  t  R
  gi|1160725   348 ALLESLEMDRLR--FPEIYERRAARYRLEPYRLKLSYILERLERTLKRND 395

                   HLLAtGi....seis.......EeAvytkvEeFLEPLELCYksLCeCGDk
                    L   G ++++  i++++++++E   yt v++F   LEL   sL   G
  gi|1160725   396 QLSDAGWkspkDAIPtdgppgsEALHYTSVDQFRNDLELIRNSL--IGTE 443

                   viADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.Y
                      +  L  lL qv  FG sL  LDiRqEs R+ D +D +t+ Le+  +Y
  gi|1160725   444 LTCE-QLDTLLHQVHIFGFSLASLDIRQESTRHSDAIDELTRFLELPQpY 492

                   ReWsEeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDs
                    e  E  R  WL+ EL+ +RPL++  +   E  ++ +  fr+L  L  +
  gi|1160725   493 GEMEESTRVAWLIEELRTRRPLIPTAVRWSETTAETMAVFRMLHRL-QEE 541

                   FG.....aYiismataPsDvLAvELLqRECgv......kqtLrvvPLFEk
                   FG++  ++Y+ism+ + sD L v LL +E g+ ++  +k +L vvPLFE
  gi|1160725   542 FGqrichSYVISMSHTASDLLEVLLLAKEAGLvdpaarKASLLVVPLFET 591

                   LADLeAAPAavekLFsiDWYinr.....idGK..qevmvGYsDsGKDAGR
                   + DL+ APA ++ LF +  Y+   +  +i+G++ qe m+GYsDs KD G
  gi|1160725   592 VEDLQRAPAVMDELFNTPLYRDLlpmvgIQGQplQELMLGYSDSNKDSGF 641

                   lsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqP
                   ls  W + +Aq  +     + Gv L lFHGRGG v RGGGP   AiL+qP
  gi|1160725   642 LSSNWEIHQAQLALQDLSSRQGVALRLFHGRGGSVSRGGGPAYQAILAQP 691

                   PDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsP
                     t++G +++t qGEv+   +   +L    L   t A +   +    +
  gi|1160725   692 SGTLQGRIKITEQGEVLASKYSLPELALYNLETVTTAVVQNSLvTNQLDA 741
```

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                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                     P W +Lm ++     E YR++v   P  v +F   tP  E  k+ i sR
  gi|1160725   742 TPSWNQLMSRLSARSREHYRALVHDNPDLVAFFQQVTPIEEISKLQISSR 791

                    PaKRkPsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    Pa+Rk + + + sLRAiPW+F Wtq RF LP W G+G A    ++ D
  gi|1160725   792 PARRKTGAkDLSSLRAIPWVFGWTQSRFLLPSWFGFGTALAEEVKADPEQ 841

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL....vaEeLk
                    l  L+ + + WPFFR  +  +Em   K D  +A  y + L++++  E
  gi|1160725   842 LDLLRRLHQRWPFFRTLISKVEMTLSKVDLDLAHHYMNSLgkpeQREAFE 891

                    PFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvf
                         +  +Y  t++l+L+i G   lL  D  L+  + LR+  i  L  +
  gi|1160725   892 AIFAVISTEYALTRKLVLEITGQPRLLGADQGLQLSVDLRNRTIVPLGFL 941

                    qAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLE
                    q   LKR+RD +     +P++s    + +   a e  +    ++   G
  gi|1160725   942 QVALLKRLRDQN----RQPPMS----ESP--GAPEDTRTYSRSELLRG-- 979

                    DtLiLtmKGiAAGmqntG<-*
                       +Lt+ GiAAGm ntG
  gi|1160725   980 --ALLTLNGIAAGMRNTG    995

gi|33863980|ref|NP_895540.1|: domain 1 of 1, from 24 to 1004: score 403.3, E = 3.9e-118
                    *->siDAqLRlLvPGKvsedekLieYDALLl.DkFLDiLqDLHGedLkEa
                           q R++  G+ +   +L++    L++D +  +L     +d  E
  gi|3386398    24    ---EQPRAIGEGQQA--GRLLQNRLELVeDLWQTVLRSECPPDQAER 65

                    vqECYEls..AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                          ls++   EG  + +    +   +  +d a+ai  A+a++    L
  gi|3386398    66 LLRLKQLSepLALEGADENSASRAIVLLIQEMDLAEAITAARAFSLYFQL 115

                    AnLAEE.ve....lAyRRRikkkkhGD.....FaDEasAttE.sDiEEtl
                     n+ E ++e+++ lA     k     D++ ++Fa      t+++   E +
  gi|3386398   116 VNILEQrIEedsyLASMSSGKENNRQDkpydpFAPPLATQTDpATFRELF 165

                    KkLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL
                     +L  +ln  P+     L+   + Lv+tAHPt  vR  +  K+ ++   L
  gi|3386398   166 ERL-RRLNVPPAQLETLLQEMDIRLVFTAHPTEIVRHTVRHKQRKVASLL 214

                    aqLsAKDvtveDKkE.LDEALHREiqAAFRtDEiRRaqPtPqDEmRaGms
                     q           kE+L   L  Ei   +RtDE+   +P   DE+ + +
  gi|3386398   215 QQFQSDPTKSTSEKEsLRLQLEEEIRLWWRTDELHQFKPSVLDEVDYALH 264

                    YiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGk
                    Y+   +++ +P+  RR  tA+        +P ++    F sW+G DRDG
  gi|3386398   265 YFQQVLFDAMPQLRRRLITAMAESYPDVHIP-QAAFCTFGSWVGSDRDG- 312

                    nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEE
                    nP vtPE+t       R +    Y++ v  L   ls+    + +     E
  gi|3386398   313 NPSVTPEITWRTACYQRQLMLERYVNAVQKLRDQLSISMQWSQVSTPLLE 362

                    lyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLA
                         +       Y E        EPYR  L    ++L  t  R   L
  gi|3386398   363 SLEMDRLR-FPEVYEERAARY-RLEPYRLKLSYTLERLKLTQHRNQQLAE 410

                    tGiseisE............eAv.ytkvEeFLEPLELCYksLCeCGDkvi
                     G    +E+ +++++  + +eA +y  v eF   LEL   sL       +
  gi|3386398   411 AGWQTPPEglnpspnlinagEALhYKSVAEFRSDLELIRNSLVSTD---L 457

                    ADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYRe
                        L  lL qv  F  sL  LDiRqEs+R+ D lD +t+ L+++ +Y +
  gi|3386398   458 SCEPLDTLLNQVHIFAFSLASLDIRQESNRHSDALDELTRYLNLpKAYGD 507

                    WsEeKRqEWLlaELkGKRPLlgsDL...PktEEvkDvldafrvLA.ELPi
                     +E+ R  WL+ EL+ +RPL++s +  +P t E   v   ++ L +E  +
  gi|3386398   508 MAENERVQWLMEELQTRRPLIPSAViwsPSTAETVAVFRMLHRLQeEFGS 557

                    DsFGaYiismataPsDvLAvELLqRECgvkqt......LrvvPLFEkLAD
                         Y+ism+ + sD L v LL +E g+  +  ++ +L vvPLFE + D
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  gi|3386398   558 RICRTYVISMSHTVSDLLEVLLLAKEAGLVDPaaghaeLLVVPLFETVED 607

                   LeAAPAavekLFsiDWYin.......ridGKqevmvGYsDsGKDAGRlsA
                   L+ APA +e L s   Y+n  ++ +++++  qe m+GYsDs KD G ls
  gi|3386398   608 LQRAPAVMEALLSSPVYRNllprvseQVQPLQELMLGYSDSNKDSGFLSS 657

                   AWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDt
                    W + +Aq  +   A + Gv L lFHGRGG vGRGGGP   AiL+qP  t
  gi|3386398   658 NWEIHQAQIALQDLANRQGVALRLFHGRGGSVGRGGGPAYQAILAQPSGT 707

                   inGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsPkPE
                   + G +++t qGEv+   +   +L    L  Ft A L   +    +   P
  gi|3386398   708 VRGRIKITEQGEVLASKYSLPELALYNLETFTTAVLQNSLvTNQLDATPS 757

                   WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaK
                   W +Lm ++A    E YR++v   P  v +F   tP  E  k+ i sRPa+
  gi|3386398   758 WNQLMTRLAGRSREHYRALVHNNPDLVAFFQQVTPIEEISKLQISSRPAR 807

                   RkPsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqk
                   Rk + + + sLRAiPW+F Wtq RF LP W GvG A    ++ D   l
  gi|3386398   808 RKSGAkDLSSLRAIPWVFGWTQSRFLLPSWFGVGTALAAEVESDADQLDL 857

                   LkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP....FG
                   L+ + + WPFFR+ +  +Em   K D  +A  y   L  E+ +   ++
  gi|3386398   858 LRRLHQRWPFFRMLISKVEMTLSKVDLDLAHHYMTSLGREDYREafnrIF 907

                   ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                   + +  +Y  t+ l+L i G   lL  DP L+  + LR+  i  L  +q
  gi|3386398   908 EIIETEYSLTRRLVLNITGQPRLLAADPALQLSVDLRNRTIVPLGFLQVA 957

                   tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    L+++RD +     +P++  +  d  +    eL++
  gi|3386398   958 LLRKLRDQN----RQPPM-NDAGDGRTYSRSELLRGA------------- 989

                   iLtmKGiAAGmqntG<-*
                   +Lt+ GiAAGm ntG
  gi|3386398   990 LLTINGIAAGMRNTG    1004

gi|113954224|ref|YP_729688.1|: domain 1 of 1, from 18 to 1001: score 403.1, E = 4.5e-118
                   *->siDAqLRlLvPGKvsedekLieYD.ALLlDkFLDiLqDLHGedLkEa
                       i       + G  +   +L++   AL+ D +  +L     ++  E
  gi|1139542    18    -IPESTQPRADGNEAGGGQLLQQRlALVEDLWRTVLRSECPPEQAEQ 63

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                         ls      + +   + L   + ++d a+ai  A+a++    L n
  gi|1139542    64 LLRMKQLSDPVLPGEHPAGTDALIDLIKGMDLAEAIAAARAFSLYFQLVN 113

                   LAEE.......velAyRRRikkkkhGDFaDEasAttE.sDiEEtlKkLvl
                   + E + ++++  e   R   +  +   Fa      tE++   E + +L
  gi|1139542   114 ILEQrieedtyLESINRSQDQAEQFDPFAPPLATQTEpATFRELFERL-R 162

                   klnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsA
                   +ln  P+     L+   + Lv+tAHPt  vR  +  K+ R+    L qL
  gi|1139542   163 RLNVPPAQLEALLQELDIRLVFTAHPTEIVRHTVRHKQRRVASLLQQLET 212

                   KDvtveDKkE.LDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEt
                   +  t+    +++   L  Ei   +RtDE+   +P   DE+ + + Y+
  gi|1139542   213 QPPTPSGATDsVRLQLEEEIRLWWRTDELHQFKPSVLDEVDYALHYFQQV 262

                   vWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvt
                   +++ +P+  RR+   L       R+P       F sW+G DRDG nP vt
  gi|1139542   263 LFNAMPQLRRRIVASLAASYPDVRVP-SSSFCTFGSWVGSDRDG-NPSVT 310

                   PEvtRDvCLLaRmmAanlYisqvEDLmFElsm...WRCndELRvRAEEly
                    E+t       R +    Yis v  L   ls++ +W   +       E+
  gi|1139542   311 TEITWRTACYQRQLMLDRYISAVQHLRNQLSIsmqWSQVSPPLLESLEMD 360

                   rtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtG
                   r    d     Y E        EPYR  L  v ++L  t  R   L   G
  gi|1139542   361 RLRFPD----VYEERATRY-RLEPYRLKLSFVLERLRLTQLRNQQLADAG 405
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```
                    iseisE.............eAv.ytkvEeFLEPLELCYksLCeCGDkviAD
                        +E+ ++ ++++ +++A +y  + eF   LEL   sL +     +
  gi|1139542   406 WRTPPEglpsftpgnapgDALhYGSIAEFRSELELIRTSLVNTD---LSC 452

                    GsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWs
                      L  lL qv  FG sL  LDiRqEs R+ D lD + + ++  ++Y
  gi|1139542   453 EPLDTLLTQVHIFGFSLAGLDIRQESTRHSDALDELSRYINPDrAYGAMD 502

                    EeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLA....ELPiDs
                    E  R  WL+ EL+ +RPL+++ +      ++ +d fr+L + ++E  +
  gi|1139542   503 EAERVAWLMEELQTRRPLIPPAVSWSAATAETVDVFRMLHrlqdEFGSRI 552

                    FGaYiismataPsDvLAvELLqRECgvkqt......LrvvPLFEkLADLe
                     G Y+ism+ + sD L v LL +E g+  ++ ++ +L vvPLFE + DL+
  gi|1139542   553 CGTYVISMSHSVSDLLEVLLLAKEAGLVDPsarhadLLVVPLFETVEDLQ 602

                    AAPAavekLFsiDWYinri.....dG..KqevmvGYsDsGKDAGRlsAAW
                     AP  +e+LF +  Y+  +++ +++G   qe m+GYsDs KD G ls  W
  gi|1139542   603 RAPEVMEHLFQTPLYRDLLpkvgtQGllLQELMLGYSDSNKDSGFLSSNW 652

                    qLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtin
                     + +Aq  +   A + G+ L lFHGRGG vGRGGGP   AiL+qP  t++
  gi|1139542   653 EIHQAQIALQDLASRQGIALRLFHGRGGSVGRGGGPAYQAILAQPSGTLQ 702

                    GslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsPkPEWR
                    G +++t qGEv+   +   +L    L   t A +   +    +   P W
  gi|1139542   703 GRIKITEQGEVLASKYSLPELALYNLETVTTAVIQNSLvTNQLDATPSWN 752

                    kLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRk
                    kLm ++A      YR++v   P  v +F   tP  E  k+ i sRPa+Rk
  gi|1139542   753 KLMSRVAKSSRRNYRALVHDNPDLVAFFQQVTPIEEISKLQISSRPARRK 802

                    PsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLk
                     + + + sLRAiPW+F Wtq RF LP W GvG A    ++ D   l  L+
  gi|1139542   803 TGTrDLSSLRAIPWVFGWTQSRFLLPSWFGVGSALSEELEADPDQLTLLR 852

                    EmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL.vaEeLkPFGk...s
                     + + WPFFR+ +  +Em   K D  +A  y   L+ aE    F k
  gi|1139542   853 TLHQRWPFFRMLISKVEMTLSKVDLDLARHYVTSLgSAEHHEAFEKiyaT 902

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    + ++Y  tk+l+L i G   lL+ DP L+  + LR+  i  L  +q   L
  gi|1139542   903 VAEEYARTKELVLAITGQERLLDADPALQLSVDLRNRTIVPLGFLQVALL 952

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    +R+RD +     +P++s    + +s   d+       ++   G     +L
  gi|1139542   953 RRLRDQN----RQPPMS----ESPSSDGDGRTYSR--SELLRG----ALL 988

                    tmKGiAAGmqntG<-*
                    t+ GiAAGm ntG
  gi|1139542   989 TINGIAAGMRNTG    1001

gi|33866579|ref|NP_898138.1|: domain 1 of 1, from 23 to 1010: score 401.5, E = 1.4e-117
                    *->siDAqLRlLvPGKvsedekLieYDALLl.DkFLDiLqDLHGedLkEa
                           q R+      +   +L++    L++D +  +L     ++  E
  gi|3386657    23    --GEQPRASGGSPGA--GRLLQHRLELVeDLWQTVLRSECPPEQSER 65

                    vqECYEls..AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                          ls++   EG+   +  e +   + s+d ++ai  A+a++    L
  gi|3386657    66 LLRLKQLSdpVALEGRDGESSSEAIVELIRSMDLSEAIAAARAFSLYFQL 115

                    AnLAEEvelAyRRRikkkkhGDFaDEasA.............ttEsDiEEt
                     n+ E          +++      DE+ A+ ++  ++  ++t  +   E
  gi|3386657   116 INILEQRIEEDSYLDSLRPSRSQDDETAApfdpfapplasqTDPATFGEV 165

                    lKkLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnC
                    + +L       P+ v   L+   + Lv+tAHPt  vR  +  K+ ++
  gi|3386657   166 FERLRRMN-VPPAQVETLLRELDIRLVFTAHPTEIVRHTVRHKQRKVASL 214

                    LaqLsAKDvtve.DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGm
                    L  L      +  D +EL   L  Ei   +RtDE+   +Pt  DE+   +
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  gi|3386657   215 LQRLQSEPALPRyDEEELRRQLEEEIRLWWRTDELHQFKPTVLDEVDSTL 264

                   sYiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDG
                    Y+   +++ +P+  RR    L         P ++    F sW+G DRDG
  gi|3386657   265 HYFQQVLFEAMPQLRRRLVSSLSRHYPDVQFP-QASFCTFGSWVGSDRDG 313

                   knPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE
                    nP vtPE+t       R +   lYi  v  L   ls+    + +
  gi|3386657   314 -NPSVTPEITWRTACYQRQLMLELYIGSVQSLRNQLSISMQWSQVAPPLL 362

                   Elyrtaardkvv KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLL
                   E     +         E        EPYR  L  + ++L  t  R   +
  gi|3386657   363 ESLEMDRLR--FPEIYERRAARYRLEPYRLKLSYILERLELTLQRNHQMS 410

                   AtGiseisEeAv.............ytkvEeFLEPLELCYksLCeCGDk
                     G    +E A + ++++ ++++  +yt +++F   LEL   sL
  gi|3386657   411 EAGWQSPPEPAAtaptdgipghealhYTAIDQFRSDLELIRNSLVS---T 457

                   viADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsY
                    +    L  lL qv  FG sL  LDiRqEs R+ D +D +ttHL+++ +Y
  gi|3386657   458 ELSCEQLDTLLNQVHIFGFSLASLDIRQESTRHSDAIDELTTHLQLpKAY 507

                   ReWsEeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDs
                       E  R  WLl EL+ +RPL+++ +   E  +     f++L  L  +
  gi|3386657   508 GAMEESERVAWLLEELQTRRPLIPAAVEWSEATAQTFAVFQMLHRLQQE- 556

                   FG.....aYiismataPsDvLAvELLqRECgv......kqtLrvvPLFEk
                   FG++  ++Y+ism+ + sD L v LL +E g+ +++ +k +L vvPLFE
  gi|3386657   557 FGqrichSYVISMSHTASDLLEVMLLAKEIGLvdpqagKASLLVVPLFET 606

                   LADLeAAPAavekLFsiDWYinri.......dGKqevmvGYsDsGKDAGR
                   + DL+ APA ++ LF +  Y+n +++ + +++  qe m+GYsDs KD G
  gi|3386657   607 VEDLQRAPAVMDGLFQTPIYRNLLpsvgvqrQPLQELMLGYSDSNKDSGF 656

                   lsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqP
                   ls  W + +Aq  +   A  +Gv L lFHGRGG v RGGGP   AiL+qP
  gi|3386657   657 LSSNWEIHQAQIALQTLASSHGVALRLFHGRGGSVSRGGGPAYQAILAQP 706

                   PDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsP
                     t++G +++t qGEv+   +G  +L    L   t A +   +    +
  gi|3386657   707 SGTLQGRIKITEQGEVLASKYGLPELALYNLETVTTAVVQNSLvTNQLDA 756

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    P W +Lm ++A    E YR++v   P  v +F   tP  E  k+ i sR
  gi|3386657   757 TPSWNQLMSRVAKRSREHYRALVHDNPDLVAFFQQVTPIEEISKLQISSR 806

                   PaKRkPsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                   Pa+Rk + + + sLRAiPW+F Wtq RF LP W GvG A    ++ D
  gi|3386657   807 PARRKTGArDLSSLRAIPWVFGWTQSRFLLPSWFGVGTALAEEVNDDPEQ 856

                   lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEe....Lk
                   l  L+ + + WPFFR+ +  +Em   K D  +A  y   L   e+++
  gi|3386657   857 LDLLRRLHQRWPFFRMLISKVEMTLSKVDLDLAHHYMSSLGNPEqrdaFE 906

                   PFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvf
                      k + d+Y  t +l+L+i G   lL  D  L+  + LR+  i  L  +
  gi|3386657   907 GIFKVIADEYGRTLKLVLEITGQSRLLGADQNLQLSVDLRNRTIVPLGFL 956

                   qAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLE
                   q   L+R+RD +     +P++s     E    +++       ++   G
  gi|3386657   957 QVALLRRLRDQN----RQPPMS-----ESPGTPEDRRTYS-RSELLRG-- 994

                   DtLiLtmKGiAAGmqntG<-*
                      +Lt+ GiAAGm ntG
  gi|3386657   995 --ALLTLNGIAAGMRNTG    1010

gi|113474661|ref|YP_720722.1|: domain 1 of 1, from 5 to 1038: score 399.8, E = 4.5e-117
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLk.Ea
                       +  +   L PG      k+   D  L  + + i+  L    L++E
  gi|1134746     5    -LHSKEITLEPGFKN--PKMTASDLFLHNR-IKIVENLWESVLRqEC 47
```

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                vqECYElsAeY......EGKkDtkKLeELGakLtsLdPaDailvAkailH
                 qE  ++    ++++++EG+       E+   +  L+  Dai  A+a+
gi|1134746    48 GQELVDILQKMrsghspEGQASDFLGSEIEQLIEKLELKDAIRAARAFAL 97

                mLnLAnLAEEv......elAyRRRikkkk...hGDFa...DEasAttEs.
                   L n+ E   +++ ++lAy   +++ k  ++ D a+++D  s   Es
gi|1134746    98 YFQLINIVEQHyeqkiqQLAYSHNNSLEKlisKDDIAkdhDTRSLRVESi 147

                ..........DiEEtlKkLvlkln..KsPeEvFeALKnqs.vDLvltAHP
                +  ++++ +++ E t+  L  +l++   P    + L n  ++ Lv+tAHP
gi|1134746   148 pvwndnrikhEGEGTFHYLFPLLQtlNVPSQLIQRLINNLdIRLVFTAHP 197

                tqsvRRsLLqKnaRiRnCLaqL.....sAKDvtveDKk..........E
                t  vRR +  K+ Ri   L qL++ ++s  +  v++ + ++  ++ + +
gi|1134746   198 TEIVRRTIRTKQRRIAKILQQLdqvneSLSESHVDEEQvnslvsswkieS 247

                LDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLRR
                L E L  Ei   +RtDE+   +P   DE+   + Y+ E +++  P   RR
gi|1134746   248 LKEQLTEEILLWWRTDELHQFKPSVLDEVETTLHYFNEVLFDATPELHRR 297

                vDtALKniGinERlPYdvP....LikFssWmGGDRDGknPRvtPEvtRDv
                   AL         PY  P++ +  kF sW+G DRDG nP  tP vt
gi|1134746   298 FKQALHS-----SFPYLKPpsynFCKFGSWVGSDRDG-NPFCTPAVTWQT 341

                CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                    R +    Y++ ++ L   ls+    ++  v  E l +  + +  +
gi|1134746   342 ACYQRQIVLEKYLNAIDRLKELLSLSLHWSD--VLPELLDSLDRDHIQMS 389

                yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLA.............
                   + W     +EPYR  L  ++ +L ntR+R   L  +++ ++++++
gi|1134746   390 EVYDQWAIRYRQEPYRLKLSYIKKRLENTRDRNARLYNgdevqrqkkevl 439

                .....tGiseisE.eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLD
                ++++++ +s+  E+  +y    +FL  L L  + L e G   +    L
gi|1134746   440 sqrqkQVLSQYQEtKSIYHSSADFLAELQLIQRNLKETG---LSCSDLEN 486

                lLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei..GsYReWsEeKR
                l+ qv  FG  L +LDiRqEs  +   +  it+ L+i + sY e sE  R
gi|1134746   487 LISQVEIFGFNLARLDIRQESSVHEAAIQEITEYLQIlpKSYIEMSEAER 536

                qEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFG.....a
                 EWL +EL  +RPL++ +LP  E   +++++fr+L EL  + FG++  +
gi|1134746   537 TEWLSTELPTRRPLIPTELPFSEKTCEIINTFRMLRELQLE-FGeeicqT 585

                YiismataPsDvLAvELLqRECgvkqt......LrvvPLFEkLADLeAAP
                Yiism+   sD L v LL  E g+  + ++ +++ vvPLFE + DL+ AP
gi|1134746   586 YIISMSRDVSDLLEVLLLAQEAGLYDPatgassIHVVPLFETVEDLRSAP 635

                AavekLFsiDWYinridG...................KqevmvGYsDsGK
                  +  LF +  Y+  + G+ ++ ++++ ++  ++ +  qevm+GYsDs K
gi|1134746   636 RVMHDLFKLSLYRAGLAGgydklskepinelvneapyLQEVMLGYSDSNK 685

                DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                D G ls  W + kAq  + Kv  ++G+ L +FHGRGG vGRGGGP   Ai
gi|1134746   686 DSGFLSSNWEIHKAQKALYKVGEEHGIALRIFHGRGGSVGRGGGPAYKAI 735

                LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHG.mnP
                L+qP   i G +++t qGEv+   +   +L    L   t A +    ++
gi|1134746   736 LAQPGKSISGRIKITEQGEVLASKYSLPHLAMFNLENVTTAVIQASlLHT 785

                PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmn
                       W ++mee+Av     YR +++     vE+F   tP  E  ++
gi|1134746   786 GFDEIETWNQIMEELAVRSRSHYRNLIYEQEDLVEFFYQVTPMPEISQLQ 835

                iGsRPaKRkPs..GGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid
                i sRPa+Rk  ++  i  LRAiPW+F+Wtq RF LP W GvG A +  ++
gi|1134746   836 ISSRPARRKNDkkKTISGLRAIPWVFSWTQSRFLLPAWYGVGTALQEFVE 885

                KD.iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva..
                K++   l+ L+  Y +WPFF   +  +Em  AK D  iA  y + L  ++
gi|1134746   886 KEpEEHLKLLQYFYVKWPFFTTAISKVEMTLAKVDLQIAHYYVRELSKpe 935
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                  ..EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYi
                  ++E      +++  +Y  t++l+L+i GH+  L+GDP L+  + LR++ i
  gi|1134746   936 drERFETLFEEITIEYHLTRNLVLQISGHQRPLDGDPDLQRSVQLRNATI 985

                  ttLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpter
                    L ++q   LKR+R    + t  P +             eL++
  gi|1134746   986 IPLGMLQVALLKRLRQ---HDTGTPGVINSRYSKS-----ELLRGA---- 1023

                  vaPGLEDtLiLtmKGiAAGmqntG<-*
                           +Lt+ GiAAGm ntG
  gi|1134746  1024 ---------LLTLNGIAAGMRNTG    1038

gi|154146696|emb|CAM83983.1|: domain 1 of 1, from 1 to 439: score 399.3, E = 6.3e-117
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541466     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541466     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541466     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541466     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541466     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541466     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541466     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541466     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541466     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tD +DAittHL+iGsYR W+Ee+RqEWL++EL+GKRPL+g+DLP+ +
  gi|1541466     1 --HTDAMDAITTHLGIGSYRAWPEERRQEWLVSELRGKRPLFGPDLPQSD 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl+afrv+AELP DsFGaYiismataPsDvLAvELLqRECgvk++L
  gi|1541466    49 EVADVLGAFRVIAELPGDSFGAYIISMATAPSDVLAVELLQRECGVKNPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADL+ A A++e LFs+DWY+ ri+GKqe+m+GYsDsGKDAG
  gi|1541466    99 RVVPLFEKLADLQQARATMELLFSVDWYKERINGKQEIMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEEi+ vA ++GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541466   149 RLSAAWQLYKAQEEIVSVAERHGVKLTIFHGRGGTVGRGGGPSHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP t+nG lRvt+qGEviE sFGEEnLCFr+LqRFtAAtLEHGmnPPvsP
  gi|1541466   199 PPNTVNGLLRVTIQGEVIEKSFGEENLCFRTLQRFTAATLEHGMNPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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                    kPEWR+L+++mA vAt+EYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541466   249 KPEWRRLLDDMATVATDEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+G AF+hA+++    l
  gi|1541466   299 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGTAFRHAMQQQAGGL 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvt+DLlEmvFAKGDPGiAaLyDkLLv  +L+PFG++
  gi|1541466   349 ATLREMYEEWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVPQDLWPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y Et+ lLL++AGHkDlLE DPYL+qrl LRdsYit
  gi|1541466   399 LRANYAETQSLLLQVAGHKDLLESDPYLRQRLILRDSYITA--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541466     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541466     - -------------    -

gi|78185499|ref|YP_377934.1|: domain 1 of 1, from 4 to 995: score 399.0, E = 7.7e-117
                    *->siDAqLRlLvP...GKvsedekLieYDALLl.DkFLDiLqDLHGedL
                       s    L    P+++G  +   +L++   +L++D +  +L     ++
  gi|7818549     4    STAHALQGEQPresGVTAGAGRLLQNRLVLVeDLWQTVLRSECPPEQ 50

                    kEavqECYEls..AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHm
                             ls++   EG+   +  e +   + ++d ++ai  A+a++
  gi|7818549    51 SARLLRLKQLSdpVALEGRDGDSTSEAIVELIRAMDLSEAIAAARAFSLY 100

                    LnLAnLAEE.ve.......lAyRRRikkkkhGDFaD.....EasAttEsD
                      L n+ E ++e+++  ++lA R+        D  D+  ++ as t  +
  gi|7818549   101 FQLINILEQrIEedsyldsLAPRKSAADDG-RDAFDpfappLASQTDPAT 149

                    iEEtlKkLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaR
                      E + +L       P+ v   L+   + Lv+tAHPt  vR  +  K+ R
  gi|7818549   150 FGEVFERLRRMN-VPPAQVEALLQELDIRLVFTAHPTEIVRHTVRHKQRR 198

                    iRnCLaqLsAKD.vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEm
                    + n L qL    ++  + K +L   L  Ei   +RtDE+   +Pt  DE+
  gi|7818549   199 VANLLQQLQSDSpMALQVKDDLRQQLEEEIRLWWRTDELHQFKPTVLDEV 248

                    RaGmsYiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGG
                       + Y+   +++ +P+  RR    L        +P ++    F sW+G
  gi|7818549   249 DSTLHYFQQVLFDAMPQLRRRLTSSLHRHYPDVQVP-QASFCTFGSWVGS 297

                    DRDGknPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELR
                    DRDG nP vt ++t       R +   lYis v  L   ls+    + +
  gi|7818549   298 DRDG-NPSVTTDITWRTACYQRQLMLELYISSVQALRNQLSISMQWSQVA 346

                    vRAEElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERa
                        E     +         E        EPYR  L  + ++L  t  R
  gi|7818549   347 PALLESLEMDRLR--FPEIYERRAARYRLEPYRLKLSYILERLERTLKRN 394

                    RHLLAtGi....seis.......EeAvytkvEeFLEPLELCYksLCeCGD
                      L   G ++++  i++++++++E   yt v++F   LEL   sL   G
  gi|7818549   395 DQLSDAGWkspkDAIPtdgppgsEALHYTSVDQFRNDLELIRNSL--IGT 442

                    kviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.
                        +  L  lL qv  FG sL  LDiRqEs R+ D +D +t+ Le+  +
  gi|7818549   443 ELTCE-QLDTLLHQVHIFGFSLASLDIRQESTRHSDAIDELTRFLELPQp 491

                    YReWsEeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiD
                    Y e  E  R  WL+ EL+ +RPL++  +   +  ++ +  fr+L  L  +
  gi|7818549   492 YGEMEESTRVAWLIEELRTRRPLIPTAVRWSDTTAETMAVFRMLHRL-QE 540

                    sFG.....aYiismataPsDvLAvELLqRECgv......kqtLrvvPLFE
                     FG++  ++Y+ism+ + sD L v LL +E g+ ++  +k +L vvPLFE
  gi|7818549   541 EFGqrichSYVISMSHTASDLLEVLLLAKEAGLvdpaarKASLLVVPLFE 590
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                    kLADLeAAPAavekLFsiDWYinr.....idGK..qevmvGYsDsGKDAG
                     + DL+ APA ++ LF +  Y+   +  +i+G++ qe m+GYsDs KD G
  gi|7818549   591 TVEDLQRAPAVMDELFNTPLYRDLlpmvgIQGQplQELMLGYSDSNKDSG 640

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     ls  W + +Aq  +     + Gv L lFHGRGG v RGGGP   AiL+q
  gi|7818549   641 FLSSNWEIHQAQLALQELSSRQGVALRLFHGRGGSVSRGGGPAYQAILAQ 690

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvs
                    P  t++G +++t qGEv+   +   +L    L   t A +   +    +
  gi|7818549   691 PSGTLQGRIKITEQGEVLASKYSLPELALYNLETVTTAVVQNSLvTNQLD 740

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                      P W +Lm ++     E YR++v   P  v +F   tP  E  k+ i s
  gi|7818549   741 ATPSWNQLMSRLSARSREHYRALVHDNPDLVAFFQQVTPIEEISKLQISS 790

                    RPaKRkPsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                    RPa+Rk + + + sLRAiPW+F Wtq RF LP W G+G A    ++ D
  gi|7818549   791 RPARRKTGAkDLSSLRAIPWVFGWTQSRFLLPSWFGFGTALAEEVKADPD 840

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL....vaEeL
                     l  L+ + + WPFFR  +  +Em   K D  +A  y + L++++  E
  gi|7818549   841 QLDLLRRLHQRWPFFRTLISKVEMTLSKVDLDLAHHYMNSLgkpeQREAF 890

                    kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnv
                          +  +Y  t++l+L+i G   lL  D  L+  + LR+  i  L
  gi|7818549   891 EAIFAVIATEYALTRKLVLEITGQPRLLGADQGLQLSVDLRNRTIVPLGF 940

                    fqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGL
                    +q   LKR+RD +     +P++s    + +   a e  +    ++   G
  gi|7818549   941 LQVALLKRLRDQN----RQPPMS----ESP--GAPEDTRTYSRSELLRG- 979

                    EDtLiLtmKGiAAGmqntG<-*
                        +Lt+ GiAAGm ntG
  gi|7818549   980 ---ALLTLNGIAAGMRNTG    995

gi|219847347|ref|YP_002461780.1|: domain 1 of 1, from 1 to 933: score 398.8, E = 8.9e-117
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                              +       e + L      L D    ++ +  G    E v
  gi|2198473     1    -------MSGRTTAGEHDLLSANIRTLGDMLGRVITEQSGAATFELV 40

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ++ e      +     L   +t+L       + ka+     L nL
  gi|2198473    41 ERVRLMAKELRNGAPPAGTHVLQDLITGLSLPQLRNLVKAFTLYFGLVNL 90

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE ve     R + ++       a A     i + +  L   +   P+
  gi|2198473    91 AEGVEQLRVLRSRDLR------NAPAPRAESIADAIELLKRHG--VPAAA 132

                    FeALKnqsvDL.vltAHPtqsvRRsLLqKnaRiRnCLaqLs..AKDvtve
                     +    q+  ++v+tAHPt s RR +L K  Ri   L  L  + + v +
  gi|2198473   133 IQEWIDQALIMpVFTAHPTESRRRTILIKLRRIFDTLIDLTfgERLVLPS 182

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    D++     + RE    + tD++R  +P   DE+  G+ Y+   +W+ +P
  gi|2198473   183 DRQSALTRIERETVGLWQTDDVRNRRPSVLDEVENGLFYFQTVLWDLIPE 232

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R    AL       R     P ++F sWmGGDRDG nP vtPEvt +
  gi|2198473   233 IYRETADALATAYPDHRWRLP-PFLRFGSWMGGDRDG-NPFVTPEVTVET 280

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      L R       i+ ++ L+ +ls     + + v      r a  + ++
  gi|2198473   281 VRLMRSAMLRYLINGIDRLITDLS--QSVQQVPVDQAIFDRIAEYHELMP 328

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaR.HLLAtGiseisEe..
                                EPYR +   +  +L nt   + +H    G    +   +
  gi|2198473   329 DAAATLNPHYRCEPYRQLCHFIQARLQNTLHYTLsHTPRWGADPPPPRlp 378

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
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                    +y +  e L  L+L   sL   G  +iADG L Dl   v    L    L
  gi|2198473   379 TIYYHSRELLADLDLIDTSLRRHGGAIIADGLLRDLRTNVAVCRLHTATL 428

                    DiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlg
                    D+Rq + R+t+ l  i    ++ ++Y    E  R   L +E++  RPL +
  gi|2198473   429 DVRQHASRHTEALTEILAGAGVVAnYAALDECERVAVLSTEIRRPRPLTP 478

                    sDLPktE.EvkDvldafrvLA....ELPiDsFGaYiismataPsDvLAvE
                      L    +  ++ +++fr+LA  ++ L  + F  Yiis +   sD LAv
  gi|2198473   479 IRLGHFSpATAETVQTFRMLAaiseQLDPEIFQTYIISTTSQVSDLLAVL 528

                    LLqRECgvkqt.....LrvvPLFEkLADLeAAPAavekLFsiDWYinri.
                    L  R+ g+ q+++ ++L +vPLFE   DL+ AP  ++ L  +  Y+ ++
  gi|2198473   529 LFCRDAGLYQPgqysrLDIVPLFETGEDLQRAPLILDELLQLPVYREHLa 578

                    ..dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                     +d  qevm+GYsDs K+ G l+A W LY+Aq E+  v  ++Gv+L  FH
  gi|2198473   579 lrDNLQEVMLGYSDSNKEGGFLAANWALYRAQVELNTVTERHGVRLRFFH 628

                    GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                    GRGG vGRGGGP   AiL+qPP t++G ++vt qGEvi   + +     r
  gi|2198473   629 GRGGAVGRGGGPAGQAILAQPPGTLHGQIKVTNQGEVISDRYLDPRTAHR 678

                    sLqRFtAAtLEHGmnPPv..sPkPEWRkLmeemAvvAtEEYRsvvvKEPR
                     L     A L  G  P + +sP P W + me+mA  A   YR +v+ +P
  gi|2198473   679 HLEQVVNAVLRAGF-PGIarSPEPAWLEAMEQMAHTARTVYRRLVYEDPD 727

                    FvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFH
                    F  YFR AtP  E  ++ iGsRP  R+ s  ie LRAiPW+F+W qtR
  gi|2198473   728 FLTYFRNATPVAELSRLRIGSRPVSRRKSDRIEDLRAIPWVFSWMQTRHT 777

                    LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                    LP W G+G A    +  D   l  L+ mY+ WPFF   lD   m+  K D
  gi|2198473   778 LPGWFGLGSALSEFVAADPHHLYVLRAMYRHWPFFTTLLDNAQMIMLKAD 827

                    PGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                      iA  y  L+   eL  +  +++ ++Y  t+ ++ +i   ++lL   P
  gi|2198473   828 MSIARSYAGLVPDQELAArIFQQIEAEYRRTEHMICQITESQELLAHQPV 877

                    LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                    L+  +R R++Yi  L  +q   L+RiR         P+   E  dE
  gi|2198473   878 LQRAIRQRNPYIDPLSYIQIELLRRIRN-------APP---EDQDEI--- 914

                    adeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                    E  L++ + GiAAG++ntG
  gi|2198473   915 -----------------ETVLLMSINGIAAGLKNTG    933

gi|225517756|ref|ZP_03764713.1|: domain 1 of 1, from 46 to 1017: score 397.0, E = 3.1e-116
                    *->siDAqLRlLvP..GKvsedekLieYDALLlDkFLDiLqDLHGe.dLk
                        +  qLR L  ++G+   d+      A+ l   L i   +   +
  gi|2255177    46    DLLGQLRDLCSpeGQATHDQTA---SAVELIEQLNINEAIRAArAFA 89

                    EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                     + q    +  eYE K+   +  + G+ +     a  i         L +
  gi|2255177    90 LYFQLINIIEQEYEQKQQLTRYSDSGT-INQEHLANIIYSTNQREDDLPV 138

                    A.nL.AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnK
                     + L+A+     +      k++G Fa              l  L  kln
  gi|2255177   139 TkELgADSLSQSWTDTTPIKQKGTFA-------------ALFPLLFKLNV 175

                    sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt
                     P+ +   +    + Lv+tAHPt  vR  +  K+  +   L  L
  gi|2255177   176 PPQQIQRLISQLDIRLVFTAHPTEIVRHTIRDKQRQVVDLLQHLDSLQNR 225

                    ....veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtv
                    +++ + + +E+ E L  Ei   +RtDE+   +Pt  DE+ + + Y+ E +
  gi|2255177   226 sggyPWEAQEVKERLLEEIRLWWRTDELHQFKPTVLDEVDYALHYFQEVL 275

                    WkGvPKFLRRvDtALKniGinERlPYdvP....LikFssWmGGDRDGknP
                    ++G+P+  +R    L         P+  P++++   F sW+G DRDG nP
  gi|2255177   276 FDGIPQLYKRLKYSL-----EQTFPWLEPpsknFCSFGSWVGSDRDG-NP 319
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                    RvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsm.WRCndELRvRAE..
                     vtPEvt       R m    Yi+ v  L+  ls++    d L    E+
  gi|2255177   320 SVTPEVTWKTACYQRKMVLGRYIQSVKQLIELLSVsMQWSDVLPDLLEsl 369

                    ElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLL
                    El +   +d v       ++q    EPYR  L  v  +L ntR+    L
  gi|2255177   370 ELDQSTMSD-VYDALALRYRQ----EPYRLKLAYVLRRLENTRDHNLALY 414

                    AtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqv
                            +  +y    eFL  L L  + L e G   +    L  l+ qv
  gi|2255177   415 SRERPANEDSPMYRSGAEFLSELRLVQRNLTETG---LSCRELENLICQV 461

                    stFGLsLvKLDiRqEseRqtDvlDAittHLei..GsYReWsEeKRqEWLl
                      F   L +LDiRqEs R+ D l  i + L++ + sY + sE +R  WL
  gi|2255177   462 EIFDFNLTQLDIRQESSRHCDALNEILEYLQVlpLSYNQLSEAQRVSWLT 511

                    aELkGKRPLlgsDLPktEEvkDvldafrvL....AELPiDsFGaYiisma
                     EL+ +RPL++ +LP  E   Dv+++frv+++ + E  i     Yiism+
  gi|2255177   512 GELQTRRPLIPGELPFSEKTNDVIETFRVVrslqQEFGINICQTYIISMC 561

                    taPsDvLAvELLqRECgvkqt......LrvvPLFEkLADLeAAPAavekL
                       sDvL v LL +E  +  +    +++rvvPLFE + DL+     ++kL
  gi|2255177   562 REVSDVLEVLLLAKEARLFDPaiavgsIRVVPLFETVEDLQRSRSVMKKL 611

                    FsiDWYinridG.........................KqevmvGYsD
                    F +  Y+  + G+ +  ++++++++++++++++++ +++ qevm+GYsD
  gi|2255177   612 FELPLYRAFLAGgyealnsentppdtqppnspssptlnpnLQEVMLGYSD 661

                    sGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtH
                    s KD G ls  W + kAq  + K+A +yG  L +FHGRGG vGRGGGP
  gi|2255177   662 SNKDSGFLSSNWEIHKAQKSLQKIAEQYGLHLRIFHGRGGSVGRGGGPAY 711

                    LAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm
                     AiL+qP   inG +++t qGEv+   +   +L    +   t A +   +
  gi|2255177   712 EAILAQPGNSINGRIKITEQGEVLASKYSLLDLALYHVETITTAVVQASL 761

                    nPPvsPkPE.WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYG
                            E+W ++mee+ +     YR +++  P F+++F   tP  E
  gi|2255177   762 LRTGFDDIEpWNEIMEELSMRSRQHYRGLIYEQPDFIDFFHQVTPIEEIS 811

                    kmniGsRPaKRkPsG..GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKh
                    ++ i sRPa R+PsG++ + sLRAiPW+F+WtqtRF LP W G+G A +
  gi|2255177   812 QLQISSRPA-RRPSGkkDLSSLRAIPWVFSWTQTRFLLPSWYGLGTALQE 860

                    AidKD.iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLy.DkLL
                     ++  +   l+ L+  Y +WPFF++ +   Em  AK D  +A  y  +L
  gi|2255177   861 FLNEQpEEHLKLLRYFYVKWPFFKMAISKAEMTLAKVDIEMAHHYvQELS 910

                    vaEeLkPFG...ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRd
                      E+   F +  +++  ++  t+dl+L i GH+ lL+GDP L+  + LR+
  gi|2255177   911 NPEDKAQFDkvfEQIASEFYLTRDLVLNITGHQRLLDGDPILQRSVQLRN 960

                    sYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnp
                      i  L  +q   LKR+R  +yk t    +                 +n
  gi|2255177   961 GTIVPLGFIQVSILKRLR--QYKNTTTSGV-----------------IN- 990

                    tervaPG.LEDtLiLtmKGiAAGmqntG<-*
                     +r++ G+L    +Lt+ GiAAGm ntG
  gi|2255177   991 -SRYSKGeLLRGALLTINGIAAGMRNTG    1017

gi|269961450|ref|ZP_06175814.1|: domain 1 of 1, from 1 to 654: score 396.9, E = 3.4e-116
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2699614     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2699614     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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                     + ++k
gi|2699614     1 ----------MNDRLK---------------------------------- 6

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|2699614     - ------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                                                    sY+ E
gi|2699614     7 ----------------------------------SYLGEG---------- 12

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                              lP d+  ++FssWmGGDRDG nP vt  vtR+v LL
gi|2699614    13 --------------LPIDARPVHFSSWMGGDRDG-NPFVTHSVTREVLLL 47

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                  +R  Aa lY++ + +L+ Elsm  Cnd +R  A + +
gi|2699614    48 SRWKAADLYLNDINELISELSMTVCNDKVRELAGDDQH------------ 85

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                           EPYR iL + R  L  t++       +G   ++  A   kv
gi|2699614    86 ---------EPYRAILKQLRSLLNETKD-ILDAKVHG-QKLAVKAPLQKV 124

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                  E+  EPL  CY+sL eCG  viA GsLLD LR v  FG+ Lv+LDiRqEs
gi|2699614   125 EQLWEPLYACYQSLNECGMGVIANGSLLDTLRRVKAFGIHLVRLDIRQES 174

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   R+ Dvl  +t+ L+iG Y +WsE+ +  +L  EL  KRPLl+ D    E
gi|2699614   175 TRHADVLSELTRYLGIGDYEQWSEQDKVAFLTNELASKRPLLPRDWEPSE 224

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   vk+vld+ +++A  P ++FGaY+isma + sDvLAv LL  E g    +
gi|2699614   225 PVKEVLDTCKIVAAQPREAFGAYVISMARTASDVLAVHLLLQEAGCPYRM 274

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   v PLFE L DL+ A A +++L  iD Y+  i+  q vm+GYsDs KDAG
gi|2699614   275 DVCPLFETLDDLNNAEAVIKQLMGIDLYRGFIQNHQMVMIGYSDSAKDAG 324

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   +sA W  Y A + ++KvA + Gv L+lFHGRGGt+GRGG P H A+Lsq
gi|2699614   325 VMSAGWAQYHAMDSLVKVAEEEGVELTLFHGRGGTIGRGGAPAHAALLSQ 374

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP  P
gi|2699614   375 PPKSLKGGLRVTEQGEMIRFKLGLPDVAVNSFNLYASAILEANLLPPPEP 424

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  k EWR+Lm+ +  v  E YRsvv  EP Fv YFR AtPElE Gk+ +GsR
gi|2699614   425 KQEWRDLMDVLSEVSCEAYRSVVRGEPDFVPYFRQATPELELGKLPLGSR 474

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKR P GG+esLRAiPWiF+W q R  LP WLG G A ++ +dK  + l
gi|2699614   475 PAKRNPNGGVESLRAIPWIFSWSQNRLVLPAWLGAGEAIQYSVDKGHQAL 524

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+Em +eWPFF   l +lEmv+ K    i   yD+ Lv   L+P G++
gi|2699614   525 --LEEMCREWPFFSTRLGMLEMVYTKCNMEISRYYDQRLVETPLQPLGDR 572

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++ +   + +L +     l+  DP+ +  +RLR+ Y+  Ln++qA  L
gi|2699614   573 LREQLQRDIKSVLNVENNENLMQSDPWGQESIRLRNIYVEPLNMLQAELL 622

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   R R                                te+ +  LE+ L++
gi|2699614   623 YRTRQ------------------------------TEEASANLEEALMV 641

                  tmKGiAAGmqntG<-*
                  t+ GiAAGm ntG
gi|2699614   642 TIAGIAAGMRNTG    654
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gi|172038735|ref|YP_001805236.1|: domain 1 of 1, from 9 to 1020: score 396.7, E = 4e-116
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                     s+   +  +     s  +  ++    L++   +++L+   G++L +
  gi|1720387     9    SLQSTVEEVNIFSTS--DLFLRQRLKLVESLWEsVLKAECGQELVDL 53

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                        +    EG+   k    +   + +L+  +ai  A+a+     L n
  gi|1720387    54 LEKLRKICSP-EGQVTDKPKTSINELIEGLELNEAIRAARAFALYFQLIN 102

                  LAE......EvelAyRR..RikkkkhGDFaDE...asAttEsDiEE....
                  + E++ ++++ +l  R +   + k     a E+++a+    +D+ E+
  gi|1720387   103 IVEqhyeqrDQQLNRRAtyQESEKARNNHAKEenkANGSVGADLLEkalv 152

                  ..........tlKkL...vlklnKsPeEvFeALKnqsvDLvltAHPtqsv
                  ++++++++++t+  L ++  +ln  P+ +   L    + Lv+tAHPt  v
  gi|1720387   153 ggtenqekggTFHWLfpqLKRLNVPPQQIQRLLEQLDIRLVFTAHPTEIV 202

                  RRsLLqKnaRiRnCLaqL.sAKD......vtveDKkE.LDEALHREiqAA
                  R  +  K+ Ri   L  L++A ++ ++ ++      E++ E L  Ei
  gi|1720387   203 RHTIRLKQRRIATLLRRLdYAEEsfrgmgLSSSWEAEsIIEQLNEEIRLW 252

                  FRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLRRvDtALKniGinE
                  +RtDE+   +P   DE+ + + Y+ E + +  P+   R   ALK
  gi|1720387   253 WRTDELHQFKPSVLDEVDYTLHYFDEVLCDALPQLSQRLQQALKANFPRI 302

                  RlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLLaRmmAanlYisqv
                  + P +    +F sW+GGDRDG nP vtPEvt       R +    Y+  +
  gi|1720387   303 KPPHNT-FCRFGSWVGGDRDG-NPFVTPEVTWRTACYQRNLILEKYLAAI 350

                  EDLmFEls...mWRCndELRvRAEElyrtaardkvvKyYiEFWKqvPPtE
                  EDL   ls++  W   +       E  r a  +     Y E       +E
  gi|1720387   351 EDLTEILSsslHWSNVSQDLLDSLERDRVAMPE----IYDELAIRY-RQE 395

                  PYRviLGdvRDKLYntRERaRHLLAtGisei.sEeA...vytkvEeFLEP
                  PYR  L  +  +L  tR+R  HL      +i  Ee ++++y   EeF
  gi|1720387   396 PYRLKLAYIEKRLETTRDRNNHLANPEKRQIlTEETppnIYHSGEEFEAE 445

                  LELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDv
                  L L  + L e G k  A   L  l+ q   FG  L +LD RqEs R+ +
  gi|1720387   446 LQLIKRNLEETGLKCQA---LENLIFQAQMFGFTLTQLDFRQESSRHSET 492

                  lDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLlgsDLPktEEvkD
                  ++ i   L++ +  Y e sE  +  WL+ EL+ +RPL++ ++P  E   +
  gi|1720387   493 IEVIANYLNVlpRPYGELSETEKVNWLVGELQTRRPLIPMEMPFDEKTIE 542

                  vldafrvL....AELPiDsFGaYiismataPsDvLAvELLqRECgv....
                   ++++r+L+  + E  ++    Yiism+   sDvL v LL +E g+ +++
  gi|1720387   543 TIETMRMLrylqQEFGVEICQTYIISMTNDVSDVLEVLLLAKEAGLydpg 592

                  ..kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG..........
                  ++  t+r+vPLFE + DL+ AP  ++ LF +  Y+  + G+ +  ++ ++
  gi|1720387   593 tsTTTIRIVPLFETVDDLKRAPEIMDALFKLTLYRAALAGgydyldeakk 642

                  ............KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKky
                  ++ ++++ ++ + qe+mvGYsDs KD G ls  W + kAq  + KvA  y
  gi|1720387   643 eqlpppelqpanLQEIMVGYSDSNKDSGFLSSNWEIHKAQKSLQKVAEPY 692

                  GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF
                  G  L lFHGRGG vGRGGGP   AiL+qP  tinG +++t qGEv+   +
  gi|1720387   693 GLALRLFHGRGGSVGRGGGPAYAAILAQPTGTINGRIKITEQGEVLASKY 742

                  GEEnLCFrsLqRFtAAtLEHGm....nPPvsPkPEWRkLmeemAvvAtEE
                     +L    L   t A +   + +++   + P   W ++mee+A  A
  gi|1720387   743 SLPELALYNLETATTAVIQASLlgsgFDDIVP---WNDIMEELASSARKA 789

                  YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs.GGiesLRAiP
                  YRs+++  P F ++F + tP  E  ++ i sRPa+Rk ++  + +LRAiP
  gi|1720387   790 YRSLIYEQPDFLDFFLSVTPIPEISQLQISSRPARRKSGkKDLSTLRAIP 839

                  WiFaWtqtRFHLPvWLGvGAAFKhAidKD.iKnlqkLkEmYkeWPFFRvt
                  W+F+Wtq RF LP W GvG A    +++++  nl+ L+  Y +WPFF++
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  gi|1720387   840 WVFSWTQSRFLLPAWYGVGTALESFLQQEpNENLKLLRYFYLKWPFFKMV 889

                    lDLlEmvFAKGDPGiAaLyDkLLva.EeLkPFG...ksLRdkYvEtkdlL
                    +  +Em   K D  iA  y k L  +E++  F +  +++ ++Y  t+d++
  gi|1720387   890 ISKVEMTLSKVDLQIAHHYVKELSQpEDIERFNkvfERISQEYHRTRDII 939

                    LkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtl
                    L i     lLEGD  L+  + LR+  i  L  +q   LKR+R    + t
  gi|1720387   940 LSINEQPKLLEGDAGLQRSVQLRNGTIVPLGFLQVSLLKRLR----QYTR 985

                    rPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqnt
                    +        +E      ++++          L    +Lt+ GiAAGm nt
  gi|1720387   986 Q--------AES-----GVIHFR---YSKEELLRGALLTINGIAAGMRNT 1019

                    G<-*
                    G
  gi|1720387  1020 G    1020

gi|254413284|ref|ZP_05027055.1|: domain 1 of 1, from 49 to 1034: score 396.6, E = 4.2e-116
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHG.edLkEa
                        + A LR L                  +   LD+   +  +     +
  gi|2544132    49    DLLASLRQLSSPEGQ-ATGFSLSSIPEVIEGLDLNAAIRAsRAFALY 94

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                     q    +   YE ++D + L    a    L+ +D   + ka    L   n
  gi|2544132    95 FQLINGVEQHYE-QRDQQLLRR--ATYNTLAGSDRTSM-KANGSSLQASN 140

                    LAEEvelAyRRRikkkkhGDFaDEasAt.tEsDiEEtlKkLvlklnKsPe
                      +E +      i  +    + D+  A +t s     +  L  +    P+
  gi|2544132   141 NGDEAKPSGSEPIADLLEKRWQDDRKAAnTNSTFHWLFPYLRNLN-VPPQ 189

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL.....sAKD
                     +   + n  + Lv+tAHPt  vR  + qK+ Ri   L qL++ ++  +
  gi|2544132   190 HIQRLIDNLDIRLVFTAHPTEIVRHTIRQKQRRISTILQQLdqaeeASRA 239

                    vtveDKkELD...EALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEt
                    +  +   E+++ +E L  Ei   +RtDE+   +Pt  DE+ + + Y+ E
  gi|2544132   240 LGLNSSWEVEdytEQLREEIRLWWRTDELHQFKPTVLDEVDYTLHYFQEV 289

                    vWkGvPKFLRRvDtALKniGinERlPYdvP....LikFssWmGGDRDGkn
                    +++ +P+   R    LK  Gi    P+  P++++  kF sW+G DRDG n
  gi|2544132   290 LFDAIPQLYHR----LKQ-GIQSSFPWLNPprknFCKFGSWVGSDRDG-N 333

                    PRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEl
                    P v PEvt       R +    Yi+ v  L   ls+    +++     +
  gi|2544132   334 PSVKPEVTWQTACYQRNLVLEKYINSVKHLNNLLSLSLHWSDVLPELLDS 383

                    yrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL...
                        +++  +    E       +EPYR  L  +  +L nt  R  HL+++
  gi|2544132   384 LEQDRSQ--IPEVYEQLAIRYRQEPYRLKLSYIQQRLENTLARNLHLsqs 431

                    ..LAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlL
                    ++L     e     +y    eFL  L L  + L e G   +    L  l+
  gi|2544132   432 qpLQPVRLETTNPCIYNSDQEFLAELQLIQRNLAETG---LSCQELETLI 478

                    RqvstFGLsLvKLDiRqEseRqtDvlDAittHLei..GsYReWsEeKRqE
                     qv  +G  L  LDiRqEs R+ D +  it  L+i +  Y e sE  R E
  gi|2544132   479 CQVEIYGFNLAHLDIRQESSRHSDTMHEITDYLQIlpKPYNELSEAERTE 528

                    WLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFG.....aYi
                    WL  EL  +RPL++++LP   E  + +++fr+L  L  + FG++  + Yi
  gi|2544132   529 WLTKELPTRRPLIPAELPFSPEACETIETFRMLRRLHQE-FGeqicqTYI 577

                    ismataPsDvLAvELLqRECgv......kqtLrvvPLFEkLADLeAAPAa
                    ism+   sD L v LL  E g+ ++ +++ +++vvPLFE + DL+ AP
  gi|2544132   578 ISMSHEASDLLEVLLLAQEAGLydpatgRSSIQVVPLFETVDDLKRAPKV 627

                    vekLFsiDWYinridG.........................KqevmvGY
                    ++ LF +  Y+  + G+ +  ++ ++  ++++++  ++ +++ qe+m+GY
  gi|2544132   628 MKSLFELPLYRACLAGgyqaledceramgdenspafpsypqpLQEIMLGY 677
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                    sDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGP
                    sDs KD G ls  W + kAq  + ++A +yG+ + +FHGRGG vGRGGGP
  gi|2544132   678 SDSNKDSGFLSSNWEIHKAQKALQQIAEDYGIAVRIFHGRGGSVGRGGGP 727

                    tHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEH
                    t  AiL+qP   i+G +++t qGEv+   +   +L    L   t A +
  gi|2544132   728 TYEAILAQPGRSIQGRIKITEQGEVLASKYSLPELALYHLETVTTAVIQA 777

                    GmnPPvsPkPE.WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElE
                     +        E+W ++mee+Av     YR  v+    F ++F   tP  E
  gi|2544132   778 SLLGSGFDNLEpWNEIMEELAVRSRQHYRGFVYEQSDFLDFFNEVTPIQE 827

                    YGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKh
                      ++ i sRP++R       sLRAiPW+F+Wtq RF LP W GvGAA K
  gi|2544132   828 ISQLQISSRPTRRGGKKDFSSLRAIPWVFSWTQSRFLLPSWYGVGAALKG 877

                    AidKD.iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLv
                     +d ++  nl+ L+  Y +WPFF++ +  +Em  AK D  iA+ y + L
  gi|2544132   878 FLDEEpEENLKLLRYFYFKWPFFKMVISKVEMTLAKVDLQIAGHYVEKLS 927

                    a....EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRd
                     ++++E      +++ +++  t +l+  i GHk lL+GDP L+  + LR+
  gi|2544132   928 HpddrERFDRLFQQISQEFNLTCELISLITGHKQLLDGDPELQRSVHLRN 977

                    sYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnp
                      i  L  +q   LKR+R  s                 s+ a + v+
  gi|2544132   978 GTIVPLGFLQVSLLKRLRQHS-----------------SQMASGFVQ--- 1007

                    tervaPG.LEDtLiLtmKGiAAGmqntG<-*
                     +r++ G+L    +Lt+ GiAAGm ntG
  gi|2544132  1008 -SRYSKGeLLRGALLTINGIAAGMRNTG    1034

gi|16330985|ref|NP_441713.1|: domain 1 of 1, from 9 to 1034: score 395.9, E = 6.8e-116
                    *->siDAqLRlLvPGKvsedekLieYDAL.LlDkFLD.iLqDLHGedLkE
                        +         G  s +e+ + Y  L++++   +++Lq   G++L +
  gi|1633098     9    GLSTNWSGNGNGSNS-EEESVLYQRLkMVEELWErVLQSECGQELVD 54

                    avqECYElsAeYEG...KkDtkKLeELGakLtsLdPaDailvAkailHmL
                       E   l    E  ++    + +  +  ++  L+  Dai  A+a+
  gi|1633098    55 LLTE-LRLQGTHEAitsEISEEVIMGITQRIEHLELNDAIRAARAFALYF 103

                    nLAnLAE...EvelAyRRRikkkkhGDFaDEa.............sAttE.
                     L n+ E++ E +   R R +  +   F + a+++++  ++++  A tE+
  gi|1633098   104 QLINIVEqhyEQNEQQRNRWEASQETNFYEQAgneeemvppsrlGASTEp 153

                    ....sDiEE......tlKkLv...lklnKsPeEvFeALKnqsvDLvltAH
                     + + D  E + + +t+  L+++  +ln  P+ + + L    + Lv+tAH
  gi|1633098   154 lpvgIDQNElqasvgTFHWLMrelKRLNVPPQHIQNLLDHLDIRLVITAH 203

                    PtqsvRRsLLqKnaRiRnCLaqLsAKD..vtveDKkELDEA......LHR
                    Pt  vR  +  K+ R+   L +L    ++vt  D     +A++   +L
  gi|1633098   204 PTEIVRHTIRRKQRRVDRILRKLDQLQgsVTGRDWLNTWDAktaiaqLTE 253

                    EiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLRRvDtALKn
                    Ei   +RtDE+   +Pt  DE+ + + Y+ E +++ vP   +R   A+K
  gi|1633098   254 EIRFWWRTDELHQFKPTVLDEVDYSLHYFDEVLFDAVPELSKRLGQAIKE 303

                    iGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLLaRmmAanl
                         R P  +    F sW+GGDRDG nP vtPEvt       R +
  gi|1633098   304 TFPHLRAP-RANFCYFGSWVGGDRDG-NPSVTPEVTWQTACYQRGLVLGK 351

                    YisqvEDLmFEl..smWRCndELRvRAEElyrtaardkvvKyYiEFWKqv
                    Y+  + +L+  l++s+  C    +v  E l +  +         E
  gi|1633098   352 YLFSLGELVAILspSLHWC----KVSQELLDSLERDRIQLPEIYEELSLR 397

                    PPtEPYRviLGdvRDKLYntRERaRHLLA....tGiseisEeAvytkvEe
                      +EPYR+ L  v  +L nt  R   L  +++++ +  ++ e  y   Ee
  gi|1633098   398 YRQEPYRMKLAYVTKRLENTLRRNNRLANpeerQTMITMPAENHYRTGEE 447

                    FLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseR
                     LE L L  + L e G   +    L  l+ q   +G  L +LD RqEs R
```

```
  gi|1633098   448 LLEELRLIQRNLTETGLTCL---ELENLITQLEVYGFNLAQLDFRQESSR 494

                   qtDvlDAittHLeiGs..YReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   + + +  i + +++  ++Y e +Ee +  WL  EL+ +RPL++ ++P  E
  gi|1633098   495 HAEAIAEIAEYMGVLTtpYEEMAEEDKLAWLGVELQTRRPLIPQEMPFSE 544

                   EvkDvldafrvL....AELPiDsFGaYiismataPsDvLAvELLqRECgv
                     ++ ++++r L++ + E  +D    Yiism+   sDvL v LL +E g+
  gi|1633098   545 RTRETIETLRTLrhlqMEFGVDICQTYIISMTNDASDVLEVLLLAKEAGL 594

                   kqt......LrvvPLFEkLADLeAAPAavekLFsiDWYinridGK.....
                     + + +++Lr+vPLFE + DL+ AP  ++ LFs+ +Y+  + G  ++ +
  gi|1633098   595 YDPatasnsLRIVPLFETVEDLKNAPGIMDSLFSLPFYRATLAGSyhslk 644

                   ........................qevmvGYsDsGKDAGRlsAAWqLYkA
                   + ++++++  + ++++   ++++ qe+mvGYsDs KD G ls  W + kA
  gi|1633098   645 elqnqppdyyqiptttallnpgnlQEIMVGYSDSNKDSGFLSSNWEIHKA 694

                   qEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRv
                   q  +  vA+ + v L lFHGRGG vGRGGGP   AiL+qP  t++G +++
  gi|1633098   695 QKSLQAVAQSHRVILRLFHGRGGSVGRGGGPAYKAILAQPAGTVDGRIKI 744

                   tvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE.WRkLmee
                   t qGEv+   +   +L    L   t A +   +        E+W ++mee
  gi|1633098   745 TEQGEVLASKYSLPELALYNLETLTTAVIQASLLKSSFDFIEpWNRIMEE 794

                   mAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs.GG
                   +A  A   YRs+++ EP F ++F   tP  E   + i sRPa+Rk ++
  gi|1633098   795 LACTARRAYRSLIYEEPDFLDFFLTVTPIPEISELQISSRPARRKGGkAD 844

                   iesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD.iKnlqkLkEmYk
                   + sLRAiPW+F+WtqtRF LP W GvG A K  +d+D++Kn++ L+  Y
  gi|1633098   845 LSSLRAIPWVFSWTQTRFLLPAWYGVGTALKSFVDQDpVKNMKLLRYFYF 894

                   eWPFFRvtlDLlEmvFAKGDPGiAaLy.DkLLvaEeLkPFG...ksLRdk
                   +WPFF + +  +Em   K D  iA+ y  +L   E+   F +  ++++++
  gi|1633098   895 KWPFFNMVISKVEMTLSKVDLTIASHYvQELSKPEDRERFDrlfQQIKQE 944

                   YvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiR
                   Y+ t+d+ ++i  H  lL+GD  L+  + LR+  i  L  +q   LKR+R
  gi|1633098   945 YQLTRDFAMEITAHPHLLDGDRSLQRSVLLRNRTIVPLGLLQISLLKRLR 994

                   DPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKG
                      +        + y  E+      L++               +Lt+ G
  gi|1633098   995 QVTQEAETSGVRYRRYSKEE------LLRGA-------------LLTING 1025

                   iAAGmqntG<-*
                   iAAGm ntG
  gi|1633098  1026 IAAGMRNTG    1034

gi|218441147|ref|YP_002379476.1|: domain 1 of 1, from 2 to 1021: score 395.1, E = 1.2e-115
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      s   q+        s  +  ++    L++   +++Lq   G++L
  gi|2184411     2    SSLVQVSTTPLQFFSTSDLFLQDRLKLVEELWeEVLQAECGQELVAL 48

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +    +  e  G+      + +   +  Ld  +a+   +a+     L n
  gi|2184411    49 LKKLRAICCE-QGQAQKALEDSITQLIEQLDLVEAVRTSRAFALYFQLIN 97

                   LAE......EvelAyRRRik....kkkhGDFaDE....asAttEsDiEE.
                   + E++ ++++ +l  R   ++++ k k G  ++ ++  +sA     +E +
  gi|2184411    98 IVEqhyeqrDQQLSRRATYQespvKTKNGNNSESpslfSSAFGANWVERs 147

                   ............tlKkL...vlklnKsPeEvFeALKnqsvDLvltAHPtq
                    +++++++++ +tl  L +   +ln  P+ +   L    + Lv+tAHPt
  gi|2184411   148 wtddnqnqqkagTLHWLfpyLKQLNVPPQQIQRLLNQLDIRLVFTAHPTE 197

                   svRRsLLqKnaRiRnCLaqLsAKDvtve........DKkELDEALHREiq
                    vR  +  K+ Ri   L +L   + t  + + +++ + + L E    Ei
  gi|2184411   198 IVRHTIRRKQRRIAHILQKLDQAEETFRgmgltnswEAEQLKEQFKEEIR 247
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                    AAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLRRvDtALKniGi
                      +RtDE+   +Pt  DE+ + + Y+ E +++  P+   R    LK  G
  gi|2184411   248 LWWRTDELHQFKPTVLDEVDYALHYFNEVLFQALPQLALRLKQTLK--GA 295

                    nERl.PYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLLaRmmAanlYi
                      Rl+P       F sW+GGDRDG nP vtPEvt       R +    Y+
  gi|2184411   296 FPRLePPKNNFCYFGSWVGGDRDG-NPFVTPEVTWATACYQRNVVIEKYL 344

                    sqvEDL..mFElsmWRCn...dELRvRAEElyrtaardkvvKyYiEFWKq
                    + v++L+++   s+  Cn  +d L     +  + +     ++  i +
  gi|2184411   345 QTVDELsnILSPSLHWCNvlpDLLDSLEKDRVQMPEIY--TQLAIRY--- 389

                    vPPtEPYRviLGdvRDKLYntRERaRHLLA....tGiseisEeAvytkvE
                       +EPYR  L  ++ +L nt +R   L  ++++  i       +y + E
  gi|2184411   390 --RQEPYRLKLAYIKKRLENTQDRNNRLANpnerLLIFKTGNPNIYHNKE 437

                    eFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEse
                    e  E L L  + L   G   +    L  l+ qv  +G  L +LD RqEs
  gi|2184411   438 ELSEELQLIRRNLEASG---LTCQELENLICQVEIYGFNLTQLDFRQESS 484

                    RqtDvlDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                     + D +  i + L+i +  Y + sE  R  WL+ ELk +RPL++ ++P
  gi|2184411   485 CHSDAINEIAEYLQIlpKPYNQLSEAERTAWLIEELKTRRPLIPQEMPFS 534

                    EEvkDvldafrvL....AELPiDsFGaYiismataPsDvLAvELLqRECg
                    E   +v++++++L+  + E   +    Yiism+   sDvL v LL  E g
  gi|2184411   535 EKTCEVIETLKMLrllqQEFGLEICHTYIISMTNDVSDVLEVMLLAQEAG 584

                    vkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinridG.....
                    +  + +++ t+r+vPLFE + DL+ AP  +  LF +  Y+  + G+ +
  gi|2184411   585 LYDpatssiTIRIVPLFETVEDLKRAPEIMRALFEMTLYRAALAGgyqyl 634

                    .....................KqevmvGYsDsGKDAGRlsAAWqLYkAqE
                     ++++++  ++ +++  ++++ qe+mvGYsDs KD G ls  W + kAq
  gi|2184411   635 akdqgqeiigelqppllqppnLQEIMVGYSDSNKDSGFLSSNWEIHKAQK 684

                    EiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtv
                     + KvAK yG+ L lFHGRGG vGRGGGP   AiL+qP  tinG +++t
  gi|2184411   685 ALQKVAKGYGIDLRLFHGRGGSVGRGGGPAYAAILAQPTGTINGRIKITE 734

                    qGEviEfsFGEEnLCFrsLqRFtAAtLEHGmn.PPvsPkPEWRkLmeemA
                    qGEv+   +   +L    L     A +   + +        W ++me++A
  gi|2184411   735 QGEVLASKYSLPELALYNLETIVTAVIQSSLLgCGFDDIQVWNEIMEDLA 784

                    vvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs.GGie
                      A   YRs+++ +P F+++F + tP  E  ++ i sRPa+Rk ++  +
  gi|2184411   785 GCARKAYRSLIYEDPDFIDFFMSVTPIPEISQLQISSRPARRKSGkKDLS 834

                    sLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD.iKnlqkLkEmYkeW
                    +LRAiPW+F+WtqtRF LP W GvG A    i++++   l+ L+  Y +W
  gi|2184411   835 TLRAIPWVFSWTQTRFLLPAWYGVGTALEQFINREpEEHLKLLRYFYLKW 884

                    PFFRvtlDLlEmvFAKGDPGiAaLyDkLLva.EeLkPFGk...sLRdkYv
                    PFFR+ +  +Em   K D  iA  y k L  +E+L  F +  +++ ++Y
  gi|2184411   885 PFFRMVISKVEMTLSKVDLQIAHHYVKELSKpEDLERFERvfnQISEEYH 934

                    EtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDP
                     t  l+L i     lL+GDP L+  + LR+  i  L  +q   LKR+R
  gi|2184411   935 RTCRLVLDITENERLLDGDPTLQRSVQLRNGTIVPLGFLQVSLLKRLRQY 984

                    sykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiA
                    + +      +   y  E+      L++               +Lt+ GiA
  gi|2184411   985 NAQ-AESGVIHFRYSKEE------LLRGA------------LLTINGIA 1014

                    AGmqntG<-*
                    AGm ntG
  gi|2184411  1015 AGMRNTG    1021

gi|146339589|ref|YP_001204637.1|: domain 1 of 1, from 11 to 933: score 394.6, E = 1.6e-115
                    *->siDAqLR..lLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLk
                       +i   +R++  +  +  e +  ++ D  Ll + L+D + D  G d+
```

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gi|1463395    11    AITEEIRpnRAADVQAMEADAQLREDIRLLGRILgDTVRDQEGADVF 57

                    EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    + v      s  +   +D +   EL   L ++  a+++ + +a++    L
gi|1463395    58 DLVERIRQTSVRFHRDEDRQARRELEQILDGMTIAETVRIVRAFSYFSHL 107

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                    An+AE+ +   R R k          + A     +  tl +  + +
gi|1463395   108 ANIAEDQNNIRRMRAKSDA------NGGAGM---LAATLAHAKSAG-FDA 147

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    +E         v  vltAHPt   R+s + ++  +   L       +t+e
gi|1463395   148 AELRKFFSTALVSPVLTAHPTEVRRKSTMDREMEVAMLLDRRERMQLTPE 197

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    +++  DEAL R +   + t  +RR++ t  DE+  G+s++  t  + vP+
gi|1463395   198 EREANDEALRRAVLTLWQTNLLRRTKLTVLDEVTNGLSFYDYTFLREVPR 247

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     L   +  L n G  E     +  ++  sW+GGDRDG nP vt Ev R
gi|1463395   248 LLCSLEDRL-NDG-AEVAGDLASFLRMGSWIGGDRDG-NPFVTAEVMRGT 294

                    CLLaRmmAanlYisqvEDLmFElsmWR....CndELRvRAEElyrtaard
                      L   +A   Y++ +  L  Els+  +  +  +ELR+ AE    t+
gi|1463395   295 LKLQSSLAMHYYLEELHLLGSELSIAAhladVSEELRALAEKSPDTSPHR 344

                    kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                                   EPYR  +  +  +L  t  +    L   is ++
gi|1463395   345 --------------RGEPYRLAVSGIYARLAATAKK----LGIEISRLPV 376

                    eAv..ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                      v +y  v e  + L++  +sL      viA G L  l R v  FG  L
gi|1463395   377 ADVapYDSVKELQDDLDVLHHSLIANNAEVIARGRLRLLRRAVDCFGFHL 426

                    vKLDiRqEseRqt.DvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRP
                     +LDiRq s  + + v + i t +   sY   sE+ R   L+ EL+  RP
gi|1463395   427 ARLDIRQNSAVHErTVAELIDTAMPGMSYLALSEDARVGLLVNELRNTRP 476

                    LlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLA
                    L+   +   +E    l+ fr  AE + +   D     iism+   sD+L
gi|1463395   477 LVSHFVKYSDETIGELELFRAAAEahatFGADVISQCIISMCKGMSDMLE 526

                    vELLqRECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                    v LL +E g+ +++++ ++ +vPLFE + DL+A    ++++ ++  Y+
gi|1463395   527 VALLLKEVGLidpsgRCAVNIVPLFETIEDLQASSGIMDRMLALHDYRRL 576

                    idGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                    +d ++  qevm+GYsDs KD G +   W LYkA   ++ +  ++ v+L l
gi|1463395   577 VDSRgavQEVMLGYSDSNKDGGFVTSGWELYKAEIHLVEIFERHHVRLRL 626

                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                    FHGRGG vGRGGGP   Ai++qP   +nG +R+t qGE+i   +   ++
gi|1463395   627 FHGRGGSVGRGGGPSYDAIIAQPGGAVNGQIRITEQGEIISSKYSNAEVG 676

                    FrsLqRFtAAtLEHGmnPPvsPkP..EWRkLmeemAvvAtEEYRsvvvKE
                       L   +AAtLE  +  P  P P++E+   m+++   A   YR +v+
gi|1463395   677 RYNLEILAAATLEASLLHPRQPAPkrEYLTAMDRLSELAFKAYRGLVYET 726

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
                      Fv+YF + t   E   +niGsRPa Rk    ie LRAiPW+F+W q R
gi|1463395   727 DGFVDYFWSSTVINEIATLNIGSRPASRKKTRAIEDLRAIPWVFSWAQCR 776

                    FHLPvWLGvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                      LP W G+G A   +  +   + +  L+E+Y+eWPFFR+ l  ++mv A
gi|1463395   777 LMLPGWYGFGSAVEaWIAENPEQGMPFLRELYQEWPFFRMLLSNMDMVLA 826

                    KGDPGiAaLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLkiAGHkDlLE
                    K    iA+ y +L+  E L+ + FG+ +R ++    + LL i G   lL
gi|1463395   827 KSSIAIASRYAELVPDEALREqiFGR-IRREWNLVIETLLDITGQERLLQ 875

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
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                  G P L   +R R +Y+  Ln +q                  +l KE+ +
  gi|1463395   876 GNPLLERSVRNRFPYLDPLNHVQV-----------------ELLKEHRAQ 908

                  nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                  n           p e+v  G+     Lt+ Gi AG+ ntG
  gi|1463395   909 N-----------PDEQVLRGIQ----LTINGISAGLRNTG    933

gi|209528283|ref|ZP_03276745.1|: domain 1 of 1, from 2 to 1035: score 394.4, E = 1.9e-115
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                     s   q    +P  v   +       LLl   L i+ DL    L+
  gi|2095282     2    SSLVQSSEPIPSAVVSSNVTAGASELLLRNRLKIVEDLWESVLR--- 45

                  qECYElsAeY..........EGKkDtkKLeELGakLtsLdPaDailvAka
                  qEC E   +   + ++ +++EG+  +     +   +  Ld   ai  A+a
  gi|2095282    46 QECGEQLVDLllqmrsmtspEGQASPDLQANVWQIIKELDINAAIRAARA 95

                  ilHmLnLAnLAE......EvelAyR.............RRikkkkhG
                  +     L n+ E++ +++E elAy + ++++ ++++ ++++R i   +h
  gi|2095282    96 FALYFQLINIVEqhyeqrEQELAYAqikqqgapespadksnRSIFETRHQ 145

                  DFaDEasAttE.........sDiE.EtlKkLvlklnK..sPeEvFeALKn
                   F+   +   E  +++++++ D +  t+  L   l++ + P  v + L n
  gi|2095282   146 RFSTAEETPVEllnqtsqrqNDRDlATFHNLFPMLQRlnVPSQVIQRLLN 195

                  qs.vDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt...veDKk..
                  q ++ Lv+tAHPt  vR  +  K+ Ri   L qL   D   ++v+ K ++
  gi|2095282   196 QLdIRLVFTAHPTEIVRHTIRTKQRRIAKILQQLDTVDESygkVDNKDpe 245

                  ..........ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEt
                   ++  ++ ++EL E L  Ei   +RtDE+   +Pt  DE+ + + Y+ E
  gi|2095282   246 atglvktwtgELQEQLTEEIRLWWRTDELHQFKPTVLDEVEYSLHYFQEI 295

                  vWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvt
                  +++ +P+   R+   L         P +    kF sW+G DRDG nP vt
  gi|2095282   296 LFDVIPQLYQRIKQTLHPC-FPHLKPPNYDFCKFGSWVGADRDG-NPSVT 343

                  PEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrta
                  PEvt       R m    Yi+ v+ L   ls+    +++     El
  gi|2095282   344 PEVTWKTACYQRGMIIDKYIQAVDHLSQLLSLSLHWSDI---LPELLESL 390

                  ardkvvKyYiEFWKqvPP...tEPYRviLGdvRDKLYntRERaRHLLAtG
                   rd       E + qv  + ++EPYR  L  +  +L ntR+R   L
  gi|2095282   391 DRD--QVQLPEVYDQVAIryrQEPYRLKLCYIHKRLQNTRDRNQRLSTSN 438

                  iseisEeAvytkvE.........eFLEPLELCYksLCeCGDkviADGsLL
                    e   e + tk   ++  ++++eFL  L L  + L   G   i    L
  gi|2095282   439 EVERERERIVTKENagslynsgsEFLKELKLIERNLLATG---IQCRDLE 485

                  DlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs..YReWsEeK
                   l+ qv  +G  L ++D+RqEs  +   l  i   L++ +++Y +  E
  gi|2095282   486 NLICQVEIYGFYLARMDMRQESSVHSTALNEIVDYLQLLArpYDDLTEAE 535

                  RqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFG.....
                  R  WL++EL+ +RPL++++LP      + +++frv+ EL  + FG++  +
  gi|2095282   536 RTLWLITELQTRRPLIPAELPFSQKTCETINTFRVMRELQQE-FGqeicq 584

                  aYiismataPsDvLAvELLqRECgvkqt......LrvvPLFEkLADLeAA
                   Yiism+   sD L v LL +E g+  + ++ ++L+vvPLFE + DL+ A
  gi|2095282   585 TYIISMSHDVSDLLEVLLLAKEAGLYDPatgignLQVVPLFETVEDLKKA 634

                  PAavekLFsiDWYinridG..............KqevmvGYsDsGKDAG
                  P  ++ LF +  Y+  + G+ ++ ++ +++ + + qe+m+GYsDs KD G
  gi|2095282   635 PSVMKDLFELPLYRALLAGgyqkyqqvsqdmnasLQEIMLGYSDSNKDSG 684

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   ls  W + kAq  +   A  y v + +FHGRGG vGRGGGP   AiL+q
  gi|2095282   685 FLSSNWEIHKAQKALQTLAESYYVSIRIFHGRGGSVGRGGGPAYKAILAQ 734

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHG.mnPPvs
                  P   inG +++t qGEv+   +   +L    L   + A +    ++
  gi|2095282   735 PGKSINGRIKITEQGEVLASKYSLSQLALYNLESVATAVIQASlLHTGFD 784
```

```
                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                        W ++mee+ v     YR++++  P  v++F   tP  E  ++ i s
  gi|2095282   785 EIEPWNQIMEELSVRSRSCYRALIYEQPDLVDFFEQVTPIQEISQLQISS 834

                    RPaKRkPs..GGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD.
                    RPa+R+  ++  i  LRAiPW+F+Wtq RF LP W GvG A    i+ ++
  gi|2095282   835 RPARRQSDkkKDISGLRAIPWVFSWTQSRFLLPSWYGVGTAIEQFIQEEp 884

                    iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva....E
                      n++ L+  Y +WPFFR tl  +Em  AK D  +A  y + L  +++++
  gi|2095282   885 QENIKLLRYFYIKWPFFRTTLSKVEMTLAKVDLEMAHHYVRELSHpkdrD 934

                    eLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittL
                         +++  ++  t++++L+i G + lL+ DP L+  +RLR+  i  L
  gi|2095282   935 RFEDLFERIAKEFNLTRQMVLEITGQQQLLDNDPVLQRSVRLRNGTIIPL 984

                    nvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaP
                      +q   L+R+R      t+   +   y   +      L++
  gi|2095282   985 GLLQVSLLQRLRHHGTSATP-GVIHSRYSKGE------LLRGA------- 1020

                    GLEDtLiLtmKGiAAGmqntG<-*
                          +Lt+ GiAAGm ntG
  gi|2095282  1021 ------LLTINGIAAGMRNTG    1035

gi|154146870|emb|CAM84122.1|: domain 1 of 1, from 1 to 439: score 393.6, E = 3.4e-115
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDv+DA+ttHL+iGsYReW E+KR EWLl+EL+GKRPLl +D+P+tE
  gi|1541468     1 --HTDVIDAVTTHLGIGSYREWDEDKRIEWLLSELRGKRPLLAPDMPQTE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvl+a+rv+AELP+DsFG+Yiismata sDvLAv LLqREC v ++L
  gi|1541468    49 EIADVLGALRVIAELPSDSFGPYIISMATATSDVLAVHLLQRECRVPKPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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                    vvPLFE+LADL+AAPA+ve+LF +DWY+ +i GKq vmvGYsDsGKDAG
  gi|1541468     99 HVVPLFERLADLQAAPASVERLFKMDWYMDQIGGKQMVMVGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAW LYkAq + ++vA kyGvKL+ FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468    149 RLSAAWALYKAQTDTARVANKYGVKLTFFHGRGGTVGRGGGPTHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGslRvt+qGEviE  FGEE+LCF +LqRFtAAtLEHG++PPvsP
  gi|1541468    199 PPDTINGSLRVTIQGEVIEHQFGEEHLCFLTLQRFTAATLEHGVHPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEW  LmeemA v tEEYRs+v+KEPRFvEYFR+AtPE+E  +mniGsR
  gi|1541468    249 KPEWSALMEEMAAVCTEEYRSIVFKEPRFVEYFRSATPETELPRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkP+GG+++LRAiPWiF+WtqtRFHLPvWLGvGAAFK A+ KD+Kn+
  gi|1541468    299 PAKRKPGGGVTTLRAIPWIFSWTQTRFHLPVWLGVGAAFKQAMTKDSKNI 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q L++mY+eWPFFRvt+DLlEmvFAKGDP iAaLyD+LLva eLkPFG++
  gi|1541468    349 QLLRDMYNEWPFFRVTVDLLEMVFAKGDPSIAALYDDLLVANELKPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR kY Et +lLL++AGHk++LEGDP L+q+lRLR++Yitt
  gi|1541468    399 LRSKYAETLQLLLQVAGHKEILEGDPILRQQLRLRNPYITT--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|154146688|emb|CAM83979.1|: domain 1 of 1, from 1 to 441: score 393.6, E = 3.5e-115
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541466     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541466     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541466     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541466     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541466     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541466     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541466     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541466     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541466     - ------------------------------------------------- -
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                    eRqtDvlDAitthLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tDv+D ittHL+iGsYReW+Ee+RqEWL++EL+G+RPL+g+DLP+tE
  gi|1541466     1 --HTDVMDTITTHLGIGSYREWPEERRQEWLVSELRGRRPLFGADLPQTE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl++f+v+AELP DsFGaYiis+ataPsDvLAvELLqREC vk++L
  gi|1541466    49 EVADVLGTFKVVAELPEDSFGAYIISLATAPSDVLAVELLQRECYVKNPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLe A A++e LFsiDWY+ ri G qe+m+GYsDsGKDAG
  gi|1541466    99 RVVPLFEKLADLERARATMELLFSIDWYKERIAGNQEIMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEEi+ vA ++GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541466   149 RLSAAWQLYKAQEEIVAVAERHGVKLTIFHGRGGTVGRGGGPSHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP tinGslRvt+qGEviE  FGEEnLCFr+LqRFtAAtLEHGm PPvsP
  gi|1541466   199 PPNTINGSLRVTIQGEVIEKTFGEENLCFRTLQRFTAATLEHGMYPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L+++mAvvAtEEYRs+v+KEPRF+EYFR+AtPE+EYG+mniGsR
  gi|1541466   249 KPEWRALLDDMAVVATEEYRSIVFKEPRFIEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi..K
                    P+KRkP GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhA++   +++
  gi|1541466   299 PSKRKPEGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAMQMQAgdR 348

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                     l  L+EmY+eWPFFRvt+DLlEmvFAKGDPGiAaLyDkLLv  +L+PFG
  gi|1541466   349 GLAALREMYDEWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVPSDLWPFG 398

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    ++LR++Y+Et+ lLL++AGH DlLE DPYLKqrl LRdsYit
  gi|1541466   399 EQLRANYKETQSLLLQVAGHDDLLENDPYLKQRLLLRDSYITA------- 441

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL

  gi|1541466     - ------------------------------------------------- -

                    iLtmKGiAAGmqntG<-*

  gi|1541466     - ---------------    -

gi|148238790|ref|YP_001224177.1|: domain 1 of 1, from 22 to 1003: score 393.2, E = 4.6e-115
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         +  + ++    v   + L +  AL+ D +  +L      +  E
  gi|1482387    22    ESEQAMAAVNDAPVG-GQLLQQRLALVEDLWQTVLRSECPAEQAERL 67

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls        +   + L + +  +d ++ai  A+a++    L n+
  gi|1482387    68 LRMKQLSDPVLPEGNAVSSDALVSLIRDMDLSEAIAAARAFSLYFQLVNI 117

                    AEE.......velAyRRRikkkkhGDFaDEasAttE.sDiEEtlKkLvlk
                     E + ++++  e   R      +   F+      tE++   E + +L  +
  gi|1482387   118 LEQrieedgyLESIVRSQDTAEQINPFTPPLATQTEpATFRELFERL-RR 166

                    lnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK
                    ln  P+     L+   + Lv+tAHPt  vR  +  K+ R+   L qL A+
  gi|1482387   167 LNVPPAQLETLLQELDIRLVFTAHPTEIVRHTVRHKQRRVASLLQQLEAQ 216

                    .DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtv
                    ++    +   +   L  Ei   +RtDE+   +P   DE+ + + Y+   +
  gi|1482387   217 tESSTFEAGTIRLQLEEEIRLWWRTDELHQFKPSVLDEVDYALHYFQQVL 266

                    WkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtP
                    ++ +P+  RR   AL        lP       F sW+G DRDG nP vt
  gi|1482387   267 FDAMPQLRRRLSSALASSYPDVQLP-PSSFCTFGSWVGSDRDG-NPSVTT 314

                    EvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaa
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                    ++t       R +    Y+s v  L   ls+    + + +   E     +
  gi|1482387   315 DITWRTACYQRQLMLERYVSAVQGLRDQLSISMQWSQVSAPLLESLEMDR 364

                    rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi...
                           Y E        EPYR  L  v ++L  t  R   L   G + +
  gi|1482387   365 LR-FPEVYEERATRY-RLEPYRLKLSFVLERLRLTQIRNQQLAEAGWrap 412

                    ..........seisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLL
                     ++  ++++++  sE   y  v eF   LEL   sL       +    L
  gi|1482387   413 adgllssnpeAPQSESLHYGSVAEFRSDLELIRTSLVSTD---LTCEPLD 459

                    DlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLe.iGsYReWsEeKR
                     lL qv  FG sL  LDiRqEs R+ D lD + + L++  +Y +  E+ R
  gi|1482387   460 TLLTQVHIFGFSLAGLDIRQESTRHSDALDEVSRYLNpDQAYGDLNEQER 509

                    qEWLlaELkGKRPLlgsDL...PktEEvkDvldafrvLA.ELPiDsFGaY
                      WLl EL+ +RPL+++ ++ +P tEE  Dv  +++ L +E  +     Y
  gi|1482387   510 VQWLLQELQTRRPLIPPSVswsPTTEETVDVFRTLHRLQdEFGSRICRTY 559

                    iismataPsDvLAvELLqRECgvkqt......LrvvPLFEkLADLeAAPA
                    +ism+ + sD L v LL +E g+ +++ ++ +L vvPLFE + DL+ AP
  gi|1482387   560 VISMSHSVSDLLEVLLLSKEAGLVEPsaghadLLVVPLFETVEDLQRAPE 609

                    avekLFsiDWYinri.....dGK..qevmvGYsDsGKDAGRlsAAWqLYk
                     +e LF +  Y+n +++ +++G++ qe m+GYsDs KD G ls  W + k
  gi|1482387   610 VMEELFQTPLYRNLLprvgsQGQplQELMLGYSDSNKDSGFLSSNWEIHK 659

                    AqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslR
                    Aq  +   A + Gv L lFHGRGG vGRGGGP   AiL+qP  t++G ++
  gi|1482387   660 AQIALQDLAARNGVALRLFHGRGGSVGRGGGPAYQAILAQPSGTLQGRIK 709

                    vtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsPkPEWRkLme
                    +t qGEv+   +   +L    L     A +   +    +   P W +Lm
  gi|1482387   710 ITEQGEVLASKYSLPELALYNLETVSTAVVQNSLvTNQLDATPSWNDLMA 759

                    emAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.
                    ++A      YR++v   P  v +F   tP  E  k+ i sRPa+Rk + +
  gi|1482387   760 RLARCSRRHYRALVHDNPDLVAFFEQVTPIEEISKLQISSRPARRKTGTr 809

                    GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYk
                     + sLRAiPW+F Wtq RF LP W GvG A    +  D   +  L+ + +
  gi|1482387   810 DLSSLRAIPWVFGWTQSRFLLPSWFGVGTALHEELVNDPDQMSLLRTLHQ 859

                    eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEe....LkPFGksLRdk
                     WPFFR+ +  +Em   K D  +A  y   L + ++++        + ++
  gi|1482387   860 RWPFFRMLISKVEMTLSKVDLDLARHYVTSLGSADhrqaFDGIYTTIAEE 909

                    YvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiR
                    Y  t+ l+L+i G   lL+ DP L+  + LR+  i  L  +q   L+R+R
  gi|1482387   910 YSLTHRLVLEITGQERLLDADPALQLSVDLRNRTIVPLGFLQVALLRRLR 959

                    DPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKG
                    D +     +P++s     E   ++d+  +    ++   G     +Lt+ G
  gi|1482387   960 DQN----RQPPMS-----ES--PSDGDGRTYSRSELLRG----ALLTING 994

                    iAAGmqntG<-*
                    iAAGm ntG
  gi|1482387   995 IAAGMRNTG    1003

gi|196256031|ref|ZP_03154569.1|: domain 1 of 1, from 47 to 1020: score 392.4, E = 7.9e-115
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGe......
                        +  +LR++   +   +  L +    L++k LD+   +   +
  gi|1962560    47    DLLIKLRAICSEQGQAQKALEDSITQLIEK-LDLNEAVRTSrafaly 92

                    .dLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailH
                     +L  +v   YE   +   ++ t   +E  ak  +++   + +  +a+
  gi|1962560    93 fQLINIVEQHYEQRDQQLSRRATYNEGESSAK-NGINGEQTSIFSSAFG- 140

                    mLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkl
                        An  E      R  +  k+      +    t   +   lK+L
  gi|1962560   141 ----ANWLE------RSLNDEKQ-----NDQKIGTFHWLFPYLKQL---- 171
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                nKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKD
                n  P+ +   L    v Lv+tAHPt  vR  +  K+ Ri   L +L   +
gi|1962560   172 NVPPQQIQRLLEQLDVRLVFTAHPTEIVRHTIRRKQRRIAHILQKLDQAE 221

                vtve........DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGms
                 t  + + +++ + +E  E L  Ei   +RtDE+   +Pt  DE+ + +
gi|1962560   222 ETFRgmgltnswEAEEAKEQLKEEIRLWWRTDELHQFKPTVLDEVDYSLH 271

                YiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGk
                Y+ E +++ +P+   R    LK      R P +     F sW+GGDRDG
gi|1962560   272 YFNEVLFEAIPQLALRLKRTLKSAFPRLRPPKNN-FCYFGSWVGGDRDG- 319

                nPRvtPEvtRDvCLLaRmmAanlYisqvEDL..mFElsmWRCn...dELR
                nP vtPEvt       R +    Yi+ v++L+++   s+  Cn  +d L
gi|1962560   320 NPFVTPEVTWATACYQRNVVIEKYIERVDELsnILSPSLHWCNvlpDLLD 369

                vRAEElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERa
                    +  + ++     +  i +      +EPYR  L  ++ +L ntR+R
gi|1962560   370 SLEKDRVQIPQVY--NQLAIRY-----RQEPYRLKLAYIKKRLENTRDRN 412

                RHLLA....tGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGs
                  L  ++++  +        y + EeF+E L L  + L   G   +
gi|1962560   413 SRLANpeerLLVFKTTNANNYQNKEEFIEELKLMRRNLESTG---LSCQE 459

                LLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei..GsYReWsE
                L  l+ qv  +G  L +LD RqEs  + D +  i + L+i +  Y +  E
gi|1962560   460 LDSLICQVEVYGFNLTQLDFRQESSNHSDAINEIAEYLQIlpKPYNQLTE 509

                eKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvL....AELPiDsF
                  R  WL+ ELk +RPL++ ++P  E   +v++++r+L++ + E   +
gi|1962560   510 AERTAWLIEELKTRRPLIPQEMPFSEKTCEVIETLRMLrqlqQEFGLEIC 559

                GaYiismataPsDvLAvELLqRECgvkq......tLrvvPLFEkLADLeA
                  Yiism+   sDvL v LL  E g+  + + ++t+r+vPLFE + DL+
gi|1962560   560 HTYIISMTNEVSDVLEVLLLAQEAGLYDpatcssTIRIVPLFETVEDLKR 609

                APAavekLFsiDWYinridG.........................Kqevm
                AP  +  LF +  Y+  + G+ ++  + ++++ ++ +++  ++++ qe+m
gi|1962560   610 APEIMRALFELTLYRATLAGgydhlaslqgenvgelkpplleptnLQEIM 659

                vGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRG
                vGYsDs KD G ls  W + kAq  + KvAK+yG  L lFHGRGG vGRG
gi|1962560   660 VGYSDSNKDSGFLSSNWEIHKAQKALQKVAKRYGLDLRLFHGRGGSVGRG 709

                GGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAt
                GGP   AiL+qP  t+nG +++t qGEv+   +   +L    L     A
gi|1962560   710 GGPAYAAILAQPTATVNGRIKITEQGEVLASKYSLPELALYNLETIVTAV 759

                LEHGmn.PPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtP
                +   + +        W ++mee+A      YR++++ EP Fv++F + tP
gi|1962560   760 IQSSLLgCGFDDIQVWNEIMEELASCSRKAYRALIYEEPDFVDFFMSVTP 809

                ElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWLGvGA
                  E  ++ i sRPa+Rk ++  + +LRAiPW+F+WtqtRF LP W GvG
gi|1962560   810 IQEISQLQISSRPARRKSGkKDLSTLRAIPWVFSWTQTRFLLPAWYGVGT 859

                AFKhAidKD.iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyD
                A    i  ++   l+ L+  Y +WPFF++ +  +Em   K D  iA  y
gi|1962560   860 ALEQFISTEpEEHLKLLRYFYLKWPFFKMVISKVEMTLSKVDLQIAYHYV 909

                kLLva....EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrl
                k L  ++++E      +++ ++Y  t  l+L+i   k lL+GDP L+  +
gi|1962560   910 KELSQpedrERFERLFEQIAQEYHRTCRLVLEITENKRLLDGDPTLQRSV 959

                RLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLv
                 LR+  i  L  +q   +KR+R  + +      +   y  E+      L+
gi|1962560   960 QLRNGTIVPLGFLQVSLIKRLRQYNAQ-AESGVINFRYSKEE------LL 1002

                kLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                +               +Lt+ GiAAGm ntG
```

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  gi|1962560  1003 RGA------------LLTINGIAAGMRNTG    1020

gi|27378066|ref|NP_769595.1|: domain 1 of 1, from 8 to 932: score 391.6, E = 1.4e-114
                  *->siDAqLRlLvPGKvs..edekLieYDALLlDkFL.DiLqDLHGedLk
                     s  A  R   P  v   e +  ++ D  Ll + L+D + D  G dL
  gi|2737806     8    SDAADSRPNRPEDVQalEADARLRDDIRLLGRILgDTVRDQEGADLF 54

                  EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                  + v      s  +   +D     EL   L s+  ++++ + +a++    L
  gi|2737806    55 DLVERIRQTSIRFHRDEDRLARRELEQILDSMSTSETVRIVRAFSYFSHL 104

                  AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                  An+AE+ +     R +                + +tl +    +   P
  gi|2737806   105 ANIAEDQNNIRQMRARTAA--------KIGGSGVLADTLAHAKAAG-IGP 145

                  eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                  +   +  K   v  vltAHPt   R+s + ++  +   L       +t +
  gi|2737806   146 DALRNFFKTALVSPVLTAHPTEVRRKSTMDREMEVASLLDRRERVALTED 195

                  DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                  +    DE L RE+   + t  +RR++ t  DE+  G+s++  t  + vP+
  gi|2737806   196 EAAASDEQLRREVLTLWQTNLLRRTKLTVLDEVANGLSFYDYTFLREVPR 245

                  FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                   +   +  L   G        +  ++  sW+GGDRDG nP vt +v R
  gi|2737806   246 LVNVLEDRLEEDG-DQAASELASFLRMGSWIGGDRDG-NPFVTADVMRGT 293

                  CLLaRmmAanlYisqvEDLmFElsmWR....CndELRvRAEElyrtaard
                    L       +Y++ +  L  Els+  +  +  +ELR  AE    t+
  gi|2737806   294 LRLQSSRVMQFYLNELHVLGSELSIAAhladVSEELRTLAERSPDTSPHR 343

                  kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                                 EPYR  +  +  +L  t E     +      +
  gi|2737806   344 --------------SGEPYRLAVSGIYARLTATAEALEVEITR--RPVGK 377

                  eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                     y  v e    L++  +sL     +viA G L   l R v  FG  L +
  gi|2737806   378 GRPYESVKELQADLDVLHRSLISNNARVIARGRLRLLRRAVDCFGFHLAR 427

                  LDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLl
                  LDiRq s  +   +  +    + G sY    E+ R   L  EL+  R L+
  gi|2737806   428 LDIRQNSAVHERTIAELMDAANPGmSYLALGEDARISLLTNELRSTRALV 477

                  gsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAvE
                   + +   +E    l+ f+  AE + +  +D+    iism+   sD+L v
  gi|2737806   478 SPFVKYSDETMGELNVFHAAAEahakFGSDAIPQCIISMCKGMSDMLEVA 527

                  LLqRECgvkqt.....LrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                  +L +E g+ ++++++ + +vPLFE + DL+A  A ++++ s+  Y+  +d
  gi|2737806   528 VLLKEVGLVHPsgrsaINIVPLFETIEDLQASSAIMDRMLSLHDYRRLVD 577

                  GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                   +++ qevm+GYsDs KD G +   W LYkA   ++ v  ++ v+L lFH
  gi|2737806   578 SRgsvQEVMLGYSDSNKDGGFVTSGWELYKAEINLVDVFERHHVRLRLFH 627

                  GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                  GRGG vGRGGGP   Ai++qP   +nG +R+t qGE+i   +   ++
  gi|2737806   628 GRGGSVGRGGGPSYDAIIAQPGGAVNGQIRITEQGEIISSKYSNAEVGRN 677

                  sLqRFtAAtLEHG.mnPPvs.PkPEWRkLmeemAvvAtEEYRsvvvKEPR
                   L   +AAtLE   ++P  s P+ E+   m+e+   A   YR +v+
  gi|2737806   678 NLEILAAATLEASlLHPRQSaPRREYLTAMDELSSLAFRAYRGLVYETDG 727

                  FvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFH
                  Fv+YF   t   E   +niGsRPa Rk    ie LRAiPW+F+W q R
  gi|2737806   728 FVDYFWASTVINEIATLNIGSRPASRKKTRAIEDLRAIPWVFSWAQCRLM 777

                  LPvWLGvGAAF.KhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                  LP W G+G A +++  +   K +  LkE+YkeWPFFR+ l  ++mv AK
  gi|2737806   778 LPGWYGFGTAVeQWIAEHPDKGMPFLKELYKEWPFFRMLLSNMDMVLAKS 827
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                    DPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                       iA+ y +L+  E L++k FG+ +R ++    + LL i G   lL G
  gi|2737806   828 SIAIASRYAELVPDEALreKIFGR-IRREWHSCIETLLDIMGQDRLLQGN 876

                    PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                    P L   +R R +Y+  Ln +q                 +l +E+ + n
  gi|2737806   877 PLLERSVRHRFPYLDPLNHVQV----------------ELLREHRAQN- 908

                    kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                             p e+v  G+     Lt+ Gi AG+ ntG
  gi|2737806   909 ----------PDEQVLRGIQ----LTINGISAGLRNTG    932

gi|88807863|ref|ZP_01123374.1|: domain 1 of 1, from 11 to 991: score 391.1, E = 1.9e-114
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           q R+ v       + L +  AL+ D +  +L      +  E
  gi|8880786    11    --SEQPRVAVAEAPVGGQLLQQRLALVEDLWQTVLRSECPAEQAERL 55

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls        +   + L + +  +d ++ai  A+a++    L n+
  gi|8880786    56 LRMKQLSDPVLPDGNAVSSDALVSLIRDMDLSEAIAAARAFSLYFQLVNI 105

                    AEE.......velAyRRRikkkkhGDFaDEasAttE.sDiEEtlKkLvlk
                     E + ++++  e   R      +   Fa      tE++   E + +L  +
  gi|8880786   106 LEQrieedgyLESIVRSQDTAEQINPFAPPLATQTEpATFRELFERL-RR 154

                    lnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK
                    ln  P+   + L+   + Lv+tAHPt  vR  +  K+ R+   L qL  K
  gi|8880786   155 LNVPPAQLENLLQELDIRLVFTAHPTEIVRHTIRHKQRRVASLLQQLETK 204

                    .DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtv
                    +D    +   +   L  Ei   +RtDE+   +P   DE+ + + Y+   +
  gi|8880786   205 sDSSAVEAGTIRLQLEEEIRLWWRTDELHQFKPSVLDEVDYALHYFQQVL 254

                    WkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtP
                    +  +P+  RR   AL        lP       F sW+G DRDG nP vt
  gi|8880786   255 FGAMPQLRRRLSSALACSYPDVQLP-PSSFCTFGSWVGSDRDG-NPSVTT 302

                    EvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaa
                    ++t       R +    Y+s v  L   ls+    + + +   E     +
  gi|8880786   303 DITWRTACYQRQLMLDRYVSAVHGLRDQLSISMQWSQVSAPLLESLEMDR 352

                    rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                           Y E        EPYR  L  v ++L  t  R   L   G
  gi|8880786   353 LR-FPEVYEERATRY-RLEPYRLKLSFVLERLRLTQIRNQQLADAGWRAP 400

                    sEeAv.............ytkvEeFLEPLELCYksLCeCGDkviADGsLL
                    ++  v  +++++++++ +y  v eF   LEL   sL       +    L
  gi|8880786   401 ADAQVaatpetpqseslhYGSVAEFRSDLELIRTSLVSTD---LTCEPLD 447

                    DlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLe.iGsYReWsEeKR
                     lL qv  FG  L  LDiRqEs R+ D lD + + L++  +Y +  E+ R
  gi|8880786   448 TLLTQVHIFGFCLAGLDIRQESTRHSDALDEVSRYLNpDEAYGDLNEQER 497

                    qEWLlaELkGKRPLlgsDL...PktEEvkDvldafrvLA.ELPiDsFGaY
                      WLl EL+ +RPL+++ ++ +  tEE  Dv  +++ L +E  +     Y
  gi|8880786   498 VNWLLQELQTRRPLIPPSVqwsSTTEETVDVFRTLHRLQdEFGSRICRTY 547

                    iismataPsDvLAvELLqRECgvkqt......LrvvPLFEkLADLeAAPA
                    +ism+ + sD L v LL +E g+ +++ ++ +L vvPLFE + DL+ AP
  gi|8880786   548 VISMSHSVSDLLEVLLLAKEAGLVEPsaghadLLVVPLFETVEDLQRAPE 597

                    avekLFsiDWYinri.....dGK..qevmvGYsDsGKDAGRlsAAWqLYk
                     +e+LF +  Y+n +++ +++G++ qe m+GYsDs KD G ls  W + k
  gi|8880786   598 VMEQLFQTPLYRNLLprvgsQGQplQELMLGYSDSNKDSGFLSSNWEIHK 647

                    AqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslR
                    Aq  +   A + G  L lFHGRGG vGRGGGP   AiL+qP  t++G ++
  gi|8880786   648 AQIALQDLAARNGLALRLFHGRGGSVGRGGGPAYQAILAQPSGTLQGRIK 697

                    vtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsPkPEWRkLme
                    +t qGEv+   +   +L    L   t A +   +    +   P W +Lm
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  gi|8880786   698 ITEQGEVLASKYSLPELALYNLETVTTAVVQNSLvTNQLDATPSWNDLMA 747

                   emAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.
                   ++A      YR++v   P  v +F   tP  E  k+ i sRPa+Rk + +
  gi|8880786   748 RLARCSRRHYRALVHDNPDLVAFFEQVTPIEEISKLQISSRPARRKTGTr 797

                   GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYk
                    + sLRAiPW+F Wtq RF LP W GvG A    ++ D   +  L+ + +
  gi|8880786   798 DLSSLRAIPWVFGWTQSRFLLPSWFGVGTALHEELENDPDQMSLLRTLHQ 847

                   eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva....EeLkPFGksLRdk
                    WPFFR+ +  +E+   K D  +A  y   L + +++E      k + ++
  gi|8880786   848 RWPFFRMLISKVEITLSKVDLDLARHYVTSLGSadhrEAFDGIYKTIAEE 897

                   YvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiR
                   Y  t+ l+L+i G   lL+ DP L+  + LR+  i  L  +q   L+R+R
  gi|8880786   898 YSLTHRLVLEITGQERLLDADPALQLSVDLRNRTIVPLGFLQVALLRRLR 947

                   DPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKG
                   D +     +P++s     E   ++d+  +    ++   G     +Lt+ G
  gi|8880786   948 DQN----RQPPMS-----ES--PSDGDGRTYSRSELLRG----ALLTING 982

                   iAAGmqntG<-*
                   iAAGm ntG
  gi|8880786   983 IAAGMRNTG    991

gi|74148786|gb|ABA00148.1|: domain 1 of 1, from 1 to 414: score 390.9, E = 2.3e-114
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7414878     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7414878     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7414878     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7414878     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                                                  sY+HEt+WkGvPKFLR
  gi|7414878     1 ----------------------------------SYFHETIWKGVPKFLR 16

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALKniGi ER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|7414878    17 RVDTALKNIGIDERVPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 65

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmAanlY sq+EDLmFElsmWRC dELRvRA+El+r ++rd   K+Yi
  gi|7414878    66 ARMMAANLYCSQIEDLMFELSMWRCSDELRVRADELHRSSKRD--AKHYI 113

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWK +PP+EPYRviLGdvRDKLY tRER+RH+LA+Gi +i+EeA yt++
  gi|7414878   114 EFWKTIPPNEPYRVILGDVRDKLYQTRERSRHMLAHGICDIPEEATYTNI 163

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   E+FLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLvKLDiRqEs
  gi|7414878   164 EQFLEPLELCYRSLCACGDRPIADGSLLDFLRQVSTFGLSLVKLDIRQES 213

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +R+tDvlDAit+HL+iGsYR+WsEe+RqEWLl+EL  KRPL+g+DLPktE
  gi|7414878   214 DRHTDVLDAITKHLDIGSYRDWSEERRQEWLLSELASKRPLFGADLPKTE 263

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dvld+f+vLAELP+D+FGaYiismataPsDvLAvELLqREC+v+q+L
  gi|7414878   264 EIADVLDTFHVLAELPSDCFGAYIISMATAPSDVLAVELLQRECKVRQPL 313
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                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAav++LFsiDWY+nri+GKqevm+GYsDsGKDAG
  gi|7414878   314 RVVPLFEKLADLEAAPAAVARLFSIDWYKNRIQGKQEVMIGYSDSGKDAG 363

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+iKvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7414878   364 RLSAAWQLYKAQEELIKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 413

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    P
  gi|7414878   414 P---------------------------------------------- 414

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|7414878     - ---------------------------------------------- -

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|7414878     - ---------------------------------------------- -

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|7414878     - ---------------------------------------------- -

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|7414878     - ---------------------------------------------- -

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|7414878     - ---------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|7414878     - -------------    -

gi|56417897|gb|AAV90837.1|: domain 1 of 1, from 9 to 995: score 390.4, E = 3.1e-114
                    *->siDAqLRlLvPGKvsedekLieYDALLl.DkFLDiLqDLHGedLkEa
                       s +A L        s  + L++    L++D +  +Lq   G+ L E
  gi|5641789     9    SAEAEL-------LSTSQSLLRQRLTLVeDIWQAVLQKECGQKLVER 48

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                              +G+        +   +  Ld  Dai  A+a+     L n
  gi|5641789    49 LNH-LRATRTADGQSLNFSPSSISELIETLDLEDAIRAARAFALYFQLIN 97

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEE.......tlKkLv..
                      E  +   R   + ++    a  ++A   s   E  +++ +t+  L ++
  gi|5641789    98 SVEQ-HYEQREQQQFRRNLASANASEANGNSVHTEiaptqagTFDWLFph 146

                    lklnKsPeEvFeALKnqs.vDLvltAHPtqsvRRsLLqKnaRiRnCLaqL
                    lk +  P    + L nq ++ Lv+tAHPt  vR  +  K+ Ri   L qL
  gi|5641789   147 LKHQNMPPQTIQRLLNQLdIRLVFTAHPTEIVRHTIRNKQRRIAGILRQL 196

                    s.....AKDvtveDKkELDEA...LHREiqAAFRtDEiRRaqPtPqDEmR
                     +++++ K +   D  E++  +++L  Ei   +RtDE+   +P   DE+
  gi|5641789   197 DqteegLKSLGTSDSWEIENIqqqLTEEIRLWWRTDELHQFKPQVLDEVD 246

                    aGmsYiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGD
                    + + Y+ E +++  P    R   ALK      ++P       F sW+GGD
  gi|5641789   247 YALHYFEEVLFDTLPELSVRLQQALKASFPTLKVP-TTNFCNFGSWVGGD 295

                    RDGknPRvtPEvtRDvCLLaRmmAanlYisqvEDL..mFElsmWRCndEL
                    RDG nP vtP+vt       R +    Yi  vE L+++  ls+   n
  gi|5641789   296 RDG-NPSVTPDVTWKTACYQRGLVLERYIASVESLsdVLSLSLHWSN--- 341

                    RvRAEElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRER
                     v  + l++  + + +             +EPYR     ++ +L nt ER
  gi|5641789   342 -VLPDLLHSSYQDQNIFPDVYQSLASRHRQEPYRLKSAYIKRRLENTLER 390

                    aRHLLAtGi....seisEeAvytkvEeFLEPLELCYksLCeCGDkviADG
                     R L      +++ e +++ vy    eFL  L L   sL +     i
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  gi|5641789   391 NRRLANMPAwenkVEAADDKVYICGQEFLADLKLIRESLVQ---TEINCA 437

                   sLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEe
                   +L  l+ qv  F   L +LD RqEs R+ D +  i   L i    + +
  gi|5641789   438 ALDKLICQVEIFSFVLTRLDFRQESTRHSDAIAEIVDYLSIAQILQRPKR 487

                   KRqEW..LlaELkGKRPLlgsDLPktEEvkDvldafrvL....AELPiDs
                   +R+   +L+ ELk +RPL++ ++   E   + +++++vL++ + E  i
  gi|5641789   488 RRKNHlgLVQELKTRRPLIPKEMHFSERTVETIQTLQVLrrlqQEFGIGI 537

                   FGaYiismataPsDvLAvELLqRECgvkqtL......rvvPLFEkLADLe
                      Yiism+   sDvL v LL  E g+  +L++ ++ r+ PLFE + DL+
  gi|5641789   538 CQTYIISMTNEVSDVLEVLLLAQEAGLYDPLtgmttiRIAPLFETVDDLR 587

                   AAPAavekLFsiDWYinridG.....................KqevmvGY
                    AP  ++ LF i  Y+  + G+ +++ +++ +++ +++  ++ qe+m+GY
  gi|5641789   588 NAPEIMQALFEIPLYRACLAGgyeppadgrcdetfgdrlvpnLQEIMLGY 637

                   sDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGP
                   sDs KD G ls  W + kAq  + +vA  yG+ L +FHGRGG vGRGGGP
  gi|5641789   638 SDSNKDSGFLSSNWEIHKAQKNLQQVADPYGIDLRIFHGRGGSVGRGGGP 687

                   tHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEH
                      AiL+qPP tinG +++t qGEv+   +   +L    L     A +
  gi|5641789   688 AYAAILAQPPNTINGRIKITEQGEVLASKYSLPDLALYHLESVSTAVIQS 737

                   GmnPP.vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElE
                    +   +      W ++me++       YR+++ EP F ++F + tP  E
  gi|5641789   738 SLLASgFDDIQPWNRIMEDLSQRSRAAYRALIYEEPDFLDFFMSVTPIPE 787

                   YGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFK
                     ++ i sRPa+Rk + + + sLRAiPW+F+Wtq RF +P W GvG A +
  gi|5641789   788 ISQLQISSRPARRKKGNkDLSSLRAIPWVFSWTQSRFLVPAWYGVGTALQ 837

                   hAidKD.iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLy.DkL
                      + D++ nl+ ++  Y +WPFFR+ +  +Em   K D  +A+ y  +L
  gi|5641789   838 GFFEEDpVENLKLMRYFYSKWPFFRMVISKVEMTLSKVDLQMASHYvHEL 887

                   LvaEeLkPFG...ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLR
                      E++  F +  +++ ++Y  tk l+L+i     lL+GD  L+  + LR
  gi|5641789   888 AEKEDIPRFEkllEQISQEYNLTKRLILEITENEALLDGDRPLQRSVQLR 937

                   dsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLn
                   +  i  L  +q   LKR+R               y  E     + +v+
  gi|5641789   938 NGTIVPLGFLQVSLLKRLR--------------QYTRET---QASIVHFR 970

                   ptervaPGLEDtLiLtmKGiAAGmqntG<-*
                           L    +Lt+ GiAAGm ntG
  gi|5641789   971 ---YSKEELLRGALLTINGIAAGMRNTG    995

gi|154146866|emb|CAM84120.1|: domain 1 of 1, from 1 to 439: score 389.5, E = 5.7e-114
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541468     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541468     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541468     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541468     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541468     - ---------------------------------------------- -
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                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541468     - ------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541468     - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541468     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541468     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tDv+DAittHL+iGsYRe  E+KR EWLl+EL+GKRPLl +D+P+tE
  gi|1541468     1 --HTDVIDAITTHLGIGSYRERDEDKRIEWLLSELRGKRPLLAPDMPQTE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++Dvl+a+rv+AELP+DsFG+Yiismata sDvL v LLqREC v ++L
  gi|1541468    49 EIADVLGALRVIAELPSDSFGPYIISMATATSDVLTVHLLQRECRVPKPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   vvPLFE+LADL+AAPA+ve+LF +DWY+ +i GKq vmvGYsDsGKDAG
  gi|1541468    99 HVVPLFERLADLQAAPASVERLFKMDWYMDQIGGKQMVMVGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAW LYkAq + ++vA kyGvKL+ FHGRGGtvGRGGGPtHLAiLsq
  gi|1541468   149 RLSAAWALYKAQTDTARVANKYGVKLTFFHGRGGTVGRGGGPTHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGslRvt+qGEviE  FGEE+LCF +LqRFtAAtLEHGm+PPvsP
  gi|1541468   199 PPDTINGSLRVTIQGEVIEHQFGEEHLCFLTLQRFTAATLEHGMHPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEW  LmeemA v tEEYRs+v+KEPRFvEYFR+AtPE+E  +mniGsR
  gi|1541468   249 KPEWSALMEEMAAVCTEEYRSIVFKEPRFVEYFRSATPETELPRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKRkP+GG+++LRAiPWiF+WtqtRFHLPvWLGvGAAFK A+ KD+Kn+
  gi|1541468   299 PAKRKPGGGVTTLRAIPWIFSWTQTRFHLPVWLGVGAAFKQAMTKDSKNI 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q L++mY+eWPFFRvt+DLlEmvFAKGDP iAaLyD+LLva+eLkPFG++
  gi|1541468   349 QLLRDMYNEWPFFRVTVDLLEMVFAKGDPSIAALYDDLLVADELKPFGEQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR kY Et +lLL++AGHk++LEGDP L+q+lRLR++Yitt
  gi|1541468   399 LRSKYAETLQLLLQVAGHKEILEGDPILRQQLRLRNPYITT--------- 439

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541468     - ------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|1541468     - -------------    -

gi|50251800|dbj|BAD27731.1|: domain 1 of 1, from 15 to 452: score 389.1, E = 7.5e-114
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                     siDAqLRlL+PGKvsed+kL+eYDALL+D+FLDiLqDLHG+ L+E+v
  gi|5025180    15    SIDAQLRLLAPGKVSEDDKLVEYDALLVDRFLDILQDLHGPHLREFV 61

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                  qECYElsAeYE  +D  +L+ELG kLtsL P+D+i+v ++++HmLnLAnL
  gi|5025180    62 QECYELSAEYENDRDEARLDELGRKLTSLPPGDSIVVSSSFSHMLNLANL 111

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AEEv++A+RRRik+k+ GDFaDEasA tEsDiEEtlK+Lv +l Ks eEv
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  gi|5025180   112 AEEVQIAHRRRIKLKR-GDFADEASAPTESDIEETLKRLVTQLGKSREEV 160

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   F+ALKnq+vDLv+tAHPtqsvRRsLLqK++RiRnCL qL+AKD+t +DK+
  gi|5025180   161 FDALKNQTVDLVFTAHPTQSVRRSLLQKHGRIRNCLRQLYAKDITADDKQ 210

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL REiqAAFRtDEiRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|5025180   211 ELDEALQREIQAAFRTDEIRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 260

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   R+DtALKniGinERlPY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|5025180   261 RIDTALKNIGINERLPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 309

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmAanlY+sq+EDLmFElsmWRC dELR+RA++l+  +++    K+Yi
  gi|5025180   310 ARMMAANLYFSQIEDLMFELSMWRCSDELRIRADDLHCSSRKA--AKHYI 357

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWKq+PP+EPYRviLG vRDKLY tRER+RHLL tG+sei+EeA +t+v
  gi|5025180   358 EFWKQIPPNEPYRVILGGVRDKLYYTRERTRHLLTTGVSEIPEEATFTNV 407

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   EeFLEPLELCY+sLC CGDk iADGsLLD
  gi|5025180   408 EEFLEPLELCYRSLCACGDKPIADGSLLD---------------------- 436

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|5025180     - ------------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|5025180     - ------------------------------------------------- -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG

  gi|5025180     - ------------------------------------------------- -

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|5025180     - ------------------------------------------------- -

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                             v v+G  i
  gi|5025180   437 ----------VNVKGGLI------------------------------- 444

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|5025180     - ------------------------------------------------- -

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                                                WL
  gi|5025180   445 -------------------------------WL----------------- 446

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                                                          L+P
  gi|5025180   447 -----------------------------------------LQP---- 449

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|5025180     - ------------------------------------------------- -

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                       DP
  gi|5025180   450 ----DPK---------------------------------------- 452

                   tmKGiAAGmqntG<-*

  gi|5025180     - -------------    -

gi|284050999|ref|ZP_06381209.1|: domain 1 of 1, from 2 to 1035: score 389.0, E = 8.4e-114
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                *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                   s   q    +P  v   +  ++   LLl   L i+ DL    L+
gi|2840509     2    SSLVQSSEPIPSAVVSSNAPVQASDLLLRNRLKIVEDLWESVLR--- 45

                qECYElsAeY..........EGKkDtkKLeELGakLtsLdPaDailvAka
                qEC E   +   + ++ +++EG+  ++    +   +  Ld   ai  A+a
gi|2840509    46 QECGEQLVDLllqmrsmtspEGQASPHLQANVWQIIKDLDINAAIRAARA 95

                ilHmLnLAnLAE......EvelAyR.................RRikkkkhG
                +     L n+ E++ +++E elAy + +++++ +++ ++++R i   +h
gi|2840509    96 FALYFQLINIVEqhyeqrEQELAYAqikhqgpaespadksnRSIFETRHQ 145

                DFaDEasAttE.........sDiE.EtlKkLvlklnK..sPeEvFeALKn
                 F+   +A  E  +++++++ D +  t+  L   l++ + P  v + L n
gi|2840509   146 RFSTAEEAPVEllnqtsrrqDDRDlATFHNLFPMLQRlnVPSQVIQRLLN 195

                qs.vDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKD............
                q ++ Lv+tAHPt  vR  +  K+ Ri   L qL   D++ ++ ++++++
gi|2840509   196 QLdIRLVFTAHPTEIVRHTIRTKQRRIAKILQQLDTVDesygkvdntnpe 245

                ...vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEt
                 +++      EL E L  Ei   +RtDE+   +Pt  DE+ + + Y+ E
gi|2840509   246 atgLVKTWTGELQEQLTEEIRLWWRTDELHQFKPTVLDEVEYSLHYFQEI 295

                vWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvt
                +++ +P+   R+   L+        P +    kF sW+G DRDG nP vt
gi|2840509   296 LFDVIPQLYQRIKQTLQP-HFPHLKPPNYDFCKFGSWVGADRDG-NPSVT 343

                PEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrta
                PEvt       R +  n Yi+ v+ L   ls+    ++  v  E l +
gi|2840509   344 PEVTWKTACYQRGLIINKYIQAVDHLNQLLSLSLHWSD--VLPELLESLD 391

                ardkvvKyYiEFWKqvPP...tEPYRviLGdvRDKLYntRERaRHLLAtG
                + +       E + qv  + ++EPYR  L  +  +L ntR+R   L
gi|2840509   392 RDQ---VQLPEVYDQVAIryrQEPYRLKLCYILKRLENTRDRNQRLSTSN 438

                iseisEeAvytkvE.........eFLEPLELCYksLCeCGDkviADGsLL
                  e   e + tk   ++  +++  FL  L L  + L   G   i    L
gi|2840509   439 EVERERERIVTKENagslyhsgaAFLKELKLIERNLMATG---IQCRDLE 485

                DlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs..YReWsEeK
                 l+ qv  +G  L ++D+RqEs  +   l  i   L++ +++Y +  E
gi|2840509   486 NLICQVEIYGFYLARMDMRQESSVHSTALNEIVDYLQLLArpYDDLTEAE 535

                RqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFG.....
                R  WL++EL+ +RPL++++LP      + +++frv+ EL  + FG++  +
gi|2840509   536 RTLWLITELQTRRPLIPAELPFSPKTCETINTFRVMRELQQE-FGqeicq 584

                aYiismataPsDvLAvELLqRECgvkqt......LrvvPLFEkLADLeAA
                 Yiism+   sD L v LL +E g+  + ++ ++L+vvPLFE + DL+ A
gi|2840509   585 TYIISMSHDVSDLLEVLLLAKEAGLYDPatgignLQVVPLFETVEDLKKA 634

                PAavekLFsiDWYinridG..............KqevmvGYsDsGKDAG
                P  ++ LF +  Y+  + G+ ++ ++ +++ + + qe+m+GYsDs KD G
gi|2840509   635 PSVMKDLFELPLYRAMLAGgyqkyeqvsqdvnasLQEIMLGYSDSNKDSG 684

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 ls  W + kAq  +   A  y + + +FHGRGG vGRGGGP   AiL+q
gi|2840509   685 FLSSNWEIHKAQKALQTLAESYHISIRIFHGRGGSVGRGGGPAYKAILAQ 734

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHG.mnPPvs
                P   inG +++t qGEv+   +   +L    L   + A +    ++
gi|2840509   735 PGKSINGRIKITEQGEVLASKYSLSQLALYNLESVATAVIQASlLHTGFD 784

                PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    W ++mee+ v     YR++++  P  v++F   tP  E  ++ i s
gi|2840509   785 EIEPWNQIMEELSVRSRSCYRALIYEQPDLVDFFEQVTPIQEISQLQISS 834

                RPaKRkPs..GGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD.
                RPa+R+  ++  i  LRAiPW+F+Wtq RF LP W GvG A    i  ++
gi|2840509   835 RPARRQSDkkKDISGLRAIPWVFSWTQSRFLLPSWYGVGTAIEQFIREEp 884
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                  iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLva....E
                    n++ L+  Y +WPFFR t+   Em  AK D  +A  y + L  +++++
  gi|2840509   885 EENIKLLRYFYIKWPFFRTTISKAEMTLAKVDLEMAHHYVRELSHpqdrD 934

                  eLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittL
                        +++  ++  t++++L+i G k lL+ DP L+  +RLR+  i  L
  gi|2840509   935 RFEDLFQRIAKEFNLTRQMVLEITGQKQLLDNDPVLQRSVRLRNGTIIPL 984

                  nvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaP
                    +q   L+R+R      t+   +   y   +      L++
  gi|2840509   985 GLLQVSLLQRLRHHGTSATP-GVIHSRYSKGE------LLRGA------- 1020

                  GLEDtLiLtmKGiAAGmqntG<-*
                        +Lt+ GiAAGm ntG
  gi|2840509  1021 ------LLTINGIAAGMRNTG    1035

gi|154146684|emb|CAM83977.1|: domain 1 of 1, from 1 to 439: score 388.8, E = 9.4e-114
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541466     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541466     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541466     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541466     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541466     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541466     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541466     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541466     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541466     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tD +DAittHL+iGsYR W+Ee+RqEWL++EL+GKRPL+g+DLP+ +
  gi|1541466     1 --HTDAMDAITTHLGIGSYRAWPEERRQEWLVSELRGKRPLFGPDLPQSD 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl++frv+AELP DsFGaYiismataPsDvLAvELLqRECgvk++L
  gi|1541466    49 EVADVLGTFRVIAELPGDSFGAYIISMATAPSDVLAVELLQRECGVKNPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADL+ A  ++e LFs+DWY+ ri+GKqe+m+GYsDsGKDAG
  gi|1541466    99 RVVPLFEKLADLQQARPTMELLFSVDWYKERINGKQEIMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEEi+ vA ++ vKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541466   149 RLSAAWQLYKAQEEIVSVAERHSVKLTIFHGRGGTVGRGGGPSHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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                    PP t+nG lRvt+qGEviE sFGEEnLCFr+LqRFtAAtLEHGmnPPvsP
  gi|1541466   199 PPNTVNGLLRVTIQGEVIEKSFGEENLCFRTLQRFTAATLEHGMNPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR+L+++mA vAt+EYRs+v++E RFvEYFR+AtPE+EYG+mniGsR
  gi|1541466   249 KPEWRRLLDDMATVATDEYRSIVFQESRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+G AF+hA+++    l
  gi|1541466   299 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGTAFRHAMQQQAGGL 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvt+DLlEmvFAKGDPGiAaLyDkLLv  +L+PFG++
  gi|1541466   349 ATLREMYEEWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVPQDLWPFGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++YvEt+ lLL++AGHkDlLE DPYL+qrl LRdsYit
  gi|1541466   399 LRANYVETQSLLLQVAGHKDLLESDPYLRQRLILRDSYITA--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541466     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541466     - -------------    -

gi|154146700|emb|CAM83985.1|: domain 1 of 1, from 1 to 438: score 388.0, E = 1.6e-113
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tD +DAittHL+iGsYR+W+Ee+RqEWL++EL+G RPL+g+DLP+ +
  gi|1541467     1 --HTDAVDAITTHLGIGSYRDWPEEQRQEWLVSELRGNRPLFGPDLPQSD 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl++frv+AELP DsFGaY+ismataPsDvLAvELLqRECgvk+++
  gi|1541467    49 EVADVLGTFRVIAELPDDSFGAYVISMATAPSDVLAVELLQRECGVKKPM 98
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                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADL+ A A++e LFs+DWY+ ridGKqe+m+GYsDsGKDAG
  gi|1541467     99 RVVPLFEKLADLQQARATMELLFSVDWYKERIDGKQEIMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAW LYkAqEEi+ vA ++GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541467    149 RLSAAWHLYKAQEEIVDVAERHGVKLTIFHGRGGTVGRGGGPSHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP t+nGslRvtvqGEviE sFGE+nLCFr+LqRFtAAtLEHGmnPPvsP
  gi|1541467    199 PPNTVNGSLRVTVQGEVIEKSFGEDNLCFRTLQRFTAATLEHGMNPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L+++m  vAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467    249 KPEWRALLDDMTEVATEEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+hA+dK    l
  gi|1541467    299 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHAMDKPA-GL 347

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvt+DLlEmvFAKGDPGiAaLyDkLLv  +L+PFG++
  gi|1541467    348 ATLREMYDEWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVPQDLWPFGEQ 397

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y Et+ lLLk+AGH DlLE DPYL+qrl LRdsYit
  gi|1541467    398 LRANYAETQSLLLKVAGHEDLLESDPYLRQRLMLRDSYITA--------- 438

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|288555580|ref|YP_003427515.1|: domain 1 of 1, from 3 to 918: score 387.4, E = 2.5e-113
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                    v + + L++ D   l   L++iL    G dL
  gi|2885555      3    ------------EVNDANTLLRNDVKKLGNILgEILVHHGGVDLLNK 37

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v    E        +D +  + L   +  L+P     v +a++    L n
  gi|2885555     38 VESIREKTKSLRQHHDQETYNALKEEIATLEPPTRQQVIRAFSIYFHLVN 87

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R R  ++      +E+     s +E  +  +  +     +
  gi|2885555     88 IAEQNHRIRRQRQYQLN-----EEGVSQPFS-LERAVSAVKELQ-PEDAV 130

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +   L   s++L++tAHPt + +R +L  + Ri   L     + +t  ++
  gi|2885555    131 MQKVLNDLSIELIITAHPTEATKRTVLETQKRISTILQEFDNQQLTKKER 180

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + L++ L  E+ A + tDE+R  +Pt  DE++ G+ Y+  t+++ +P
  gi|2885555    181 RRLEDSLFNEVTALWQTDELRHRKPTVLDEVKNGLHYFNQTLFEVIPEVH 230

                    RRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDvC
                       +  L     n +  + vP+ ++F sW+GGDRDG nP vtPEvt +
  gi|2885555    231 QELEVQLDEQFPNHK--WSVPnFLHFGSWIGGDRDG-NPNVTPEVTWETL 277

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     L R +    Y + + DLm  +s       + +  E l++  a +
  gi|2885555    278 KLQRRLVLKKYKESLVDLMKRFS--QTTTRVQISDELLQSVEADE---AN 322

                    YiEFWKqvP.PtEPYR....viLGdvRDKLYntRERaRHLLAtGiseisE
                    Y+E     P  tE YR++ +viL  +R              A G  +
  gi|2885555    323 YLEDGEEWPiETELYRrkfqVILKRIR--------------AVGKED--- 355

                    eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
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                     A y + Ee L  L L   s  +          L  l+Rqv  FG  L
  gi|2885555   356 KAAYQNAEELLADLNLIKESAEQHQPANRTLKTLRKLIRQVQLFGFHLAT 405

                    LDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLl
                    LDiR  s  +   +  i + ++i + Y +  Ee +   L   L+  RPLl
  gi|2885555   406 LDIRNHSGEHEAAITEILRAVQITdDYASLTEEEKLTILQDVLRDPRPLL 455

                    gsDLPktEEvkDvldafrvL....AELPiDsFGaYiismataPsDvLAvE
                           E ++v+  f ++++ + E  + s   Y++sm+ + sD L v
  gi|2885555   456 LLKEDYSKETQEVIKVFDMIkqahREFGSRSIEVYLVSMTQSSSDLLEVL 505

                    LLqRECgvkqt.........LrvvPLFEkLADLeAAPAavekLFsiDWYi
                    LL +E g+ + + +++ +++L v PL E + DL A P  ++ LF +D Y+
  gi|2885555   506 LLAKEAGIYRLhadgtvdsgLHVAPLLETVDDLVAGPRIMKTLFEMDVYR 555

                    nridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                    n++  ++++qe+m+GYsD  KD G l A W+L+kAq Ei  +AK+y v+L
  gi|2885555   556 NHLSERgnhQEIMLGYSDGSKDGGTLTANWKLFKAQQEIHDMAKDYQVRL 605

                    vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                      FHGRGG  GRGGGP    iLsqP +t+   +++t qGEv+   +  E+
  gi|2885555   606 KFFHGRGGSLGRGGGPLNRSILSQPAETLGDGVKITEQGEVLSSRYLLED 655

                    LCFrsLqRFtAAtLEHGmnPPv......sPkPEWRkLmeemAvvAtEEYR
                    + +r L   + A LE      +++++++s k  W + mee        Y
  gi|2885555   656 IAYRNLEQAASALLEASASSQIqtkkghSRKEAWEEAMEEASKHSLKKYQ 705

                    svvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiF
                    s+v+ +  F  YF+ AtP  E G +niGsRP  Rk s   e LRAiPW+F
  gi|2885555   706 SLVFGDQDFLTYFKQATPLNELGALNIGSRPMSRKGSQRFEDLRAIPWVF 755

                    aWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLl
                    aWtq R  +P W   G       +    nl  L+EmY++WPFF  t+  l
  gi|2885555   756 AWTQSRQMIPAWYAAGTGLSAFANESEENLALLREMYNNWPFFHSTINNL 805

                    EmvFAKGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGH
                     m   K D   A  y +L+   e+ ++ FG+ + ++Y  tk++LLki
  gi|2885555   806 QMALMKADLKTAKEYMNLVEDQEIadRIFGD-ISEEYIRTKEILLKISES 854

                    kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                     +lL+  P ++  +  R++Y+  Ln +q             v l   +sK
  gi|2885555   855 EELLDHSPNIQESVHRRNPYVDPLNFLQ-------------VDL---ISK 888

                    EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      A+En  ++deL+               +Lt+ G+AAG+ ntG
  gi|2885555   889 MRAEEN--PSDELMTEV-------------LLTISGVAAGLVNTG    918

gi|158426293|ref|YP_001527585.1|: domain 1 of 1, from 4 to 931: score 386.8, E = 3.8e-113
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       ++ A +     G     ++ ++ D  Ll + L+D + +  G+ + E
  gi|1584262     4    AVWAVVSEQEAGGPD-KDQPLRDDIRLLGRILgDTVREQEGDAIYEL 49

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      s  +    D    +EL a L s+ P  a+ + +a++    LAn
  gi|1584262    50 VETIRQTSIRFHRDADEAARQELNALLESMTPEVAVQIIRAFSYFSHLAN 99

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+ +   R R +          +sA     +   l +    +    +E
  gi|1584262   100 IAEDQHHSRRNRAHAVA-------GSAPRPGTLANALARAEKAG-IGAAE 141

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                             v  vltAHPt   R+s + ++  i   L        t+++
  gi|1584262   142 LRAFFDAALVSPVLTAHPTEVRRKSTMNREMEIADLLDLKERLQATPQEA 191

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +E DE L R +   + t  +R+ + t  DE+  G+sY+  t    vP+ L
  gi|1584262   192 REQDEKLRRAVLTLWQTALLRKFKLTVLDEVQNGLSYYDYTFLAEVPRLL 241

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                       +  L      E      P ++  sW+GGDRDG nP vt +v R+
  gi|1584262   242 CALEDHLAEQEGGEPGAELPPFLRIGSWIGGDRDG-NPFVTADVLRETVR 290
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                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                      R     +Y++qv  L+ Els+      L +  E+l   a r
  gi|1584262   291 QHRDRVMAFYLEQVGLLVTELSL---AKRLVAVSEDLTALAERS--GDRA 335

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv..y
                     E       +EPYR  L  +  +L  t    +          +E+   +y
  gi|1584262   336 PEH-----REEPYRLALVGIHNRLKATVAAQKAADDGKTMGAAEDGHlpY 380

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     +   F   L++ Y+sL   G  ++A G L  + R v  FG  L  LD+R
  gi|1584262   381 PDAAAFRADLDILYRSLMANGSAILARGRLRHVRRAVDSFGFHLASLDLR 430

                    qEseRqt.DvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    q s+ + + v D + +      Y    Ee R   L aEL   RPL  + L
  gi|1584262   431 QNSDVHErTVADLLEQAAPGTNYHALDEEARIAVLRAELTNPRPLASPFL 480

                    PktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAvELLqR
                      tEE +  l  +r  AE + +L        iis a   sD+L   LL +
  gi|1584262   481 SYTEETRSELAILRTAAEaharLGKTVIPNAIISKAEGISDMLELALLLK 530

                    ECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid...G
                    E g+ + ++  ++ v+PLFE + DL+A    +++L ++  Y+  +d+++G
  gi|1584262   531 EVGLvsatgESAINVIPLFETIGDLQACGPVMDRLLALPEYRALVDsrgG 580

                    KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                     qevm+GYsDs KD G +s  W LYkA   +i v  ++ vKL lFHGRGG
  gi|1584262   581 EQEVMLGYSDSNKDGGFVSSGWELYKAEIALIEVFARHKVKLRLFHGRGG 630

                    tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                     vGRGGGP   AiL+qP   + G +R+t qGE+i   +   +   r L
  gi|1584262   631 SVGRGGGPSYDAILAQPAGAVSGQIRITEQGEIISSKYSNPENGRRNLEI 680

                    FtAAtLEHGm..nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEY
                       AtLE  + +    sP+PE+   mee+   A   YRs+v+  P F +Y
  gi|1584262   681 LVSATLESTLleAEQASPRPEFLAAMEELSKTAFTAYRSLVYETPGFEDY 730

                    FRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvW
                    F + t   E   +niGsRPa R     ie+LRAiPW+F+W q R  LP W
  gi|1584262   731 FWSSTVISEIATLNIGSRPASRNKTRAIEALRAIPWVFSWSQCRLMLPGW 780

                    LGvGAAFKhAid.KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                     G+G A    ++ + +  +  L+ mY+eWPFFR  l  ++mv  K    +
  gi|1584262   781 YGFGTAIAAFVEaRPVDGIAFLQSMYREWPFFRTLLSNMDMVLSKSSLAV 830

                    AaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                    A+ y +L+  EeL+ +   ++ ++Y+     LL i G k lLE  P L
  gi|1584262   831 ASRYAELVPDEELRTrIFSRISAEYQSAITSLLAIMGQKKLLEANPLLDR 880

                    rlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkade
                     +R R +Y+  Ln +q   LK  R                d     +d
  gi|1584262   881 SIRNRFPYLDPLNHIQVELLKLHR----------------SDAG---SDH 911

                    LvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +++                Lt+ Gi AG+ n G
  gi|1584262   912 VLHGI-------------QLTINGISAGLRNSG    931

gi|154146702|emb|CAM83986.1|: domain 1 of 1, from 1 to 438: score 386.6, E = 4.4e-113
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|1541467     - ------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tD +DAittHL+iGsYR+W+Ee+RqEWL++EL+  RPL+g+DLP+ +
  gi|1541467     1 --HTDAVDAITTHLGIGSYRDWPEEQRQEWLVSELQCNRPLFGPDLPQSD 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl++frv+AELP DsFGaY+ismataPsDvLAvELLqRECgvk+++
  gi|1541467    49 EVADVLGTFRVIAELPEDSFGAYVISMATAPSDVLAVELLQRECGVKKPM 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADL+ A A++e LFs+DWY+ ri+GKqe+m+GYsDsGKDAG
  gi|1541467    99 RVVPLFEKLADLQQARATMELLFSVDWYKERINGKQEIMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEEi+ vA ++ vKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541467   149 RLSAAWQLYKAQEEIVDVAERHSVKLTIFHGRGGTVGRGGGPSHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP t+nGslRvtvqGEviE sFGEEnLCFr+LqRFtAAtLEHGmnPPvsP
  gi|1541467   199 PPNTVNGSLRVTVQGEVIEKSFGEENLCFRTLQRFTAATLEHGMNPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L+++mA vAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWRALLDDMATVATEEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+hA+d     l
  gi|1541467   299 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHAMDTPG-GL 347

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+EmY+eWPFFRvt+DLlEmvFAKGDPGiAaLyDkLLv  +L+PFG++
  gi|1541467   348 ATLREMYEEWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVPQDLWPFGEQ 397

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y Et+ lLLk+AGH DlLE DPYL+qrl LRdsYit
  gi|1541467   398 LRANYGETQSLLLKVAGHNDLLESDPYLRQRLMLRDSYITA--------- 438

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|222526644|ref|YP_002571115.1|: domain 1 of 1, from 13 to 933: score 385.9, E = 7.3e-113
                   *->siDAqLRlL..vPGKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                       + A +R+L+++ G+v                   i q  HG +
  gi|2225266    13    -LSANIRALgdALGRVI------------------IGQ--HGSEALA 38
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                avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                 v     ++ +          + L   +  Ld      + ka+     L
gi|2225266    39 LVEQVRRMAKDLRNAPTNTDPQALPQLIADLDLPQLRSLVKAFTLYFGLV 88

                nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                nLAE ve     R + ++    a    A   +D  E lK+  +     P+
gi|2225266    89 NLAEGVERLRVLRARDLR---HAPAPRAESIADAIELLKRHGVPA---PA 132

                EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLs..AKDvtv
                 + e L    +  vltAHPt s RR +L K  Ri   L  L  + + v +
gi|2225266   133 -IQEWLDHALIMPVLTAHPTESRRRTILIKLRRIFDTLVDLTfgERLVLP 181

                eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                 D++     + REi   +  D++R  +P   DE+  G+ ++   +W+  P
gi|2225266   182 ADRQAALTRIEREIVGLWQSDDVRNRRPSVLDEVENGLFFFQTVLWELLP 231

                KFLRRvDtALKniGinE..RlPYdvPLikFssWmGGDRDGknPRvtPEvt
                   R +  AL+      + RlP   P ++F sWmGGDRDG nP vtPEvt
gi|2225266   232 HIYREMSDALQAAYPDHpwRLP---PFLRFGSWMGGDRDG-NPFVTPEVT 277

                RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk
                 +   L R       i+ ++ L+ +ls     + ++v    + r a
gi|2225266   278 VETVRLMRSAMLRYLIDCLDRLITDLS--QSVQQVKVDTAIIDRIAEYRE 325

                vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAt.Gise..i
                ++             EPYR +   +  +L nt   +       Gi  +
gi|2225266   326 LMPDAAATLNPHYRCEPYRQLCHFIQARLHNTLQYTLDYTPRwGIDPplA 375

                sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                    +y +  e L  L+L   sL + G   iA+G L D+   v    L
gi|2225266   376 RRPDIYYHSRELLADLDLIDASLRNNGSTLIAEGLLRDVRTLVAVCHLHT 425

                vKLDiRqEseRqtDvlDAittHLe.iGsYReWsEeKRqEWLlaELkGKRP
                  LD+Rq + R+t  l  i    + +  Y    E  R   L  E++  RP
gi|2225266   426 ATLDVRQHASRHTAALSEILAAAGvVDDYEALDEAERIAVLSVEIRRPRP 475

                LlgsDLPktE.EvkDvldafrvLA....ELPiDsFGaYiismataPsDvL
                L +s L    +  ++ + +frv+A  ++ L  + F  Yiis +   sD L
gi|2225266   476 LTPSRLSHFSpATAETIHTFRVIAaiseQLDPEIFQTYIISTTSQVSDLL 525

                AvELLqRECgvkqt.....LrvvPLFEkLADLeAAPAavekLFsiDWYin
                Av LL R+ g+ q+++ ++L +vPLFE   DL+ APA ++ L  +  Y+
gi|2225266   526 AVLLLCRDAGLYQPgqasqLHIVPLFETGDDLQRAPALLDELLRLPVYRE 575

                ri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                ++  +d  qevm+GYsDs K+ G ++A W LY+Aq E+  v  ++Gv+L
gi|2225266   576 HLalrDNLQEVMLGYSDSNKEGGFVAANWALYRAQVELTAVTDRHGVRLR 625

                lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                lFHGRGG vGRGGGP   AiL+qPP t++G ++vt qGE+i   + +
gi|2225266   626 LFHGRGGAVGRGGGPAGQAILAQPPGTLHGQIKVTDQGEMISDRYLDPRT 675

                CFrsLqRFtAAtLEHGmnPPvs..PkPEWRkLmeemAvvAtEEYRsvvvK
                  r L     A L  G  P ++++P P W   meemA  A   YR +v+
gi|2225266   676 AHRHLEQVVNAVLRAGF-PGMArqPEPTWLAAMEEMATTARTVYRQLVYE 724

                EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                +P F  YFR+AtP  E+ ++ iGsRP  R+ s  ie LRAiPW+F+W q
gi|2225266   725 DPDFLIYFRSATPVAEFNRLRIGSRPVSRRKSDRIEDLRAIPWVFSWMQS 774

                RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                R  +P W G+G A    ++ D   l  L+ mY+ WPFF   lD   m+
gi|2225266   775 RHTIPGWFGLGSALEAFVEADPHHLHLLRTMYQHWPFFSTLLDNAQMIML 824

                KGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEG
                K D  iA  y  L+    L  +  +++  ++  t+ ++ +i    DlL
gi|2225266   825 KADMNIARAYASLVPDRHLAErIFQRIESEFRRTERMICQITERNDLLAH 874

                DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                 P L+  +R R++Yi  L  +q   L+R+R               A+ +
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  gi|2225266   875 QPVLQRAIRQRNPYIDPLSFVQIELLRRLR----------------AAPP 908

                   skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                +    LE  L++ + GiAAG++ntG
  gi|2225266   909 --------------EEQGELETVLLMSINGIAAGLKNTG    933

gi|154146690|emb|CAM83980.1|: domain 1 of 1, from 1 to 438: score 385.0, E = 1.3e-112
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541466     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541466     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541466     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541466     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541466     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541466     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541466     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541466     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541466     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +t+ +DAittHL+iGsYR+W+Ee+RqEWL++EL+G RPL+g+DLP+ E
  gi|1541466     1 --HTEAVDAITTHLGIGSYRDWPEEQRQEWLVSELRGNRPLFGPDLPQSE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl++frv+A+LP DsFGaY+ismataPsDvLAvELLqRECgvk+++
  gi|1541466    49 EVADVLGTFRVIADLPGDSFGAYVISMATAPSDVLAVELLQRECGVKKPM 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADL+ A A++e LFs+DWY+ ri+GKqe+m+GY DsGKDAG
  gi|1541466    99 RVVPLFEKLADLQQARATMELLFSVDWYKERINGKQEIMIGYPDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEEi+ vA ++GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541466   149 RLSAAWQLYKAQEEIVSVAERHGVKLTIFHGRGGTVGRGGGPSHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP t+nGslRvtvqGEviE sFGEEnLCFr+LqRFtAAtLEHGmnPPvsP
  gi|1541466   199 PPNTVNGSLRVTVQGEVIEKSFGEENLCFRTLQRFTAATLEHGMNPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L+++mA vAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541466   249 KPEWRALLDDMATVATEEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRk +GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+hA+d  +  l
  gi|1541466   299 PSKRKTGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHAMDTPS-GL 347
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                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvt+DLlEmvFAKGDPGiAaLyDkLLv E+L+PFG++
  gi|1541466   348 ATLREMYDEWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVPEDLWPFGEQ 397

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y Et+ lLL++AGH DlLE DPYL+qrl LR sYit
  gi|1541466   398 LRANYAETQSLLLQVAGHNDLLESDPYLRQRLMLRGSYITA--------- 438

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541466     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541466     - -------------    -

gi|30248603|ref|NP_840673.1|: domain 1 of 1, from 2 to 933: score 384.3, E = 2.2e-112
                    *->siDAqLRlLvPGKvs..edekLieYDALllDkFL.DiLqDLHGedLk
                       s+      ++P K  ++e +  ++ D  Ll + L+D + +L Ge +
  gi|3024860     2    SLNTR-ANIIPEKNTpnEKDYPLREDIRLLGRMLgDTIRELEGETMF 47

                    EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                      v      s  +   +D     EL + L  L   ++i v +a++    L
  gi|3024860    48 NLVETIRQTSVRFRRDQDEAAEHELDTILNHLSHKETIAVVRAFSYFSLL 97

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                     n+AE+ +   RRR +++  G    ++s t        l+++v k+
  gi|3024860    98 SNIAEDLHHNRRRRAHLRA-GSPPQDGSVTL------ALQRVVKKG-IDA 139

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    e   +      +  vltAHPt   RRs+L  + +i   L       +t++
  gi|3024860   140 EQLQNFFASALISPVLTAHPTEVQRRSILDYQLKIQRLLKERDRTQLTPN 189

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    + +  +E L   iq  + t  +R  + t qDE+  G+ Y+H t  + +P
  gi|3024860   190 EMRHNEEDLRSAIQTLWQTRVLRSVRLTVQDEIENGLIYYHYTFLRQIPY 239

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                       + +  L    +    P  +  ++  sW+GGDRDG nP vt  +
  gi|3024860   240 IYAKLEDILER-HMDKAAPRIASFLRIGSWIGGDRDG-NPFVTHQIMLHA 287

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                          +   +Yis vE +   +s+      +    E l +ta
  gi|3024860   288 AERHSALILDFYISEVERIGQTMSLSERLIKVSSDLEGLASTAPGL--PA 335

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL..LAtGiseisEeA
                      i+        EPYR +   +  +L  t   +RHL++   G  +
  gi|3024860   336 SRID--------EPYRRVFLGIHARLIAT---SRHLgsSIRGCCQENNAE 374

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                     y +  eF+  L++  +sL +     +A G+L Dl R    FG  L  LD
  gi|3024860   375 PYADSAEFVHDLDIVIRSLRQHRSDRLAQGALRDLRRAADVFGFHLAPLD 424

                    iRqEseRqtDvlDAittH..LeiGsYReWsEeKRqEWLlaELkGKRPLlg
                    +Rq s  +  v+  + + ++ +   Y e s   R EWLlaEL+  R L+
  gi|3024860   425 MRQHSKIHEQVISELYEKntRDDRNYLEMSRSERVEWLLAELRHPRSLVT 474

                    sDLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvEL
                    s     +  +  l  +++ AE+ ++ +  +   Yiismat    +L v L
  gi|3024860   475 SFSDFSDVTQGELRILKMAAEIQrrfgHAALPNYIISMATGVVHILEVAL 524

                    LqRECgv.......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                    L +E g+ + +++++ t+ ++PLFE + DL+     ++ LFs+  Y+  +
  gi|3024860   525 LLKEAGLlqfgddpRSTVNIIPLFETIDDLRGCASVMDELFSLPDYRKLL 574

                    ...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                     ++d  qevm+GYsDs KD G +   W +YkA  E+ +v  ++Gv+L lF
  gi|3024860   575 lsrDNLQEVMLGYSDSNKDGGFVTSNWEIYKAEIELTRVFDRHGVRLRLF 624

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGGtvGRGGGP    iL+qPP  + G +R t qGEvi   + + ++
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  gi|3024860   625 HGRGGTVGRGGGPSYQGILAQPPGSVSGQIRLTEQGEVIASKYTDPEIGR 674

                   rsLqRFtAAtLEHGm...nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKE
                   r L    AAt+E  + +++      P + ++mee+   A   YR +v+K
  gi|3024860   675 RNLETLVAATIESTLldrDAVHYHAPHYHQIMEELSSSACAAYRDLVYKT 724

                   PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
                   P F  +F   tP  E   + iGsRP+ RkPs  ie LRAiPW+F+W   R
  gi|3024860   725 PGFKQFFLESTPIREIAGLHIGSRPTSRKPSDKIEDLRAIPWVFSWSLNR 774

                   FHLPvWLGvGAAFKhAidK...DiKnlqkLkEmYkeWPFFRvtlDLlEmv
                     +P W G+G A    +++ +++   l++L+EmY++WPF    l  ++mv
  gi|3024860   775 TMIPGWYGFGTAVENFVQQagnEQEALKQLQEMYRTWPFLQTLLSNMDMV 824

                   FAKGDPGiAaLyDkLLvaEeLk.PFGksLRdkYvEtkdlLLkiAGHkDlL
                     K D GiA+ y +L+   eL++    s+R +++   ++L  i G  +lL
  gi|3024860   825 LSKSDLGIASRYAELVTDPELRqSVFTSIRTEWELCMKWLFAITGYSELL 874

                   EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                      P L   +R+R +Yi  Ln +q   L+R R
  gi|3024860   875 QDNPTLARSIRIRTPYIDPLNHLQIELLRRYR------------------ 906

                   EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     s   d+ v+              + Lt+ G+A G+ n G
  gi|3024860   907 --SGDDDDTVRRA------------IHLTINGVATGLRNSG    933

gi|154146680|emb|CAM83975.1|: domain 1 of 1, from 1 to 439: score 383.9, E = 2.8e-112
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541466     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541466     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541466     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541466     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541466     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541466     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541466     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541466     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541466     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tD +DAittHL+iGsYR W+E  RqEWL++EL+GKRPL+g+DLP+tE
  gi|1541466     1 --HTDAMDAITTHLGIGSYRAWPEAARQEWLVSELRGKRPLFGPDLPQTE 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl++frv+AELP DsFGaYiismataPsDvLAvELLqRECgvk++L
  gi|1541466    49 EVADVLGTFRVIAELPPDSFGAYIISMATAPSDVLAVELLQRECGVKKPL 98
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                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADL+ A A++e LFsiDWY+ ri GKqe+m+GYsDsGKDAG
  gi|1541466     99 RVVPLFEKLADLQGARATMELLFSIDWYKERIAGKQEIMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEEi+ vA + Gv+L++FHGRGGtvGRGGGP HLAiLsq
  gi|1541466    149 RLSAAWQLYKAQEEIVDVAARNGVRLTIFHGRGGTVGRGGGPSHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                     P tinGslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGmnPPvsP
  gi|1541466    199 LPNTINGSLRVTVQGEVIEKSFGEEHLCFRTLQRFTAATLEHGMNPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR+L+++mAvvAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541466    249 KPEWRDLLNDMAVVATEEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkP GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF h +    + l
  gi|1541466    299 PSKRKPDGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFEHSMLTSDRGL 348

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvt+DLlE+vFAKGDPGiAaLyDkLLv E+L+P G++
  gi|1541466    349 DALREMYDEWPFFRVTIDLLEVVFAKGDPGIAALYDKLLVPEDLWPIGEQ 398

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y  t+ lLL++AGH DlLE DPYLKqrl LR sYit
  gi|1541466    399 LRANYTKTQSLLLQVAGHDDLLENDPYLKQRLMLRYSYITA--------- 439

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541466     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541466     - -------------    -

gi|218288887|ref|ZP_03493138.1|: domain 1 of 1, from 1 to 906: score 383.2, E = 4.4e-112
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                   +++d  L +   +L D   ++L +  G+ + + v
  gi|2182888     1    -------------MANDAPLHRDIRVLGDLLGEVLVEQCGQRVFDHV 34

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          +  +     ++    L a + +++P     v +a++    L nL
  gi|2182888    35 ESIRMAAKAFRADPSPETRAALQAAVSAVEPEHRNDVIHAFSVYFQLVNL 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE     +R R ++       D ++        Et++ L  ++  + +++
  gi|2182888    85 AEQ---NHRLRRHRDY-----DRSQQVLRGSFRETMRTLADRG-MTADDI 125

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L+   ++LvltAHPt + RR +L K+++i   L  +     t+ +
  gi|2182888   126 ESLLREVGIELVLTAHPTEALRRTVLDKHTKIAAFLEDMDDPRKTPRELD 175

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     L E +  Ei A + t  +R+ + t  DE+R G+ ++   +++  P+
  gi|2182888   176 VLRERIRTEIVALWQTRSVRKQRITVLDEVRNGLYFLDQILFDVLPRVHQ 225

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    + + A+        l    PLi+F sWmGGDRDG nP vt ++t    +L
  gi|2182888   226 KLEQAVEE-QFGRQLLELPPLIRFGSWMGGDRDG-NPNVTSDITWQTLVL 273

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                       +A n Y +++ +L  +ls+    +  R+ A+E    +
  gi|2182888   274 HCDLALNKYEQKLRELGRDLSV----SVDRAGADEDLLASLEG------- 312

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                             EPYR ++  + ++L ntR R      +G  e  +   y
  gi|2182888   313 ------ENDEPYRALINRMLERLANTRRR-----LHG--ERVDGPYYASP 349

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E  +E +E   +sL     + + D  L  +L q   FG  +v LDiRq s
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  gi|2182888   350 EAMMEDVERMARSLAHHRGQRMVDAWLRPFLLQLRIFGFHMVTLDIRQHS 399

                   eRqtDvlDAittHLe.iGsYReWsEeKRqEWLlaELkGKRPL.....lgs
                     +   +  + +  + +  Y +  Ee R   L   L   RP++++ ++ s
  gi|2182888   400 GVHEQAVAELLQTAGlVDDYASLGEEERVRVLSECLASPRPIrnpyhVYS 449

                   DLPktEEvkDvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLqRE
                   DL  t E   vld +r   E+    +   Y+ism+   sD L v LL +E
  gi|2182888   450 DL--TTEALAVLDCVRRGHEtFGPRCVQDYLISMTQGASDLLEVLLLAKE 497

                   Cgv..........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                    g+ + +++++ ++k  L vvPLFE + DLe A   +  LF    Y+ ++
  gi|2182888   498 SGLfgwpdgpkappKSELNVVPLFETIEDLESAAGIMRSLFENPVYRRHL 547

                   dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                   + ++ +qe+m+GYsDs KD G l A W LY Aq  +i+ A +yGv++  F
  gi|2182888   548 EMRgwqQEIMLGYSDSNKDGGYLTANWSLYMAQKHLIRLAEEYGVRIKFF 597

                   HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                   HGRGG  GRGGGP    iL+qP + + G +++t qGEvi + +G   +
  gi|2182888   598 HGRGGALGRGGGPVEQSILAQPTEALRGHVKITEQGEVISQRYGHPGIAE 647

                   rsLqRFtAAtL....EHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvK
                   rsL   +AA L + +    +     +P W  Lm++   +    YR +v+
  gi|2182888   648 RSLESSAAAVLvgatREDTEEWAERHPRWFALMDRASEISFRAYRKLVFE 697

                   EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                    P F EYF  AtP  E GkmniGsRP++R  s  ie LRAiPW+F+Wtq
  gi|2182888   698 HPAFLEYFHRATPIDEIGKMNIGSRPSRRSQSARIEDLRAIPWVFSWTQS 747

                   RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                   R  LP W G+G A    +  D + l  L+ mY+ WPFFR  +D l m  A
  gi|2182888   748 RHLLPAWYGFGSAIEAIMREDPRALEDLRRMYEVWPFFRTLVDNLQMALA 797

                   KGDPGiAaLyDkLL..vaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE
                   K D  +A  y +L ++  E + P    + ++Y  t+  +L i G + lL+
  gi|2182888   798 KADMLVAREYAQLAgeAGEAVFPL---IEEEYARTERAVLDITGYRQLLD 844

                   GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                     P ++  + LR++Y+  L  fq   L  +R        r  ls E  +
  gi|2182888   845 NKPVIRESISLRNPYVDPLSFFQVRLLADLR--------RDNLSPEEREA 886

                   nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   +   ad L  +n                  GiAAG+ ntG
  gi|2182888   887 E--LADALQTIN-----------------GIAAGLRNTG    906

gi|154146710|emb|CAM83990.1|: domain 1 of 1, from 1 to 438: score 382.8, E = 6.2e-112
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ---------------------------------------------- -
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                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tD +DAittHL+iGsYR+W+Ee+RqEWL+ EL+G RPL+g+DLP+ +
  gi|1541467     1 --HTDTVDAITTHLGIGSYRDWPEEQRQEWLVNELRGNRPLFGPDLPQSD 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl++frv+AELP DsFGaY+ismataPsDvLAvELLqRECgvk+++
  gi|1541467    49 EVADVLGTFRVIAELPADSFGAYVISMATAPSDVLAVELLQRECGVKKPM 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADL+ A A++e LFs +WY+ ridGKqe+m+GYsDsGKDAG
  gi|1541467    99 RVVPLFEKLADLQQARATMELLFSCEWYKERIDGKQEIMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAW LYkAqEEi+ vA ++GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541467   149 RLSAAWHLYKAQEEIVDVAERHGVKLTIFHGRGGTVGRGGGPSHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP t+nGslRvtvqGEviE sFGE+ LCFr+LqRFtAAtLEHGmnPPvsP
  gi|1541467   199 PPNTVNGSLRVTVQGEVIEKSFGEDSLCFRTLQRFTAATLEHGMNPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L+++mA vAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWRALLDDMATVATEEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+hA+dK    l
  gi|1541467   299 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHAMDKPG-GL 347

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+EmY+eWPFFRvt+DLlEmvFAKGDPGiAaLyDkLLv  +L+PFG++
  gi|1541467   348 ATLREMYDEWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVPQDLWPFGEQ 397

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y Et+ lLLk+AGH DlLE DPYL+qrl LRdsYit
  gi|1541467   398 LRANYAETQSLLLKVAGHDDLLESDPYLRQRLMLRDSYITA--------- 438

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|86750702|ref|YP_487198.1|: domain 1 of 1, from 11 to 933: score 382.4, E = 8.2e-112
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +A           e e  ++ D  Ll + L+D + D  G  + +
  gi|8675070    11    --EALPNRADDSAALEAETRLRNDIRLLGRILgDTVRDQEGAAVFDL 55

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v      s  +    Dt    EL a L ++  +D++ + +a++    LAn
  gi|8675070    56 VEGIRQTSIRFHRDDDTTARRELEAILDGMSASDTVKIVRAFSYFSHLAN 105

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  +AE+ +     R+           +sA     +  tl +    +    +E
  gi|8675070   106 IAEDQNNIRQMRVGSTA-------GSAPRAGMLAKTLAHARADG-IGAAE 147

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  K   v  vltAHPt   R+s + ++  i   L       +t+e+
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```
  gi|8675070   148 LRDFFKTALVSPVLTAHPTEVRRKSTMDREMQIAALLDERERVQLTPEEW 197

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +  +E L R +   ++t  +RR++ t  DE+  G+s++  t  + vP
  gi|8675070   198 EQNEEQLRRAVVTLWKTNLLRRTKLTVLDEVTNGLSFYDYTFLREVP--- 244

                    RRvDtALKn.iGinERlPYdvPLikFs...sWmGGDRDGknPRvtPEvtR
                     R   AL  ++G  E    d+ L  F + +sW+GGDRDG nP vt Ev
  gi|8675070   245 -RLHCALEDqLGGGEGAEADAELASFLrmgSWIGGDRDG-NPFVTAEVLH 292

                    DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                        L       +Y++ + +L  Els+    + L +  +E+   a r
  gi|8675070   293 GTLQLQSARVLRFYLDELHELGSELSL---ASHLVAISDEVRALAERS-- 337

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                                 EPYR  +  +  +L  t  + R  +    + + E
  gi|8675070   338 -----PDHSPHRRHEPYRLAVSGIYARLAATAAKLR--IDSIRAPVGEAE 380

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                     y  v +F   L+   +sL      viA G L  l R    FG  L  LD
  gi|8675070   381 AYASVHDFKADLDAIHRSLVAHNAGVIARGRLRQLRRAADCFGFHLASLD 430

                    iRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgs
                    +Rq s  +   +  +       s Y e  E+ R   L aEL+  RPL
  gi|8675070   431 MRQNSAVHERTIAELMNAAHPASaYLEIGEDARIALLTAELRSARPLTSI 480

                    DLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                     +   +++ +E++   +a +  A     +    iism+   sD L v +L
  gi|8675070   481 FVKYSDetvgELAVLHEAAQAHATYGAAAIPQCIISMTKGVSDLLEVAVL 530

                    qRECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid..
                     +E g+ +++++ ++ +vPLFE + DL+A  A +++L  i  Y+  +d++
  gi|8675070   531 LKEVGLidpsgRSAINIVPLFETIEDLQASSAIMDRLLGIPEYRRLVDsr 580

                    .GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    +G qevm+GYsDs KD G +   W LYkA   +i +  ++G++L lFHGR
  gi|8675070   581 gGVQEVMLGYSDSNKDGGFVTSGWELYKAEIGLIEIFEHHGIRLRLFHGR 630

                    GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                    GG vGRGGGP   Ai++qP   +nG +R+t qGE+i   +   ++    L
  gi|8675070   631 GGSVGRGGGPSYDAIVAQPGGAVNGQIRITEQGEIITSKYSNREVGRNNL 680

                    qRFtAAtLEHGmnPP..vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFv
                       tAAtLE  +  P++v+P+ ++ + me++  +A   YR +v+    Fv
  gi|8675070   681 EILTAATLEASLLQPkrVAPQRDYLDAMEQLSAMAFKAYRGLVYETDGFV 730

                    EYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLP
                    +YF   t  +E   +niGsRPa Rk    ie LRAiPW+F+W q R  LP
  gi|8675070   731 DYFWASTVITEISTLNIGSRPASRKKTRAIEDLRAIPWVFSWAQCRLMLP 780

                    vWLGvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                     W G+G A   +      K +  L+ mY+eWPFFR  l  ++mv  K
  gi|8675070   781 GWYGFGSAVEaWIAAHPDKGVPFLRSMYQEWPFFRTLLSNMDMVLSKSSL 830

                    GiAaLyDkLLvaEeLk..PFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                    GiA+ y +L+  E L+++ FG+ +R+++    d LL i GH  lL G P
  gi|8675070   831 GIASRYAELVPDETLRreIFGR-IRAEWHASVDGLLAIMGHDKLLQGNPL 879

                    LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                    L   +R R +Y+  Ln +q   L+  R      t  P       dE+
  gi|8675070   880 LDRSIRHRFPYLDPLNHVQVQLLREHR------THDP-------DEQ--- 913

                    adeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                          L             + Lt+ Gi AG+ n G
  gi|8675070   914 -----ILR-----------GIQLTINGISAGLRNSG    933

gi|291612738|ref|YP_003522895.1|: domain 1 of 1, from 4 to 922: score 382.3, E = 8.6e-112
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                              + +P  +s  +  ++ D  Ll + L+D L +  Ge+
  gi|2916127     4    -------ISAPADISSKDIPLRDDVRLLGRILgDTLREQEGEETYKL 43
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                vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                +      +  +   +D +  e L   L  L P+++++v +a++    L n
gi|2916127    44 IESVRRAAVRFRKTQDEQDGELLEQMLDQLSPTETLVVVRAFSYFSQLTN 93

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                +AE+ +   R R ++k        +s   +  +   l +L  k     +
gi|2916127    94 IAEDLHHNRRHRAHLKA-------GSPPKDGTLQLALDRLEEKK-IDKDT 135

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    L    v  vltAHPt   R+s+L  +  i   La     D+t++D
gi|2916127   136 LQSFLNSALVSPVLTAHPTEVQRKSILDCHLIISSLLANRDRVDMTPDDL 185

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                 E +EALHR +   + t  +R a+    DE+R G+ Y+H t    +PK
gi|2916127   186 AENEEALHRFVLILWQTRMMRTAKLNVRDEIRNGLEYYHYTFLAEIPKLY 235

                RRvDtALK.niGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   +  L +      ++P   PL++  sW+GGDRDG nP vt +v  D
gi|2916127   236 ANLEKQLEsRFDKDIKVP---PLLRVGSWIGGDRDG-NPFVTHDVMTDAV 281

                LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    ++A   Y++    L   ls+    d L     El + +
gi|2916127   282 REHSILALEYYLNETHLLGTRLSL---TDRLVEVTPELRKLSDAS-PDNV 327

                YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                ++         EPYR  L  +  +L  t     H   +     +    y
gi|2916127   328 FVRL------DEPYRRALILIYSRLTATAKHLGHDTSHLRPVDAHAQPYA 371

                kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   +F+  L++   sL   G   +A G L  l R v  FG  L  LD+Rq
gi|2916127   372 TAQDFIADLDVMIDSLFKHGAVYLARGRLANLRRAVEVFGFYLAPLDMRQ 421

                EseRqtDvlDAittH.LeiGsYReWsEeKRqEWLlaELkGKRPLlg....
                 s      +  +  H+ +   Y +  E  ++  Ll  L+  + Ll + ++
gi|2916127   422 HSAILEQTVSELFSHsSGKANYSDLDEAGKRSVLLEALQSGKILLAdikr 471

                .sDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqR
                 sD+P+  E++ +  a ++       +    iis + a sD+L v L+
gi|2916127   472 ySDVPQS-ELRIMQAAAEIHRRFGHGALPNHIISKTDAVSDMLEVALMLQ 520

                ECgvkq...tLrv..vPLFEkLADLeAAPAavekLFsiDWYinridGK..
                  g+ q+++tL v+ +PLFE + DL+     ++ LFsi WY+  +  +++
gi|2916127   521 QFGLLQdgdTLHVniIPLFETIEDLRGGASIMDELFSIPWYRKLLSSRgn 570

                .qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                +qevm+GYsDs KD G l A W LYkA  E++Kv  k+G+ L lFHGRGG
gi|2916127   571 tQEVMLGYSDSNKDGGYLTANWELYKAEVELVKVFAKHGIELRLFHGRGG 620

                tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                tvGRGGGP   AiL+qPP  +nG +R+t qGEvi   +   ++  r L
gi|2916127   621 TVGRGGGPSYDAILAQPPGSVNGQIRITEQGEVISSKYSNPEIGRRNLET 670

                FtAAtLEHGm..nPP.vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvE
                  AAt+E  + ++P +    PE+ ++me +   A   YR +v+  P F +
gi|2916127   671 LIAATIEATLldHPHnADGDPEYMRIMEALSLDAFAAYRKLVYETPGFTD 720

                YFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPv
                YF  AtP  E   +niGsRP+ Rk s  ie LRAiPW+F+W   R  LP
gi|2916127   721 YFFTATPIREIAELNIGSRPSSRKASDRIEDLRAIPWVFSWGLNRVMLPG 770

                WLGvGAAFKhAidKDiKn.lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPG
                W G+G A K  i+++   +l++L+ mYk+W FFR  +  ++mv  K D G
gi|2916127   771 WFGFGSAVKQFIQREGDAgLKQLQAMYKNWAFFRGMMSNMDMVLSKSDMG 820

                iAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                iA  y +L+   eL+++ FG  + ++++ t ++L  + G   lL   P
gi|2916127   821 IAWRYAELVQDIELrdRIFG-AINNEWEATIEMLFAVTGATTLLQDNPAF 869

                KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                   l  R +Yi  Ln +q   L R R               A +n
gi|2916127   870 ARSLLTRTPYIDPLNHLQVALLHRHR----------------AGDN---- 899
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                  deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                  de vk              + Lt+ GiA G+ n G
  gi|2916127   900 DEKVKRA------------IHLTINGIATGLRNSG    922

gi|154146714|emb|CAM83992.1|: domain 1 of 1, from 1 to 438: score 382.0, E = 1e-111
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tD +DAittHL+iGsYReW+Ee+RqEWL++EL+GKRPL+g++LP+ +
  gi|1541467     1 --HTDAVDAITTHLGIGSYREWPEERRQEWLVSELRGKRPLFGPELPQSD 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl++frv+AELP DsFGaY+ismataPsDvLAvELLq ECgvk++L
  gi|1541467    49 EVADVLGTFRVIAELPGDSFGAYVISMATAPSDVLAVELLQLECGVKKPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADL+ A A++e LFs+DWY+ ri+GKqe+m+GYsDsGKDAG
  gi|1541467    99 RVVPLFEKLADLQQARATMELLFSVDWYKGRINGKQEIMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEEii vA ++GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541467   149 RLSAAWQLYKAQEEIIGVAERHGVKLTIFHGRGGTVGRGGGPSHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP t+nGslRvtvqGEviE sFGEEnLCFr+LqRFtAAtLEHGmnPPvsP
  gi|1541467   199 PPNTVNGSLRVTVQGEVIEKSFGEENLCFRTLQRFTAATLEHGMNPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR+L+++mA v tEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWRRLLDDMATVSTEEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+hA+++    l
  gi|1541467   299 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHAMQQPG-GL 347

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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                     L+EmY+eWPFFRvt+DLlEmvFAKGDP iAaLyD+LLv  +L+PFG++
  gi|1541467   348 ATLREMYDEWPFFRVTIDLLEMVFAKGDPRIAALYDNLLVPQDLWPFGEQ 397

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y Et+ lLL++AGH DlLE DPYL+qrl LRdsYit
  gi|1541467   398 LRANYAETQSLLLQVAGHDDLLENDPYLRQRLMLRDSYITA--------- 438

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|254422587|ref|ZP_05036305.1|: domain 1 of 1, from 8 to 1032: score 381.8, E = 1.2e-111
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           L+  vP     d  L +    + + +  +L D  G++L
  gi|2544225     8    --ASDLKPAVPAVATHDRLLRRRLKSVEETWASVLEDECGPSLVALL 52

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        l A  +G+  +     +   +  L+ +Dai +A+a+     L n+
  gi|2544225    53 TRLRRLCAP-DGQANAANASPVLQLIEELELSDAIKMARAFALYFQLINI 101

                   A.................EEvelAyRRRikkkkhGDFaDEasAtt.....
                    +++ ++++++++ +   EE e+A    i+     D+ D       +++
  gi|2544225   102 VeqhyeqrgqqqqyraayEEAEIAAGHSIEDYAAADYNDADASQQasqsa 151

                   .....EsDiEEtlKkL..............vlklnKsPeEvFeALKnqs
                   ++ ++ s + Et++  ++ ++ ++     ++  +ln  P+ +   L
  gi|2544225   152 ngfngQSAVAETIRTAdslrdvgtfywlfptLKRLNVPPKMIQRLLDQLD 201

                   vDLvltAHPtqsvRRsLLqKnaRiRnCLaqLs.....AKDvtve...DKk
                   v Lv+tAHPt  vR  +  K+ Ri   L qL +++++A+ +   ++ + +
  gi|2544225   202 VRLVFTAHPTEIVRHTIRDKQRRISEILRQLDreeegARALSLAsswEIQ 251

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    L   L  Ei   +RtDE+   +P   DE+ + + Y+   +++  P+
  gi|2544225   252 ALQKQLVEEIRLWWRTDELHQFKPSVLDEVEFTLHYFDVVLFDTLPQLRQ 301

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   R+  AL       R P +    +F sW+G DRDG nP vtP vt
  gi|2544225   302 RICRALEGTFPSLR-PPQHGFCRFGSWVGSDRDG-NPSVTPQVTWKTANY 349

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    R m    Yi  v  L   ls+    +E+     E     + + +   Y
  gi|2544225   350 QRNMVLGKYIASVQNLTQRLSLSLHWSEILSELLESLEKDQTQ-MPEIYE 398

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi.........sei
                   E       +EPYR  L  +  +L nt ER++ L    + ++++++ +se+
  gi|2544225   399 ELAIRY-RQEPYRLKLAYIEQRLINTLERSKKLYNGDYlqeretnldSEL 447

                   sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                   s    y   E+FL  L L    L e     +    L +l+ qv  +G  L
  gi|2544225   448 SSGRLYRFGEDFLYELKLIQTNLKE---TNMVCRELEELIAQVEIYGFNL 494

                   vKLDiRqEseRqtDvlDAittHLeiGs..YReWsEeKRqEWLlaELkGKR
                    +LDiRqEs R+ D +  +t  L++  ++Y +  E  + +WL+ EL+ +R
  gi|2544225   495 AQLDIRQESTRHSDTIGEVTDYLGLLDkpYNDLDEAEKTDWLIRELSTRR 544

                   PLlgsDLPktEEvkDvldafrvLAELPiDsFG.....aYiismataPsDv
                   PL++ +LP  +   + + +fr++  L  + FG++  ++Yiism+ + sD
  gi|2544225   545 PLIPGELPFSDKASETIATFRMVRKLHRE-FGhsicqSYIISMSHTASDL 593

                   LAvELLqRECgvkqt......LrvvPLFEkLADLeAAPAavekLFsiDWY
                   L v LL +E g+  ++++ + L++vPLFE + DL+ AP  +++L+ +  Y
  gi|2544225   594 LEVALLAKEAGLFDPttgigaLKIVPLFETVEDLRRAPKVMKQLWELPLY 643

                   inridG..................KqevmvGYsDsGKDAGRlsAAWqLYk
                   +  ++G+ +  +  + ++++ ++  qevm+GYsDs KD G ls  W + k
  gi|2544225   644 RAMLQGgyeamevvkakpdeaetaLQEVMLGYSDSNKDSGFLSSNWEIHK 693
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                    AqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslR
                    Aq  +   A  y + L +FHGRGG vGRGGGP   AiL+qP   ++G ++
  gi|2544225   694 AQQALQALAEGYSIALRIFHGRGGSVGRGGGPAYEAILAQPGRSVDGRIK 743

                    vtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE.WRkLme
                    +t qGEv+   +   +L    L   t A +   +        E W ++me
  gi|2544225   744 ITEQGEVLASKYNLPDLALYNLETVTTAVIQGSVLGSSFDGIEaWNEIME 793

                    emAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGG
                    e+Av     YR++++  P  vE+F   tP  E  ++ i sRPa+R
  gi|2544225   794 ELAVRSRQHYRALIYEQPDLVEFFHQVTPIQEISQLQISSRPARRGGKKN 843

                    iesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD.iKnlqkLkEmYk
                    ++ LRAiPW+F+WtqtRF LP W GvG A K  id  +   +++L+  Y
  gi|2544225   844 LDGLRAIPWVFSWTQTRFLLPSWYGVGTALKEFIDAQpTEHIKQLRYFYA 893

                    eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLv....aEeLkPFGksLRdk
                    +WPFF++ +  +Em  AK D  iA  y + L +++++E+ +   +++ ++
  gi|2544225   894 KWPFFKMVISKVEMTLAKVDLQIAQHYVNQLSseekSEDFQKMFDQIAAE 943

                    YvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiR
                    +  t++ +L i  H  lL+GDP L++ + LR+  i  L  +q   LKR+R
  gi|2544225   944 FYLTREVVLTITDHTNLLDGDPSLQKSVQLRNGTIVPLSFLQVALLKRLR 993

                    DPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPG.LEDtLiLtmK
                                 Ey ++        v     +r++ G+L    +Lt+
  gi|2544225   994 --------------EYGNDA-------VTGRVRSRYSKGeLLRGALLTIN 1022

                    GiAAGmqntG<-*
                    G+AAGm ntG
  gi|2544225  1023 GVAAGMRNTG    1032

gi|154146678|emb|CAM83974.1|: domain 1 of 1, from 1 to 438: score 381.3, E = 1.7e-111
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541466     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541466     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541466     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541466     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541466     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541466     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541466     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541466     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541466     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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                     +tD lDAitt L+iGsYReW+Ee+RqEWL++EL+GKRPL+g++LP+ +
  gi|1541466     1 --HTDALDAITTYLGIGSYREWPEERRQEWLVSELRGKRPLFGPELPQSD 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl++frv+AELP DsFGaYiismataPsDvLAvELLqRECgvk++L
  gi|1541466    49 EVADVLGTFRVIAELPGDSFGAYIISMATAPSDVLAVELLQRECGVKKPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADL+ A A++e LFs+DWY+ ri+GKqe+m+GYsDsGKDAG
  gi|1541466    99 RVVPLFEKLADLQQARATMELLFSVDWYKERINGKQEIMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEEi+ vA ++GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541466   149 RLSAAWQLYKAQEEIVGVAERHGVKLTIFHGRGGTVGRGGGPSHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP t+nGslRvtvqGEviE sFGEEnLCFr+LqRFtAAtLEHGmnPPvsP
  gi|1541466   199 PPNTVNGSLRVTVQGEVIEKSFGEENLCFRTLQRFTAATLEHGMNPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR+L+++mA vAt+EYRs+v +EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541466   249 KPEWRRLLDDMATVATDEYRSIVHREPRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+hA+ +    l
  gi|1541466   299 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHAM-RQPGGL 347

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+ mY+eWPFFRvt+DLlEmvFAKGDPGiAaLyDkLLv  +L+PFG++
  gi|1541466   348 ATLRQMYDEWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVPQDLWPFGEQ 397

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y Et+ lLL++A H DlLE DPYL+qrl LRdsYit
  gi|1541466   398 LRANYAETQSLLLQVAAHDDLLESDPYLRQRLMLRDSYITA--------- 438

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541466     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541466     - -------------    -

gi|218248219|ref|YP_002373590.1|: domain 1 of 1, from 10 to 1024: score 381.2, E = 1.8e-111
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       si   + +           L +   L+ + +  +L    G++L +
  gi|2182482    10    SIVEEINIFSTSDLF----LRQRLKLVEELWEAVLRAECGQELVDLL 52

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    +    +    EG+        + a++  L+  ++i  A+a+     L n+
  gi|2182482    53 KQLRTMCSP-EGQLTDITQTPITAVIEQLELNESIRAARAFALYFQLINI 101

                    AEEvelAyRRRikkkkhGDFaDE....asAttEs.................
                     E  +    R  ++ +   + D ++++a+   Es+++++ +++  +++
  gi|2182482   102 VE--QHYEQRDQQLTRRANYCDIdskpANNHGESstnpsighhlverswm 149

                    DiEE......tlKkL...vlklnKsPeEvFeALKnqsvDLvltAHPtqsv
                    D E ++++++t+  L ++   ln  P+ +   L    + Lv+tAHPt  v
  gi|2182482   150 DSENtsekggTFHWLfphLKELNVPPQQIQRLLDQLDIRLVFTAHPTEIV 199

                    RRsLLqKnaRiRnCLaqLsAKDvtve........DKkELDEALHREiqAA
                    R  +  K+ Ri n L  L   +    + + +++ + +   E L  Ei
  gi|2182482   200 RHTIRRKQRRIVNILRRLDRAEEAFRgmglsnswEAQSAIEQLTEEIRLW 249

                    FRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLRRvDtALKniGinE
                    +RtDE+   +P   DE+ + + Y+ E +++  P+   R    LK
  gi|2182482   250 WRTDELHQFKPSVLDEVDYALHYFDEVLFEVLPQLSQRLQQSLKSSFPWL 299

                    RlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLLaRmmAanlYisqv
                    R P +    +F sW+GGDRDG nP vtPEvt       R m    Y++ +
  gi|2182482   300 RPPKNT-FCRFGSWVGGDRDG-NPFVTPEVTWKTACYQRNMVLKKYLESI 347
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                    EDLmFElsmWRCndELRvRAEElyrtaardkvvKyYiEFWKqvP.PtEPY
                     DL   ls     + +     +l     rd+v    i     +    EPY
  gi|2182482   348 RDLTEILSASLHWSNV---SQDLLDSLERDRVQMPEIYDELAIRyRHEPY 394

                    RviLGdvRDKLYntRERaRHLLA....tGiseisEeAvytkvEeFLEPLE
                    R  L   +  +L ntR+R   L  +++++ +    Ee +y   EeF   LE
  gi|2182482   395 RLKLAYIEKRLQNTRDRNNRLANpdqrQQLLYREEENIYHSGEEFWQELE 444

                    LCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlD
                    L  + L e G   +    L  lL q   FG  L +LD Rq+s R+ D ++
  gi|2182482   445 LIKRNLEETGLNCL---ELNNLLIQAEMFGFNLTQLDFRQDSSRHADAIE 491

                    AittHLei..GsYReWsEeKRqEWLlaELkGKRPLlgsDL....PktEEv
                     i + L+i +  Y + sE  +  WL+ ELk +RPL++  ++ ++P   E
  gi|2182482   492 EIAEYLNIlpKPYTQLSEAEKTQWLIQELKTRRPLIPTGMqfkkPENSET 541

                    kDvldafrvL.AELPiDsFGaYiismataPsDvLAvELLqRECgv.....
                     + l+ +r L+ E   +    Yiism+   sDvL v LL +E g+ ++ +
  gi|2182482   542 VETLQMLRYLqQEFGLEICQTYIISMTNYVSDVLEVLLLAKEAGLydpat 591

                    .kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG...........
                    +  t+r+vPLFE + DL+ AP  +e LF +  Y+  + G+ ++ ++++++
  gi|2182482   592 sTTTIRIVPLFETVDDLKRAPEVMEDLFKLPLYRASLAGgydqlqpsetp 641

                    .................KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiK
                    +++  ++ + +  ++++ qe+mvGYsDs KD G ls  W + kAq  +
  gi|2182482   642 sqgavkslnlpalqptnLQEIMVGYSDSNKDSGFLSSNWEIHKAQKALQN 691

                    vAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEv
                    +A++yGv L lFHGRGG vGRGGGP   AiL+qP  tinG +++t qGEv
  gi|2182482   692 MAQRYGVDLRLFHGRGGSVGRGGGPAYAAILAQPSSTINGRIKITEQGEV 741

                    iEfsFGEEnLCFrsLqRFtAAtLEHGm....nPPvsPkPEWRkLmeemAv
                    +   +   +L    L     A +   + +++   + P   W ++me++A
  gi|2182482   742 LASKYSLGDLALYNLETVSTAVIQASLlgsgFDDINP---WNEIMEDLAE 788

                    vAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs.GGies
                     A   YR +++  P F ++F + tP  E  ++ i sRPa+Rk ++  + s
  gi|2182482   789 RARKAYRGLIYEQPDFLDFFLSVTPIPEISQLQISSRPARRKSGkADLSS 838

                    LRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD.iKnlqkLkEmYkeWP
                    LRAiPW+F+Wtq RF LP W GvG A +  +d ++  nl+ L+  Y +WP
  gi|2182482   839 LRAIPWVFSWTQSRFLLPAWYGVGTALQSFVDEEpEENLKLLRYFYLKWP 888

                    FFRvtlDLlEmvFAKGDPGiAaLy.DkLLvaEeLkPFG...ksLRdkYvE
                    FF++ +  +Em   K D  iA  y  +L  aE+   F +  +++ ++Y
  gi|2182482   889 FFKMVVSKVEMTLSKVDLQIAHHYvRELSKAEDKERFErvfEEISQEYHR 938

                    tkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPs
                    t+d +L i  H+ lL+ D  L+  + LR+  i  L  +q   LKR+R  s
  gi|2182482   939 TRDVILNITNHQRLLDSDLSLQRSVQLRNGTIVPLGFLQVALLKRLRQYS 988

                    ykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAA
                     +      +   y  E+      L++               +Lt+ GiAA
  gi|2182482   989 NQ-AQSGVIHFRYSKEE------LLRGA-------------MLTINGIAA 1018

                    GmqntG<-*
                    Gm ntG
  gi|2182482  1019 GMRNTG    1024

gi|257093120|ref|YP_003166761.1|: domain 1 of 1, from 1 to 918: score 381.2, E = 1.8e-111
                    *->siDAqLRlLvPGKvsedekL.ieYDALLlDkFL.DiLqDLHGedLkE
                                      ed +L+++ D  Ll + L+D L    Ge   E
  gi|2570931     1    ---------MTEAFPEDKDLpLREDIRLLGRLLgDTLRAQEGEATFE 38

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                     v      +  +   +D+   +EL a L sL    +  v +a++H   LA
  gi|2570931    39 LVERIRVSAIRFHRDEDSGARQELAAILDSLSRDQTQTVVRAFSHFSHLA 88

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
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                n+AE+ +   R R ++         +s      +   l +    +    +
gi|2570931    89 NIAEDQHHIRRSRAHLIA-------GSPPHAGSLAHALARARAAG-CDVA 130

                EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                  +      s+  vltAHPt   R+s L  +  i   L       +t+++
gi|2570931   131 QLYGFFDDASIVPVLTAHPTEVQRKSTLNGQRAIAHLLHRRDNSRLTPDE 180

                KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                ++ LDE L R + A + t  +R ++    DE+  G+sY+  t  +  P+
gi|2570931   181 QESLDEGLRRAVLALWQTRMLRTTRLMVLDEVANGLSYYDYTFLRELPRL 230

                LRRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDv
                    +  L       R   + P+ ++  sWmGGDRDG nP vt  vtR
gi|2570931   231 YCWLEDHLAAAD-GGRPASELPgFLQLGSWMGGDRDG-NPFVTAPVTRAA 278

                CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                  L    A  + ++ +  L  Els+    + L    + l++ a +
gi|2570931   279 LRLQSACALRFHLDEIHALGAELSL---AEGLVSVSDALQSLADSS---- 321

                yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL..LAtGiseisEeA
                            EPYR  L  +  +L  t   aR L++L      + E A
gi|2570931   322 ---PDTAAARSDEPYRRALTGIYARLAAT---ARKLdgLEPERHPVGESA 365

                vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                 y +  eF   L++  +sL   G + +A G L  l R    FG  L  LD
gi|2570931   366 PYANCGEFAADLDVIHRSLVANGSQLLARGRLRTLRRAARVFGFHLAALD 415

                iRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgs
                +Rq se +  v+  + +    G +YRe  E  R E Ll E++  RPL  s
gi|2570931   416 LRQNSEVHERVVGELLEAASPGTnYREHDEAGRVELLLREISSTRPLASS 465

                DLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAvELL
                 L   +E +  l+ fr  A+ ++   + +   Yiis +   sD L v LL
gi|2570931   466 HLAYSDETRGELEIFRTAADahraFGSQAVQNYIISKTDGVSDLLEVALL 515

                qRECgvkqt......LrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                 +ECg+  +++++  + +vPLFE + DL+  P  ++ + s+  Y+  +
gi|2570931   516 LKECGLLLPqsrelaVNIVPLFETIPDLRNCPRVMDEVLSLPAYRRLVAS 565

                K...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                +++ qevm+GYsDs KD G l   W LY+A   ++ v  ++GvKL lFHG
gi|2570931   566 RgdlQEVMLGYSDSNKDGGFLTSGWELYRAEIALVEVFARHGVKLRLFHG 615

                RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                RGG vGRGGGP   AiL+qP   ++G lR t qGEvi   +   ++  r
gi|2570931   616 RGGSVGRGGGPSYQAILAQPGGAVQGRLRLTEQGEVIASKYSNPEVGRRN 665

                LqRFtAAtLEHGm..nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                L   + A LE  +   P  +P+PE+ + m  +   A   YR +v+    F
gi|2570931   666 LEILASAVLEATLlaAPDPAPQPEYLEAMAMLSQSAYRAYRGLVYETEGF 715

                vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                  YF   t   E  ++niGsRPa Rk    ie LRAiPW+F+W q R  L
gi|2570931   716 ERYFWESTVIAEIAHLNIGSRPASRKKTTAIEDLRAIPWVFSWAQCRLML 765

                PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                P W G+G A +  +      l  L+ m +eW FFR  l  ++mv AK D
gi|2570931   766 PGWYGFGTAVREFLAVHPEGLEVLQRMHHEWGFFRTLLSNMDMVLAKTDL 815

                GiAaLyDkLLvaEeLk.PFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                 iAa y +L+    L+     +L+++++ t d LL i G + lLE  P L
gi|2570931   816 AIAARYAELVTDPALRaAIFPRLKAEWQATIDALLAISGQQCLLEDNPLL 865

                KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                   +R R +Y+  Ln +q   ++R+R                A  +
gi|2570931   866 ARSIRNRFPYLDPLNHLQIELIRRLR----------------AGNE---- 895

                deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                de vk             + Lt+ GiAAG+ n G
gi|2570931   896 DERVKRA------------IHLTINGIAAGLRNSG    918
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gi|154146706|emb|CAM83988.1|: domain 1 of 1, from 1 to 438: score 381.1, E = 2e-111
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tD +DAittHL+iGsYReW+E++RqEWL++EL+G+RPLlg DLP+ E
  gi|1541467     1 --HTDAMDAITTHLGIGSYREWPEQRRQEWLVSELSGRRPLLGYDLPQSE 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl++frv+AELP DsFGaYiismataPsDvLAvELLqRECgvk++L
  gi|1541467    49 EVADVLGTFRVIAELPGDSFGAYIISMATAPSDVLAVELLQRECGVKKPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkL DL+ A A++e LFs+DWY+ ri+GKqe+m+GYsDsGKDAG
  gi|1541467    99 RVVPLFEKLTDLQQARATMELLFSVDWYRERINGKQEIMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEEi+ vA ++GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541467   149 RLSAAWQLYKAQEEIVGVAERHGVKLTIFHGRGGTVGRGGGPSHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP t+nGslRvtvqGEviE sFGEEnLCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541467   199 PPNTVNGSLRVTVQGEVIEKSFGEENLCFRTLQRFTAATLEHGMHPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L+++m  vAt+EYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWRSLLDDMGSVATDEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+hA++     l
  gi|1541467   299 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHAMQHPT-GL 347

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+EmY+eWPFFRvt+DLlEmvFAKGDPGi aLyD+LLv E+L+PFG++
  gi|1541467   348 ATLREMYDEWPFFRVTIDLLEMVFAKGDPGIDALYDELLVPEDLRPFGEQ 397

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR +Y E + lLL++AGH DlLE DPYLKqrl LRdsYit
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  gi|1541467   398 LRVNYAEIQRLLLQVAGHDDLLESDPYLKQRLMLRDSYITA--------- 438

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|126658238|ref|ZP_01729388.1|: domain 1 of 1, from 5 to 1016: score 380.6, E = 2.8e-111
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                       s+   +  +     s  +  ++    L++   +++L+   G++L +
  gi|1266582     5    SLQSTVEEVNIFSTS--DLFLRQRLKLVESLWEsVLKAECGQELVDL 49

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                     +    +    EG+   k    +   + +L+  +ai  A+a+     L n
  gi|1266582    50 LKKLRKICSP-EGQVTDKPKTSINELIEGLELNEAIRAARAFALYFQLIN 98

                    LAE.................EvelAyRRRikkkkhGDFaDEasAttEsDi
                    + E++ ++++++ +++ + +E e A    +k  k+G  +  a+    + +
  gi|1266582    99 IVEqhyeqrdqqlnrratyqESEKARNNNVKEEKKGNGSVGADLLEKALV 148

                    EE........tlKkL...vlklnKsPeEvFeALKnqsvDLvltAHPtqsv
                     E++++++++t+  L ++  +ln  P+ +   L    + Lv+tAHPt  v
  gi|1266582   149 GEtenqekggTFHWLfpqLKRLNVPPQQIQRLLEQLDIRLVFTAHPTEIV 198

                    RRsLLqKnaRiRnCLaqLsAKDvtve........DKkELDEALHREiqAA
                    R  +  K+ Ri   L  L   +    + + +++ + + + E L  Ei
  gi|1266582   199 RHTIRLKQRRIATLLRRLDQAEEAFRgmglssswEAESIIEQLNEEIRLW 248

                    FRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLRRvDtALKniGinE
                    +RtDE+   +P   DE+ + + Y+ E + +  P+  +R   ALK
  gi|1266582   249 WRTDELHQFKPSVLDEVDYTLHYFDEVLCDALPQLSKRLQQALKANFPRI 298

                    RlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLLaRmmAanlYisqv
                    + P +     F sW+GGDRDG nP vt ++t       R +    Y+  v
  gi|1266582   299 KPPHNN-FCSFGSWVGGDRDG-NPFVTTDITWRTACYQRNLILEKYLVAV 346

                    EDLmFEls...mWRCndELRvRAEElyrtaardkvvKyYiEFWKqvPPtE
                    EDL   ls++  W   +       E  r a  + +       ++q    E
  gi|1266582   347 EDLTEILSsslHWSNVSQDLLDSLERDRVAMPE-IYDDLAIRYRQ----E 391

                    PYRviLGdvRDKLYntRERaRHLLAtGisei.sEeA...vytkvEeFLEP
                    PYR  L  +  +L  tR+R   L      +i sEe ++++y    eF
  gi|1266582   392 PYRLKLAYIEKRLETTRDRNNYLANPEKRQIlSEETppnIYHSGAEFEAE 441

                    LELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDv
                    L L  + L + G k  A   L  l+ q   FG  L +LD RqEs R+ +
  gi|1266582   442 LQLIKRNLEDTGLKCQA---LENLIFQAQMFGFTLTQLDFRQESSRHSET 488

                    lDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLlgsDLPktEEvkD
                    ++ i   L++ +  Y e sE  +  WL+ EL+ +RPL++ ++P  E   +
  gi|1266582   489 IEVIANYLNVlpRPYGELSETEKVNWLIGELQTRRPLIPMEMPFDEKTIE 538

                    vldafrvL....AELPiDsFGaYiismataPsDvLAvELLqRECgv....
                     ++++r+L+  + E  ++    Yiism+   sDvL v LL +E g+ +++
  gi|1266582   539 TIETMRMLrylqQEFGVEICQTYIISMTNDVSDVLEVLLLAKEAGLydpg 588

                    ..kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG..........
                    ++  t+r+vPLFE + DL+ AP  ++ LF +  Y+  + G+ +  ++ ++
  gi|1266582   589 tsTTTIRIVPLFETVDDLKRAPEIMDALFKLPLYRAALAGgydyldeakk 638

                    ............KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKky
                    ++ ++++ ++ + qe+mvGYsDs KD G ls  W + kAq  + KvA  y
  gi|1266582   639 eqlpspelqpanLQEIMVGYSDSNKDSGFLSSNWEIHKAQKSLQKVAEPY 688

                    GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF
                    G  L lFHGRGG vGRGGGP   AiL+qP  tinG +++t qGEv+   +
  gi|1266582   689 GLALRLFHGRGGSVGRGGGPAYAAILAQPTGTINGRIKITEQGEVLASKY 738
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                    GEEnLCFrsLqRFtAAtLEHGm....nPPvsPkPEWRkLmeemAvvAtEE
                       +L    L   t A +   + +++   + P   W ++mee+A  A
  gi|1266582   739 SLPELALYNLETATTAVIQASLlgsgFDDIVP---WNEIMEELASSARKA 785

                    YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs.GGiesLRAiP
                    YRs+++  P F ++F + tP  E  ++ i sRPa+Rk ++  + +LRAiP
  gi|1266582   786 YRSLIYEQPDFLDFFLSVTPIPEISQLQISSRPARRKSGkKDLSTLRAIP 835

                    WiFaWtqtRFHLPvWLGvGAAFKhAidKD.iKnlqkLkEmYkeWPFFRvt
                    W+F+Wtq RF LP W GvG A    +++++  nl+ L+  Y +WPFF++
  gi|1266582   836 WVFSWTQSRFLLPAWYGVGTALENFLQQEpDENLKLLRYFYLKWPFFKMV 885

                    lDLlEmvFAKGDPGiAaLy.DkLLvaEeLkPFG...ksLRdkYvEtkdlL
                    +  +Em   K D  iA  y ++L   E++  F +  +++ ++Y  t+d++
  gi|1266582   886 ISKVEMTLSKVDLQIAHHYvEELSQPEDIERFEkvfEQISQEYNRTRDII 935

                    LkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtl
                    L i     lLEGD  L+  + LR+  i  L  +q   LKR+R    + t
  gi|1266582   936 LSINEQPKLLEGDTGLQRSVQLRNGTIVPLGFLQVSLLKRLR----QYTR 981

                    rPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqnt
                    +        +E      ++++          L    +Lt+ GiAAGm nt
  gi|1266582   982 Q--------AES-----GVIHFR---YSKEELLRGALLTINGIAAGMRNT 1015

                    G<-*
                    G
  gi|1266582  1016 G    1016

gi|154146676|emb|CAM83973.1|: domain 1 of 1, from 1 to 438: score 379.5, E = 6.1e-111
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541466     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541466     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541466     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541466     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541466     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541466     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541466     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541466     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541466     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tD +DAittHL+iGsYReWsEe+RqEWL++EL+GKRPL+g+DLP+ +
  gi|1541466     1 --HTDAMDAITTHLGIGSYREWSEERRQEWLVSELRGKRPLFGPDLPQSD 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl++frv+AELP+DsFGaYiismataPsDvLAvELLqRECgvk++L
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  gi|1541466    49 EVADVLGTFRVIAELPSDSFGAYIISMATAPSDVLAVELLQRECGVKKPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADL+ A  ++e LFs+DWY+ ri+GKqe+m+GYsDsGKDAG
  gi|1541466    99 RVVPLFEKLADLQQARPTMELLFSVDWYKERINGKQEIMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEEi+ vA ++GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541466   149 RLSAAWQLYKAQEEIVGVAERHGVKLTIFHGRGGTVGRGGGPSHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP t+nGslRvt+qGEviE sFGEEnLCFr+LqRFtAAtLEHGmnPPvsP
  gi|1541466   199 PPNTVNGSLRVTIQGEVIEKSFGEENLCFRTLQRFTAATLEHGMNPPVSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR+L+++mA vAt  YRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541466   249 KPEWRRLLDDMATVATGKYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvW+G+GAAF+hA+++    l
  gi|1541466   299 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWMGFGAAFRHAMQQPG-GL 347

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+EmY+eWPFFRvt+DLlEmvFAKGDPGiAaLyD LLv  +L+PFG+
  gi|1541466   348 ATLREMYDEWPFFRVTIDLLEMVFAKGDPGIAALYDGLLVPQDLRPFGDL 397

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++YvEt+ lLL++AGHkDlLE DPYL+qrl LRdsY t
  gi|1541466   398 LRANYVETQSLLLQVAGHKDLLESDPYLRQRLMLRDSYTTA--------- 438

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541466     - -------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541466     - -------------    -

gi|239993151|ref|ZP_04713675.1|: domain 1 of 1, from 1 to 662: score 379.0, E = 8.5e-111
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                  +                 D + +L G
  gi|2399931     1    -------------MP-----------------DFMRELDGR-----L 12

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    E YE+s
  gi|2399931    13 NEDYEVS------------------------------------------ 19

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2399931     - -------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2399931     - -------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2399931     - -------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                                lP d+  ++FssWmGGDRDG nP vt  vt  v LL
  gi|2399931    20 --------------LPLDASPVQFSSWMGGDRDG-NPFVTSKVTEQVLLL 54

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aR  Aa l+   ++ L  Elsm+ Cnd LR +          d
  gi|2399931    55 ARKRAAKLFAIDLDRLQVELSMYDCNDALREKV--------GD------- 89

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                          +EPYR +L    DK   tR+     LA    + s
  gi|2399931    90 -------ANEPYRALLRPLVDKFIATRDGISDYLAGKNPDTSN--WVESD 130
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                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    +e +EPL LCY+sL +CG +v+A G LLD +R    FG+ L +LD+Rq+s
  gi|2399931   131 DELIEPLMLCYQSLLDCGMQVVANGLLLDTIRRARVFGIHLLRLDVRQDS 180

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+ Dv   +t+ L++G Y +WsE  +q +Ll EL  KRPL+++     +
  gi|2399931   181 ERHADVFSELTRYLGLGDYAQWSEADKQAFLLRELGSKRPLFPAQWDASD 230

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    +vk+vld+ +v+A      FG Yiisma  PsDv+Av LL  E gv  ++
  gi|2399931   231 DVKEVLDTCKVIAKHSKHGFGIYIISMASEPSDVMAVQLLLQESGVDWPM 280

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +v PLFE L DL+  P  + kL siDWY+  + G+q vm+GYsDs KDAG
  gi|2399931   281 PVAPLFETLDDLNNSPDVMRKLLSIDWYRGYVKGRQFVMIGYSDSAKDAG 330

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     l+A W  Y+ qE ++ +A ++ v L+lFHGRGGt+GRGG P H Ai sq
  gi|2399931   331 ALAAGWAQYQSQEALVAIADEFDVSLTLFHGRGGTIGRGGLPAHAAIYSQ 380

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  ++G  Rvt qGE i + FG  +L  rsL  ++ A +E  + PP +P
  gi|2399931   381 PPGSLDGGFRVTEQGETIRYKFGMPKLAKRSLGIYASAIIEAMLFPPPAP 430

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    k EWR+L+  mA    + YR+ v  +  Fv YFR+AtPE E Gk+ +GsR
  gi|2399931   431 KEEWRELITAMAAQGRDNYRATVRHDKEFVPYFRVATPEQELGKLPLGSR 480

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkP GGiesLRAiPWiFaW qtR  LP WLGv  A      K   n
  gi|2399931   481 PAKRKPQGGIESLRAIPWIFAWAQTRLVLPSWLGVMRAIDSV--KTPENE 528

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    + + Em+ eWPF+R  l +l+mvF K DP i   yD+ Lv  eLk FG+
  gi|2399931   529 KVVNEMFSEWPFYRSRLSMLDMVFHKADPRISEAYDERLVPKELKHFGEA 578

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR + +E    LL i G  D++  DP  K  + +R +Y+  L  +q   L
  gi|2399931   579 LRSELKESISSLLAITGDGDIMKNDPQGKESMEIRAAYLQPLHYLQIELL 628

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     RiR                A ++          n        LE  +++
  gi|2399931   629 DRIRK---------------AGDD--------AQN------TSLERAMMV 649

                    tmKGiAAGmqntG<-*
                    t+ GiA Gm ntG
  gi|2399931   650 TIAGIAIGMRNTG    662

gi|283848041|ref|ZP_06365460.1|: domain 1 of 1, from 1 to 921: score 378.4, E = 1.3e-110
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                              +    K s    L++ D   l   L++iL    G +L
  gi|2838480     1    ------MIQTEDKNS----LLRNDVKKLGNILgEILVHHGGISLFNK 37

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v E  E+  +       +  + L  k+ sL+      v +a++    L n
  gi|2838480    38 VEEIREMTKDLRKNYNEEAYNKLKEKINSLEAPTRQNVIRAFSIYFHLVN 87

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   RRR  ++       E        iE  +  +        +
  gi|2838480    88 IAEQNHRIRRRRQYQLE------EDHVVQPVSIESAVLSMKEHN-YDRDV 130

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +   L   s++L++tAHPt +++R +L  + Ri   L q     +t  +K
  gi|2838480   131 IQKVLNDLSIELIITAHPTEAAKRTILEIQKRISDILKQFDNPILTKREK 180

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L+E L  E+ A + tDE+R  +Pt  DE++ G+ Y+ Et+++  P
  gi|2838480   181 LSLEESLFNEVTALWQTDELRHRKPTVIDEVKNGLYYFDETLFDVLPEIH 230

                    RRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDvC
                       +  L     n    + vP+ ++F sW+GGDRDG nP vtPE+t +
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  gi|2838480   231 QELEDQLDSYFPNSE--WKVPnFLHFGSWIGGDRDG-NPNVTPEITWETL 277

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     L R +A   Y + + DLm  +s     +  Rv   E    +  d
  gi|2838480   278 RLQRKLALKKYKQAIVDLMRKFS----QSTSRVTISEDLISSVED---EE 320

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                     i F K+    E + v     R K      R + +        s e  y
  gi|2838480   321 RI-FLKK---GETWPVDSEIYRRKFAIMQKRIKYV------GQSTEIGYS 360

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    + Ee L+ L +  ks  +         sL  l+Rqv  FG  L  LDiR
  gi|2838480   361 HAEELLDDLKMIHKSAQNHQSSHHKLKSLEKLMRQVELFGFHLATLDIRN 410

                    EseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgsDLP
                     s  +   +  i + ++i + Y   +E+ +   L   L+  RP++
  gi|2838480   411 HSGEHESAIAEILKSVNITdDYSALPEDEKINILNDVLQDPRPVMLFHGD 460

                    ktEEvkDvldafrvL....AELPiDsFGaYiismataPsDvLAvELLqRE
                       E ++v+  f+++++ + E  + s   Y++sm+ + sD L v +L +E
  gi|2838480   461 YSRETQEVIKVFQMIkeahEEFGSRSIQVYLVSMTQSASDLLEVLVLAKE 510

                    Cgvkqt.........LrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                     g+ + + ++  +++L v PL E + DL A    +++LF +D Y+n+++
  gi|2838480   511 AGIYRLhadgyvesgLHVAPLLETIDDLVAGAEIMKQLFQMDVYRNHLEE 560

                    K...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                    ++++qe+m+GYsD  KD G l A W+L+kAq Ei  +AK++ v+L  FHG
  gi|2838480   561 RgnhQEIMLGYSDGSKDGGTLTANWKLFKAQQEIHDMAKEFNVRLKFFHG 610

                    RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                    RGG  GRGGGP    iLsqP +t+   +++t qGEv+   +   ++ +r
  gi|2838480   611 RGGSLGRGGGPLNRSILSQPVETLGDGVKITEQGEVLSSRYLLQDIAYRN 660

                    LqRFtAAtLEHGmnPPvsPkPE......WRkLmeemAvvAtEEYRsvvvK
                    L     A LE   +   s   ++ ++++W   me++  v  E Y s+v+
  gi|2838480   661 LEQASSALLEASAKVAGSNDHDhfreksWELAMEDISKVSLEKYQSLVFG 710

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                    +  F  YF+  tP  E   +niGsRP KRk s   e LRAiPW+FaWtq
  gi|2838480   711 DQDFLTYFKQTTPLRELAALNIGSRPMKRKGSERFEDLRAIPWVFAWTQC 760

                    RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                    R  LP W   G   +  + K+  nl  L+ mY++WPFF vt+  l m
  gi|2838480   761 RQNLPAWYAAGSGLQAFVSKEKENLSLLQTMYQQWPFFEVTINNLQMALL 810

                    KGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlLE
                    K D   A  y +L+    ++++ FG+ + ++Y  t++ LL+i G  +lL+
  gi|2838480   811 KADLTTAKEYINLIEDKAIgdRIFGN-ITEEYHRTREVLLQITGNNELLD 859

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                      P ++     R++Y+  Ln +q   ++++R                 dE
  gi|2838480   860 HTPNIQESFHRRNPYVDPLNFLQVDLIQKMRS---------------LDE 894

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +  + +eL+               +Lt+ G+AAG+ ntG
  gi|2838480   895 EDPQMEELLTEV-------------LLTISGVAAGLLNTG    921

gi|114331035|ref|YP_747257.1|: domain 1 of 1, from 2 to 933: score 377.4, E = 2.6e-110
                    *->siDAqLRlLvPGKvs..edekLieYDALLlDkFL.DiLqDLHGedLk
                       s+   L  +vP K  + e ++ ++ D  Ll + L+D + +L Ge +
  gi|1143310     2    SLNT-LANIVPEKDTslEKDHPLREDIRLLGRMLgDTIRELEGEPMF 47

                    EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    + v      +  +   +D +   EL + L  L   ++  v +a++    L
  gi|1143310    48 DLVETIRQTAVRFRREQDEEAGKELDTILNHLSHKETTAVVRAFSYFSLL 97

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                     n+AE+ +   RRR +++  G    ++s t        l ++v k+
  gi|1143310    98 SNIAEDLHHNRRRRAHLRA-GSPPQDGSVTL------ALERVVAKG-INT 139
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                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    +   +      +  vltAHPt   RRs+L  + +i   L       +t++
  gi|1143310   140 QQLENFFAEALISPVLTAHPTEVQRRSILDYQLKIQRLLKERDRTQLTPN 189

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    + +  +E L   iq  + t  +R  + t qDE+  G+ Y+H t  k +P
  gi|1143310   190 ELRHNEEDLRSAIQTLWQTRVLRSVRLTVQDEIENGLIYYHYTFLKQIPY 239

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                       +++  L    +    P  +  ++  sW+GGDRDG nP vt  +
  gi|1143310   240 IYAKIEDILER-HMDKAAPCIASFLRIGSWIGGDRDG-NPFVTHQIMLHA 287

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                          +    Yi+ vE +   +s+      +    E l +ta
  gi|1143310   288 AERHSALILDYYIEEVEKIGQAMSLTERLIKVTSELEGLASTAPGL--PA 335

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv.
                      i+        EPYR +   +  +L  t   +R L  +   +  E+  +
  gi|1143310   336 SRID--------EPYRRVFLGMHTRLIAT---SRYLSPHVGRQYQENTAe 374

                    .ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                    +y +  eF+  L++  +sL +     +A G++ Dl R v  FG  L  LD
  gi|1143310   375 pYADSAEFVHDLDIVIRSLKQHQSNKLAQGAIRDLRRAVDVFGFHLASLD 424

                    iRqEseRqtDvlDAittH..LeiGsYReWsEeKRqEWLlaELkGKRPLlg
                    +Rq s  +  v+  + + +  +   Y +     R EWLlaELk   PL+
  gi|1143310   425 MRQHSKIHEQVVSELYEKnaQDNRNYPDLTRAERAEWLLAELKRSHPLVS 474

                    sDLPktEEvkDvldafrvLAELPiDsFG.....aYiismataPsDvLAvE
                    s     +  +  l  +r+ AE+    FG+   + Yiismat    +L
  gi|1143310   475 SLSDYSDITQGELRILRMAAEI-QRRFGhvalpNYIISMATGVIHILEAA 523

                    LLqRECgv.......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                    LL +E g+ + ++  + t+ ++PLFE + DL+     +e LFs+  Y+
  gi|1143310   524 LLLKEAGLlqfgeaaRSTVNIIPLFETIDDLRGCANVMEELFSLPEYRKM 573

                    idGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                    +  +++ qevm+GYsDs KD G +   W + kA  E+ Kv  ++Gv+L l
  gi|1143310   574 LRSRsnlQEVMLGYSDSNKDGGFVTSNWEIHKAEIELTKVFNRHGVRLRL 623

                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                    FHGRGGtvGRGGGP    iL+qPP  +nG +R t qGEvi   + + ++
  gi|1143310   624 FHGRGGTVGRGGGPSYQGILAQPPGSVNGQIRLTEQGEVIASKYTDPEIG 673

                    FrsLqRFtAAtLEHGm...nPPvsPkPEWRkLmeemAvvAtEEYRsvvvK
                     r L    AAt+E  + +++      P   ++mee+   A   YR +v+K
  gi|1143310   674 RRNLETLVAATIESTLldrDAIHCHTPQCYQIMEELSASAYAAYRDLVYK 723

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                     P F  +F   tP  E   + iGsRP+ RkPs  ie LR iPW+F+W
  gi|1143310   724 TPNFTQFFQESTPIREIAGLHIGSRPTSRKPSNKIEDLRTIPWVFSWSLN 773

                    RFHLPvWLGvGAAFKhAidKD...iKnlqkLkEmYkeWPFFRvtlDLlEm
                    R  +P W G+G A    +++ +++   l +++ mY++WPFF   l  ++m
  gi|1143310   774 RTMIPGWYGFGTAVENFVQQAgntQDVLIQMQKMYRTWPFFQTLLSNMDM 823

                    vFAKGDPGiAaLyDkLLvaEeLkPFG.ksLRdkYvEtkdlLLkiAGHkDl
                    v AK D GiA+ y +L+   eL+ +    +R +++   ++L  i GH +l
  gi|1143310   824 VLAKSDLGIASRYAELVTDSELRQYVfTAIRTEWELCVKWLFAITGHTEL 873

                    LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                    L   P L   +R+R +Yi  +n +q   L+R R
  gi|1143310   874 LQDNPTLARSIRIRTPYIDPMNHLQVELLRRYR----------------- 906

                    dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       s   d+ ++             + Lt+ G+A G+ n G
  gi|1143310   907 ---SGDDDDAIRRA-----------IHLTINGVATGLRNSG    933

gi|163764698|ref|ZP_02171753.1|: domain 1 of 1, from 1 to 922: score 377.2, E = 3e-110
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                              ++P    + + +++ D   l k L+D+L    Ge L
```

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gi|1637646     1    --------MAPLNEQDPNMMLRSDVNKLGKILgDVLRHHGGEALFNE 39

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v E  E+        D     EL  ++  L       v +a+     L n
gi|1637646    40 VEEIREMTKALRKSYDEANEKELKKRIENLKSPMRQQVIRAFAIYFHLVN 89

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE  +   R R  + k       ++    s iE  +   + k  K Pe
gi|1637646    90 IAEQHHRIRRSRQYRMK------RGENIQPSSIEAAIVN-IQKE-KYPET 131

                    vF.eALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    v ++ L   s++L++tAHPt + +R +L  + Ri   L q     +t  +
gi|1637646   132 VIqQVLDDSSIELIMTAHPTEATKRTILEIQKRISYILEQFDNPALTEKE 181

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    +++ +E L  E+ A + tDE+R  +Pt  DE++ G+ Y+  t+++  P
gi|1637646   182 REDHEESLINEVTALWHTDELRFKKPTVIDEVKNGLYYFDTTLFDVLPAV 231

                    LRRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDv
                       ++  L          + vP+ i+F sW+GGDRDG nP vtPEvt +
gi|1637646   232 HQEIEEQLERYYPDQ--DFKVPnFIHFGSWIGGDRDG-NPFVTPEVTWET 278

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE.Elyrtaardkvv
                      L R +    Y + + +Lm  +s     +  Rv  ++E   t  +
gi|1637646   279 LNLQRDLTLRKYEESITELMRRFS----QSTTRVDIDpEFIETMEQY--E 322

                    KyYiEFWKqvP.PtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe.
                    K Y+      P  tE YR +LG++R      R R      tG+ +++Ee
gi|1637646   323 KKYMKKSETWPvTTEIYRRMLGAIRK-----RIRQVGKTNTGY-DVAEEl 366

                    .AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                     A    v e      L  + L +          L  ++Rqv  FG  L
gi|1637646   367 lADLRYVRENALKHQLPNQKLKQ----------LNKMIRQVELFGFHLAT 406

                    LDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLl
                    LD+R  s  +   +  i + ++i  +Y++  Ee ++  L   Lk  RPL+
gi|1637646   407 LDVRNHSGEHETAIAEILKVVGITEdYKSLDEEEKMTILENALKDPRPLM 456

                    gsDLPktEEvkDvldafrvL....AELPiDsFGaYiismataPsDvLAvE
                           EE +++   f+++++ + E    s   Y++sm+ + sD L v
gi|1637646   457 LLNEDYSEETREIFKVFQMIkdahEEFGQRSIEVYLVSMTQSASDLLEVL 506

                    LLqRECgvkq.........tLrvvPLFEkLADLeAAPAavekLFsiDWYi
                    +L +E g+ + + +++ ++ L v PL E + DL A PA +++LF +D Y+
gi|1637646   507 VLAKEAGIYRlhadgsvdsNLHVAPLLETVDDLMAGPAIMKRLFEMDIYR 556

                    nridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                     ++  ++++qe+m+GYsD  KD G l A W+L+ Aq  i  +AK+y v+L
gi|1637646   557 THLGERgdhQEIMLGYSDGSKDGGTLTANWKLFEAQAKIHNMAKDYNVRL 606

                    vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                      FHGRGG  GRGGGP    i+sqP +t+   +++t qGEv+   +   +
gi|1637646   607 KFFHGRGGSLGRGGGPLNRSIVSQPAETLGDGVKITEQGEVLSSRYLLGD 656

                    LCFrsLqRFtAAtLEHGmnPPvsP.......kPEWRkLmeemAvvAtEEY
                    + Fr L   + A LE   n   sP+++ + ++P W + mee+       Y
gi|1637646   657 IAFRNLEQAASALLEASANVYASPgdschirRPQWEEAMEEISKASLSKY 706

                    RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWi
                     s+v+K+P F  YF+  tP  E   +niGsRP  Rk s   e LRAiPW+
gi|1637646   707 QSLVFKDPDFLTYFKETTPLNELKELNIGSRPMSRKGSERFEDLRAIPWV 756

                    FaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDL
                    FaWtq R  LP W   G       +    nl  L++mY++WPFF  t+
gi|1637646   757 FAWTQCRQMLPAWYASGTGLAAYGKASEENLELLQDMYQNWPFFHSTINN 806

                    lEmvFAKGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAG
                    l m   K D   A  y kL+   e++++ +G+ +  ++  tk++LLki G
gi|1637646   807 LQMALMKADLFAAKEYVKLVKDQEMgqRIYGE-IEKEFNLTKEMLLKISG 855

                    HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
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                     lL+  P ++  + LR++Y+  Ln +q   + ++R+ s         s
  gi|1637646   856 SEQLLDFTPNIRDSVHLRNPYVDPLNFLQVDLIEKMRESS---------S 896

                    KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     E  +E          L             ++Lt+ G+AAG+ ntG
  gi|1637646   897 EERTEEL---------LT-----------EVLLTISGVAAGLLNTG    922

gi|186685513|ref|YP_001868709.1|: domain 1 of 1, from 47 to 1037: score 376.9, E = 3.7e-110
                    *->siDAqLRlLvP..GKvsede.....kLieY....DALLlDkFLDiLq
                        +  qLR L  ++G+  +d+ ++  kLie  + ++A+   +   +
  gi|1866855    47    DLLRQLRDLCSpeGQATNDQassavKLIEQlninEAIRAARAFALYF 93

                    DLHGedLkEavqECYElsAeYEGKkDtkKLeELGak.LtsLdPaDailvA
                     L     +E+ q    ls  YE   ++   e    ++  s +  D   v
  gi|1866855    94 QLINIIEQEYEQR-QQLS-RYEAETEPTDSERASNVnYSSNQREDDAPVS 141

                    kailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKk
                    k i   L   n  E  ++       k k G Fa              l
  gi|1866855   142 KGIAAELLAKNYLEKAQV-------KPK-GTFA-------------ALFP 170

                    LvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq
                       k n  P+ +   +    v Lv+tAHPt  vR  +  K+  +   L +
  gi|1866855   171 YLFKQNVPPQQIQRLIAHLDVRLVFTAHPTEIVRHTIRDKQRQVVQLLQK 220

                    LsAKDvtve........DKkELDEALHREiqAAFRtDEiRRaqPtPqDEm
                    L   +    +++++   +  ++ E L  Ei   +RtDE+   +Pt  DE+
  gi|1866855   221 LDTLENHAGgtgggyawEAADVREQLLEEIRLWWRTDELHQFKPTVLDEV 270

                    RaGmsYiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGG
                     + + Y+ E +++G+P+  +R    L n       P       F sW+G
  gi|1866855   271 DYALHYFQEVLFDGIPQLYKRFKHTLSNT-FPWLEPPSKNFCSFGSWVGS 319

                    DRDGknPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndEL.
                    DRDG nP vtPEvt       R m    Yi+ v  L+  ls+    +++
  gi|1866855   320 DRDG-NPSVTPEVTWQTACYQRKMVLGRYIQSVKNLIELLSVSMHWSDVl 368

                    ..RvRAEElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntR
                    ++     El +   ++ v       ++q    EPYR  L  v  +L ntR
  gi|1866855   369 pdLLESLELDQSQLSE-VYDALALRYRQ----EPYRLKLAYVLKRLENTR 413

                    ERaRHLLAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsL
                    +R   L         +   y   ++FL  L +  + L e G   +    L
  gi|1866855   414 DRNLALYNRETPKNQDSPLYRSGDDFLAELRMIQRNLTETG---LSCRDL 460

                    LDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei..GsYReWsEe
                      l+ qv  FG  L +LDiRqEs R+ D l  i + L+i +  Y e sEe
  gi|1866855   461 ENLICQVEIFGFNLTQLDIRQESSRHADALNEILQYLQIlpQPYNELSEE 510

                    KRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvL....AELPiDsFG
                    ++  WL  EL+ +RPL++++LP  E   Dv+++frv+++ + E
  gi|1866855   511 QKVAWLTGELQTRRPLIPAELPFSEKTNDVIETFRVVrslqQEFGLNICQ 560

                    aYiismataPsDvLAvELLqRECgvkq......tLrvvPLFEkLADLeAA
                     Yiism+   sDvL v LL +E  +  +    +t++vvPLFE + DL+
  gi|1866855   561 TYIISMCRDVSDVLEVLLLAKEARLFDpaiavgTIQVVPLFETVEDLQRS 610

                    PAavekLFsiDWYinridG.............................
                       + kLF +  Y+  + G+ +++++++   ++++++  ++ ++ ++ ++
  gi|1866855   611 RSVMRKLFELPLYRALLAGgyeqtktesvvvdenssslaspappaspasp 660

                    ..........KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGv
                     +++++ +++ qevm+GYsDs KD G ls  W + kAq  + ++A  y +
  gi|1866855   661 apspspltpnLQEVMLGYSDSNKDSGFLSSNWEIHKAQKSLQQIAEGYDI 710

                    KLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGE
                     L +FHGRGG vGRGGGP   AiL+qP   inG +++t qGEv+   +
  gi|1866855   711 NLRIFHGRGGSVGRGGGPAYEAILAQPGHSINGRIKITEQGEVLASKYSL 760

                    EnLCFrsLqRFtAAtLEHGmnPPvsPkPE.WRkLmeemAvvAtEEYRsvv
                     +L    +   t A +   +        E+W ++mee+A      YR+++
  gi|1866855   761 LDLALYHMETITTAVIQASLLRTGFDDIEpWNEIMEELAARSRQHYRALI 810
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                    vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG..GiesLRAiPWiFa
                    +  P Fv++F   tP  E  ++ i sRPa R+PsG++ + sLRAiPW+F+
  gi|1866855   811 YEQPDFVDFFHQVTPIEEISQLQISSRPA-RRPSGkkDLSSLRAIPWVFS 859

                    WtqtRFHLPvWLGvGAAFKhAidKD.iKnlqkLkEmYkeWPFFRvtlDLl
                    WtqtRF LP W GvG A +  ++ ++   l+ ++  Y +WPFF++ +
  gi|1866855   860 WTQTRFLLPSWYGVGTALQEFLNAEpEEHLKLMRYFYVKWPFFKMVISKA 909

                    EmvFAKGDPGiAaLy.DkLLvaEeLkPFGk...sLRdkYvEtkdlLLkiA
                    Em  AK D  +A  y  +L  +E+   F k  +++  ++  t+dl+Lki
  gi|1866855   910 EMTLAKVDMQMAHHYvQELSQSEDQLRFAKvfdQIASEFYLTRDLVLKIT 959

                    GHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhl
                     H  lL+GDP L+  + LR+  i  L  +q   LKR+R           +
  gi|1866855   960 DHNQLLDGDPVLQRSVQLRNGTIVPLGFIQVSLLKRLRQSMNTNATSGVI 1009

                    sKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       y   +      L++               +Lt+ GiAAGm ntG
  gi|1866855  1010 HSRYSKGE------LLRGA-------------LLTINGIAAGMRNTG    1037

gi|154146698|emb|CAM83984.1|: domain 1 of 1, from 1 to 440: score 375.8, E = 7.6e-110
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541466     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541466     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541466     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541466     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541466     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541466     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541466     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541466     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541466     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tD +DAittHL+iGsYR+W+E +RqEWL++EL+G RPL+g DLP  +
  gi|1541466     1 --HTDAMDAITTHLGIGSYRDWPEARRQEWLVSELRGNRPLFGDDLPHSD 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk.qt
                    Ev+Dvl++frv+AELP DsFGaYiismataPsDvLAvELLq ECgvk+++
  gi|1541466    49 EVADVLGTFRVIAELPGDSFGAYIISMATAPSDVLAVELLQQECGVKeKP 98

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    LrvvPLFEkLADL+ A A++e LFsiDWY+ ri+GKqe+m+GYsDsGKDA
  gi|1541466    99 LRVVPLFEKLADLQQARATMELLFSIDWYKERINGKQEIMIGYSDSGKDA 148

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
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                    GRlsAAWqLYkAqEEi+ vA ++GvKL++FHGRGGtvGRGGGP HLAiLs
  gi|1541466   149 GRLSAAWQLYKAQEEIVGVAERHGVKLTIFHGRGGTVGRGGGPSHLAILS 198

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP t+nGslRvtvqGEviE sFGEE+LCFr+LqRFtAAtLEHGm PPv+
  gi|1541466   199 QPPGTVNGSLRVTVQGEVIEKSFGEEHLCFRTLQRFTAATLEHGMSPPVA 248

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                    PkPEWR Lm++mAvvAtEEYR +v++EPRFvEYFR AtPE+EYG+mniGs
  gi|1541466   249 PKPEWRALMDDMAVVATEEYREIVFREPRFVEYFRRATPETEYGRMNIGS 298

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                    RP+KRk +GGiesLRA+PWiFaWtqtRFHLPvWLG+GAAF+hA++K
  gi|1541466   299 RPSKRKVGGGIESLRAVPWIFAWTQTRFHLPVWLGFGAAFRHAMEKQPGG 348

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                    l  L+EmY+eWPFFRvt+DLlEmvFAKGDPGiA LyDkLLv  +L+PFG+
  gi|1541466   349 LATLREMYEEWPFFRVTIDLLEMVFAKGDPGIAELYDKLLVPQDLWPFGE 398

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    +LR++Y Et+ lLL++AGH DlLE DPYL+qrl LRdsYit
  gi|1541466   399 QLRANYAETQSLLLQVAGHEDLLESDPYLRQRLMLRDSYITA-------- 440

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi

  gi|1541466     - ------------------------------------------------ -

                    LtmKGiAAGmqntG<-*

  gi|1541466     - --------------    -

gi|115523808|ref|YP_780719.1|: domain 1 of 1, from 11 to 927: score 375.8, E = 7.9e-110
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                         DA  R         ++  ++ D  Ll + L+D + D  Ged+ +a
  gi|1155238    11    --DALPRSGEDAAAIAEDARLRDDIRLLGRILgDTVRDQEGEDVFDA 55

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      s  +    D    +EL     +L    ++ + +a++    LAn
  gi|1155238    56 VERIRQTSIRFHRDNDQPARDELVELFDGLSTPATLRIVRAFSYFSHLAN 105

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAE+ +     R  +++        +      +  tl +    +  s +E
  gi|1155238   106 LAEDQN---NIRQMRLQ--------NGARPGSLVATLAHARAVG-ISAKE 143

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                             v  vltAHPt   R+s + ++  i   L       +t+e+
  gi|1155238   144 LRHFFETALVSPVLTAHPTEVRRKSTMDREMEIARLLDRRERLQMTPEEI 193

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +  +E L R +   + t  +RR++ t  DE+  G+s++     + vP+
  gi|1155238   194 EQHEELLRRAVLTLWQTNMLRRTKLTVLDEVANGLSFYDYAFLHEVPRLH 243

                    RRvDtALK.niGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                       +  L +  G  E l   +  ++  sW+GGDRDG nP vt Ev R
  gi|1155238   244 GVLEDKLNdDDGAGEEL---ASFLRMGSWIGGDRDG-NPFVTAEVMRGTL 289

                    LLaRmmAanlYisqvEDLmFElsmWR....CndELRvRAEElyrtaardk
                     L    A   Y++ +  L  Els+  +  +  dELR+ AE    t+
  gi|1155238   290 RLQSRRALRHYLDELHALGSELSIAAhladISDELRALAENSPDTSPHR- 338

                    vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei...
                                  EPYR  + ++  +L  t  R       Gi +i+ +
  gi|1155238   339 ------------AGEPYRLAVSAIYARLAATAHR------LGIDDIrap 369

                    .sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                     +E A y +  e    L++  +sL      viA G L  l R v  FG
  gi|1155238   370 vAESAPYAEPAELKADLDVLHRSLVANNSAVIARGRLRSLRRAVDCFGFH 419

                    LvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKR
                    L  LD+Rq s  +   +  +      G+sY    Ee R   L aEL+  R
  gi|1155238   420 LASLDMRQNSAVHERTMAELIDKAMPGkSYMAMNEEARIALLAAELRSPR 469
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                    PLlgsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDv
                    PL  + +   EE  D l  fr  AE    +FG+   ++ iism+   sD
  gi|1155238   470 PLASPFVKYSEETVDELAVFRAAAE-AHATFGPaaipqCIISMTKGVSDL 518

                    LAvELLqRECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYi
                    L v +L +E g+ ++ ++ ++ vvPLFE + DL+AA   +++L  +  Y+
  gi|1155238   519 LEVVVLLKEVGLvdpagRSAINVVPLFETIEDLQAAAGIMDRLLGLHDYR 568

                    nrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                      +d+++G qevm+GYsDs KD G +   W LYkA  E+ K+  ++Gv++
  gi|1155238   569 RLVDsrgGVQEVMLGYSDSNKDGGFVTSGWELYKAEIELLKIFEHHGVRM 618

                    vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                     lFHGRGG vGRGGGP   AiL+qP   +nG +R+t qGE+i   +   +
  gi|1155238   619 RLFHGRGGSVGRGGGPSYDAILAQPAGAVNGQIRITEQGEIITSKYSNPE 668

                    LCFrsLqRFtAAtLEHGmnPPv..sPkPEWRkLmeemAvvAtEEYRsvvv
                    +    L   +AAtLE  +  P  ++P   + k m+e+   A   YR +v+
  gi|1155238   669 VGRNNLEVLAAATLEASLLQPRlgAPCVGYLKAMDEISALAFKAYRGLVY 718

                    KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                        F +YF + t  +E   +niGsRPa Rk    ie LRAiPW+F+W q
  gi|1155238   719 ETEGFEDYFWSSTVITEIATLNIGSRPASRKKTHKIEDLRAIPWVFSWAQ 768

                    tRFHLPvWLGvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                     R  LP W G+G A   +      + +  L+E+ +eWPFFR  l  ++mv
  gi|1155238   769 CRLMLPGWYGFGSAVEaWVKAHPEQGMAYLQELNREWPFFRTLLSNMDMV 818

                    FAKGDPGiAaLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLkiAGHkDl
                      K    iA+ y +L+  E L+   FG+ ++ ++      LL i GH+ l
  gi|1155238   819 LSKSSIAIASRYAELVADEKLRAaiFGR-IKREWHSSIAALLAIMGHQRL 867

                    LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                    L G P L   +R R +Y+  Ln +q   LK  RD
  gi|1155238   868 LQGNPRLERSIRHRFPYLDPLNHVQVELLKQHRDHA----------V 904

                    dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    dE+         L             + +t+ Gi AG+ n G
  gi|1155238   905 DEQ--------ALR-----------GIQITINGISAGLRNSG    927

gi|20196766|emb|CAC86387.1|: domain 1 of 1, from 1 to 398: score 374.9, E = 1.4e-109
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2019676     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2019676     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2019676     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                           svDLv+tAHP qs+RRsLLqKnaRiRnCL+qLsAKDvtveDKk
  gi|2019676     1 -------SVDLVFTAHPMQSARRSLLQKNARIRNCLTQLSAKDVTVEDKK 43

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmR+GmsYiHEtvW+GvPKFLR
  gi|2019676    44 ELDEALHREIQAAFRTDEIRRAQPTPQDEMRYGMSYIHETVWNGVPKFLR 93

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinERlPYdvPLikF+sWmGGDRDG nPRvtPE+tRDvCLL
  gi|2019676    94 RVDTALKNIGINERLPYDVPLIKFCSWMGGDRDG-NPRVTPEMTRDVCLL 142

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    +RmmAanlYi+qvEDLmFElsmWRCndELR+RAEE+++t+a++kv+KyYi
  gi|2019676   143 SRMMAANLYINQVEDLMFELSMWRCNDELRARAEEVQSTPASKKVTKYYI 192

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
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                    EFWKq+PP+EPYRviLG+vRDKLYntRERaRHLLAtG+seisE+Av+tk+
  gi|2019676   193 EFWKQIPPNEPYRVILGAVRDKLYNTRERARHLLATGFSEISEDAVFTKI 242

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFLEPLELCYksLCeCGDk+iADGsLLDlLRqv+ FGLsLvKLDiRqEs
  gi|2019676   243 EEFLEPLELCYKSLCECGDKAIADGSLLDLLRQVFAFGLSLVKLDIRQES 292

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+tDv+DAittHL+iGsYR+W+E+KR+EWL++ELkGKRPLl++DLP tE
  gi|2019676   293 ERHTDVIDAITTHLGIGSYRSWPEDKRMEWLVSELKGKRPLLPPDLPLTE 342

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dv++a+rvLAELPiDsFG+Yiism+taPsDvLAvELLqRECg++qtL
  gi|2019676   343 EIADVIGAMRVLAELPIDSFGPYIISMCTAPSDVLAVELLQRECGIRQTL 392

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLF
  gi|2019676   393 PVVPLF---------------------------------------------- 398

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|2019676     - ------------------------------------------------- -

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

  gi|2019676     - ------------------------------------------------- -

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|2019676     - ------------------------------------------------- -

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|2019676     - ------------------------------------------------- -

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|2019676     - ------------------------------------------------- -

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|2019676     - ------------------------------------------------- -

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|2019676     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|2019676     - -------------    -

gi|163848702|ref|YP_001636746.1|: domain 1 of 1, from 13 to 939: score 374.1, E = 2.5e-109
                    *->siDAqLRlL..vPGKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                        + A +R+L+++ G+v                    i q  HG +
  gi|1638487    13    -LSANIRALgdALGRVI-----------------IGQ--HGSEALA 38

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                     v     ++ +          + L   +  Ld      + ka+     L
  gi|1638487    39 LVEQVRRMAKDLRNAPTNTDPQALPQLIADLDLPQLRSLVKAFTLYFGLV 88

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    nLAE ve     R + ++    a    A   +D  E lK+  +     P+
  gi|1638487    89 NLAEGVERLRVLRARDLR---HAPAPRAESIADAIELLKRHGVPA---PA 132

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLs..AKDvtv
                     + e L    +  vltAHPt s RR +L K  Ri   L  L  + + v +
  gi|1638487   133 -IQEWLDHALIMPVLTAHPTESRRRTILIKLRRIFDTLVDLTfgERLVLP 181

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                     D++     + REi   +  D++R  +P   DE+  G+ ++   +W+  P
  gi|1638487   182 ADRQAALTRIEREIVGLWQSDDVRNRRPSVLDEVENGLFFFQTVLWELLP 231
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                    KFLRRvDtALKniGinE..RlPYdvPLikFssWmGGDRDGknPRvtPEvt
                       R +  AL+      + RlP   P ++F sWmGGDRDG nP vtPEvt
  gi|1638487   232 HIYREMSDALQAAYPDHpwRLP---PFLRFGSWMGGDRDG-NPFVTPEVT 277

                    RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk
                     +   L R       i+ ++ L+ +ls     + ++v    + r a
  gi|1638487   278 VETVRLMRSAMLRYLIDCLDRLITDLS--QSVQQVKVDTAIIDRIAEYRE 325

                    vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAt.Gise..i
                    ++             EPYR +   +  +L nt   +       Gi  +
  gi|1638487   326 LMPDAAATLNPHYRCEPYRQLCHFIQARLHNTLQYTLDYTPRwGIDPplA 375

                    sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                        +y +  e L  L+L   sL + G   iA+G L D+   v    L
  gi|1638487   376 RRPDIYYHSRELLADLDLIDASLRNNGSTLIAEGLLRDVRTLVAVCHLHT 425

                    vKLDiRqEseRqtDvlDAittHLe.iGsYReWsEeKRqEWLlaELkGKRP
                      LD+Rq + R+t  l  i    + +  Y    E  R   L  E++  RP
  gi|1638487   426 ATLDVRQHASRHTAALSEILAAAGvVDDYEALDEAERIAVLSVEIRRPRP 475

                    LlgsDLPktE.EvkDvldafrvLA....ELPiDsFGaYiismataPsDvL
                    L +s L    +  ++ + +frv+A  ++ L  + F  Yiis +   sD L
  gi|1638487   476 LTPSRLSHFSpATAETIHTFRVIAaiseQLDPEIFQTYIISTTSQVSDLL 525

                    AvELLqRECgvkqt.....LrvvPLFEkLADLeAAPAavekLFsiDWYin
                    Av LL R+ g+ q+++ ++L +vPLFE   DL+ APA ++ L  +  Y+
  gi|1638487   526 AVLLLCRDAGLYQPgqasqLHIVPLFETGDDLQRAPALLDELLRLPVYRE 575

                    ri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                    ++  +d  qevm+GYsDs K+ G ++A W LY+Aq E+  v  ++Gv+L
  gi|1638487   576 HLalrDNLQEVMLGYSDSNKEGGFVAANWALYRAQVELTAVTDRHGVRLR 625

                    lFH......GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                    lFH++++  GRGG vGRGGGP   AiL+qPP t++G ++vt qGE+i
  gi|1638487   626 LFHgrggavGRGGAVGRGGGPAGQAILAQPPGTLHGQIKVTDQGEMISDR 675

                    FGEEnLCFrsLqRFtAAtLEHGmnPPvs..PkPEWRkLmeemAvvAtEEY
                    + +     r L     A L  G  P ++++P P W   meemA  A   Y
  gi|1638487   676 YLDPRTAHRHLEQVVNAVLRAGF-PGMArqPEPTWLAAMEEMATTARTVY 724

                    RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWi
                    R +v+ +P F  YFR+AtP  E+ ++ iGsRP  R+ s  ie LRAiPW+
  gi|1638487   725 RQLVYEDPDFLIYFRSATPVAEFNRLRIGSRPVSRRKSDRIEDLRAIPWV 774

                    FaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDL
                    F+W q R  +P W G+G A    ++ D   l  L+ mY+ WPFF   lD
  gi|1638487   775 FSWMQSRHTIPGWFGLGSALEAFVEADPHHLHLLRTMYQHWPFFSTLLDN 824

                    lEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGH
                      m+  K D  iA  y  L+    L  +  +++  ++  t+ ++ +i
  gi|1638487   825 AQMIMLKADMNIARAYASLVPDRHLAErIFQRIESEFRRTERMICQITER 874

                    kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                     DlL   P L+  +R R++Yi  L  +q   L+R+R
  gi|1638487   875 NDLLAHQPVLQRAIRQRNPYIDPLSFVQIELLRRLR-------------- 910

                    EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      A+ +              +    LE  L++ + GiAAG++ntG
  gi|1638487   911 --AAPP-------------EEQGELETVLLMSINGIAAGLKNTG    939

gi|148656870|ref|YP_001277075.1|: domain 1 of 1, from 11 to 952: score 374.0, E = 2.7e-109
                    *->siDAqLRlLvPGKvsedekLieYDA.LLlDkFLDiLqDLHGedLkEa
                        + A +R L  G      ++i+  A+    + ++ L  L G++L+
  gi|1486568    11    RLSATIRFL--GNLL--GEVIRNQAgEEAFRLVEQLRTL-GKELRNG 52

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                               E  +    L  L +++t    +D   v ka+     L n
  gi|1486568    53 -----------EPDRADASLRALASQMTV---TDVQTVIKAFNAYFLLVN 88

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
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                LAE ++     R+  ++  + a  +   tEs i   +  +      s
gi|1486568    89 LAEQMQ-----RVWILRDREQASPTAPRTES-IAAAIAEIHAHN-VSAVT 131

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                v e L    +  v+tAHPt + RR  L K  R    La L  +
gi|1486568   132 VQEWLETARIQPVFTAHPTEARRRTALEKVRR----LATLLDRRSGGLQG 177

                kELDEALHR...EiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                 EL+E   R ++Ei   + tDE+R  +Pt  DE++ G+ Y+   +++ +P
gi|1486568   178 FELEENTLRireEIVSLWQTDEVRVVKPTVIDEVKNGLFYFESGLFDLIP 227

                KFLRRvDtALKni..GinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                +  R  + AL+   +    R+P   PL+++ +WmGGDRDG nP vt  vt
gi|1486568   228 RLYRELEYALRTAypDHEWRVP---PLLRYGAWMGGDRDG-NPNVTHAVT 273

                RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk
                     L R  A    i  +E+L   l          v  E   + a
gi|1486568   274 LQTVRLLRAAAVQRHITTIEELSHRLG--QSTRQAPVSEELRASLANDAA 321

                vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisE
                +     +   q  P E YR     +R+KL  t   a   +L  G s+ +
gi|1486568   322 LFPDVADMLTQRNPYELYRQKCTYIREKLLRTLNDANTAsLDWGRSDPPP 371

                eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                +  y + ++ L  L +  +sL      v+ADG+L Dl+Rqv  FGL
gi|1486568   372 NGAYLRSDDLLADLRVMEQSLRANNAAVVADGALRDLIRQVEVFGLHTAT 421

                LDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLl
                LDiRq seR+t  l  +    ++ ++Y    E  R + L  E+   RPL+
gi|1486568   422 LDIRQHSERHTAALAEVLASAGVCAdYTALNETERIDLLSREIGNPRPLI 471

                gsDLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAvE
                ++ L    +  +v+++fr+   +L  L  ++   Yi+sm+   sD LA
gi|1486568   472 PAHLDYSPDTVEVIQTFRtiaaILNRLSPEAIETYIVSMTRGASDLLAPL 521

                LLqRECgvkqt.....LrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                LL +E g+ ++ + ++L + PLFE  ADL      +e   s+  Y+ ++
gi|1486568   522 LLAKEAGLFRPfrfsrLNIAPLFETGADLTCCDTILEACLSLPVYRDHLA 571

                GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                 +++ qevm+GYsDs KD G ++A W LY+Aq  +    ++yG+ + lFH
gi|1486568   572 LRgnlQEVMIGYSDSNKDVGYVAANWALYQAQRKLRDFGRRYGIHMRLFH 621

                GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                GRGG +GRGGGP   AiL+qPP  i   +++t qGEvi   +G   L  r
gi|1486568   622 GRGGAIGRGGGPANHAILAQPPGSIGNQIKITEQGEVIADRYGLPLLAHR 671

                sLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFv
                 +     A L  G+     P  EW + +e++A      YR++v+    Fv
gi|1486568   672 HIEQVMNAVLRAGLLQRDDPPAEWMQALERLADLSQRHYRALVYERNDFV 721

                EYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLP
                 YF   tP +E  ++niGsRPa R+  G ie LRAiPW+F+W q R  LP
gi|1486568   722 PYFHNVTPITEISRLNIGSRPASRRNTGRIEDLRAIPWVFSWMQSRHTLP 771

                vWLGvGAAFKhAidK.........DiKn.............lqkLk
                 W G+G A    + K+++ + + ++D+ n ++++++++ ++  ++l  L+
gi|1486568   772 GWYGMGFALETFVYKgdgidldmsgDSGNvtgdgttdhvgsaidrLALLQ 821

                EmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL.vaEeLkPFGksLRd
                EmY  W FFRv +D   m+  K D  iAa y +L +  E        +Rd
gi|1486568   822 EMYARWSFFRVMIDNAQMILGKADLHIAARYAELApDREAAASIFAAIRD 871

                kYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRi
                +Y  t  ++ +iA    lL+  P L+  +  R++Yi  +  +q   L+R+
gi|1486568   872 EYGRTDRMIRQIARIERLLDNSPVLQHSIQRRNPYIDPMSYLQIELLRRL 921

                RDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmK
                R                 + +    d+  +          +ED ++L +
gi|1486568   922 R-----------------AAP----DGPQHAA--------IEDAILLSIS 942
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                  GiAAGmqntG<-*
                  G+AAG+ ntG
  gi|1486568   943 GLAAGLMNTG    952

gi|209884453|ref|YP_002288310.1|: domain 1 of 1, from 9 to 916: score 373.3, E = 4.4e-109
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       DAqLR+     +           Ll + L+D + D  G d+ +
  gi|2098844     9    RADAQLRA----EIR-----------LLGRILgDTVRDHEGTDVFDL 40

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v      s  +   +D + L EL a L +   a+++ + +a++    LAn
  gi|2098844    41 VESIRQASIRFHRDEDVSALHELEAMLNGRSIAETVRIVRAFSYFSHLAN 90

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  +AE+        i++ +    +D + At    +  t+ +    +  s e
  gi|2098844    91 IAED-----QNHIRQTR--NHSDAGLATAATTLAGTVDRACDAG-FSKEQ 132

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +      v  vltAHPt   R+s + ++  i   La      +t e+
  gi|2098844   133 LRDFFNDALVSPVLTAHPTEVRRKSTIDREMEIAELLADRDRTQMTSEEL 182

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   E DE L R +   + t  +RR++ t  DE+  G+s++  t  k  P+ +
  gi|2098844   183 AENDEQLRRCVATLWQTNLLRRTKLTVLDEVQNGLSFYDYTFLKQLPRLI 232

                  RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                     +  L      +     +  ++  sW+GGDRDG nP vt +v R
  gi|2098844   233 NLLEDRLTPEDDDD--DELASFLRMGSWIGGDRDG-NPFVTADVLRGTLQ 279

                  LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                  +      n+Yi+ +  L  Els+      L     El+    r   v
  gi|2098844   280 MQCERVMNFYIEELQQLYGELSL---AVPLVKISQELKTLCERSPDVSVH 326

                  iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGise.isEeAvyt
                   +        EPYR  +  +  +L  t   aR L    +  ++ E   y
  gi|2098844   327 RD-------REPYRRAVNGIYARLKAT---ARGLDVDTVGRpVDEVDPYP 366

                  kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                  +vE F + L++  +sL e G +viA G L  l R v  FG  L  LD+Rq
  gi|2098844   367 NVEAFSDDLDIIHRSLVENGSRVIARGRLRRLRRAVDCFGFHLASLDLRQ 416

                  EseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgsDLP
                   s  +   +  + +    G +Y + sEe R   L  ELk  RPL+ + +
  gi|2098844   417 NSAVHERTIAELFEVAASGTdYLSLSEEERCKLLARELKTVRPLISPFVS 466

                  ktEEvkDvldafrvLAELPiDsFG.....aYiismataPsDvLAvELLqR
                    EE    ld +r  AE     FG++  +  i+sma   sD+L + +L +
  gi|2098844   467 YSEETTSELDVLRAAAEAHAQ-FGrkvirQSIVSMAEGISDILEIAVLLK 515

                  ECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid...G
                  E g+ +++++  +  vPLFE + DL+     +++  s+  Y+  +d+++G
  gi|2098844   516 EAGLidpngRSHINLVPLFETIEDLRNCAGIMDRALSLPEYRRLVDsrgG 565

                  KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                   qevm+GYsDs KD G +   W LYkA   ++ v  k  v+L lFHGRGG
  gi|2098844   566 LQEVMLGYSDSNKDGGFVTSGWELYKAEISLVDVFAKQNVRLRLFHGRGG 615

                  tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                   vGRGGGP   A+L+qP    +nG +R t qGE+i   +   ++  + L
  gi|2098844   616 SVGRGGGPSYEAVLAQPGGAVNGQIRLTEQGEIISSKYSNPEVGRQNLEI 665

                  FtAAtLEHGmnPPv..sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEY
                   +AAtLE  +  P +++P+ E+   mee+   A   YR +v+    F +Y
  gi|2098844   666 LAAATLEASLLQPQhsAPREEYLAAMEELSALAFASYRGLVYETEGFEDY 715

                  FRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvW
                  F   t   E   +niGsRP+ R  +  ie LRAiPW+F+W q R  LP W
  gi|2098844   716 FWASTVINEISTLNIGSRPSSRSKAKRIENLRAIPWVFSWAQCRLMLPGW 765

                  LGvGAAF.KhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                   G+G A + +  +   K l  L+E+Y+eWPFFR+ l  ++mv  K    +
```

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  gi|2098844   766 YGFGSAVtEWLGKNPDKGLDFLRELYREWPFFRMLLSNMDMVLSKSSIAV 815

                   AaLyDkLLvaEeLk.PFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                   A+ y +L+    L++   +++R++++   ++LLki     lL   P L
  gi|2098844   816 ASRYADLVPDKTLRdTIFQRIRAEWQSSINWLLKIMDQERLLGHNPLLER 865

                   rlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkade
                    +R R +Y+  Ln +q   LK  R               A  +   ++
  gi|2098844   866 SIRHRFPYLDPLNHVQVEFLKAHR----------------AKNE--DPQV 897

                   LvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   L  +               +t+ Gi AG+ n G
  gi|2098844   898 LRGIQ--------------ITINGISAGLRNSG    916

gi|154146712|emb|CAM83991.1|: domain 1 of 1, from 1 to 438: score 373.0, E = 5.2e-109
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tD +DAittHL+iGsYReW+Ee+RqEWL++EL+G+RPL+g+ LP+
  gi|1541467     1 --HTDAMDAITTHLGIGSYREWPEEQRQEWLVSELRGRRPLFGPHLPQSG 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dv+++frv+AELP DsFGaYiismat PsDvLAvELLqRECgvk++L
  gi|1541467    49 EVADVIGTFRVIAELPDDSFGAYIISMATVPSDVLAVELLQRECGVKRPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADL+  PA++e LFsiDWY+ ri GKqe+m+GYsDsGKDAG
  gi|1541467    99 RVVPLFEKLADLQQGPATMELLFSIDWYKQRIGGKQEIMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEEi+ vA  +GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541467   149 RLSAAWQLYKAQEEIVGVAELHGVKLTIFHGRGGTVGRGGGPSHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP t+nGslRvt+qGEviE sFGEE LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1541467   199 PPNTVNGSLRVTIQGEVIEKSFGEESLCFRTLQRFTAATLEHGMKPPVSP 248
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                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR+L++ mA v tEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KPEWRRLLDVMAAVSTEEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+hA +     l
  gi|1541467   299 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHAAETPG-GL 347

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvt+DLlEmvFAKGDPGiAaLyD+LLv ++L+PFG++
  gi|1541467   348 AALREMYDEWPFFRVTIDLLEMVFAKGDPGIAALYDNLLVPDDLRPFGEQ 397

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y Et+ lLL++AGHkDlLE DPYL+qrl LRdsYit
  gi|1541467   398 LRANYAETQSLLLQVAGHKDLLESDPYLRQRLMLRDSYITA--------- 438

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146682|emb|CAM83976.1|: domain 1 of 1, from 1 to 436: score 372.9, E = 5.7e-109
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541466     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541466     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541466     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541466     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541466     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541466     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541466     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541466     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541466     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tD +DAittHL  GsYReW+Ee+RqEWL++EL+GKRPL+g DLP+ +
  gi|1541466     1 --HTDAMDAITTHL--GSYREWPEEQRQEWLVSELRGKRPLFGTDLPQSD 46

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl++frv+AELP DsFGaYiismataPsDvLAvELLqRECgvk++L
  gi|1541466    47 EVADVLGTFRVIAELPDDSFGAYIISMATAPSDVLAVELLQRECGVKRPL 96

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADL+  PA++e L siDWY+ ri GKqe+m+GYsDsGKDAG
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  gi|1541466    97 RVVPLFEKLADLHQGPASMELLLSIDWYKERIGGKQEIMIGYSDSGKDAG 146

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEEi+ vA ++GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541466   147 RLSAAWQLYKAQEEIVGVAERHGVKLTIFHGRGGTVGRGGGPSHLAILSQ 196

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP t+nGslRvt+qGEviE sFGEEnLCFr+LqRFtAAtLEHGmnPPvsP
  gi|1541466   197 PPNTVNGSLRVTIQGEVIEKSFGEENLCFRTLQRFTAATLEHGMNPPVSP 246

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR+L+++mA v tEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541466   247 KPEWRRLLDDMAAVSTEEYRSIVFREPRFVEYFRSATPETEYGRMNIGSR 296

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+hA +     l
  gi|1541466   297 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHAAQT-ADGL 345

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+EmY+eWPFFRvt+DLlEmvFAKGDPGiAaLyDkLLv ++L+PFGk+
  gi|1541466   346 ATLREMYDEWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVPDDLRPFGKQ 395

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y Et+ lLL++AGH DlLE DPYL+qrl LRdsYit
  gi|1541466   396 LRANYAETESLLLQVAGHSDLLESDPYLRQRLMLRDSYITA--------- 436

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541466     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541466     - -------------    -

gi|111024131|ref|YP_707103.1|: domain 1 of 1, from 1 to 918: score 372.9, E = 5.7e-109
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                             +  P      e L e   LL      i+ +  G+++ + v
  gi|1110241     1    ------MIETPREAT--EPLREDIRLLGGILGQIVREQAGDSVFDLV 39

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         s  +  ++      +L    t +  +D+i v +a++H   LAnL
  gi|1110241    40 EKARVES--FRVRRSEIDRADLADMFTQVSTSDTIPVIRAFSHFALLANL 87

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AE+++   RR ++          ++   +s +  t+ kL        + v
  gi|1110241    88 AEDIHRERRRAVHVAA-------GEPAPDSTLTATFAKLDAAH-LDSAVV 129

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    +AL+   v  v+tAHPt   RR +   ++Ri   +       +t  +
  gi|1110241   130 ADALRGALVSPVITAHPTETRRRTVFETQSRITELMRYRERTALTESETA 179

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ++D  L R i   + t  iR ++   qDE+  G+ Y+   +++ vPK
  gi|1110241   180 DVDVRLRRQILTLWQTALIRLSRLRIQDEIEVGLRYYDAALFEVVPKINA 229

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                       AL+       l  + P+++  sW+GGDRDG nP vt Ev R
  gi|1110241   230 ELRGALRSRWPDADLGRE-PILRPGSWIGGDRDG-NPYVTDEVVRQATTR 277

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   a   A    +  +E L  Elsm          A  +  t+a d +
  gi|1110241   278 AAATALEHHLGELETLERELSM---------SARLVTVTPALD-LLAAAS 317

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaR.....HLLAtGiseisEeA
                            EPYR  +  +R +L  t  R  ++ ++H L  G+      A
  gi|1110241   318 QDDSPFRADEPYRRAIRGIRGRLTATAHRILgeapdHGLDLGL------A 361

                   vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                    y    + L+ L++   sL   GD  iAD  L  l   v  FG  L  LD
  gi|1110241   362 PYDTPRQMLDELDVVDDSLRRGGDGTIADDGLANLRDSVEVFGFHLSGLD 411
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                    iRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgs
                    +Rq s+ +  v+  +    ++ + Y + sE+ R E L aEL+ +RPL  +
  gi|1110241   412 MRQNSDVHETVVAELLAWAGVHpDYPSLSEDERVELLSAELSTRRPLTTA 461

                    DLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAvELL
                         E  +  l  ++  AE  ++L   +   Yiism+t+ sD+L   +L
  gi|1110241   462 NAEFSELTAKELAILQAGAEavrtLGAGAVPNYIISMCTSVSDMLEAAVL 511

                    qRECgvkq.........tLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                     +E g+  +++++ ++ ++ +vPLFE + DL+   A++e    +  Y+
  gi|1110241   512 LKEVGLLDpgsgeapscPVGIVPLFETIEDLQQGAATLEATLEVPIYRAL 561

                    idGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                    +  ++++qevm+GYsDs KD G l+A W LY+A  +++  A+k G++L l
  gi|1110241   562 VTSRgdsQEVMLGYSDSNKDGGYLAANWALYRAELDLVDAARKTGIRLRL 611

                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                    FHGRGGtvGRGGGP   AiL+qPP  + GslR+t qGEvi   + E  L
  gi|1110241   612 FHGRGGTVGRGGGPSYEAILAQPPGAVAGSLRITEQGEVIAAKYAEPRLA 661

                    FrsLqRFtAAtLEHGmnPPvs....PkPEWRkLmeemAvvAtEEYRsvvv
                     r L    AAtLE  +      +++  P +R +++e+A  A   Y  +v
  gi|1110241   662 QRNLETLLAATLEATLLDVEGlgddAEPAYR-ILDELAALARRAYGELVH 710

                    KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                      P FvEYF + tP  E G +niGsRPa Rk    i  LRAiPW+ +W q
  gi|1110241   711 ETPGFVEYFEMSTPVAEIGALNIGSRPASRKQTTSISDLRAIPWVLSWSQ 760

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     R  LP W G GAAF    + D + +  L  +Y++WPFFR  l  l mv
  gi|1110241   761 SRVMLPGWYGTGAAFEEWTQGDPQRVATLSRLYEKWPFFRTVLSNLAMVM 810

                    AKGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlL
                     K D G+Aa y +L+  EeL+++ FGk + ++ + t  +   i G   l
  gi|1110241   811 SKSDMGLAARYAELVPDEELrrRVFGK-IAEEHERTIRMYKAITGNDTLF 859

                    EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                       P L   +  R +Y+  Ln +q   L+R R                A
  gi|1110241   860 ADNPGLERSVHNRFPYLEPLNHLQVELLRRYR----------------AG 893

                    EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    ++s +    ++L                 m G+A  + n G
  gi|1110241   894 DDSDQTRRGIQLT----------------MNGLATALRNSG    918

gi|226366371|ref|YP_002784154.1|: domain 1 of 1, from 1 to 918: score 371.9, E = 1.2e-108
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                              +  P      e L e   LL      i+ +  G+ + + v
  gi|2263663     1    ------MIETPREAT--EPLREDIRLLGGILGQIVREQAGDGVFDLV 39

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          s  +  ++      EL    t +  +Dai v +a++H   LAnL
  gi|2263663    40 EKARVES--FRVRRSEIDRAELADMFTEVSTSDAIPVIRAFSHFALLANL 87

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+    +R R +  +       ++   +s +  t+ kL        + v
  gi|2263663    88 AED---NHRERRRAVH----VAAGEPAPDSTLTATFAKLDAAH-LGSDVV 129

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     +AL+   v  v+tAHPt   RR +   ++Ri   +       +t  +
  gi|2263663   130 ADALRGALVSPVITAHPTETRRRTVFETQTRITELMRYRERTALTESETA 179

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ++D  L R i   + t  iR ++   qDE+  G+ Y+   +++ vPK
  gi|2263663   180 DVDVRLRRQILTLWQTALIRLSRLRIQDEIEVGLRYYDAALFEVVPKINA 229

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                        AL+       l  + P+++  sW+GGDRDG nP vt Ev R
  gi|2263663   230 ELRSALRSRWPDADLGRE-PILRPGSWIGGDRDG-NPYVTDEVVRQATTR 277

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    a   A    + q+E L  Elsm          A  +  t+a d +
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  gi|2263663   278 AAATALEHHLGQLETLERELSM---------SARLVAVTPALD-LLAAAS 317

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaR.....HLLAtGiseisEeA
                              EPYR  +  +R +L  t  R  ++ ++H L  G+      A
  gi|2263663   318 QDDSPFRADEPYRRAVRGIRGRLTATAHRILgeapdHGLDLGL------A 361

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                     y    + L+ L++   sL   GD  iAD  L  l   v  FG  L  LD
  gi|2263663   362 PYDSPRQMLDELDVVDDSLRRGGDGTIADDGLATLRDSVEVFGFHLSGLD 411

                    iRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgs
                    +Rq s+ +  v+  +    ++ ++Y + sE+ R E L aEL+ +RPL  +
  gi|2263663   412 MRQNSDVHETVVAELLAWAGVHAdYPSLSEDERVELLSAELSTRRPLTTA 461

                    DLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAvELL
                         E  +  l  ++  A+  ++L   +   Yiism+t+ sD+L   +L
  gi|2263663   462 NAEFSELTAKELAILQAGADavrtLGAGAVPNYIISMCTSVSDMLEAAVL 511

                    qRECgvkq.........tLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                     +E g+  +++++ ++ ++ +vPLFE + DL+   A++e    +  Y+
  gi|2263663   512 LKEVGILDpgsgeapscPVGIVPLFETIEDLQQGAATLEATLEVPIYRAL 561

                    idGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                    +  +++ qevm+GYsDs KD G l+A W LY+A  +++  A+k G++L l
  gi|2263663   562 VSARgdaQEVMLGYSDSNKDGGYLAANWALYRAELDLVDAARKTGIRLRL 611

                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                    FHGRGGtvGRGGGP   AiL+qPP  + GslR+t qGEvi   + E  L
  gi|2263663   612 FHGRGGTVGRGGGPSYEAILAQPPGAVAGSLRITEQGEVIAAKYAEPRLA 661

                    FrsLqRFtAAtLEHGmnPPvs....PkPEWRkLmeemAvvAtEEYRsvvv
                     r L    AAtLE  +      +++  P +R +++e+A  A   Y  +v
  gi|2263663   662 QRNLETLLAATLEATLLDVEGlgddAEPAYR-ILDELAALARRAYGELVH 710

                    KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                      P FvEYF + tP  E G +niGsRPa Rk    i  LRAiPW+ +W q
  gi|2263663   711 ETPGFVEYFEMSTPVAEIGALNIGSRPASRKQTTSIADLRAIPWVLSWSQ 760

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     R  LP W G GAAF    + D   +  L  +Y++WPFFR  l  l mv
  gi|2263663   761 SRVMLPGWYGTGAAFEEWTQGDPERVATLSRLYETWPFFRTVLSNLAMVM 810

                    AKGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlL
                     K D G+Aa y +L+  EeL+++ FGk + ++ + t  +   + G   l
  gi|2263663   811 SKSDMGLAARYAELVPDEELrrRVFGK-IAEEHERTIRMYKAVTGNDTLF 859

                    EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                       P L   +  R +Y+  Ln +q   L+R R               A
  gi|2263663   860 ADNPGLERSVHNRFPYLEPLNHLQVELLRRYR----------------AG 893

                    EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    ++s +    ++L                 m G+A  + n G
  gi|2263663   894 DDSDQTRRGIQLT----------------MNGLATALRNSG    918

gi|258512100|ref|YP_003185534.1|: domain 1 of 1, from 1 to 906: score 371.6, E = 1.5e-108
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                +++d  L +   +L D   ++L +  G  + + v
  gi|2585121     1    -------------MANDAPLHRDIRVLGDLLGEVLVEQCGRRVFDHV 34

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          +  +     ++    L a + +++P     v +a++    L nL
  gi|2585121    35 ESIRLAAKAFRADPSPETRAALQAAVSAVEPEHRNDVIHAFSVYFQLVNL 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE     +R R ++       D ++        Et++ L  ++  + +++
  gi|2585121    85 AEQ---NHRLRRHRDY-----DRSQQVLRGSFRETMRTLADRG-MTADDI 125

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L+   ++LvltAHPt + RR +L K+++i   L  +     t+ +
  gi|2585121   126 ESLLREVGIELVLTAHPTEALRRTVLDKHTKIAAFLEDMDDPRKTPRELD 175
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                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     L E +  Ei A + t  +R+ + t  DE+R G+ ++   +++  P+
  gi|2585121   176 VLRERIRTEIVALWQTRSVRKQRITVLDEVRNGLYFLDQILFDVLPRVHQ 225

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    + + A+        l    PLi+F sWmGGDRDG nP vt ++t    +L
  gi|2585121   226 KLEQAVEE-QFGRQLLELPPLIRFGSWMGGDRDG-NPNVTSDITWQTLVL 273

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEE..lyrtaardkvvKy
                       +A n Y +++ +L  +ls+    +  R+ A+E+ l +    +
  gi|2585121   274 HCDLALNKYEQKLRELGRDLSV----SVDRAGADEdlLASLGGEN----- 314

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                              EPYR ++  + ++L ntR R      +G  e  +   y
  gi|2585121   315 ----------DEPYRALINRMLERLANTRRR-----LHG--ERVDGPDYA 347

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                      E  +E +E   +sL     + + D  L  +L q   FG  +v LDiRq
  gi|2585121   348 SPEAMMEDVERMARSLAHHRGQRMVDAWLRPFLLQLRIFGFHMVTLDIRQ 397

                    EseRqtDvlDAittHLe.iGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                     s  +   +  + +  + +  Y +  Ee R   L   L   RP+  +
  gi|2585121   398 HSGVHEQAVAELLQTAGlVDDYTSLGEEERVRVLSECLASPRPIRNPYHV 447

                    ...ktEEvkDvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLqRE
                     ++ t E   vld +r   E+    +   Y+ism+   sD L v LL +E
  gi|2585121   448 ysdVTTEALAVLDCVRRGHEtFGPRCVQDYLISMTQGASDLLEVLLLAKE 497

                    Cgv...........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                     g+ + ++++  ++k  L vvPLFE + DLe A   +  LF    Y+ ++
  gi|2585121   498 SGLfgwpdgpmappKSDLNVVPLFETIEDLESAAGIMRSLFENPVYRRHL 547

                    dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                    + ++ +qe+m+GYsDs KD G l A W LY Aq  +i+ A  yGv++  F
  gi|2585121   548 EMRgwqQEIMLGYSDSNKDGGYLTANWSLYMAQKHLIRLAEAYGVRIKFF 597

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGG  GRGGGP    iL+qP + + G +++t qGEvi + +G   +
  gi|2585121   598 HGRGGALGRGGGPVEQSILAQPTEALRGHVKITEQGEVISQRYGHPGIAE 647

                    rsLqRFtAAtL....EHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvK
                    rsL   +AA L + +    +     +P W +L+++   +    YR +v+
  gi|2585121   648 RSLESSAAAVLvgatREDSEEWAERHPRWFRLLDRASEISFRAYRKLVFE 697

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                     P F EYF  AtP  E GkmniGsRP++R  s  ie LRAiPW+F+Wtq
  gi|2585121   698 HPAFLEYFHRATPIDEIGKMNIGSRPSRRSQSARIEDLRAIPWVFSWTQS 747

                    RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                    R  LP W G+G A    +  D + l  L+ mY+ WPFFR  +D l m  A
  gi|2585121   748 RHLLPAWYGFGSAIEAIMREDPRALEDLRRMYEVWPFFRTLVDNLQMALA 797

                    KGDPGiAaLyDkLL..vaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE
                    K D  +A  y +L ++  E + P    + ++Y  t+  +L i G + lL+
  gi|2585121   798 KADMLVAKEYAQLAgeAGEAVFPL---IEEEYARTERAVLDITGYRQLLD 844

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                      P ++  + LR++Y+  L  fq   L  +R  +        ls E  +
  gi|2585121   845 NRPVIRESISLRNPYVDPLSFFQVRLLADLRTDN--------LSPEEREA 886

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +   ad L  +n                  GiAAG+ ntG
  gi|2585121   887 E--LADALQTIN-----------------GIAAGLRNTG    906

gi|251827845|ref|ZP_04830919.1|: domain 1 of 1, from 4 to 922: score 371.3, E = 1.8e-108
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                +P  +s  +   + D  Ll + L+D L +  Ge
  gi|2518278     4    -------FSAPADISSKDLPFREDVRLLGRILgDTLREQEGEATFQL 43

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      +  +   +D +  e L   L +L P++++ v +a++    L n
```

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gi|2518278    44 VENVRRSAVRFRKTQDERDGEQLEQMLDALSPSETLAVVRAFSYFSQLTN 93

                 LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                 +AE+ +   R R ++k        +s      +   l ++  k   sPe
gi|2518278    94 IAEDLHHNRRHRAHLKA-------GSSPKNGSLMLALDRIEEKQ-VSPEA 135

                 vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                 +   L    +  vltAHPt   R+s+L  +  i   L+     ++t+++
gi|2518278   136 MQAFLDSALISPVLTAHPTEVQRKSILDCHLIISSLLSNRDRIEMTPDEL 185

                 kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  E + AL R +   + t  +R a+ t  DE+R G+ ++  t    +PK
gi|2518278   186 AENENALRRFVLILWQTRMLRTAKLTVRDEIRNGLEFYRYTFLTEIPKLY 235

                 RRvDtALKn.iGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    +  L  +     ++P    L+k  sW+GGDRDG nP vt +v
gi|2518278   236 ANLEKQLEArFDKDIKIP---ALLKVGSWIGGDRDG-NPFVTHDVMQYAV 281

                 LLaRmmAanlYisqvEDLmFEls....mWRCndELRvRAEElyrtaardk
                      +A   Y++    L   ls ++++    dELR+  +     a +
gi|2518278   282 QQHSELAFEHYLNETHILGTRLSltdrLVDVSDELRAMSDASPDNAVSR- 330

                 vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                               EPYR  L  +  +L  t  +  H + +
gi|2518278   331 -------------TDEPYRRALIMIYSRLSATAGKLGHEISHLPPVDKAA 367

                 AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                 A y    +F+  L++   sL   G   +A G L  l R    FG  L  L
gi|2518278   368 APYATPAQFIADLDVLIESLNRHGAIYLARGRLANLRRSAEIFGFHLAPL 417

                 DiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlg
                 D+Rq s  +   +  +  H ++ ++Y e  E  R+E Ll+ L+  +PL+g
gi|2518278   418 DMRQHSAIHEQTVSELLAHSGVMAnYSELDEAARREILLTTLQAAKPLMG 467

                 .....sDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvE
                 + ++ sD+ +  E++ +  a  +       +    iis a a sD+L
gi|2518278   468 kidqySDIAQS-ELRIMQAAADIHQRFGRAALPNHIISKADAVSDMLELA 516

                 LLqRECgv...kqtLr..vvPLFEkLADLeAAPAavekLFsiDWYinrid
                 L+     + +++ +L  +++PLFE + DL+     ++ LF+i +Y+  +
gi|2518278   517 LMLQQVNLlegRDALHinIIPLFETIEDLRSCGPIMDELFAIPYYRQLLA 566

                 GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                  ++++qevm+GYsDs KD G + A W LYkA  E++Kv  kyGv L lFH
gi|2518278   567 CRgntQEVMLGYSDSNKDGGYITANWELYKAELELVKVFAKYGVELRLFH 616

                 GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                 GRGGtvGRGGGP   AiL+qPP  +nG +R+t qGEvi   +   ++  r
gi|2518278   617 GRGGTVGRGGGPSYEAILAQPPGSVNGQIRITEQGEVISSKYSNPEIGQR 666

                 sLqRFtAAtLEHGm...nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEP
                  L    AAt+E  + +++   s  PE+ ++me +   A   YR +v+  P
gi|2518278   667 NLETLVAATMEATLlhhHGADSAMPEFHRIMEALSLDAFAAYRKLVYETP 716

                 RFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRF
                  F EYF  AtP  E   +niGsRP+ R+ s  ie LRAiPW+F+W   R
gi|2518278   717 GFTEYFFTATPIREIAELNIGSRPSARRASDRIEDLRAIPWVFSWGLNRT 766

                 HLPvWLGvGAAFKhAidKDiKn.lqkLkEmYkeWPFFRvtlDLlEmvFAK
                  LP WLG+G A K  i ++   +l +L+ mY+eWPFFR  +  ++mv  K
gi|2518278   767 LLPGWLGFGSAVKQFIAREGDDgLAQLQTMYREWPFFRGLMSNMDMVLSK 816

                 GDPGiAaLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLkiAGHkDlLEG
                  D GiA+ y  L+   e++ + FG  +  ++++t +lL  +     lL
gi|2518278   817 TDMGIASRYAALVEDVEMREriFG-AIHSEWQDTVELLFSVTRNDALLQE 865

                 DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                  P     l  R +Yi  Ln +q   L   R                + n
gi|2518278   866 NPSFARSLLSRTPYIDPLNHLQVALLEHHR-----------------AGN 898

                 skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
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                      deLvk              + Lt+ GiA G+ n G
  gi|2518278   899 ---TDELVKRA------------IHLTINGIATGLRNSG    922

gi|71907389|ref|YP_284976.1|: domain 1 of 1, from 1 to 918: score 370.4, E = 3.3e-108
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                          +    P K    ++ ++ D  Ll + L+D + +  Ge++ ++
  gi|7190738     1    -----MHDASPSK----DEPLRTDIRLLGRILgDTVREQEGESVFDI 38

                     vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDai.lvAkailHmLnLA
                     v      +  +    D+   +EL a L  L P+D+ + v +a++  L LA
  gi|7190738    39 VERVRQTAVRFARDGDPAARDELAALLDPL-PGDTTqAVVRAFSYFLQLA 87

                     nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                     n+AE+ +   RRR + +        +s   E  +   l  L      sPe
  gi|7190738    88 NIAEDEHHIRRRRAHDLA-------GSPPREGSLIFALDALSTAA-VSPE 129

                     EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                      + +      v  vltAHPt   R sL+  +  +   L q     +t+e+
  gi|7190738   130 AIADFFAHAVVAPVLTAHPTEVQRQSLIRNHRDLAHLLDQRERLQMTPEE 179

                     KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                       E D AL   i   +    +R  +    DE++ G+ Y+ Et +   P+
  gi|7190738   180 EAENDLALANAILTLWQSRMLRPVRLKVLDEVKNGITYFKETFFTELPRL 229

                     LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                            L+     E+     P  +  sW+GGDRDG nP vt ++ R+
  gi|7190738   230 YIQATEQLQK-RYPEKTWALPPFFRVGSWIGGDRDG-NPFVTADILREAL 277

                     LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                      L    A n Y++ v +L  El +    ++L v+      t+    +  +
  gi|7190738   278 RLQSSAALNHYLNEVHELGGELPL----SDLLVKV-----TPELLALAEH 318

                     YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                       +   q    EPYR  L  +  +L  t  Ra         ei     y
  gi|7190738   319 STDHSPQ-RADEPYRRALSGIYARLAAT-ARALDQFEPVRHEIGHATPYD 366

                     kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                       +     L L   sL   G   +A G L  lLR v  FG  L  +D+Rq
  gi|7190738   367 TPDALRADLKLLANSLKLNGSAKLAGGRLRRLLRGVQIFGFHLAPIDLRQ 416

                     EseRqt.DvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                      s+ + + v + +        Y   sE  R   L+ E++  RPL+ + L
  gi|7190738   417 NSDVHArSVAELLAGAGRCPDYEALSEAERIKLLVDEISTPRPLYSPYLN 466

                     ktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvELLqRE
                       EE +  l  f    EL ++ ++ +    iis +   sD L   LL +E
  gi|7190738   467 YSEETQGELAIFFAARELRqkygSAALPNCIISKTDGVSDLLELALLLKE 516

                     Cgvkqt.......LrvvPLFEkLADLeAAPAavekLFsiDWYinridGK.
                      g+  ++ +++ ++ ++PLFE + DL+   A+++ +F+i  Y+  i G++
  gi|7190738   517 SGLLLPgakpqlkVNIIPLFETIEDLQKSAATMAGVFAIPAYRELIAGRg 566

                     ..qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRG
                     ++ evm+GYsDs KD G l   W LYkA  E++++  ++Gv+L lFHGRG
  gi|7190738   567 deHEVMLGYSDSNKDGGFLTSGWELYKAEIELARIFGQHGVRLRLFHGRG 616

                     GtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLq
                     G vGRGGGPt  AiL+qP   + G +R t qGEvi   +G  +   r L
  gi|7190738   617 GSVGRGGGPTYHAILAQPAGAVAGQIRLTEQGEVISTKYGNADTGRRNLE 666

                     RFtAAtLEHGm...nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFv
                        AAtLE  +++++  v P   +  +m+e+   A   YR +v+  P F
  gi|7190738   667 VLLAATLEASLtdhENRVEPAEQFHAVMDELSARAFNAYRGLVYETPGFT 716

                     EYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLP
                      YFR  t   E   +niGsRPa Rk s  ie LRAiPW+F+W q R  LP
  gi|7190738   717 TYFRQSTVVSEIASLNIGSRPASRKASERIEDLRAIPWVFSWAQCRLMLP 766

                     vWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPG
                      W G+GAA    ++     l  L+ m + WPFF+  l  ++mv AK D
  gi|7190738   767 GWYGFGAAVEGYLQANPAGLATLRRMVHAWPFFKSLLSNMDMVLAKTDLA 816
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                    iAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLK
                    iA+ y +L+   eL+ +   ++++++  t++ LL i    + L   P L
  gi|7190738   817 IASRYAELVADVELREhIFSRIKAEWALTRQHLLAILEQDEFLADNPLLA 866

                    qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                      l LR +Y+  Ln +q   LKR R                A +
  gi|7190738   867 RSLQLRSPYMDPLNHLQVELLKRHR----------------AGDT----- 895

                    eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                            er a G+     Lt+ GiA G+ n G
  gi|7190738   896 -------DERLARGIH----LTINGIASGLRNSG    918

gi|90423192|ref|YP_531562.1|: domain 1 of 1, from 7 to 929: score 370.3, E = 3.4e-108
                    *->siD..AqLRlLv..PGKvsedekLieYDALLlDkFL.DiLqDLHGed
                        iD+ Aq   ++++P  + ed +L + D  Ll + L+D + D  Ge
  gi|9042319     7    PIDpiAQKTPVAedPAAIDEDARLRD-DIRLLGRILgDTVRDQEGEG 52

                    LkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmL
                    + ++v      s  +    D     EL a L +L   D++ + +a++
  gi|9042319    53 VFDVVERIRQTSIRFHRDNDKPARSELEAILDGLSTPDTVRIVRAFSYFS 102

                    nLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnK
                     LAn+AE+        i++ +    a  +     s +  tl +    +
  gi|9042319   103 HLANIAED-----QNNIRQMR----ALSGTPRPGS-VVGTLAHARAVG-I 141

                    sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt
                    s +E         v  vltAHPt   R+s + ++  +   L       +t
  gi|9042319   142 SAQELRRFFAHALVSPVLTAHPTEVRRKSTMDREMEVAGLLDRRERLQMT 191

                    veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGv
                     e+    +E L R +   + t  +RR++ t  DE++ G+s++     + v
  gi|9042319   192 AEEVAQHEEQLRRAVLTLWQTNMLRRTKLTVLDEVKNGLSFYDHSFLREV 241

                    PKFLRRvDtALK.niGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                    P+     +  L +  G  E l   +  ++  sW+GGDRDG nP vt Ev
  gi|9042319   242 PRLHGLLEDRLNdDDGRDEEL---ASFLRMGSWIGGDRDG-NPFVTAEVM 287

                    RDvCLLaRmmAanlYisqvEDLmFElsmWR....CndELRvRAEElyrta
                    R    L    A  +Y++ +  L  Els+  +  +  d+LR  AE    t+
  gi|9042319   288 RGALRLQSTRALRFYLDELHALGSELSIAAhladVSDDLRLLAERSPDTS 337

                    ardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGise
                                      EPYR  +  +  +L  t  + +
  gi|9042319   338 PHR--------------SGEPYRLAVSGIYARLAATAHKLKFDDIRAPVG 373

                    isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                     +E   y +  eF   L++  +sL      viA G L  l R v  FG
  gi|9042319   374 AAEP--YADPQEFKADLDVLHRSLIANQASVIARGRLRQLRRAVDCFGFH 421

                    LvKLDiRqEseRqtDvl.DAittHLeiGsYReWsEeKRqEWLlaELkGKR
                    L  LD+Rq s  +   +++ i   +   sY    Ee R   L  EL+  R
  gi|9042319   422 LASLDMRQNSAVHERTMtELIDAAMPGKSYMAMNEEARIALLAGELRSTR 471

                    PLlgsDLPktEEvkDvldafrvLAELPiDsFG.....aYiismataPsDv
                    PL  + +   EE    l  fr  AE    +FG++  +  iism+   sD+
  gi|9042319   472 PLASPFVKYGEETLGELAVFRTAAE-AHAAFGhtvisQCIISMCKGVSDM 520

                    LAvELLqRECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYi
                    L v LL +E g+ ++ ++ ++ vvPLFE + DL+A    +++L s+  Y+
  gi|9042319   521 LEVVLLLKEVGLvdhagRSAINVVPLFETIEDLQASAGIMDRLLSLHDYR 570

                    nrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                      +d+++G qevm+GYsDs KD G +   W LYkA  E++Kv  ++Gv+L
  gi|9042319   571 RLVDsrgGVQEVMLGYSDSNKDGGFVTSGWELYKAEIELVKVFEHHGVRL 620

                    vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                     lFHGRGG vGRGGGP   AiL+qP   +nG +R+t qGE+i   +   +
  gi|9042319   621 RLFHGRGGSVGRGGGPSYDAILAQPGGAVNGQIRITEQGEIITSKYSNAE 670

                    LCFrsLqRFtAAtLEHGmnPP..vsPkPEWRkLmeemAvvAtEEYRsvvv
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                    +    L   +AAtLE  +  P++ +P+ E+ + me++   A   YR +v+
  gi|9042319   671 VGRNNLEILAAATLEASLLMPrqSAPRAEYLDAMEQLSSFAFKAYRGLVY 720

                    KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                        F +YF   t  +E   +niGsRPa Rk    ie LRAiPW+F+W q
  gi|9042319   721 ETEGFEDYFWASTVITEIATLNIGSRPASRKKTHKIEDLRAIPWVFSWAQ 770

                    tRFHLPvWLGvGAAFKhAidKD.iKnlqkLkEmYkeWPFFRvtlDLlEmv
                     R  LP W G+G A    ++  + K +  L+E+Y+eWPFFR  l  ++mv
  gi|9042319   771 CRLMLPGWYGFGSAVEAFVKEHpDKGMAFLQELYREWPFFRTLLSNMDMV 820

                    FAKGDPGiAaLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLkiAGHkDl
                     AK    iA+ y +L+  E+L+   FG+ +R+++    + LL i     l
  gi|9042319   821 LAKSSIAIASRYAELVPDEQLRQaiFGR-IRAEWHGSIQALLDIMQQDRL 869

                    LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                    L   P L   +R R +Y+  Ln +q   LK  R
  gi|9042319   870 LQSNPRLERSIRNRFPYLDPLNHVQVELLKEHR----------------- 902

                    dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       s+  de v               + Lt+ Gi AG+ n G
  gi|9042319   903 ---SHAIDEKVLRG-----------IQLTINGISAGLRNSG    929

gi|158337676|ref|YP_001518852.1|: domain 1 of 1, from 4 to 1012: score 370.3, E = 3.6e-108
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                        +      Lv       e L+     +++  L+++L D  G++L +
  gi|1583376     4    TLNRNHPQLVQPNRL--ESLLLHRIKVIEDLLEgVLRDECGQELVDL 48

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                          +    EG+  t    E+  ++  L+  +ai  A+a+     L n
  gi|1583376    49 LRQLRSMCSP-EGQAPTVPETEVLKVVEKLELDEAIRAARAFALYFQLIN 97

                    LAE.....EvelAyRRR......ikkkkhGDFaD..EasAttEsDiEE..
                    + E++ ++E  +   R   +++++ +   G  a++ E  A    ++ E++
  gi|1583376    98 IVEqhyeqEESIVRTRGaitsspVALPNVGGSAEraENHANGQTELPEhs 147

                    ............tlKkL...vlklnKsPeEvFeALKnqsvDLvltAHPtq
                      +   ++++ +t+  L ++  +ln  P  + + ++n  + Lv+tAHPt
  gi|1583376   148 ifdailrepnagTFTWLfpkLKQLNVPPRHIQNIIQNLDIQLVFTAHPTE 197

                    svRRsLLqKnaRiRnCLaqLsAKDvtve.......DKkELDEALHREiqA
                     vR  +  K+ Ri   L +L   +    ++++++ +   L   L  E+
  gi|1583376   198 IVRQTIRAKQRRIAKILGKLDEAEAGLAnntrsnwEVDALQAQLTEEVRF 247

                    AFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLRRvDtALKniGin
                     +RtDE+   +Pt  DE+ + + Y+ E +++ +P+   R    LK
  gi|1583376   248 WWRTDELHQFRPTVLDEVEYSLHYFREVLFDAIPQLYHRLSLNLKQ-AFP 296

                    ERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLLaRmmAanlYisq
                       P      kF sW+G DRDG nP vtP++t       R +    Yi+
  gi|1583376   297 KLQPPRYNFCKFGSWVGSDRDG-NPAVTPDITWQTSCYQRNLVLEKYIQS 345

                    vEDLmFElsmWRCndELRvRAE......Elyrtaardkvv KyYiEFWKqv
                    v  L+  l +    +E+    E++ +++ l+     d   +  i F
  gi|1583376   346 VNKLINLLTLSQYWSEVPPGLEkslgqdQLQMPEVYD---RLSIRFL--- 389

                    PPtEPYRviLGdvRDKLYntRER.aRHLLAtGise......isEeAvytk
                       EP+R  L  +  +L ntR+R+        +s + +++++ E+  y
  gi|1583376   390 --GEPFRFKLSYILKRLENTRDRnQQQAQLIDFSHpihpqgMNEQIYYPA 437

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      +FL  L +    L   G   i    L  l+ qv  FG  L +LDiRqE
  gi|1583376   438 AQNFLAELRVVQENLQATG---INCQELDTLIGQVEIFGFNLTQLDIRQE 484

                    seRqtDvlDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    s  + D l  i   L+i +  Y e sE  R EWL  EL+ +RPL++ DLP
  gi|1583376   485 SSCHSDALTEIVNYLQIlpKPYNELSESERLEWLTQELQTRRPLIPHDLP 534

                    ktEEvkDvldafrvL....AELPiDsFGaYiismataPsDvLAvELLqRE
                      +  ++ +++fr++++ + E  ++    Yiism+   sD L v LL +E
  gi|1583376   535 FSDKTQELINTFRMIrrlqEEFGVEICRTYIISMSHDASDLLEVLLLAKE 584
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                    Cgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinr.idGK.
                     g+  +++ ++tL v+PLFE + DL+ AP  + +LF + +Y+n  +d +
  gi|1583376   585 SGLFDpttasgTLHVIPLFETVDDLQRAPGVMTQLFDLTFYRNYlVDAQa 634

                    .............qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyG
                    +++++++++ + qe+m+GYsDs KD G ls  W +YkAq  +   A  yG
  gi|1583376   635 sqepssnpplslQEIMLGYSDSNKDSGFLSSNWEIYKAQQRLQETAEPYG 684

                    vKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFG
                    v L +FHGRGG vGRGGGP   AiL+qP   +nG +++t qGEv+   +
  gi|1583376   685 VSLRIFHGRGGSVGRGGGPAYEAILAQPGYSVNGRIKITEQGEVVASKYS 734

                    EEnLCFrsLqRFtAAtLEHGmnPPvsPkPE.WRkLmeemAvvAtEEYRsv
                      +L    L     A +   +        E+W ++me++       YR++
  gi|1583376   735 LPELALYNLETISTAVIQSSLLRSTMDSIEpWHEIMEDLSARSRKRYRAL 784

                    vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG..GiesLRAiPWiF
                    +      v++F   tP  E  ++   +RPa+R+   ++ +e LRAiPW+F
  gi|1583376   785 IHEQEDLVDFFYEVTPINEISQLQHAARPARRRADNrrTLEGLRAIPWVF 834

                    aWtqtRFHLPvWLGvGAAFKhAid.KDiKnlqkLkEmYkeWPFFRvtlDL
                    +Wtq RF LP W GvG A +  +d+K    l  L+  Y +WPFF++ +
  gi|1583376   835 SWTQSRFLLPAWYGVGTALQDFLDeKSAEHLTLLQYFYGKWPFFKMVISK 884

                    lEmvFAKGDPGiAaLy.DkLLvaEeLkPFG...ksLRdkYvEtkdlLLki
                    +Em  AK D  iA  y  +L  +E++  F +  +++ ++Y  t++++ ki
  gi|1583376   885 VEMTLAKVDLQIAHHYlQELTSSEDVDRFErlfEQIAQEYYLTREMVSKI 934

                    AGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPh
                     G + lL+GDP LK  + LR+  i  L  +q   LKR+R  +++   r
  gi|1583376   935 TGNQQLLDGDPNLKRSVHLRNGTIVPLGFLQVSLLKRLR--QHQRQDRVA 982

                    lsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-
                    l      E      +L++              +Lt+ GiAAGm ntG
  gi|1583376   983 LGAGNVSEK-----DLLRGA------------LLTINGIAAGMRNTG   1012

                    *

  gi|1583376     -   -

gi|37519983|ref|NP_923360.1|: domain 1 of 1, from 2 to 939: score 370.1, E = 3.9e-108
                    *->siDAqLRlLvPGKvsedekLieYDAL.LlDkFL.DiLqDLHGedLkE
                         D  + l + G  s   +    D ++L+++ L+ +     G dL E
  gi|3751998     2    NWDTPIDLAAAGSPSALSHQSLRDNIeLVEQLLrQVAAQEGGGDLVE 48

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                         +    +        + +E  a +  L    ++l  +a++    L
  gi|3751998    49 LLDRLWASHQD--------RTGEGLALIRELSLEKSVLAIRAFSIYFQLI 90

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+ E  +   R+R +++     aD a+      + + +K L +
  gi|3751998    91 NIVE--QHHERKRLRLQA-SFSADTAQPGSFCWLFDEMKSLGVST----P 133

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    E+   L+   v Lv+tAHPt  vRR +  K+ Ri   L  L    +
  gi|3751998   134 EIERVLQQLDVRLVFTAHPTEIVRRTIRTKHRRIVHLLDDLD-NALSEWQ 182

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    ++ +   +  Ei   +RtDE+   +Pt  DE+   + Y+ E +++ +P+
  gi|3751998   183 QQQVHTTMLEEIRIWWRTDELHQVRPTVLDEVAHTVHYFEEVLFEAMPRV 232

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                           L                +F sW+G DRDG nP v   vt
  gi|3751998   233 RSELVRCLDMFHPSLTRSLGT-FCRFGSWVGSDRDG-NPSVNALVTWKTA 280

                    LLaRmmAanlYisqvEDLmFElsmWRCn..dELRvRAEElyrtaardkvv
                       R      Yi  vE L   ls+   n++++L    E  +r
  gi|3751998   281 CHQRSRVLAKYIKSVERLRDLLSLAEGNppQDLLLALEQDQRDLGEV--- 327

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtG...iseisE
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                      E +  v  +EPYR  L  + ++L  tRER   L  +G++++s+  E
  gi|3751998   328 ---YERYSVVYLQEPYRLKLSYILERLEHTRERNAWLEVHGpqrLSQPDE 374

                   eA...vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                       + y +  e L  L L  + L   G   i    L  l+ qv  FG
  gi|3751998   375 PGwlhYYRHAHELLAELHLLRQCLRTTG---IGCRPLETLIDQVEVFGFH 421

                   LvKLDiRqEseRqtDvlDAittHLeiGs..YReWsEeKRqEWLlaELkGK
                   L  LD+Rq+s R+ D l  +   L + +++Y e  E+ R EWL+ EL+
  gi|3751998   422 LAGLDVRQDSTRHEDTLTEVSAKLRLTAtpYAELDEQARLEWLVRELQTL 471

                   RPLlgsDLPktEEvkDvldafrvLA....ELPiDsFGaYiismataPsDv
                   RPL++++LP     ++ +++fr++ + ++E  ++    Yiism+   sD
  gi|3751998   472 RPLIPAELPFSARTEETIQTFRMIRrlqkEFGSEICHTYIISMSKQASDL 521

                   LAvELLqRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWY
                   L v LL  E g+  + ++++tL vvPLFE + DL+ AP  +e+LFs+  Y
  gi|3751998   522 LEVLLLAEEAGLFDpatgtgTLMVVPLFETVEDLRNAPHVLEQLFSLPLY 571

                   inridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvK
                   +  +   ++ qevm+GYsDs KD G ls  W ++ Aq  i +vA+++Gv+
  gi|3751998   572 RCYLTCHqnlQEVMLGYSDSNKDSGFLSSSWEIFLAQQHIQQVARRHGVQ 621

                   LvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEE
                   L +FHGRGGtvGRGGGP   AiL+qP  t+ G +++t qGEv+   +
  gi|3751998   622 LRIFHGRGGTVGRGGGPSYQAILAQPDGTVSGRIKITEQGEVLASKYSLF 671

                   nLCFrsLqRFtAAtLEHGmnPPvsP.kPEWRkLmeemAvvAtEEYRsvvv
                   +L    +   tAA +   + P   P+   W   ++e+  vA   YR +v+
  gi|3751998   672 ELAAFNIETVTAAVIQASVLPTSPPgSRNWELRLQELSDVARRTYRQLVY 721

                   KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                       F+++F   tP  E  ++ i sRP++R     + sLRAiPW+F+Wtq
  gi|3751998   722 EQEGFIDFFCHVTPIDEISQLQISSRPSRREGRRDLASLRAIPWVFSWTQ 771

                   tRFHLPvWLGvGAAFKhAidKD.iKnlqkLkEmYkeWPFFRvtlDLlEmv
                    RF L  W G+G A    i   + +nl  L+ mY++WPFFR  +  +Em
  gi|3751998   772 SRFLLQAWYGLGTALDGFIRCNrERNLAELRSMYRQWPFFRTLISKVEMT 821

                   FAKGDPGiAaLyDkLLvaEeLkPFGks....LRdkYvEtkdlLLkiAGHk
                    AK D  +Aa y + L   e    G+     + ++ + t++ +L i  H+
  gi|3751998   822 LAKVDLQVAANYVQELLPKEHEHTGECifalIAAELERTRECVLAITEHR 871

                   DlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKE
                    lLE  P L+  + LR++ i  L  +qA  LK +R  +     +P
  gi|3751998   872 QLLEDNPPLQRSIALRNATIAPLGYLQATLLKYLRYEN----RQPR---- 913

                   yAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        s   +eL++               +Lt+ GiAAGm ntG
  gi|3751998   914 -----SYSRNELLRGA-------------LLTINGIAAGMRNTG    939

gi|148243189|ref|YP_001228346.1|: domain 1 of 1, from 6 to 992: score 369.1, E = 8.1e-108
                   *->siDAqLRlLvPGKvsedekLieYDAL.LlDkFLDiLqDLHGedLkEa
                      s     R+  P    e  + +    L+ l   L+++ +L G+ L+
  gi|1482431     6    STASTSRM--PASQTETVQPVGRRTLrQLNERLELVEELWGNVLRSE 50

                   v...qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLn
                    +++q    l      ++D    + +   + ++d ++ai  A+a++
  gi|1482431    51 CppeQAARVLQLKQLCREDETS-DQIIDLIVAMDLSEAIAAARAFSLYFQ 99

                   LAnLAEEvelAyRRRikkkkhGDFaDEasAtt......EsDiEEtlKkLv
                   L n+ E  ++   R          a+ a   t +++    D   t+++L
  gi|1482431   100 LVNILEQ-HIEEDRYLATMSQDNIAEAAISDTlnghlaNHDQPATFQRLF 148

                   lkl...nKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLa
                    +l+  n  P      L+   v Lv+tAHPt  vR  +  K+ R+   +
  gi|1482431   149 QRLralNVPPGLLEPLLRELDVRLVFTAHPTEIVRHTVRHKHRRVAHLIQ 198

                   qLsA...KDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGm
                    L   ++     +D++ L   L  Ei   +RtDE+   +P   DE+ + +
  gi|1482431   199 RLEGlndENDSFDDRQGLRQQLLEEIRVWWRTDELHQFKPSVLDEVDYAL 248
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                    sYiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDG
                     ++   +++ +P    R+  ALK     +  P +     F sW+G DRDG
  gi|1482431   249 HFFQQVLFQAMPLLHERIRKALKD-SYPDVTPPEDGFCTFGSWVGSDRDG 297

                    knPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE
                     nP vtPE+t       R +    Y+s v  L   ls+    + +
  gi|1482431   298 -NPSVTPEITWRTACYQRQLMLERYLSSVRNLRNQLSISMQWSQVSPALL 346

                    Elyrtaardkvv KyYiEFWKqvPPt...EPYRviLGdvRDKLYntRERaR
                    E     +       + E + ++    + EPYR  L  v  +L  t ER
  gi|1482431   347 ESLEMDRLR-----FPEIYEKLAARyrlEPYRLKLCYVLQRLELTHERNA 391

                    HLLAtGi.seis.............EeAvytkvEeFLEPLELCYksL
                     L   G +s +s +++++++ +++ +++ e  y    +F   LEL   sL
  gi|1482431   392 QLSELGWeSPLSatepeeqtlsssltpqQELHYSTYQDFRSDLELVRTSL 441

                    CeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHL
                       G   +    L  lL qv  FG  L  LDiRqEs R+ + l  +t+ L
  gi|1482431   442 EATG---LSCEPLNRLLSQVQIFGFCLASLDIRQESTRHSEALAELTRYL 488

                    ei.GsYReWsEeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLA
                    +++  Y    E +R EWLl  L+ +RPL++      +  ++    f++L
  gi|1482431   489 QLpQDYEAMEEPQRVEWLLEQLQTRRPLIPTGPLWSDATAETFAVFQMLR 538

                    ELPiDsFG.....aYiismataPsDvLAvELLqRECgvkqt......Lrv
                     L  + FG++  + Y+ism+ + sD L v LL +E g+  + +++++L+v
  gi|1482431   539 RL-QEEFGqricrTYVISMSHTESDLLEVLLLAKEAGLVDPvegttrLQV 587

                    vPLFEkLADLeAAP....AavekLFsiDWYinridGKqevmvGYsDsGKD
                    +PLFE + DL+ AP+  +A +++ F       n     qevm+GYsDs KD
  gi|1482431   588 IPLFETVEDLRCAPevmgAVMARPFYKRLLANEEVPLQEVMLGYSDSNKD 637

                    AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                     G ls  W + +Aq  +     ++ + L +FHGRGG v RGGGP   AiL
  gi|1482431   638 SGFLSSNWEIHRAQIALQSLCSEHNISLRIFHGRGGSVSRGGGPAYQAIL 687

                    sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHG.mnPP
                    +qP  t++G +++t qGEv+   +   +L    L   t A L    +
  gi|1482431   688 AQPSGTLKGRIKITEQGEVLASKYALPELALYNLETVTTAVLQNSlLSSG 737

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni
                    v   P W +Lme++A      YR++v   P  v +F   tP  E  k+ i
  gi|1482431   738 VDDTPSWNELMERLASRSRQHYRALVHEHPDLVAFFEQVTPIEEISKLQI 787

                    GsRPaKRkPsG.GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD
                     sRPa+R+ + + + sLRAiPW+F Wtq RF LP W GvGAA +  +  D
  gi|1482431   788 SSRPARRRTGArDLSSLRAIPWVFGWTQSRFLLPSWFGVGAAIREELGDD 837

                    iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLy.DkLLvaEeLk
                       l  L+ +Y+ WPFFR+ +  +Em  AK D  +A  y D L  a+
  gi|1482431   838 GEQLDTLRTLYQRWPFFRMLISKVEMTLAKVDLSLAKYYvDSLGSADRAD 887

                    PFGk...sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittL
                     F +    + ++Y  tk+l+Lki GH  lL+GDP L+  + LR+  i  L
  gi|1482431   888 AFQEifaTIAAEYSLTKELVLKITGHERLLDGDPPLQLSVELRNRTIVPL 937

                    nvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaP
                      +q   L+R+R  +     +P++     +E          L  t  ++
  gi|1482431   938 GFLQVALLRRLRNQN----RQPPM-----NES--------DLSDTRTYSR 970

                    G.LEDtLiLtmKGiAAGmqntG<-*
                    G+L    +Lt+ GiAAG+ ntG
  gi|1482431   971 GeLLRGALLTINGIAAGLRNTG    992

gi|154244275|ref|YP_001415233.1|: domain 1 of 1, from 1 to 926: score 368.7, E = 1.1e-107
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                          A   + +PG     ++ ++ D  Ll + L+D + +  Ge++ +
  gi|1542442     1    MTSAVWSIEAPGDEEVKDRPLREDIRLLGRILgDTVREQEGEEVFDL 47

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
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                v      s  +    D    eELGa L  L    a+ + +a++    LAn
gi|1542442    48 VERIRQTSIRFHRDDDETAREELGALLEQLSSQRAVDIIRAFSYFSHLAN 97

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                +AE+ +   R R +          +sA     +   l +   ++   P+
gi|1542442    98 IAEDEHHIRRNRAHAIA-------GSAPRAGSLAYSLARAEALG-IGPQQ 139

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  e      +  vltAHPt   R+s L ++  i   L        t+ ++
gi|1542442   140 LTEFFSGAHMSPVLTAHPTEVRRKSTLNREMEIAALLDRRERVVPTPAEQ 189

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                +  +E L R +   + t  +RR + t  DE+  G+sY+  t     P+
gi|1542442   190 EQDEETLRRAVLTLWQTALLRRIKLTVLDEVANGLSYYDYTFLSELPRLY 239

                RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                  ++  +   G    lP     ++  sW+GGDRDG nP vt +v ++
gi|1542442   240 CSIEDHVSQGGSEVALP---SFLRIGSWIGGDRDG-NPFVTADVLKETVR 285

                LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                + R      Y + + +L  Els+      L     El   aar
gi|1542442   286 VHRDRILAHYEQELTELGAELSL---GARLIKVSPELAELAARS------ 326

                iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLL.....AtGiseisEe
                     q   +EPYR  L  v  +L   R  aRHL ++ ++ t   +
gi|1542442   327 -PDRSQEHREEPYRLALAYVLGRL---RLTARHLKgeapeGTEAEDAGSL 372

                AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                A y +       L++ Y sLC+ G kv+A G L  l R v  FG  L  +
gi|1542442   373 APYVNAAALKADLDIIYASLCDNGSKVLARGRLRLLRRAVDCFGFHLACI 422

                DiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlg
                D+Rq s+ +  v+  + + +  G +Y    Ee R   Ll EL   RPL
gi|1542442   423 DLRQNSDVHERVVADLFEKVAPGTnYVGLDEEARIALLLQELATARPLAS 472

                sDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAvEL
                + L   +E +  l  +r+ AE ++ L  +     iis a   sD L v L
gi|1542442   473 PFLAYEDETQSELAILRMAAEahraLGREVIPNCIISKAEGVSDLLEVAL 522

                LqRECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                L +E g+ + ++  +L ++PLFE + DL+     ++++ s+  Y+  +
gi|1542442   523 LLKEVGLvtaegTTALNIIPLFETIGDLQVCAKVMDRVLSLPAYRKLVSS 572

                K...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                ++++qevm+GYsDs KD G +   W LYkA   +i v + + v+L lFHG
gi|1542442   573 RgdeQEVMLGYSDSNKDGGFVTSGWELYKAEIGLIEVFRAHNVRLRLFHG 622

                RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                RGG vGRGGGP   AiL+qP   +nG +R+t qGE+i   +   ++  r
gi|1542442   623 RGGSVGRGGGPSYDAILAQPGGAVNGQIRITEQGEIIASKYSNPDMGRRN 672

                LqRFtAAtLEHGmnPPv..sPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                L     AtLE  +  P  ++P+ E+   mee+   A   YR +v+    F
gi|1542442   673 LEILVSATLEASLLQPQfnAPRTEFLTAMEEISDTAFSAYRNLVYETEGF 722

                vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                 +YF + t   E   +niGsRPa R     ie LRAiPW+F+W q R  L
gi|1542442   723 EDYFWSSTVISEIATLNIGSRPASRAKTRSIEKLRAIPWVFSWAQCRLML 772

                PvWLGvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                P W G+G A   +A  +    l  L+ mY+eWPFFR  l  ++mv  K
gi|1542442   773 PAWYGFGSAVEaFAERRPDYGLSFLQAMYREWPFFRTQLSNMDMVLSKSS 822

                PGiAaLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLkiAGHkDlLEGDP
                  iA+ y +L+   eL+ + FG+ +R++Y+ t +++L i G + lLE  P
gi|1542442   823 LAIASRYAELVPDVELRTqiFGR-IRAEYERTIKYVLAIMGQQKLLEDNP 871

                YLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnsk
                 L   +R R +Y+  Ln +q   L+  R               A+
gi|1542442   872 LLDRSIRNRFPYLDPLNHLQIELLRQHR----------------ANSGDD 905
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                  kadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                  k    ++L                 + Gi AG+ n G
  gi|1542442   906 KVLHGIQLS----------------INGISAGLRNSG    926

gi|154146692|emb|CAM83981.1|: domain 1 of 1, from 1 to 438: score 368.0, E = 1.7e-107
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541466     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541466     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541466     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541466     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541466     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541466     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541466     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541466     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541466     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    + D +DAittHL+iGsYR+W+Ee+RqEWL+ EL+G RPL+g+DLP+ +
  gi|1541466     1 --HIDAVDAITTHLGIGSYRDWPEEQRQEWLVNELRGNRPLFGPDLPQSD 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl++frv+ ELP DsFGaY+ismataPsDvLAvELLqRECgvk ++
  gi|1541466    49 EVADVLGTFRVISELPADSFGAYVISMATAPSDVLAVELLQRECGVKTPM 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADL+ A A++e LFsiDWY+ ri+GKqe+m+GYsDsGKDAG
  gi|1541466    99 RVVPLFEKLADLQQARATMELLFSIDWYKERINGKQEIMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAW LYkAqEEi+ vA ++GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541466   149 RLSAAWYLYKAQEEIVDVAEQHGVKLTIFHGRGGTVGRGGGPSHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP t+nGslRvt+qGEviE sFGE+ LCFr+LqRFt AtLEHGmnPPvsP
  gi|1541466   199 PPNTVNGSLRVTIQGEVIEKSFGEDSLCFRTLQRFTVATLEHGMNPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L+++mA vAt EYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541466   249 KPEWRALLDDMATVATKEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+hA+dK    l
  gi|1541466   299 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHAMDKPG-GL 347

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+EmY+eWPFFRvt+DLlEmvFAKGDPGiAaLyDkLLv  +L+PFG++
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  gi|1541466   348 ATLREMYDEWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVPRDLWPFGEQ 397

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y Et+ lLLk+AGH  lLE DPYL+qrl LRdsYit
  gi|1541466   398 LRANYAETQSLLLKVAGHENLLESDPYLRQRLLLRDSYITA--------- 438

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541466     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1541466     - -------------    -

gi|154146704|emb|CAM83987.1|: domain 1 of 1, from 1 to 438: score 366.2, E = 6e-107
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tD +DAittHL+iGsYReW+Ee+RqEWL++EL+GKRPL+g+DLP+ +
  gi|1541467     1 --HTDAMDAITTHLGIGSYREWPEEQRQEWLVSELRGKRPLFGPDLPQSD 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dv+++frv+AELP DsFG+YiismataPsDvLAvELLqRECgvk++L
  gi|1541467    49 EVADVIGTFRVIAELPDDSFGSYIISMATAPSDVLAVELLQRECGVKRPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADL+  PA++e LFsiDWY+ ri GKqe+m+GYsDsGKDAG
  gi|1541467    99 RVVPLFEKLADLQQGPATMELLFSIDWYKQRIGGKQEIMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEEi+ vA ++GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541467   149 RLSAAWQLYKAQEEIVGVAERHGVKLTIFHGRGGTVGRGGGPSHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP t+nGslRvt+qGEviE sFGEEnLCFr+LqRFtAAtLEHGmn PvsP
  gi|1541467   199 PPNTVNGSLRVTIQGEVIEKSFGEENLCFRTLQRFTAATLEHGMNQPVSP 248
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                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR+L+++m  v tEEYR +v++EPRFvEYFR At E+EYG+mniGsR
  gi|1541467   249 KPEWRRLLDDMTAVSTEEYRPIVFQEPRFVEYFRAATLETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+hA +     l
  gi|1541467   299 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHAAETPG-GL 347

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvt+DLlEmvFAKGDPGiAaLyDkLLv ++L+PF ++
  gi|1541467   348 AALREMYDEWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVPDDLRPFDEQ 397

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Yv t+ lLL++AGHkDlLE DPYL+qrl LRdsYit
  gi|1541467   398 LRANYVATQSLLLQVAGHKDLLESDPYLRQRLMLRDSYITA--------- 438

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|67923850|ref|ZP_00517310.1|: domain 1 of 1, from 5 to 1016: score 365.8, E = 7.7e-107
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s+   +  +     s d  L +   L+   +  +L+   G +L +
  gi|6792385     5    SLQSTVEEVNIFSTS-DLFLRQRLELVESLWESVLKAECGLELVDLL 50

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    +    +s   EG+   +    +   +  L+  +ai   +a+     L n+
  gi|6792385    51 KKLRKISSP-EGQVTDQPKTSINELIEELELNEAIRATRAFALYFQLINI 99

                    AE......EvelAyR........RRikkkkhGDFaD.........EasAt
                     E++ ++++ +l  R++ +++++ R   +k G+ + ++  + +  E
  gi|6792385   100 VEqhyeqrDQQLNRRstyqesekARENYQK-GEKSTnglvgadllEKALV 148

                    tEsDiEE...tlKkL...vlklnKsPeEvFeALKnqsvDLvltAHPtqsv
                     E    E+++t+  L ++  +ln  P+ +   L    + Lv+tAHPt  v
  gi|6792385   149 GETKSQEkggTFHWLfpqLKRLNVPPQQIQRLLEQLDIRLVFTAHPTEIV 198

                    RRsLLqKnaRiRnCLaqLsAKDvtve........DKkELDEALHREiqAA
                    R  +  K+ Ri   L  L   +    + + +++ + + + E L  Ei
  gi|6792385   199 RHTIRLKQRRIATLLRRLDQAEEAFRgmglssswEAESIIEQLNEEIRLW 248

                    FRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLRRvDtALKniGinE
                    +RtDE+   +P   DE+ + + Y+ E +    P+   R   AL+
  gi|6792385   249 WRTDELHQFKPSVLDEVDYTLHYFDEVLCSALPQLSQRLQQALQANFPRI 298

                    RlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLLaRmmAanlYisqv
                    + P +    +F sW+GGDRDG nP vt +vt       R +    Y+  v
  gi|6792385   299 KPPHNT-FCRFGSWVGGDRDG-NPFVTTDVTWRTACYQRNLILEKYLAAV 346

                    EDLmFEls...mWRCndELRvRAEElyrtaardkvvKyYiEFWKqvPPtE
                    EDL   ls++  W   +       E  r a  + +       ++q    E
  gi|6792385   347 EDLTEILSsslHWSNVSQDLLDSLERDRVAMPE-IYDQLAIRYRQ----E 391

                    PYRviLGdvRDKLYntRERaRHLLA..tGiseisE..eAvytkvEeFLEP
                    PYR  L  +  +L  tR+R  HL  +++G   + E++e +y    eF
  gi|6792385   392 PYRLKLAYIQKRLEHTRDRNNHLANpeQGQVLVEEtpENIYHSGVEFEAE 441

                    LELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDv
                    L L  + L e G k  A   L  l+ q   FG  L +LD RqEs R+ +
  gi|6792385   442 LQLIKRNLEETGLKCQA---LENLIFQAQMFGFTLTQLDFRQESSRHSET 488

                    lDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLlgsDLPktEEvkD
                    +  i   L+i +  Y e sE  +  WL+ EL+ +RPL++ ++P  E   +
  gi|6792385   489 IQTIASYLNIlpTPYEELSEAEKVNWLVGELQTRRPLIPMEMPFDEKTIE 538

                    vldafrvL....AELPiDsFGaYiismataPsDvLAvELLqRECgv....
                     ++++r+L++ + E  i+    Yiism+   sDvL v LL +E g+ +++
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  gi|6792385   539 TVETMRMLrhlqQEFGIEICQTYIISMTNDVSDVLEVLLLAKEAGLydpg 588

                   ..kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG..........
                   ++  t+r+vPLFE + DL+ AP  +e LF +  Y+  + G+ +  +++++
  gi|6792385   589 tsTTTIRIVPLFETVDDLKRAPEIMEALFKLPLYRTALAGgydyldedkk 638

                   .............KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKky
                   ++ ++++ ++ + qe+mvGYsDs KD G ls  W + kAq  + K+A  +
  gi|6792385   639 eqlpppqlqpanLQEIMVGYSDSNKDSGFLSSNWEIHKAQKSLQKIAEPH 688

                   GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF
                      L lFHGRGG vGRGGGP   AiL+qP  tinG +++t qGEv+   +
  gi|6792385   689 NLALRLFHGRGGSVGRGGGPAYAAILAQPTGTINGRIKITEQGEVLASKY 738

                   GEEnLCFrsLqRFtAAtLEHGmn.PPvsPkPEWRkLmeemAvvAtEEYRs
                      +L    L   t A +   + +        W  +mee+A  A   YRs
  gi|6792385   739 SLPELALYNLETATTAVIQGSLLgSGFDDIDPWNGIMEELASSARKAYRS 788

                   vvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiF
                   +++  P F ++F + tP  E  ++ i sRPa+Rk ++  + +LRAiPW+F
  gi|6792385   789 LIYEQPDFLDFFLSVTPIPEISQLQISSRPARRKSGkKDLSTLRAIPWVF 838

                   aWtqtRFHLPvWLGvGAAFKhAidKD.iKnlqkLkEmYkeWPFFRvtlDL
                   +Wtq RF LP W GvG A    +++++  nl+  k  Y +WPFF++ +
  gi|6792385   839 SWTQSRFLLPAWYGVGTALEGFLQQEpEENLKLFKYFYLKWPFFKMVISK 888

                   lEmvFAKGDPGiAaLyDkLLva.EeLkPFG...ksLRdkYvEtkdlLLki
                   +Em   K D  iA  y k L  +E++  F +  +++ ++Y  t +++L i
  gi|6792385   889 VEMTLSKVDLQIAHHYVKELSNpEDIERFEkvfERISEEYHRTCEIILSI 938

                   AGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPh
                    G   lLEGD  L+  + LR+  i  L  +q   LKR+R    + t +
  gi|6792385   939 TGQPKLLEGDAGLQRSVQLRNGTIVPLGFLQVSLLKRLR----QYTRQ-- 982

                   lsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-
                         +E      ++++          L    +Lt+ GiAAGm ntG
  gi|6792385   983 ------AES-----GVIHFR---YSKEELLRGALLTINGIAAGMRNTG   1016

                   *

  gi|6792385     -   -

gi|154146708|emb|CAM83989.1|: domain 1 of 1, from 1 to 439: score 365.8, E = 8e-107
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ---------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ---------------------------------------------------- -
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                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +tD +DAittHL+ GsYR W+Ee+R EWL++EL+GKRPL+g+DLP+ +
  gi|1541467     1 --HTDAMDAITTHLGNGSYRAWPEERRLEWLISELRGKRPLFGPDLPQSD 48

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  Ev+Dvl++frv+AELP DsFGaYiismataPsDvLAvELLqRE gvk++L
  gi|1541467    49 EVADVLGTFRVIAELPGDSFGAYIISMATAPSDVLAVELLQREYGVKNPL 98

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADL+ A A++e LFs+DWY+ ri+GKqe+m+GYsDsGKDAG
  gi|1541467    99 RVVPLFEKLADLQQAHATMELLFSVDWYKERINGKQEIMIGYSDSGKDAG 148

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEEi+ vA ++Gv L++FHGRGGtvGRGGGP HLAiLsq
  gi|1541467   149 RLSAAWQLYKAQEEIVGVAERHGVELTIFHGRGGTVGRGGGPSHLAILSQ 198

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP t+nGslRvt+qGEviE sFGEEnLCFr+LqRFtAAtLEHGmnPPvsP
  gi|1541467   199 PPNTVNGSLRVTIQGEVIEKSFGEENLCFRTLQRFTAATLEHGMNPPVSP 248

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  k EW +L+++mA vAt+EYRs+v++E RFvEYFR+AtPE+EYG+mniGsR
  gi|1541467   249 KLEWHRLLDDMATVATDEYRSIVFQESRFVEYFRSATPETEYGRMNIGSR 298

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+hA+++    l
  gi|1541467   299 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHAMQQQAGGL 348

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+EmY+eWPFFRvt+DLlEmvFAKGDP iAaLyDkLLv  +L+PFG++
  gi|1541467   349 ATLREMYDEWPFFRVTIDLLEMVFAKGDPSIAALYDKLLVPQDLWPFGEQ 398

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++YvEt+ lLL++AGH  lLE DPYL+qrl LRdsYit
  gi|1541467   399 LRANYVETQSLLLQVAGHDNLLESDPYLRQRLMLRDSYITA--------- 439

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|154146686|emb|CAM83978.1|: domain 1 of 1, from 1 to 438: score 365.1, E = 1.3e-106
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541466     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541466     - ------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541466     - ------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541466     - ------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|1541466     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541466     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541466     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541466     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541466     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     +tD +DAi   L+iGsYReW+Ee+RqEWL++EL+GKRPL+gs+LP+ +
  gi|1541466     1 --HTDAVDAIMMRLGIGSYREWPEERRQEWLVSELRGKRPLFGSELPQSD 48

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl++frv+AELP DsFGaYiismataPsDvLAvELLqRECgvk++L
  gi|1541466    49 EVADVLGTFRVIAELPADSFGAYIISMATAPSDVLAVELLQRECGVKRPL 98

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   rvvPLFEkLADL+   A++e LFs+DWY+ ri+GKqe+m+GYsDsGKDAG
  gi|1541466    99 RVVPLFEKLADLQQVRATMELLFSVDWYKERINGKQEIMIGYSDSGKDAG 148

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEEi+ vA ++ vKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541466   149 RLSAAWQLYKAQEEIVGVAERHSVKLTIFHGRGGTVGRGGGPSHLAILSQ 198

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP t+nGslRvtvqGEviE sFGEEnLCFr+LqRFtAAtLEHGmnPP sP
  gi|1541466   199 PPNTVNGSLRVTVQGEVIEKSFGEENLCFRTLQRFTAATLEHGMNPPGSP 248

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR+L+++mA vAt+EYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541466   249 KPEWRRLLDDMATVATDEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 298

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+hA+d+    l
  gi|1541466   299 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHAMDQPG-GL 347

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+EmY+eWPFFRvt+DLlEmvFAKGDPGiAaLyDkLLv  +L PFG++
  gi|1541466   348 ATLREMYDEWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVPQDLLPFGDQ 397

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR +Y Et+ +LL++AGH DlLE DPYL+qrl LRdsYit
  gi|1541466   398 LRVNYAETQSFLLQVAGHDDLLESDPYLRQRLMLRDSYITA--------- 438

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541466     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1541466     - -------------    -

gi|74316648|ref|YP_314388.1|: domain 1 of 1, from 1 to 939: score 364.3, E = 2.3e-106
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                             + +P     d++L     LL      +L    Ged+ Eav
  gi|7431664     1    -------MNAPQNLLTDDDLRAQVKLLGTLLGQVLLQFAGEDVFEAV 40

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          A+   ++D ++  EL a + ++  +   lv +a++    L n+
  gi|7431664    41 ETLRRGFADLQQQEDQQRRSELMAMIDAMPAGKIELVVRAFSSYFMLVNV 90
```

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                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AEE   A+R R + + hG    E+s       + tl  L  ++    +
gi|7431664    91 AEE-SFAHRNRRRMLSHGMTLWEGS------FDHTLADLKAQG--LSAGT 131

                FeALKnq.svDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                 + L n      v+tAHPt + RR+++    Ri     qL+   + v+D+
gi|7431664   132 LQGLINRlHFAPVFTAHPTEARRRAVMEAMRRIFLICDQLYSPSLGVNDQ 181

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                +EL+  L  Eiq  +RtDE+R a+    DE+R G+ Y+ E +++ vPK
gi|7431664   182 RELEAQLAAEIQIMWRTDELRSAKLEVRDEVRNGLYYVRESLFEAVPKAY 231

                RRvDtAL.KniGin..ERlPYdvP.LikFssWmGGDRDGknPRvtPEvtR
                   + AL+K  G+n++   P  vP+ i+F sW+GGDRDG nP vt +vt
gi|7431664   232 SFFERALrKHYGVNgdGAAPISVPsFIRFGSWIGGDRDG-NPFVTADVTE 280

                DvCLLaRmmAanlYisqvEDLmFEl...smWRCndE.LRvRAEElyrtaa
                         A   Y   v +L   l+++s W   + +   R  E
gi|7431664   281 WTVHTQMQAALDEYRARVRELRQTLthsSGWCTPSApFLERLAEYEAEFG 330

                rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                 +     +     q+   EPYR +   +  +L          LA   s
gi|7431664   331 EQ----VFRGTAVQIYSREPYRRMAAMMLARLDANLSYVHQCLADVPSFT 376

                sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                s  A y +   FL  L L   sL   GD++iA   L  l+R v  FG  L
gi|7431664   377 SHLA-YEDAAAFLADLYLIRDSLISHGDRIIAMQDLQALIRLVESFGFHL 425

                vKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRP
                 +LDiRqEs  +t  + A+ + ++    Y+   E  R   L a      P
gi|7431664   426 LQLDIRQESTIHTRTVAAVLQQIDPDfDYKGADEAERLKRLSAWTGHIDP 475

                LlgsDLPktEEvkDvldafrvLAELPi....DsFGaYiismataPsDvLA
                +   D    +E ++ +  fr +A L ++ +++ FG Yiism+ + s v+
gi|7431664   476 IEIDDSLLDDEARETVAVFRRMAKLKSevgdEVFGTYIISMTHSASHVME 525

                vELLqRECgvk........qtLrvvPLFEkLADLeAAPAavekLFsiDWY
                v LL R  g+ +++++     + v PLFE + DL+   A ++ L s   Y
gi|7431664   526 VMLLARLVGLCghngdawfCRILVAPLFETVDDLQRSQAILDELLSNKVY 575

                inri..dG.KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvK
                +  +  dG++qevm+GYsDs KD G l+  W LY+Aq  ii   +++Gv
gi|7431664   576 RALVaaDGnRQEVMLGYSDSCKDGGILASNWNLYQAQLSIIALTRRHGVE 625

                LvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFG..
                  lFHGRGGtvGRGGGPtH AiLsqPP t+nG ++ t qGE++ + + ++
gi|7431664   626 CRLFHGRGGTVGRGGGPTHEAILSQPPGTVNGEIKFTEQGEMLYYKYSnp 675

                .....EEnLCFrsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEE
                ++ + E  +    L +  A  L    +  v    ++ + m ++A
gi|7431664   676 etanyEIGMGVTGLLKASATLLK---KCEVRYPQDYLDWMRDIAAAGETT 722

                YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiP
                YR+++   P F++YF   tP +E G +niGsRP+ Rk + + + s+RAiP
gi|7431664   723 YRALIAT-PGFIDYFYENTPVTEIGTLNIGSRPSHRKKADrSLGSIRAIP 771

                WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                W+F W q R  LP W G+G A K  +d+    l  L+ mY eWPFFR  l
gi|7431664   772 WVFGWAQSRHTLPAWYGIGSALKSFVDQHPEGLAHLRAMYAEWPFFRGLL 821

                DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                  + m   K D  iA  y +L          + + d++  t   + ++A
gi|7431664   822 SNVQMALTKADMEIAEEYARLCDHPGTPDIYRAIADEFALTVAGVKQVAQ 871

                HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                   lLE    L   +  R +Yi  +n +q   LKR R  s
gi|7431664   872 IENLLEDNQPLALSISRRRPYIDPINHIQVRLLKRYRSESV--------- 912

                KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                  +  E+      L  L                +  iAAGm ntG
gi|7431664   913 --WESEQ---DSWLTPLK--------------RSINAIAAGMRNTG    939
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gi|262202294|ref|YP_003273502.1|: domain 1 of 1, from 18 to 945: score 362.7, E = 6.6e-106
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                     si   + +   G+     + ++ D  Ll   L+D++ +  G+++ E
  gi|2622022    18    SIVDHITVDDEGRAL--TEPLREDIRLLGGLLgDVIREHSGDEVFEL 62

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v E   ++A +  ++     +EL     ++     + v +a++    LAn
  gi|2622022    63 V-EAARVAA-FRIRRNEIDRGELADMFSGVSLDVVMPVIRAFSNFALLAN 110

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  LAE+++   RR i+++        ++   +s +  t+ kL   +    e
  gi|2622022   111 LAEDIHRERRRAIHLRA-------GDPPQDSSLAATYTKLAEAG-LDDEQ 152

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  v  AL   +v  v+tAHPt   RRs+   + Ri   +   s  ++t+ +
  gi|2622022   153 VGRALADATVVPVITAHPTETRRRSVFEAQNRITELMRYRSRSELTPAED 202

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +  A+ R i   + t  iR  + t qDE+R G+ Y+    ++ vPK
  gi|2622022   203 DVVIKAIRRQILTLWQTALIRLERLTIQDEIRSGLRYYDASFFDVVPKIN 252

                  RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    v   L+       l  d P+i+  sW+GGDRDG nP vt E+
  gi|2622022   253 TSVRASLRAAYPDAGLA-DDPMIRMGSWIGGDRDG-NPFVTDEIVEMATT 300

                  LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                  La   A    +s +  L  Elsm     +      El   +a d
  gi|2622022   301 LAARTAIGHHLSELHKLAEELSMSTRLMDPGEALYELAGVPADD------ 344

                  iEFWKqvPPtEPYRviLGdvRDKLYntRERa...RHLLAtGiseisEeAv
                           EP+R  L  +R +L  t     ++  + A  +  +
  gi|2622022   345 ------PKADEPFRLALRHIRSRLATTATEMfgeEVMKAADLFLVNGKPA 388

                  ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                  y +  e L  L++   +L    D ++AD  LL l   v tFG  L  LD+
  gi|2622022   389 YADAAELLADLDVIDAALRHGKDDILADDRLLTLRESVRTFGFNLSGLDM 438

                  RqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgsD
                  Rq s+ + +v+  +    ++ + Y +  E+ R   L  EL+ +RPL  +D
  gi|2622022   439 RQNSDMHEEVIAELLAWAGVHpDYASLDEDERVAILSEELQKRRPLTRPD 488

                  LPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLq
                      E   +E+  v  a r +A     +   Yiism+t+ sD+L   +L
  gi|2622022   489 ADLSElavkELGIVRAAARAVATFGPQAVPNYIISMCTSVSDMLEPMILL 538

                  RECgvkq..........tLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                  +E g+   + ++++ ++t+r+vPLFE + DL+    ++     + +Y+
  gi|2622022   539 KEAGLIDidaesgtltsTVRIVPLFETIEDLQQGATTLLAALDLPFYRGL 588

                  id...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                  +d++ G qe+m+GYsDs KD G ++A W LY+   +++  A k G++L l
  gi|2622022   589 VDsqaGMQEIMLGYSDSNKDGGYMAANWALYRGELDLVEAAAKAGIRLRL 638

                  FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                  FHGRGGtvGRGGGP   AiL+qPP  ++GslR+t qGE+i   + E
  gi|2622022   639 FHGRGGTVGRGGGPSYDAILAQPPGAVQGSLRITEQGEIIAAKYAEPVSA 688

                  FrsLqRFtAAtLEHGm..nPPvsPkPE.WRkLmeemAvvAtEEYRsvvvK
                   r L    AAt+E  + +   +    E+   +m+e+A  A   Y  +v
  gi|2622022   689 ERNLETLLAATIESSLldVEGLGDDSEdAYAIMDELAALARSAYSKLVHD 738

                  EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                   P FvEYF   tP  E G +niGsRPa Rk    i  LRAiPW+ +Wtq
  gi|2622022   739 TPGFVEYFTTSTPLSEIGALNIGSRPASRKQTEKISDLRAIPWVLSWTQS 788

                  RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                  R  LP W G G AF   i      l  L+  Y eWPFFR  +  +  v A
  gi|2622022   789 RAMLPGWYGTGSAFAEWIGDSDDRLATLQRYYTEWPFFRSVMSNMAQVLA 838

                  KGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlLE
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                  K D  +A  y +L+  EeL++k FG  +  + + t  +  ki G  DlL
  gi|2622022   839 KSDMNLAHRYAQLVPDEELrdKVFG-MIVGEHERTIAMYSKITGTDDLLA 887

                  GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                      LK  +  R +Y+  Ln +q   L+R R  +              dE
  gi|2622022   888 DNAALKRSVYNRFPYLEPLNLLQVELLRRFRAGD--------------DE 923

                  nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                  +              r+  G+     Ltm G+A  + n G
  gi|2622022   924 P--------------RIRRGIQ----LTMNGLATALRNSG    945

gi|54023896|ref|YP_118138.1|: domain 1 of 1, from 5 to 923: score 362.3, E = 9e-106
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      i+    +  P +       i++   +l    D + D  G+++ + +
  gi|5402389     5    RIETEQDATRPLRDD-----IRFLGGVLG---DTIRDHEGPEVFDLI 43

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   E   + A +  +++      +   L ++d a a+ + +a++  + LAnL
  gi|5402389    44 -ERVRIEA-FRVRREEVGRSAVAEMLRGVDIAVALPLIRAFSYFVLLANL 91

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AE+++   RR ++          ++   +s +  t++kL        + v
  gi|5402389    92 AEDIQRDRRRAVHVAA-------GEPPQDSSLAATYRKLDAAA-LDAAAV 133

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   + L    v  v+tAHPt   RR +   ++Ri   L     +   + ++
  gi|5402389   134 ADLLSDALVSPVITAHPTETRRRTVFDAQTRITE-LMRARQRATDPAERA 182

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   L+  + R +   +Rt  iR a+   qDE+  G+ Y+  t+++ +P
  gi|5402389   183 ALESRIRRQVLSLWRTALIRLARLRIQDEIAVGLRYYELTLFDVIPAINA 232

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   v  AL+       l    P+++  sW+GGDRDG nP vt Ev R
  gi|5402389   233 EVRAALRARWPGADL-LARPILRPGSWIGGDRDG-NPYVTAEVVRHAATQ 280

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                  a  +A   Y+  + +L   ls+      +  R  El      d
  gi|5402389   281 AAGVALRRYLAELVELAKTLSLSARLVPVTPRVAELAAAGYPD------- 323

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                           EPYR  L  +R +L  t +R            ++   y
  gi|5402389   324 ---PATHGDEPYRRALHHIRVRLSATADRVLDAPVPEAVAEPDAQPYAGP 370

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   eFL+ L+    sL   GD  +AD  L  l   v tFG  L  LD+Rq s
  gi|5402389   371 REFLDDLDAIDASLRASGDGLLADDRLAALRHAVETFGFHLQGLDMRQNS 420

                  eRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                  e +  v+  +    ++ ++Y + +E+ R E L aEL+ +RPLlg+
  gi|5402389   421 EVHEQVVAELLAWAGVHpAYGDLPEDARVELLAAELRTRRPLLGPHARLS 470

                  EEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvELLqREC
                  E  +  ++ +r  A   +D+FG++  ++Yiism+t+ sD+L   LL +E
  gi|5402389   471 EQAAKEVGIVRA-AKQVVDTFGPeavpnYIISMCTSVSDMLEAALLLKEG 519

                  gvkq.........tLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                  g+  ++ ++++++ t+ +vPLFE + DL A  A+++    +  Y+  +
  gi|5402389   520 GLLDpgapegspscTVNIVPLFETIEDLGAGAATLAAALEVPVYRELVAA 569

                  ...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                   + +qevm+GYsDs KD G l+A W LY+A  +++ vA+k G++L lFHG
  gi|5402389   570 agmRQEVMLGYSDSNKDGGYLAANWALYRAELDLVEVARKTGIRLRLFHG 619

                  RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                  RGGtvGRGGG    AiL+qP   + G+lR t qGEvi   + E     r
  gi|5402389   620 RGGTVGRGGGRSYDAILAQPAGAVRGALRLTEQGEVIAAKYAEPGAAHRN 669

                  LqRFtAAtLE......HGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvK
                  L    A tLE++  +  G+     P  E   Lm+e+A  A   Y  +v
  gi|5402389   670 LESLIAGTLEstlldvEGLGADAEPAYE---LMDELAALARAAYARLVHE 716
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                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                     P FvEYFR  tP  E G +niGsRPa RkP   +  LRAiPW+ aW q
  gi|5402389   717 TPGFVEYFRQSTPVAEVGDLNIGSRPASRKPTNSVSDLRAIPWVMAWSQA 766

                    RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                    R  LP W G GAA    +  D   l +L ++Y+ WPFFR  l  l  v A
  gi|5402389   767 RVMLPGWYGTGAALEEWVGGDPGRLARLTDLYRRWPFFRTVLSNLAQVMA 816

                    KGDPGiAaLyDkLLvaEeLk..PFGksLRdkYvEtkdlLLkiAGHkDlLE
                    K D  iAa y +L+    L+++ FG  +R++   t  +   i GH  lL
  gi|5402389   817 KSDLDIAARYAELVDDAALRdqIFG-MIREEHARTLRMHAAITGHDQLLA 865

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                        L   +  R +Y+  Ln +q   L+R+R
  gi|5402389   866 DNRSLAESIHNRFPYLEPLNQMQVELLRRLR------------------- 896

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     s    eLvk              ++Ltm G+A  + n G
  gi|5402389   897 -SGDDSELVKRG------------ILLTMNGLATALRNSG    923

gi|156742348|ref|YP_001432477.1|: domain 1 of 1, from 2 to 938: score 362.0, E = 1.1e-105
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s     R     + s     i++   Ll    D++ +  Ge     v
  gi|1567423     2    SHTPHNRRHESERLS---ATIRFLGNLLG---DVIREQAGEAAFQLV 42

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         l  e       +   EL      +  aD  +v ka+     L nL
  gi|1567423    43 ERLRTLGKELRNGAPDRADAELRMMAARMTVADIQIVIKAFNAYFLLVNL 92

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE ++  +  R + +k   + D      Es i   +  L   +      +
  gi|1567423    93 AEQMQRVWVLRDRERK---YPDTPRP--ES-IAAAIAELHACG-IPATTI 135

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     e L    +  v+tAHPt + RR  L K  R+   L      D+    ++
  gi|1567423   136 QEWLDTACIQPVFTAHPTEARRRTALEKVRRLATLLDE-RTGDLHGFVRE 184

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    E    +  Ei   + tDE+R  +Pt  DE++ Gm Y+   +++ +P+  R
  gi|1567423   185 ENTMRIREEIVSLWQTDEVRVVKPTVIDEVKNGMFYFESGLFDLIPRLYR 234

                    RvDtALKni..GinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                      + AL+   +    R+P   PL+++ +WmGGDRDG nP vt  vt
  gi|1567423   235 ELEYALRTTypTHEWRVP---PLLRYGAWMGGDRDG-NPNVTHTVTIQAV 280

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     + R  A    i  vE+L   l          v  E   + a    +
  gi|1567423   281 RMMRAAAIERHIAAVEELSHRLG--QSVRQAPVSDELRESLAHDASLFPE 328

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEeAvy
                      +      P E YR     +R+KL  t + aR  +L  G s+ +    y
  gi|1567423   329 VADMLARRNPYELYRQKCTYIREKLIRTLDYARTAsLDWGRSDSPPKGAY 378

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                        + L+ L +  +sL      ++A G+L Dl+Rq   FGL    LDiR
  gi|1567423   379 FSRTDLLDDLHVMERSLLSNNAAIVANGALRDLIRQAEVFGLHTATLDIR 428

                    qEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgsDL
                    q seR+t  l  +    ++ ++Y    E  R E L  E++  RPL++  L
  gi|1567423   429 QHSERHTAALAEVLAAAGVCAdYTALNEIERIELLSREIENPRPLIPTRL 478

                    PktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAvELLqR
                        +  +v+ +fr   ++L  L  ++    i+sm+   sD LA  LL +
  gi|1567423   479 DYSPDTVEVIATFRavasILERLSPEAVETCIVSMTRGASDLLAPLLLAK 528

                    ECgvkqtLr.....vvPLFEkLADLeAAPAavekLFsiDWYinridGK..
                    E g+ ++ r ++ ++ PLFE  ADL      +e    +  Y+n++  ++
  gi|1567423   529 EAGLFRPFRfsrlsMAPLFETGADLACCDEVLEACMRLPIYRNHLALRgf 578

                    .qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
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                     qevm+GYsDs KD G  +A W +Y+Aq  +    +++G+++ lFHGRGG
  gi|1567423   579 vQEVMIGYSDSNKDVGYAAANWAIYQAQRKLRDFGRRHGIQMRLFHGRGG 628

                     tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                      +GRGGGP   AiL+qPP  i   +++t qGEvi   +G   L  r +
  gi|1567423   629 AIGRGGGPANHAILAQPPGSIGNQIKITEQGEVIADRYGLPLLAHRHIEQ 678

                     FtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                        A L  G+     P  EW + +e++A      YR++v+    Fv YFR
  gi|1567423   679 VINAVLRAGLLQRDDPPDEWTQALERLAALSQRHYRALVYERSDFVPYFR 728

                     lAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG
                       tP  E  ++niGsRPa R+    ie LRAiPW+F+W q R  LP W G
  gi|1567423   729 NVTPIAEISRLNIGSRPASRRNTERIEDLRAIPWVFSWMQSRHTLPGWYG 778

                     vGAA...FKhAidK......DiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                     +G A ++F +A ++++ +++ i  l  L+EmY  W FFRv +D   m+
  gi|1567423   779 LGFAletFVYAGEQsdasgsAIDRLALLQEMYARWSFFRVMIDNAQMILG 828

                     KGDPGiAaLyDkLLvaEe.LkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                     K D  iA+ y +L    +        +R++Y+    ++ ++A    lL+
  gi|1567423   829 KADLHIASRYAELAPDQNaAAAIFAAIREEYQRASRMIRQVARIERLLDN 878

                     DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                      P L+  +  R++Yi  +  +q   L+R+R                + +
  gi|1567423   879 APVLQHSIQRRNPYIDPMSYLQIELLRRLR-----------------AAP 911

                     skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                         d+  +          +ED ++L + G+AAG+ ntG
  gi|1567423   912 ----DGPDHAA--------IEDAILLSISGLAAGLMNTG    938

gi|145224288|ref|YP_001134966.1|: domain 1 of 1, from 14 to 937: score 361.3, E = 1.8e-105
                     *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                         i A  R  v        + ++ D  Ll   L+D + +  G+++ +
  gi|1452242    14    PIGAVQRTQVGREAT---EPMREDIRLLGTILgDTVREQNGDEVFDL 57

                     vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                     v E   + A +  ++      ++      +d   ai v +a+ H   LAn
  gi|1452242    58 V-ERARVEA-FRVRRSEIDRADMAKLFDDVDVHRAIPVIRAFTHFALLAN 105

                     LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     +AE+++   RRRi+          ++   +s ++ t+ kL   +
  gi|1452242   106 VAEDIHRERRRRIHEAA-------GEPPQDSRLDATYLKLDDAG-LDAGA 147

                     vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL.aqLsAKDvtveD
                     v +AL    v  v+tAHPt   RR +   + Ri   ++  L   D t  D
  gi|1452242   148 VADALAGALVSPVITAHPTETRRRTVFDTQHRITELMrLRLHGHD-TSPD 196

                     KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                      ++++  L R i   + t  iR ++   qDE+  G+ Y+   +++ +P+
  gi|1452242   197 GRDVEQELRRHILTLWQTALIRLSRLKIQDEIETGLRYYEAALFEVIPQV 246

                     LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                        v  AL+     E    + P+++  sW+GGDRDG nP vt Ev R
  gi|1452242   247 NAEVRAALQQ-RFPEAGLLEQPIVRPGSWIGGDRDG-NPNVTAEVVRLAT 294

                     LLaRmmAanlYisqvEDLmFElsm....WRCndELRvRAEElyrtaardk
                       a   A   Y+  +  L  Elsm+ +     dEL + A+  +  a+ d
  gi|1452242   295 GSAAYTALAHYFAELTGLEQELSMsarlVHITDELAALADSCHEPARAD- 343

                     vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                                   EPYR  L  v  +L  t             ++  e
  gi|1452242   344 ---------------EPYRRALRVVHARLTATAQQILDRQPEHELDLGME 378

                     AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                       y    e L+ L++   sL   G  v+AD  L  l   v  FG  L  L
  gi|1452242   379 P-YAAPGELLDDLDVIDASLRANGSAVLADDRLGRLREAVRVFGFHLSGL 427

                     DiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlg
                     D+Rq s+ + +v+  +    ++ s+Y + sE+ R E L aEL  +RPL
  gi|1452242   428 DMRQNSDVHEEVVAELLAWAGVHSdYTSLSEDDRVEVLAAELATRRPLTS 477
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                    sDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvE
                    +D    E  +  ld +   A   +  FG++  ++Yiism+ + sD+L
  gi|1452242   478 PDADLSELARKELDIVAAAAR-AVHVFGPqavpnYIISMCQSVSDMLEAA 526

                    LLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsiDWYin
                    +L +E g+   +++++  ++ +vPLFE + DL+     +e    +  Y+
  gi|1452242   527 ILLKEAGLLDassehpyaPVGIVPLFETIDDLQRGSSILEAALELPLYRG 576

                    ridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                     +  ++++qevm+GYsDs KD G l+A W LY+A  E++   +k G++L
  gi|1452242   577 LVSARgdsQEVMLGYSDSNKDGGYLAANWALYRAELELVESSRKTGIRLR 626

                    lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                    lFHGRGGtvGRGGGP   AiL+qPP  ++GslR+t qGEvi   + E  +
  gi|1452242   627 LFHGRGGTVGRGGGPSYDAILAQPPGAVQGSLRITEQGEVIAAKYAEPRI 676

                    CFrsLqRFtAAtLEHG...mnPPvsPkPEWRkLmeemAvvAtEEYRsvvv
                      r L    AAtLE    +m+          ++++++A  A   Y  +v
  gi|1452242   677 AHRNLETLLAATLEATlldMEGLGDLAGTAYEVLDDLAARAQRAYAELVH 726

                    KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                      P Fv+YF+  tP  E G +niGsRP+ RkP   i  LRAiPW+ aW q
  gi|1452242   727 DTPGFVDYFKASTPVSEIGALNIGSRPTSRKPTTSISDLRAIPWVLAWSQ 776

                    tRFHLPvWLGvGAAFKhAi...dKDiKnlqkLkEmYkeWPFFRvtlDLlE
                     R  LP W G G AF   ++++d     lq L+++Y+ WPFF   l  +
  gi|1452242   777 SRVMLPGWYGTGTAFEDYVgdgDDAEARLQVLQDLYRRWPFFATVLSNMA 826

                    mvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtkdlLLkiAGHkD
                     v AK D G+Aa y +L+  EeL++   +++ d+   t  +   i GH D
  gi|1452242   827 QVLAKSDLGLAAHYSELVEDEELrRRVFDKIVDEHARTIRMHRLITGHED 876

                    lLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEy
                    lL   P L   +  R +Y+  Ln +q   L+R R
  gi|1452242   877 LLADNPSLARSVFNRFPYLEPLNHLQVELLRRYRS--------------- 911

                    AdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     dE+     +Lv+              ++Ltm G+A  + n G
  gi|1452242   912 GDED-----DLVQRG------------ILLTMSGLATALRNSG    937

gi|91976353|ref|YP_569012.1|: domain 1 of 1, from 16 to 933: score 360.6, E = 2.8e-105
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                             R+     + ed +L + D  Ll + L+D + D  G  + +
  gi|9197635    16    ------RADDSAFIEEDTRL-RNDIRLLGRILgDTVRDQEGSAVFDL 55

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      s  +   +D     EL a L  +  +D++ + +a++    LAn
  gi|9197635    56 VERIRQTSIRFHRDEDKPARRELEAILDDMSASDTVKIVRAFSYFSHLAN 105

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+        i++ + G  +  +sA     +  tl +    +     E
  gi|9197635   106 IAED-----QNNIRQMRAG--STAGSAPRAGMLAKTLAHAREEG-IGARE 147

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      e  K   v  vltAHPt   R+s + ++  +   L q     +t ++
  gi|9197635   148 LREFFKTALVSPVLTAHPTEVRRKSTMDREMEVAALLDQRERLQLTADEW 197

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                       +E L R +   ++t  +RR++ t  DE+  G+s++  t  + vP+
  gi|9197635   198 AQNEEQLRRAVVTLWKTNLLRRTKLTVLDEVANGLSFYDYTFLREVPRLH 247

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                       +  L       E     +  ++  sW+GGDRDG nP vt Ev
  gi|9197635   248 SALEDQLGGGEGGEAEEELASFLRMGSWIGGDRDG-NPFVTAEVLQGTLR 296

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L       +Y++ + +L  Els+    + L    E++   a r
  gi|9197635   297 LQSARVLRFYLDELHELGSELSL---ASHLAPITEDVRLLAERS------ 337

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
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                          EPYR  +  +  +L  t   a+  +    + + E  +y +
  gi|9197635   338 -PDHSPHRRHEPYRLAVSGIYARLAAT--AAKLKIDSVRAPVGEAEIYAN 384

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                   v eF   L+    sL      viA G L  l R    FG  L  LD+Rq
  gi|9197635   385 VQEFKADLDAIHYSLTKYNAGVIARGRLRQLRRAADCFGFHLASLDMRQN 434

                   seRqtDvlDAittHLe.iGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   s  +   +  +     +  sY    E+ R   L  EL+  RPL    +
  gi|9197635   435 SAVHERTMGELMDAARpTSSYLALDEDERIALLTGELRSARPLTSIFIKY 484

                   tEEvkDvldafrvLAELPi....DsFGaYiismataPsDvLAvELLqREC
                    +E    l  ++  A   +  ++ +    iism+   sD L v +L +E
  gi|9197635   485 SDETVGELAVLHEAARAHSiygeAAIPQCIISMTKGVSDLLEVAVLLKEV 534

                   gv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid...GKq
                   g+ +++++ ++ +vPLFE + DL+A  A +++L +i  Y+  +d+++G q
  gi|9197635   535 GLidpsgRCAINIVPLFETIEDLQACAAIMDRLLAIPEYRRLVDsrgGVQ 584

                   evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                   evm+GYsDs KD G +   W LYkA   +  v  ++Gv+L lFHGRGG v
  gi|9197635   585 EVMLGYSDSNKDGGFVTSGWELYKAEIGLLDVFEHHGVRLRLFHGRGGSV 634

                   GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                   GRGGGP   Ai++qP   +nG +R+t qGE+i   +   ++    L   t
  gi|9197635   635 GRGGGPSYDAIVAQPGGAVNGQIRITEQGEIITSKYSNREVGRNNLEILT 684

                   AAtLEHGmnPP..vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                   AAtLE  +  P++ +P+ ++ + me++   A   YR +v+    Fv+YF
  gi|9197635   685 AATLEASLLQPrrSAPHHDYLEAMEQLSALAFKAYRGLVYETDGFVDYFW 734

                   lAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG
                   + t   E   +niGsRPa Rk    ie LRAiPW+F+W q R  LP W G
  gi|9197635   735 SSTVINEISTLNIGSRPASRKKTRAIEDLRAIPWVFSWAQCRLMLPGWYG 784

                   vGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                   +G A   +  +   K    L+ mY+eWPFFR+ l  ++mv  K    iA+
  gi|9197635   785 FGSAVEaWVAEHPDKGTAFLQSMYQEWPFFRMLLSNMDMVLSKSSIAIAS 834

                   LyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                    y +L+  EeL++k FG+ +R ++    d LL i GH  lL G P L
  gi|9197635   835 RYADLVPDEELrhKIFGR-IRIEWHASVDSLLAIMGHERLLQGNPLLERS 883

                   lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                   +R R +Y+  Ln +q                 +l +E+   +
  gi|9197635   884 IRHRFPYLDPLNHVQV-----------------QLLREHRTHD------- 909

                   vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       p e+v  G+     Lt+ Gi AG+ n G
  gi|9197635   910 ----PDEQVLRGIQ----LTINGISAGLRNSG    933

gi|154146716|emb|CAM83993.1|: domain 1 of 1, from 1 to 438: score 360.6, E = 2.9e-105
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541467     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541467     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541467     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541467     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541467     - ---------------------------------------------- -
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                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541467     - ------------------------------------------------ -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541467     - ------------------------------------------------ -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541467     - ------------------------------------------------ -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541467     - ------------------------------------------------ -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +tD lDAittHL+iGsYR+W+Ee+RqEWL++EL+GKRPL+g++LP+ E
  gi|1541467      1 --HTDYLDAITTHLGIGSYRDWPEERRQEWLVSELRGKRPLFGPELPQSE 48

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvl++frv+ ELP DsFGaY+ismataPsDvLAvELLqRECgvk++L
  gi|1541467     49 EVADVLGTFRVIVELPGDSFGAYVISMATAPSDVLAVELLQRECGVKKPL 98

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADL+ A A++e LFs+DWY+ ri GKqe+m+GYsDsGKDAG
  gi|1541467     99 RVVPLFEKLADLQQARATMELLFSVDWYKERIGGKQEIMIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLY+AqEEi+ vA ++GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541467    149 RLSAAWQLYRAQEEIVGVAERHGVKLTIFHGRGGTVGRGGGPSHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP t+nGslRvtvqGEvi+ sFGEE LCFr+LqRFtAAtLEHGmnPP++P
  gi|1541467    199 PPSTVNGSLRVTVQGEVIDKSFGEESLCFRTLQRFTAATLEHGMNPPIAP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kP WR+L++emA v t+EYRs+v++EPRFvEYFR+A PE+EYG+mniGsR
  gi|1541467    249 KPGWRRLLDEMAAVSTDEYRSIVFREPRFVEYFRSAMPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkP+GGiesLRAiPWiFaWtqtRFHLPvWLG+G AF+hA+++    l
  gi|1541467    299 PSKRKPGGGIESLRAIPWIFAWTQTRFHLPVWLGFGTAFRHAMEQ-LAGL 347

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+eWPFFRvt+DLlEmvFAKGDPGiAaLyDkLLv E+L+PFG++
  gi|1541467    348 AMLREMYDEWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVPEDLWPFGEQ 397

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y E + lLL++AGH +lLE DPYL+qrl LR sYit
  gi|1541467    398 LRANYAERQSLLLQVAGHDELLENDPYLRQRLMLRGSYITA--------- 438

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541467     - ------------------------------------------------ -

                    tmKGiAAGmqntG<-*

  gi|1541467     - -------------    -

gi|257067921|ref|YP_003154176.1|: domain 1 of 1, from 24 to 942: score 359.4, E = 6.6e-105
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        iDA LR+ v  + s          LL       L D HG+++ + v
  gi|2570679     24    HIDAPLRATVR-RLS---------TLL----GGALADQHGQEMLDLV 56

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         l  e          +++  +L  L    a  + +a++    LAn
  gi|2570679     57 EQVRKLTKEAKSADSEASAQDVQKRLAELPIEQATALTRAFSQYFLLANA 106

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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                AE v   yR R    +            Es +  t++ +        +
gi|2570679   107 AEQV---YRVRALDER---------PSAESWVPRTVRDIHEEV--GTDGL 142

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                 +A+    v Lv+tAHPt + RR++L K  Ri   L      + t+e ++
gi|2570679   143 QQAVDSLDVRLVFTAHPTEASRRAVLTKLRRISDILGE-DTEEGTPERRR 191

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                  D  L   i   + tDE+RR +PtPqDE R  + Y+ E   + +P  L
gi|2570679   192 Q-DRDLAELIETLWQTDELRRQRPTPQDEARNALYYLREIFRHTMPEMLD 240

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     L+  G n R   +vPL +F sW+GGDRDG nP vt  vtR+v  L
gi|2570679   241 DLREELRAHGANLR-DDQVPL-RFGSWIGGDRDG-NPFVTAQVTREVLKL 287

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy..
                       + i+ + +L+ Els+    +EL    EEl    a d   ++++
gi|2570679   288 QAETSIDFAIEVISELILELSV---SSELTGEDEELRASLAED--LQHns 332

                .YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                +  E  + +  +EPYR  LG++R KL  tRER R   A+          y
gi|2570679   333 eVDEVQQELYHEEPYRLKLGAMRSKLNATRERIRTGEAH-----VHGRDY 377

                tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                 +  e  E   +   +L   G    ADG L          GL L  LD+R
gi|2570679   378 SDSAELQEDFRVLREALHRHGGERAADGTLAIAQQVLAASGLNLATLDVR 427

                qEseRqtDvlDAittHLeiGs..YReWsEeKRqEWLlaELkGKRPLlgsD
                  se++ Dvl  +   ++   ++Y e s e R   L  EL  +RPL+gs
gi|2570679   428 EHSEKHHDVLSRLFDRVGELDrpYAELSREERTTVLGRELGSRRPLVGSA 477

                LPktEEvkD..vldafrvLAELP.......iDsFGaYiismataPsDvLA
                +   E   D+    +++v  E+ + ++  +      Yiism+    DvLA
gi|2570679   478 ITEDESTLDdaTRTTYNVFREIRdahrlygTSVIETYIISMTHGADDVLA 527

                vELLqRECgv.........kqtLrvvPLFEkLADLeAAPAavekLFsiDW
                  LL RE g+ +  ++++++  +  vPL E + +L+ A   ++ L s
gi|2570679   528 AALLAREAGLlsiagseerRADIGFVPLLEEVSELRHAGEILDELLSDPS 577

                Yin..ridG.KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGv
                Y+   r+ G++qevm+GYsD  KDAG +   W + +Aq  +   A ++Gv
gi|2570679   578 YREivRLRGdRQEVMLGYSDGNKDAGVITSQWEIHQAQRSLRDTAARHGV 627

                KLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGE
                 L lFHGRGG vGRGGGPt  AiL+qP   ++G ++ t qGEvi   +
gi|2570679   628 TLRLFHGRGGSVGRGGGPTYDAILAQPYGVLEGEIKFTEQGEVISDKYML 677

                EnLCFrsLqRFtAAtLE.HGmn.PPvsPkPEWRkLmeemAvv...AtEEY
                  L    L    AA LE+  +++ P  P     +  + m  v+++    Y
gi|2570679   678 PSLARENLDLSLAAVLEgSALHtAPRTPAETLERFGDVMQSVsdsSFARY 727

                RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPW
                R +v  E    EYF +AtP    G +niGsRP+KR  s +G++ LRAiPW
gi|2570679   728 RTLVDDE-NLPEYFVSATPVEQLGDLNIGSRPSKRTTSEkGLDGLRAIPW 776

                iFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlD
                +F Wtq R  +P W G G   K A +        L+EmY+ W FFR  +
gi|2570679   777 VFGWTQSRQIVPGWFGAGSGLKAAREAGLEP--DLHEMYRSWHFFRTVIS 824

                LlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGH
                 +Em  AK D  iAa y + Lv E L+   +++R++Y+     + ++ G
gi|2570679   825 NVEMTLAKTDMQIAAHYVHSLVPERLWYLFDRIREEYELSVAEIERLTGV 874

                kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                  lL+  P LK  l +Rd Y+  +  +q   L+R R
gi|2570679   875 LGLLDNQPVLKRTLSVRDRYLDPISYMQVAMLQRAR-------------- 910

                EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                  A+              +e+ +P L   L+ t+ G+AAG++ntG
gi|2570679   911 --AATA-----------RGEELSPELQRALLTTINGVAAGLKNTG    942
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gi|118467879|ref|YP_887412.1|: domain 1 of 1, from 1 to 933: score 358.5, E = 1.2e-104
                  *->siDAqLRlLvP.GKvs......edekLieYDALLlDkFL.DiLqDLH
                       D    +L P G v +++ ++e  + ++ D  Ll   L+D + +
  gi|1184678     1    MADSNDTALEPfGSVQrthigrEASEPMREDIRLLGAILgDTVREQN 47

                    GedLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkail
                    Ge++ + v      s  +  ++      EL     ++d   ai v +a+
  gi|1184678    48 GEEVFDLVERARVES--FRVRRSEIDRSELADMFSGVDAHQAIPVIRAFT 95

                    HmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlk
                    H   LAn+AE+++   RR ++          +    +s +  t++kL
  gi|1184678    96 HFALLANVAEDIHRERRRAVHVAA-------GKPPQDSSLAATYRKLDAA 138

                    lnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK
                         + v + L    v  v+tAHPt   RR +   + Ri   +
  gi|1184678   139 D-LDVDKVADTLTGALVSPVITAHPTETRRRTVFDTQHRITELMRLRLHG 187

                    DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvW
                        +D ++++  L R i   + t  iR ++    DE+  G+ Y+    +
  gi|1184678   188 HTRTDDNRDIETELRRHILTLWQTALIRLSRLKISDEIETGLRYYEAAFF 237

                    kGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPE
                    + +P+    v  AL+      +l  + P+++  sW+GGDRDG nP vtPE
  gi|1184678   238 DVIPQVNAEVRDALRKRWPDAKL-LEEPILRPGSWIGGDRDG-NPNVTPE 285

                    vtRDvCLLaRmmAanlYisqvEDLmFElsm....WRCndELRvRAEElyr
                    v R     a  +A   Y++q+  L  Elsm+ +  +    L + A+  +
  gi|1184678   286 VVRHATGRAAYVALAHYFEQITALEQELSMsarlVKVTPALAALADACHE 335

                    taardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntR.....ERaRHL
                     a+ d               EPYR  L  +  +L  t ++  +E   H
  gi|1184678   336 PARAD----------------EPYRRALRVIHARLTSTAreildEQPEHG 369

                    LAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                    L  G+      A      eFL  L+    sL   G +v+AD  L  l
  gi|1184678   370 LDLGLPRYQTPA------EFLADLDAVDGSLRANGSRVLADDRLGRLREA 413

                    vstFGLsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLl
                    v  FG  L  LD+Rq s+ + +v+  +    ++ + Y + sE +R E L
  gi|1184678   414 VRVFGFHLSGLDMRQNSDVHEEVVAELLAWAGVHpDYTSLSEPQRVELLA 463

                    aELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGa.....Yiism
                    aE+  +RPL+       E  +  l+ +   A   +  FG++  ++Yiism
  gi|1184678   464 AEIATRRPLIREGAELSELAQKELGIVAAAAR-AVKVFGPqavpnYIISM 512

                    ataPsDvLAvELLqRECgvkq.........tLrvvPLFEkLADLeAAPAav
                    + + sD+L   +L +E g+   +++++  ++ vvPLFE + DL+     +
  gi|1184678   513 CQSVSDMLEAAVLLKEAGLLDisgstpyaPVGVVPLFETIDDLQRGSSIL 562

                    ekLFsiDWYinri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEii
                    e    +  Y+  ++ +dG qevm+GYsDs KD G  l+A W LY+A  +++
  gi|1184678   563 EAALDLPEYRTMVdarDGHQEVMLGYSDSNKDGGYLAANWALYRAELDLV 612

                    KvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGE
                      A+k G++L lFHGRGGtvGRGGGP   AiL+qPP  ++GslR+t qGE
  gi|1184678   613 ESARKTGIRLRLFHGRGGTVGRGGGPSYDAILAQPPGAVKGSLRITEQGE 662

                    viEfsFGEEnLCFrsLqRFtAAtLEHGm..nPPvsPkPE.WRkLmeemAv
                    vi   + E  +  r L    AAtLE  + +   +    E+  ++++e+A
  gi|1184678   663 VIAAKYAEPRIAHRNLETLLAATLEASLldVEGLGEEAEpAYQVLDELAA 712

                    vAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesL
                     A   Y  +v   P FvEYF+  tP  E G +niGsRP+ RkP   i  L
  gi|1184678   713 LAQRAYSELVHETPGFVEYFKTSTPVSEIGALNIGSRPTSRKPTTSIADL 762

                    RAiPWiFaWtqtRFHLPvWLGvGAAFKhAi..dKDiKnlqkLkEmYkeWP
                    RAiPW+ aW q R  LP W G G AF   i++d D   l  L+++Y  WP
  gi|1184678   763 RAIPWVLAWSQSRVMLPGWYGTGSAFENWIgtDPDGARLRVLQDLYARWP 812

                    FFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkd
                    FFR  l  +  v AK D G+Aa y +L+   +L+ +  +++ ++   t
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  gi|1184678   813 FFRTVLSNMAQVLAKADMGLAARYSELVEDADLRArVFDKIVAEHDRTIR 862

                   lLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykv
                   +   i G  DlL     L   +  R +Y+  Ln +q   L+R R
  gi|1184678   863 MHRLITGQDDLLADNAALARSVFNRFPYLEPLNHLQVELLRRYR------ 906

                   tlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmq
                                s + deLv+              ++Ltm G+A  +
  gi|1184678   907 --------------SGETDELVQRG------------ILLTMSGLATALR 930

                   ntG<-*
                   n G
  gi|1184678   931 NSG    933

gi|168700529|ref|ZP_02732806.1|: domain 1 of 1, from 2 to 920: score 358.2, E = 1.5e-104
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                +v+  +k +  D  Ll   L+  +  L G+   +
  gi|1687005     2    ------------QVA-AQKALGADIRLLGNLLgQAIRRLGGDAAFDL 35

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                     E    + e      +     L  +L  Ld      + +a++    L n
  gi|1687005    36 EEEVRAAAKELRASPSPDAARRLRDRLGTLDVPALRGLIRAFSVFFDLIN 85

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   LAE        R +  +  D a   +A  Es +    ++ v        E
  gi|1687005    86 LAEQQARVRALRHRAAR-PDPARAENA--ESALQSIARRGVPVE-----E 127

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   v + L    v  v+tAHP  + RRs+L K a +   L +L     t+ ++
  gi|1687005   128 VADHLARALVVPVFTAHPSEARRRSVLEKLAAVAQLLDKLEYGQPTPSER 177

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     L +A+  E+ A + tD +R a+P   DE+R  +  +   + + vPK
  gi|1687005   178 DALTDAIAEEVEALWLTDAVRSARPSVLDEVRQVLGVVEARLLDVVPKVY 227

                   RRvDtALKniGinE..RlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                   R+ + AL  +  n ++R+P     ++F sW+GGDRDG +P vt  vt +
  gi|1687005   228 RKLESALEKVYPNHgrRVP---AFLQFGSWIGGDRDG-HPNVTHAVTAEA 273

                   CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                     L        Y++ +E L   ls         +    l    a d
  gi|1687005   274 VRLQQETVLAHYLQRIEALGGKLSH---SAPFVAAGPSLAASLAAD---A 317

                   yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaR.HLLAtGi.seisEeA
                     +    q  P EPYR     + +KL  t    R+H    G +++ +
  gi|1687005   318 KLLPGVAQGKPGEPYRAKCLMIAEKLRRTLAFVRtHADDWGAdAQAPPAG 367

                   vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                   vy    e L  L L    L   G  + ADG++ D++R v  FGL L  LD
  gi|1687005   368 VYVGRGELLADLTLIADDLRRAGATASADGAVRDFIRLVEVFGLHLLTLD 417

                   iRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgs
                   iRq s R+      +    ++ + Y   s + R   L  EL+  RPL+++
  gi|1687005   418 IRQHSARHEAATAEVLAAAGVCpNYAALSADERFAVLAKELESSRPLVPA 467

                   DLPktEEvkDvldafrvLAEL....PiDsFGaYiismataPsDvLAvELL
                    LP t +  +v+ +fr +A + +++  ++ G Yiis +t P   L v L
  gi|1687005   468 HLPFTPDTTEVVRTFRTMAAVleqrCPEALGTYIISSTTEPVHLLEVLLF 517

                   qRECgvkqt......LrvvPLFEkLADLeAAPAavekLFsiDWYinrid.
                    RE  + ++ ++ +++ vvPLFE L  L+ A   v +L  +  Y+ +++
  gi|1687005   518 AREARLFRPaegvsrIDVVPLFEALEPLRSARRIVTRLLELPVYRRQVEl 567

                   ..GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                   ++ +qevm+GYsDs K+ G l  AW LY+Aq E+    +  Gv +  FHG
  gi|1687005   568 rgNRQEVMIGYSDSNKESGFLQSAWALYRAQAELTELGRGAGVTIQFFHG 617

                   RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                   RGG vGRGGGP   AiL+qP  t++G +R+t qGE+i   +G   +  r
  gi|1687005   618 RGGAVGRGGGPANYAILAQPKGTVDGRIRITEQGEMIADRYGHPAVAERH 667
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                    LqRFtAAtLEHGm.nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFv
                    L     A L    ++      P W   ++ +A  A   YR +v+ +P F
  gi|1687005   668 LEQVLDAVLRTSFpDAAEGADPKWLAALDALADSARKHYRGLVYEDPGFL 717

                    EYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLP
                     YF  At   E   + iGsRPa+R  +  ie LRAiPW+F+W q R  LP
  gi|1687005   718 TYFEQATCIGEIAELKIGSRPARRSGARSIEELRAIPWVFSWMQSRHTLP 767

                    vWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPG
                     W G+G A    +      l +L +mY  WPF+R  +D   m+ AK D
  gi|1687005   768 GWFGLGSAVAEFLRANPDGLAMLSDMYARWPFWRTLIDNSQMILAKADMV 817

                    iAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLK
                    iA Ly +L+    L  +   ++  +Y    d + +i G   lLE  P L
  gi|1687005   818 IARLYADLVTDQALAArIYGRIEGEYRAAVDAVCRITGQSALLERSPVLG 867

                    qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                      +  R++Y+  L  +q   L R+R                   +s + +
  gi|1687005   868 TSIERRNPYVDPLSFIQLVLLDRLRN-----------------QSGPRE 899

                    eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    eLv           LE      + G+A G++ntG
  gi|1687005   900 ELVTAV--------LE-----SINGVASGLKNTG    920

gi|289209281|ref|YP_003461347.1|: domain 1 of 1, from 3 to 946: score 357.7, E = 2.2e-104
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         D   R L      +d +L     L  +    ++  L G+ + +av
  gi|2892092     3    QTDLDDRFLP-----KDKELRARVRLFGELLGNVIRKLEGQTVFDAV 44

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                                 +D++  + L a +t  d a +  v +a++    L n+
  gi|2892092    45 EKLRRGFVSLRKDEDPQLRQRLMADITHFDAALTERVIRAFSIYFSLVNI 94

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEE +l yR R  +      + E   t   D   tl+ L   +  + +E
  gi|2892092    95 AEE-DLFYRWRRAQVS----SGEPLWTGSFD--QTLRELHNEG-VTAAEL 136

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L       v+tAHPt + RR  +  + R+      L   ++  e+++
  gi|2892092   137 ERLLAELHYQPVFTAHPTEARRRTTMENQRRVFETADRLNQPELGEEERR 186

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     + E L   iq  +Rt E+R  +P  qDE+++G+ Y+ E +++ +P+  R
  gi|2892092   187 LIIEELETQIQLLWRTNEVRVKKPQVQDEIKYGLFYFEESLFEAIPQSYR 236

                    RvDtALKni.Gi..nERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRD
                      + A++ i G+++   lP  +P  ++F sW+GGDRDG nP vtPEvt
  gi|2892092   237 FLEKAIRRIyGVhpDGSLPVRIPaFLHFGSWIGGDRDG-NPNVTPEVTEL 285

                    vCLLaRmmAanlYisqvEDL..mFElsmWRCndELRvRAEElyrtaardk
                     C La       Yi  v  L+++   s + C        E l +  a
  gi|2892092   286 ACRLAMEQVLREYIKRVNHLrnVLTHSAYMCQPS----QEFLDSLDADSN 331

                    vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                    +              EPYR  L  +R +L  t E     +    + ++ +
  gi|2892092   332 IANAVFHGASDRFESEPYRRKLYIMRYRLRETLETVCRRIQGEAAVLPTN 381

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y + + FL  L L   sL   GD+ iA G+L Dl+R v t G  L  L
  gi|2892092   382 SAYADADAFLQDLNLIRDSLISHGDRNIASGALTDLIRLVETCGFHLHHL 431

                    DiRqEseRqtDvlDAittHLe.iGsYReWsEeKRqEWL........laEL
                    D+RqEs  + + +  + + L +   Y    E  Rq  L++    + la+L
  gi|2892092   432 DVRQESTVHGEAVAQLLQQLApEVDYNTLDESDRQKVLsdliaapaLADL 481

                    kGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvL
                       R  l      t  v +v++a+r   E+  D  G Y+ism+ a s vL
  gi|2892092   482 N--REALDEGALETLRVFEVIQAMR--REIGPDGIGTYVISMTHAASHVL 527

                    AvELLqRECgvk.........qtLrvvPLFEkLADLeAAPAavekLFsiD
                     v LL R  g+ ++++++++   Lr+ PLFE + DL      +e L s
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  gi|2892092   528 EVLLLGRLAGLAgedesgepfCHLRISPLFETIEDLLHVEDVLEGLLSNP 577

                   WYinridG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyG
                    Y   +  +++ q+vm+GYsDs KD G l+  W LY Aq  i+ +  ++G
  gi|2892092   578 VYARLLTAsgnVQDVMLGYSDSCKDGGILASSWNLYEAQKKIVGITDRFG 627

                   vKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFG
                   v+  lFHGRGGtvGRGGGPtH  iL+qPP t++G ++ t qGEv+ + +
  gi|2892092   628 VRCQLFHGRGGTVGRGGGPTHESILAQPPATVQGRIKFTEQGEVLSYKYS 677

                   EEnLCFrsLqRFtAAtLEHGmnPPvsP....kPEWRkLmeemAvvAtEEY
                     +     L    A  L       + P ++++ E+R  m+e+A    + Y
  gi|2892092   678 NAETAVYELG-MGATGLMLASRSLIRParqdRDEYRATMDELARAGEDAY 726

                   RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGie.sLRAiPW
                   R ++ + P   +YF   tP  E G +niGsRP+ R+     ++s+RAiPW
  gi|2892092   727 RDLIDRTPGILDYFYEITPVQEIGFLNIGSRPSHRRKTDRSKsSIRAIPW 776

                   iFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlD
                   +F W q R  LP W G+G A       D   l +L+ mY+eWPFFR  l
  gi|2892092   777 VFGWAQSRHTLPAWYGIGSALEQWRGEDPARLEQLQRMYQEWPFFRSLLS 826

                   LlEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAG
                      m   K D   Aa y +L     L  +   ++R++   t + +L++A
  gi|2892092   827 NCQMALTKADMRTAAEYARLCSDPALAErLYSRVREEHTRTVNEVLRVAR 876

                   HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                      l++  P L   l  R++Y+  Ln +q   L+               s
  gi|2892092   877 LDNLMDETPLLARSLQRRNPYLDPLNSIQIHLLRE--------------S 912

                   KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   + + +     ad     n      P L   L+  +  iAAGm ntG
  gi|2892092   913 RQFDAQADDDAD-----N------PWLS-PLLRSINAIAAGMRNTG    946

gi|226306521|ref|YP_002766481.1|: domain 1 of 1, from 3 to 925: score 357.2, E = 3.1e-104
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         A LR   P      e L e   LL      i+ +  G+++ + v
  gi|2263065     3    TETASLRE-TPREAT--EPLREDIRLLGGILGQIVREQAGDNVFDLV 46

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         s  +  ++      EL +    +   Dai v +a++H   LAnL
  gi|2263065    47 ERARVES--FRVRRSEIDRAELVSLFAEISTDDAIPVIRAFSHFALLANL 94

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AE+++   RR i+          ++   +s +  t+ kL        + v
  gi|2263065    95 AEDIHRERRRAIHVNA-------GEPPRDSTLAATYTKLDAAD-IDSATV 136

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    eAL+   v  v+tAHPt   RR +   ++Ri   +       + v +
  gi|2263065   137 EEALRGALVSPVITAHPTETRRRTVFETQSRITELMRYRERTALSVAETA 186

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ++D  L R i   + t  iR ++   qDE+  G+ Y+   +++ +PK
  gi|2263065   187 DVDLQLRRQILTLWQTALIRLSRLRIQDEIEVGLRYYDAALFEVIPKINA 236

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    v  AL+       l    P+++  sW+GGDRDG nP vt E+
  gi|2263065   237 EVRKALRTRWPDAGL-LPEPILRPGSWIGGDRDG-NPYVTGEIVQRATSR 284

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   a   A    ++ +E L  Elsm      +    + l +t+  d
  gi|2263065   285 AAATALEHHLEELEHLERELSMSARLVSVTPELDLLASTSGDD------- 327

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaR.HLLAtGiseisEeAvytk
                            EPYR  +  +R +L  t     + L A+G s+   eA yt+
  gi|2263065   328 ---SAFRADEPYRRAIRGIRGRLSATALTVLgELPAHG-SDDGLEA-YTD 372

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     +    L +   sL   GD  iAD  L  l   v  FG  L  LD+Rq
  gi|2263065   373 PAQLQRDLGIIDTSLRRFGDETIADDRLDRLREAVEVFGFHLSGLDMRQN 422
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                    seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgsDLP.
                    se +  v+  +    ++ s+Y + +E  R E L aEL  +RPL  +D
  gi|2263065   423 SEVHESVVAELLAWAGVHSdYTSLPEADRVELLSAELTTRRPLTSPDAEf 472

                    ...ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqREC
                    ++  t E++ +    + +  L   +   Yiism+t+ sD+L   +L +E
  gi|2263065   473 selTTKELAIMAAGAKAVRVLGAGAVPNYIISMCTSVSDMLEAAVLLKEV 522

                    gvkq.........tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK
                    gv  ++ +++++ ++ +vPLFE + DL+    ++     i  Y+  +  +
  gi|2263065   523 GVLDpgvgsepscPIGIVPLFETIEDLQGGADTLLATLDIPIYRAIVRSR 572

                    ...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    +++qevm+GYsDs KD G l+A W LY+A  +++  A+k G++L lFHGR
  gi|2263065   573 gdsQEVMLGYSDSNKDGGYLAANWALYRAELDLVDAARKSGIRLRLFHGR 622

                    GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                    GGtvGRGGGP   AiL+qPP  + GslR+t qGEvi   + E  L  r L
  gi|2263065   623 GGTVGRGGGPSYEAILAQPPGAVAGSLRITEQGEVIAAKYAEPRLAHRNL 672

                    qRFtAAtLEHGm...nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                        AAt+E  + + +   s       +++e+A  A   Y  +v   P F
  gi|2263065   673 ETLIAATIESTLldvEGLGSDADAAYAVLDELAALARTAYSELVHDTPGF 722

                    vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                    v YF   tP  E G +niGsRPa Rk    i  LRAiPW+ +W q R  L
  gi|2263065   723 VQYFEASTPVAEIGALNIGSRPASRKQTKAISDLRAIPWVLSWSQSRVML 772

                    PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                    P W G GAAF   id D   l  L  +Y++WPFFR  l  + mv  K D
  gi|2263065   773 PGWYGTGAAFERWIDGDDTRLATLTGLYEKWPFFRTVLSNMAMVMSKSDL 822

                    GiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                    G+Aa y +L+   eL+++ FG  + d+ + t  +   i G   l
  gi|2263065   823 GLAARYADLVPDAELrdRVFG-MITDEHERTIRMYKAITGNENLFADNSG 871

                    LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                    L   +  R +Y+  Ln +q   ++R R                dE
  gi|2263065   872 LERSVHNRFPYLEPLNHLQVELIRRYRS---------------GDES--- 903

                    adeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                              ++v  G+     Ltm G+A  + n G
  gi|2263065   904 ----------DQVRRGIQ----LTMNGLATALRNSG    925

gi|283779027|ref|YP_003369782.1|: domain 1 of 1, from 15 to 942: score 356.6, E = 4.8e-104
                    *->siDAqLRl.LvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkE
                        i A+   +++P  vs  ++L++ D  +l   L++++ +  G++
  gi|2837790    15    YIHAKGGFeMAP--VS--NELLRRDVRMLGDMLgEVMTEAAGPEALA 57

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                     v E   l A      D     EL  k+ sL  +Da +vA+a++    LA
  gi|2837790    58 LVEEIRQL-ARRRRSGDHTAEPELAEKIASLSMSDARIVARAFSIFFDLA 106

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    nLAE+     R Ri+ ++  +         Es i   + +L   +  s +
  gi|2837790   107 NLAED-----RHRIRVLRSREQELHPVSLSES-IGAAIGRLKESG-FSAA 149

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    E   A+    ++Lv+tAHP  + RRs+  K  R+R  L  L   D+ + +
  gi|2837790   150 ETQRAIDKMLIELVFTAHPSEAKRRSIRAKLRRMRHALQELDRTDLLPRE 199

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    +  L+  +  E+   + tD +R ++Pt  +E+  G+s i   +W+ vP+
  gi|2837790   200 RARLESRIRTELTVLWQTDFLRPSRPTVLEEVERGLS-ITPRLWEVVPQV 248

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                       +  AL      E +     L +F sWmGGDRDG nP vt  +t+
  gi|2837790   249 YASMRLALDTHYPGEGIRPGLFL-RFGSWMGGDRDG-NPNVTAPITKQTL 296

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    +  R  A    isq   L   +  +   +   + A+        +   K+
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  gi|2837790   297 VWLRERA----ISQHLALTKTMYDFLSISVREIDADSTLNKGLEEASQKW 342

                   ..YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                   ++  E    + P E YR  +  +R +L      +     t    i+E
  gi|2837790   343 pgLAEALSELAPLEVYRRWVTMIRWRL------SQSSATTSCTSIPEGG- 385

                   ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                   y + Ee    L     sL     + +AD  L   L     FGL L +LD+
  gi|2837790   386 YRDGEELFADLKAMQDSLRSHHSRLLADSELQRWLDLTTVFGLHLTRLDV 435

                   RqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaELkGKRPLlgsD
                   Rq++ R  +v+  i    +i   Y + +E  R   L   +     L
  gi|2837790   436 RQDARRYREVMTEILSVAGIvENYADLPEAERCAALSRSIPWDHDLDREK 485

                   L.PktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLqRE
                   L+P   E  D    +r+ +A     + G  +is++  PsDvL v  L R
  gi|2837790   486 LsPLALETLDLFLVLRdAIAVFGPSCIGGHVISLTQCPSDVLNVLWLWRW 535

                   Cgvkqt.........LrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                    + k  ++++ +++++Lr++PLFEk+ DL+ AP ++  +     Y+ ++
  gi|2837790   536 AQSKAVrdssvpttdeLRIIPLFEKIDDLRNAPETMTSILEHPLYREHVT 585

                   ...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                   + + +q +mvGYsDs KD G l+A W LY+Aq  + +vA ++Gv+++ FH
  gi|2837790   586 rvgDRQIIMVGYSDSTKDGGYLAACWGLYQAQSGLQQVAHDHGVQVTFFH 635

                   GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                   GRGG  GRGGGP    iLs PP+ ++G lR t qGEv+   + + ++ Fr
  gi|2837790   636 GRGGSLGRGGGPAARGILSLPPEALDGTLRLTEQGEVLAERYDDTQVAFR 685

                   sLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFv
                    L   t AtL     P v  kP W  +me + v     YR +v   P F+
  gi|2837790   686 HLEQVTWATLVASALPGVQVKPSWLSMMETLSVQSFKAYRELV-DQPGFI 734

                   EYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLP
                    +F  AtP  E   + iGsRP++R+    +  LRAiPW+F+Wtq R  +P
  gi|2837790   735 AFFAAATPIDEIENLPIGSRPSRRRGERTLGDLRAIPWVFSWTQNRCMIP 784

                   vWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPG
                    W G+G A      KD    q + EmY+ WPF   t+D   +  AK D
  gi|2837790   785 AWYGLGTALSEVKYKDRTAWQTICEMYRLWPFMQATIDNAMLALAKADMY 834

                   iAaLyDkLLvaEeLkPFGksLRdkYvE.tkdlLLkiAGHkDlLEGDPYLK
                   iA  y +L      +    +L ++  ++t++ LL + G  +lL   P+ +
  gi|2837790   835 IAQHYSELAEDPAQRQVCWELIARERDrTRQALLDLVGGSELLSKNPWFQ 884

                   qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                     + +R++Yi  Ln +q   L+R R       l P        E   +a+
  gi|2837790   885 GSIEVRNPYIDPLNLIQIELLRRRR------SLTP--------EA--PAN 918

                   eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   e  +L           D L Lt++GiAAGm  tG
  gi|2837790   919 EAEQLR----------DMLRLTVQGIAAGMRTTG    942

gi|34495510|ref|NP_899725.1|: domain 1 of 1, from 1 to 898: score 356.5, E = 5.1e-104
                   *->siDAqLRlLvPGKvsedekLieYDALL..lDkFL.DiLqDLHGedLk
                                +se +k +   A L  lD+ L++++ +  G  +
  gi|3449551     1    -------------MSEHDKDLPLRADLacLDRLLsEVVGEQEGAVVS 34

                   EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    avq               ++ +E    L  L+P  a  + +a      L
  gi|3449551    35 GAVQAI-----------ALRRGDERSHPLPQLAPEAAASLLRACGLYAQL 73

                   AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                    n+AE+ +   RRR +++        +sA     +   l++L   +  s
  gi|3449551    74 FNIAEDLHHNRRRRAHQLA-------GSAPQQGSLPRALQRLRQDG-VSF 115

                   eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                       + L    v  +ltAHPt   R s+L  +  +R  L+qL A D+t+e
  gi|3449551   116 HALHQLLSHAKVGAILTAHPTEVQRQSVLDGHRAVRRFLSQLNAADLTPE 165
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                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    +++ L+  L R i A + t EiR  + t  DE+  G++Y     ++  P
  gi|3449551   166 EREALEAKLKRAILALWQTSEIRHFKMTVRDEITNGVAYHPLAFFEALPA 215

                    FLRRvDtALKni.GinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                      RR +  +  + G   RlP     i+  sW+GGDRDG nP v     R
  gi|3449551   216 LYRRLEREIGQLwGEEARLP---SFIRVGSWIGGDRDG-NPNVDAGLLRH 261

                    vCLLaRmmAanlYisqvEDLmFEls....mWRCndELRvRAEElyrtaar
                             A   Y++ +  L  Els ++++     E+ + AE     a +
  gi|3449551   262 AVTRQSQQAFEYYLQELKSLYRELSlssrLVEAGAEVLALAEQSPDQAVS 311

                    dkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseis
                                   +EPYR  L  +  KL   R  aR
  gi|3449551   312 R--------------GEEPYRRALATMQGKL---RATARLRGVELACRWD 344

                    EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                    E A y +  e +  L     sL   G   +ADG L  l+R v  FG  L+
  gi|3449551   345 ERAPYRDHRELIQDLASLSASLRAHGSALLADGRLSRLIRSVDVFGFFLM 394

                    KLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLl
                     LD+Rq +  +  v+  +    ++  YR   E  R   L+ EL   R L+
  gi|3449551   395 PLDLRQHAAVHEGVVAELFSAAGLEEYRALDEAARVRVLIRELATPRLLF 444

                    gsDLPktEEvkDvldafrvLAELPiD....sFGaYiismataPsDvLAvE
                     + L   E  +  l  fr  A +  D + ++ G  iis + + sD+LA
  gi|3449551   445 SPYLRYGEQAEKELAIFREAAAIQRDfgveAIGQCIISNCASVSDILALA 494

                    LLqRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYin
                    LL +E g+ + ++++++ ++  vPLFE +ADLe   A +  LF++ WY+
  gi|3449551   495 LLCKEAGLirledgqpRASVNLVPLFETIADLENSEAVMRALFALPWYKQ 544

                    ridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                     +d +++ qevm+GYsDs KD G l   WqL++A   ++Kv  + G +L
  gi|3449551   545 LLDSRervQEVMLGYSDSNKDGGYLTSQWQLWQAETRLVKVFADAGARLQ 594

                    lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                    lFHGRGG vGRGGGP   Ai++qP   + G +R+t qGEvi   + +  +
  gi|3449551   595 LFHGRGGSVGRGGGPSYEAIVAQPAGSVAGRIRITEQGEVITAKYSDPAI 644

                    CFrsLqRFtAAtLEHGmnPPvsPkPEW.RkLmeemAvvAtEEYRsvvvKE
                      r L    AAtLE  +     P  E +  L +e+   A   YR++v
  gi|3449551   645 AGRNLEALVAATLEASLGN--IPGGEVdTALFDELSASAFAAYRALV-ET 691

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
                    P F+ YF  AtP +   ++niGsRPa Rk    i  LRAiPW+F+W q R
  gi|3449551   692 PGFMQYFLEATPVTAIARLNIGSRPASRKSLSSIGDLRAIPWVFSWSQSR 741

                    FHLPvWLGvGAAFKhAidKDiKn.lqkLkEmYkeWPFFRvtlDLlEmvFA
                      LP W GvG A    ++K    +l kL+ +Y+  PFF v l  +E v A
  gi|3449551   742 LMLPGWFGVGSAVAAYVQKHGDAgLAKLQHLYRHSPFFQVMLSNMEQVLA 791

                    KGDPGiAaLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLkiAGHkDlLE
                    K D GiA  + +L+   eL  + FG  + +++  t+d    i G  +lLE
  gi|3449551   792 KADLGIARRFSELVADRELAArlFG-AIEAEWRKTHDAFFAITGQAELLE 840

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                    G P L+  l  R +++  L  +qA  L R+R                +E
  gi|3449551   841 GNPTLRRSLETRLPFLDALGLLQADLLARLR-----------------AE 873

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +    d L  +               Lt+ G  AG+ ntG
  gi|3449551   874 P-DDEDTLYAIH--------------LTINGTSAGLRNTG    898

gi|108799375|ref|YP_639572.1|: domain 1 of 1, from 22 to 946: score 356.3, E = 5.6e-104
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        i    R  v    s   + ++ D  Ll   L+D + +  Ged+ +
  gi|1087993    22    PIGSVTRTEVGREAS---EPMREDIRLLGAILgDTVREQNGEDVFDL 65

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      s  +  ++      EL     ++    ai v +a+ H   LAn
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gi|1087993    66 VERARVES--FRVRRSEIDRAELAGLFDGIGVRAAIPVIRAFTHFALLAN 113

                 LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                 +AE+++   RR ++          ++   +s +  t+ kL +      +E
gi|1087993   114 VAEDIHRERRRAVHVAA-------GEPPQDSSLAATYAKLDSAQ-LDSDE 155

                 vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK.DvtveD
                 v  AL    v  v+tAHPt   RR +   + Ri   L  L A +  t +D
gi|1087993   156 VSAALSGALVSPVITAHPTETRRRTVFDTQHRITE-LMRLRAHgHETTDD 204

                 KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                  ++++  L R i   + t  iR ++   qDE+  G+ Y+    ++ +P+
gi|1087993   205 GRDIELELRRHILTLWQTALIRLSRLKIQDEIETGLRYYRAAFFEVIPRV 254

                 LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    v  AL+       l    P+++  sW+GGDRDG nP vt Ev R
gi|1087993   255 NAEVRSALQTRWPDADL-LAEPILRPGSWIGGDRDG-NPNVTAEVVRQAT 302

                 LLaRmmAanlYisqvEDLmFElsm....WRCndELRvRAEElyrtaardk
                   a   A   Y+  +  L  Elsm+ +     dEL + A+  +  a+ d
gi|1087993   303 SRAAYTAFEHYFAELTGLEQELSMsarlVHVSDELAALADACHEAARAD- 351

                 vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntR.....ERaRHLLAtGis
                               EPYR  L  +  +L  t  +  +    H L  G+
gi|1087993   352 ---------------EPYRRALRVIHGRLTATAleildNQPEHELDLGLE 386

                 eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                   +  A      e L  L++   sL   G  v+AD  LL l   v  FG
gi|1087993   387 RYATPA------ELLADLDVIDASLRGHGSAVLADDRLLRLREAVRVFGF 430

                 sLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaELkGK
                  L  LD+Rq s+ + +v+  +    +++  Y + +E  R + L++EL  +
gi|1087993   431 HLSGLDMRQNSDVHEEVVAELLAWAGVhDDYASLPESDRIDLLVSELATR 480

                 RPLlgsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsD
                 RPL        E  +  ld +r  A   +  FG++  ++Yiism+ + sD
gi|1087993   481 RPLTSQKAELSELARKELDIVRAGAR-AVRVFGPqavpnYIISMCESVSD 529

                 vLAvELLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsi
                 +L   +L +E g+   +++++  ++ +vPLFE + DL+     +e    +
gi|1087993   530 MLEAAILLKEAGLLDvsddepyaPVGIVPLFETIDDLQRGSSILEAALDL 579

                 DWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKky
                   Y+  +  ++++qevm+GYsDs KD G l+A W LY+A  +++   +k
gi|1087993   580 PLYRGMVTARgdsQEVMLGYSDSNKDGGYLAANWALYRAELDLVESSRKT 629

                 GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF
                 G++L lFHGRGGtvGRGGGP   AiL+qPP  +nGslR+t qGEvi   +
gi|1087993   630 GIRLRLFHGRGGTVGRGGGPSYDAILAQPPGAVNGSLRITEQGEVIAAKY 679

                 GEEnLCFrsLqRFtAAtLE......HGmnPPvsPkPEWRkLmeemAvvAt
                  E  +  r L    AAtLE++  +  G+     P  E   +++++A  A
gi|1087993   680 AEPRIAHRNLETLVAATLEstlldvEGLGDEAGPAYE---VLDDLAARAQ 726

                 EEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAi
                   Y  +v   P Fv+YF+  tP  E G +niGsRPa RkP   i  LRAi
gi|1087993   727 RAYAELVHETPGFVDYFKASTPVSEIGALNIGSRPASRKPTTSISDLRAI 776

                 PWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn....lqkLkEmYkeWPF
                 PW+ +W q R  LP W G G AF   i      ++++l  L+++Y+ WPF
gi|1087993   777 PWVLSWSQSRVMLPGWYGTGSAFEQYIAEGAAEsedrLGVLQDLYRRWPF 826

                 FRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtkdl
                 FR  l  +  v AK D G+Aa y +L+  E+L++   +++ d+ + t  +
gi|1087993   827 FRTVLSNMAQVLAKSDLGLAARYSELVEDEDLrRRVFDKIADEHERTIRM 876

                 LLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvt
                    i G  DlL   P L   +  R +Y+  Ln +q   L+R R
gi|1087993   877 HRLITGQDDLLADNPALARSVFNRFPYLEPLNHLQVELLRRYR------- 919

                 lrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqn
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                            E+    deLv+              ++Ltm G+A  + n
  gi|1087993   920 ---------SGED----DELVQRG------------ILLTMSGLATALRN 944

                  tG<-*
                   G
  gi|1087993   945 SG    946

gi|288793906|ref|ZP_06399624.1|: domain 1 of 1, from 11 to 928: score 355.7, E = 8.6e-104
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       DA LR+ +                Ll +    L    G  L + v
  gi|2887939    11    --DAALRADIRRLGT-----------LLGQ---TLARQEGRPLLDLV 41

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                      E+ A+       + +     +L +Ld +    +A+a++    LAn+
  gi|2887939    42 E---EIRAQV-----RSDVPAAAQRLAGLDVTTGTKLARAFSTYFHLANI 83

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   E v+ A   R ++  hG + D a            K +  ++    eE+
  gi|2887939    84 TEQVHRARDLRRRRATHGGWLDQAA-----------KMIAERG-VPAEEI 121

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt..veD
                    A +  +v  v+tAHPt ++RRs+L K   +   L    A  +  +  D
  gi|2887939   122 AAAARRLAVRPVFTAHPTEAARRSILSKLRAVADELDTETANAILygASD 171

                  KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                         L   +   + tDE+R  +P P DE R  + Y+ +   +  P+
  gi|2887939   172 EGPANRRLAELLDLMWQTDELRLDRPDPTDEARNAIYYLRDLYAEAAPQV 221

                  LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                  L      L+ +G+ E  P   PL  F  W+GGDRDG nP vtP vtR+v
  gi|2887939   222 LDDLADTLRTLGV-ETSPTSRPL-SFGTWIGGDRDG-NPFVTPVVTREVL 268

                  LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                   +            +++L+ E+s+ R     R RA  l   a   k
  gi|2887939   269 RIQHEHGIAATEKAMDELITEVSVSR-----RLRAVSLDLSASLAKDLDA 313

                  YiEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                    E  ++++ v  +EPYR     v+ KL ntRER R    +    ++
  gi|2887939   314 LPEVaprFRRVNAEEPYRLKARCVKAKLANTRERLRADTPH----VPGRD 359

                  vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                   y    e +  LEL   sL     +  A G L   +R vs FGL L  +D
  gi|2887939   360 -YRGSSELIADLELLRASLARNSGQLTAVGRLASAIRTVSAFGLHLATMD 408

                  iRqEseRqtDvlDAittHL.eiGsYReWsEeKRqEWLlaELkGKRPLlgs
                  iR  +e++ +vl  + + ++e+  Y   s   R   L  EL G+RPL
  gi|2887939   409 IREHAEKHHEVLAQLYEAVgEVSDYPALSRLERTKLLADELTGRRPLSTQ 458

                  DLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvEL
                  D P tE  +   d f  + E   D FG++  ++Yiism+    DvLA  +
  gi|2887939   459 DSPLTESARKTFDVFAAIRE-AQDRFGPeviesYIISMTLGVDDVLAAVV 507

                  LqRECgv......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                  L RE g+ + ++++  + +vPL E  A+L+A    ++ L s+  Y+  +
  gi|2887939   508 LAREAGLvdvhsgRARIGIVPLLETPAELNAGGELLDELLSLPAYRALVA 557

                  GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                   +++ qevm+GYsDs K+AG     W + +Aq  +  vA ++Gv L lFH
  gi|2887939   558 ARgdvQEVMLGYSDSNKEAGITTSQWSIHRAQRSLRDVAARHGVHLRLFH 607

                  GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                  GRGGtvGRGGGPtH AiL+qP  t++G+++vt qGEvi   +    L
  gi|2887939   608 GRGGTVGRGGGPTHDAILAQPYGTLDGAIKVTEQGEVISDKYTLPALARE 657

                  sLqRFtAAtLEHGm.....nPPvsPkPEWRkLmeemAvvAtEEYRsvvvK
                   L    AA L   + ++ +  P      W   m+ +   A   YRs+v
  gi|2887939   658 NLELTVAAVLQATLlhtapRQPAEMLERWDAAMDVVSSSAFRSYRSLV-E 706

                  EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtq
                  EP    YF   tP    G +niGsRPaKR   G G+  LRAiPW+F Wtq
  gi|2887939   707 EPDLPAYFWASTPTELLGALNIGSRPAKRPNTGaGLSGLRAIPWVFGWTQ 756
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                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                    tR  +P W GvG     A  +       L Em ++W FFR  l  +Em+
  gi|2887939   757 TRQIVPGWFGVGSGL--AAARAAGLADVLAEMNRNWHFFRTFLSNVEMML 804

                    AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                     K D  iA  y + Lv   L+P  +++ ++Y+ tk+ +L +     lL+
  gi|2887939   805 TKTDLTIARRYVETLVPKKLHPIFDKIEQEYELTKQEVLAVTAAPALLDN 854

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                     P L+  l +Rd Y+  L  +q   L+  R+
  gi|2887939   855 SPVLQRTLAVRDTYLEPLHHLQVALLRQYRE------------------- 885

                    skkadeLvkLnptervaP....GLEDtLiLtmKGiAAGmqntG<-*
                    s  a   v   p+ r aP++++ LE  L+ t+ GiAAGm ntG
  gi|2887939   886 SGAAGRAVVTAPGGRRAPndgtALERALLTTVNGIAAGMRNTG    928

gi|75676463|ref|YP_318884.1|: domain 1 of 1, from 3 to 928: score 355.2, E = 1.2e-103
                    *->siDAqLRlLvPGKvsed.ekLieYDALLlDkFL.DiLqDLHGedLkE
                       s+    R+  P   + d +  ++ D  Ll + L+D + D  G++  +
  gi|7567646     3    SLMPLPRAGQPESDAADlDARLRDDIRLLGRILgDTVRDREGPEAFD 49

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                     v      s  +    D     EL a L ++   +++lv +a++    LA
  gi|7567646    50 LVERIRQTSIRFHRDDDKPARRELEAILDGMSTDETVLVVRAFSYFSHLA 99

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE+ +     R + +        + A     +  tl      +  s +
  gi|7567646   100 NIAEDQNNIRQMRSQTLA-------GGARHQGRLAHTLACARKAG-FSAA 141

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    E  +      v  vltAHPt   R+s + ++  +   L       +t+++
  gi|7567646   142 ELRDFFDSAVVSPVLTAHPTEVRRKSTIDREMEVAALLDRRERMQLTPDE 191

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                     +  +E L R +   + tD +RR++ t  DE+  G+s++  t  + vP+
  gi|7567646   192 YEASEEQLRRAVLTLWQTDLLRRTKLTVLDEVANGLSFYDYTFLREVPRL 241

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                        +  L            +  ++  sW+GGDRDG nP vt +v R
  gi|7567646   242 HCMLEDRLHDPEESSAANEIASFLRIGSWIGGDRDG-NPFVTADVMRGTL 290

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                              Y++ + +L  Els+     +L     El + a r   +
  gi|7567646   291 HWQVSRILRHYLDELHELGRELSL---AADLTDVSPELSSLAERSADTSP 337

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vy
                              EPYR  +  +  +L  t   a  L A  +      A+ y
  gi|7567646   338 HRR-------SEPYRLAVSGIYARLSAT---AVKLKADTLRPPYGAApPY 377

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                        eF   L++  +sL      viA G L  l R    FG  L  LD+R
  gi|7567646   378 ASAAEFSADLDILHHSLTANNSEVIARGRLRKLRRAADCFGFHLACLDLR 427

                    qEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgsDL
                    q s  +   +  +      G+sY    Ee R   Ll EL+  RPL  + +
  gi|7567646   428 QNSTVHERTIAELLAAASPGtSYLTLDEEARIVLLLRELRSARPLTSPFI 477

                    PktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAvELLqR
                       EE +  l  f+  AE +++L  D+    i+sm+   sD L v LL +
  gi|7567646   478 TYSEETQGELAVFHAAAEahgtLGPDAIPQCIVSMTEGISDLLEVALLLK 527

                    ECgvkqt.....LrvvPLFEkLADLeAAPAavekLFsiDWYinrid...G
                    E  +  +++++ + +vPLFE + DL+A    +++L s+  Y+  +d+++G
  gi|7567646   528 EADLVDPtghsaINIVPLFETIEDLQACAGIMDRLLSLPEYRALVDsrgG 577

                    KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                     qevm+GYsDs KD G +   W LYkA   ++ v  ++ v+L lFHGRGG
  gi|7567646   578 LQEVMLGYSDSNKDGGFVTSGWELYKAEIGLVEVFERHKVRLRLFHGRGG 627

                    tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
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                     vGRGGGP   AiL+qP   +nG +R+t qGE+i   +   ++    L
  gi|7567646   628 SVGRGGGPSYDAILAQPGGAVNGQIRITEQGEIISSKYSNAEVGRSNLEI 677

                     FtAAtLEHGmnPP..vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEY
                      +AAtLE  +  P++ +P  E+ + me +   A   YR +v+  P F +Y
  gi|7567646   678 LAAATLEASLLQPrqSAPSLEYLDAMESLSSLAYKAYRNLVFETPGFEDY 727

                     FRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvW
                     F   t   E   +niGsRPa Rk    ie LRAiPW+F+W q R  LP W
  gi|7567646   728 FWASTVINEISTLNIGSRPASRKKTRRIEDLRAIPWVFSWAQCRVMLPGW 777

                     LGvGAAFKhAidKD.iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                      G+G A    i+  + K +  L+E+Y eWPFFR+ l  ++mv AK    i
  gi|7567646   778 YGFGSAVEAWIESHpDKGMAFLQELYGEWPFFRMLLSNMDMVLAKSSIAI 827

                     AaLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLK
                     A+ y +L+   eL+   FG+ +R ++  t d LL i G   lL G P L
  gi|7567646   828 ASRYADLVPDVELREaiFGR-IRREWHLTIDKLLAIMGQERLLAGNPLLE 876

                     qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                       +R R +Y+  Ln +q   LK  R                A+ +
  gi|7567646   877 RSIRNRFPYLDPLNHVQVELLKDHR----------------AQCE----- 905

                     eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                             e+v  G+     Lt+ Gi AG+ n G
  gi|7567646   906 -------DEQVLRGIQ----LTINGISAGLRNSG    928

gi|154146694|emb|CAM83982.1|: domain 1 of 1, from 1 to 438: score 355.1, E = 1.3e-103
                     *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1541466     -    ------------------------------------------------ -

                     qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1541466     - ------------------------------------------------ -

                     AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1541466     - ------------------------------------------------ -

                     FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1541466     - ------------------------------------------------ -

                     ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1541466     - ------------------------------------------------ -

                     RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1541466     - ------------------------------------------------ -

                     aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1541466     - ------------------------------------------------ -

                     EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1541466     - ------------------------------------------------ -

                     EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1541466     - ------------------------------------------------ -

                     eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                       +t+ +DAittH +iGsYR+W+Ee+RqE L++EL+  RPL+g+DLP+ +
  gi|1541466     1 --HTEAVDAITTHPGIGSYRDWPEEQRQERLVSELQCNRPLFGPDLPQSD 48

                     EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                     Ev+Dvl++frv+AELP DsFGaY+ismataPsDvLAvELLqRECgvk ++
  gi|1541466    49 EVADVLGTFRVIAELPEDSFGAYVISMATAPSDVLAVELLQRECGVKMPM 98
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                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADL+ A A++e LFs DWY+ ri+GKqe+ +GYsDsGKDAG
  gi|1541466     99 RVVPLFEKLADLQQARATMELLFSNDWYKERINGKQEITIGYSDSGKDAG 148

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEEi+ vA ++GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1541466    149 RLSAAWQLYKAQEEIVGVAERHGVKLTIFHGRGGTVGRGGGPSHLAILSQ 198

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP t+nG lRvtvqGEviE sFGE nLCFr+LqRFtAAtLEHGmnPPvsP
  gi|1541466    199 PPNTVNGLLRVTVQGEVIEKSFGEANLCFRTLQRFTAATLEHGMNPPVSP 248

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L+++mA vAtEEYRs+v++EPRFvEYFR+AtPE+EYG+mniGsR
  gi|1541466    249 KPEWRALLDDMATVATEEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSR 298

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRk +GGiesLRAiPWiFaW qtRFHLPvWLG+GAAF+hA+dK    l
  gi|1541466    299 PSKRKAGGGIESLRAIPWIFAWSQTRFHLPVWLGFGAAFRHAMDKPG-GL 347

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvt+DLlEmvFAKGDPGiAaLyDkLLv  +L+PFG++
  gi|1541466    348 ATLREMYDEWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVPQDLWPFGEQ 397

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y Et+ lLLk+AGH DlLEGDPYL+qrl LRdsYit
  gi|1541466    398 LRANYAETESLLLKVAGHEDLLEGDPYLRQRLMLRDSYITA--------- 438

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1541466     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1541466     - -------------    -

gi|77164288|ref|YP_342813.1|: domain 1 of 1, from 14 to 957: score 352.7, E = 7e-103
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       ++  q     P +   d +L     L       ++q   Ge +  av
  gi|7716428     14    ALQDQTGNTTPWR---DKELRARVKLFGNLLGQVIQNQSGEKVFAAV 57

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                            +   K+ + K   L   +  L+      v +a++    LAn+
  gi|7716428     58 EALRKGYINLRKKENSDKRIQLLRLIDTLNVEKITQVVRAFSIYFSLANI 107

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEE   Ay  R ++++     D +        EEtl+ L   +  sPe
  gi|7716428    108 AEE---AYQHRQRQRR----IDAGGPLWRGSFEETLRELRKSG-ISPEQL 149

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L n +   v+tAHPt + RR ++    +i      L    +   + +
  gi|7716428    150 QIMLDNLAYIPVITAHPTEAKRRTVMEHLRKIFLASKLLDETRLSQREEE 199

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     L   L R iq  ++tDE+R  +P  qDE+  G+ Y+   +++ vP   R
  gi|7716428    200 TLHRQLERQIQVLWKTDEVRAHRPQVQDEIINGLFYFKVSLFQAVPETYR 249

                    RvDtALKni...GinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRD
                      + A+  + ++ + E     vP+ ++F sW+GGDRDG nP vtPEvt
  gi|7716428    250 QLEEAINKVygdMLPESTTLRVPsFLHFGSWIGGDRDG-NPNVTPEVTAM 298

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                       L   mA   Yi  +  L   l        L      l     +d
  gi|7716428    299 AVRLQMRMALQHYIACITKLTRILTH---SIPLIRPSTALTESINQD--L 343

                    KyYiEFWKqvP...PtEPYRviLGdvRDKLY.ntRERaRHLLAtGiseis
                        E ++  P++   EPYR  L  +R +L +n R   R LL       +
  gi|7716428    344 SDCPETFRGDPdrfSREPYRRKLYLMRYRLMdNLRAVERYLLPEIQPTPP 393

                    EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
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                      y   E+FLE L L   sL   GD  iA G L Dl+R v  FG  L
  gi|7716428   394 QGVGYPSEEKFLEDLCLLRDSLSSHGDGNIAAGELQDLIRLVESFGFYLL 443

                   KLDiRqEseRqtDvlDaittHLeiG.sYReWsEeKRqEWLlaELkGKRPL
                   KLD+RqEs R+t+ +  + +HL++ +sY + sE  R   L   L
  gi|7716428   444 KLDVRQESGRHTEAVAELVKHLDLHpSYLDLSETERLGLLSEQLAREEET 493

                   lgsDLPktEEvkDvldafrvLAELPiD....sFGaYiismataPsDvLAv
                          t   ++ ld f+v+A +  + +++ FG Y+ism+ a s v+ v
  gi|7716428   494 TIQRERLTPATRETLDLFHVMAQMRQEvsprVFGHYVISMTHAASHVMEV 543

                   ELL........qRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYi
                     L+   +  + R  + +  L++ PLFE + DLe     +  L     Y+
  gi|7716428   544 MYLgylaglagRRRGQWHCGLQISPLFETIEDLEHIEPVMTALLDDPSYR 593

                   nridG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                     ++  +++qevm+GYsDs KD G l+  W+LY Aq  +       Gv
  gi|7716428   594 ALLQAagnQQEVMIGYSDSCKDGGILASSWKLYDAQKKVTGLTDSRGVDC 643

                   vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                    +FHGRGGt+GRGGGPt  AiLsqP  t++G ++ t qGEv+   +   +
  gi|7716428   644 RIFHGRGGTIGRGGGPTFDAILSQPQGTVHGQIKFTEQGEVLSSRYSNPE 693

                   LCFrsLqRFtAAtLEHG...mnPPvsPkPEWRkLmeemAvvAtEEYRsvv
                        L       +   +  ++PP   k ++  +++ +       YR
  gi|7716428   694 TAIYELNMGISGLIKAStclVQPPQEEKRDYLGIIDSLVETGEQTYREFT 743

                   vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaW
                    +   F +YF  AtP  E G +niGsRP  Rk + +  +s+RAiPW+F W
  gi|7716428   744 EQTSGFQDYFYEATPVNEIGLLNIGSRPPHRKKGDrSKNSVRAIPWVFGW 793

                   tqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEm
                    q R   P W G+G A           l kL+ mY+eWP+FR  l    m
  gi|7716428   794 AQARHTFPAWYGIGSALEKWRAGAPDRLAKLQTMYEEWPYFRALLSNTQM 843

                   vFAKGDPGiAaLyDkL.LvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDl
                     AK +  iA  y  L L  E  +     L ++Y+ t   +L+i G + l
  gi|7716428   844 SLAKAELHIAQQYAGLcLDPETGQKIFALLSAEYQRTVTQVLHIVGAHTL 893

                   LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                   LE  P L   l  Rd+Y+  Ln +q   LKR RDP  ++t+
  gi|7716428   894 LEENPPLALSLQRRDPYLDPLNHIQLTLLKRTRDP--RITP--------- 932

                   dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    E+  + + L              D L+  +  iAAGm ntG
  gi|7716428   933 -EE--REAWL--------------DPLLRSINAIAAGMRNTG    957

gi|254434134|ref|ZP_05047642.1|: domain 1 of 1, from 11 to 954: score 352.7, E = 7e-103
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      ++  q     P +   d +L     L       ++q   Ge +  av
  gi|2544341    11    ALQDQTGNTTPWR---DKELRARVKLFGNLLGQVIQNQSGEKVFAAV 54

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                           +   K+ + K   L   +  L+      v +a++    LAn+
  gi|2544341    55 EALRKGYINLRKKENSDKRIQLLRLIDTLNVEKITQVVRAFSIYFSLANI 104

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEE   Ay  R ++++     D +        EEtl+ L   +  sPe
  gi|2544341   105 AEE---AYQHRQRQRR----IDAGGPLWRGSFEETLRELRKSG-ISPEQL 146

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      L n +   v+tAHPt + RR ++    +i      L    +   + +
  gi|2544341   147 QIMLDNLAYIPVITAHPTEAKRRTVMEHLRKIFLASKLLDETRLSQREEE 196

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    L   L R iq  ++tDE+R  +P  qDE+  G+ Y+   +++ vP   R
  gi|2544341   197 TLHRQLERQIQVLWKTDEVRAHRPQVQDEIINGLFYFKVSLFQAVPETYR 246

                   RvDtALKni...GinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRD
                     + A+  + ++ + E     vP+ ++F sW+GGDRDG nP vtPEvt
  gi|2544341   247 QLEEAINKVygdMLPESTTLRVPsFLHFGSWIGGDRDG-NPNVTPEVTAM 295
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                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                       L   mA   Yi  +  L   l        L      l     +d
  gi|2544341   296 AVRLQMRMALQHYIACITKLTRILTH---SIPLIRPSTALTESINQD--L 340

                    KyYiEFWKqvP...PtEPYRviLGdvRDKLY.ntRERaRHLLAtGiseis
                        E ++  P++   EPYR  L  +R +L +n R   R LL       +
  gi|2544341   341 SDCPETFRGDPdrfSREPYRRKLYLMRYRLMdNLRAVERYLLPEIQPTPP 390

                    EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                        y   E+FLE L L   sL   GD  iA G L Dl+R v  FG  L
  gi|2544341   391 QGVGYPSEEKFLEDLCLLRDSLSSHGDGNIAAGELQDLIRLVESFGFYLL 440

                    KLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPL
                    KLD+RqEs R+t+ +  + +HL++ +sY + sE  R   L   L
  gi|2544341   441 KLDVRQESGRHTEAVAELVKHLDLHpSYLDLSETERLGLLSEQLAREEET 490

                    lgsDLPktEEvkDvldafrvLAELPiD....sFGaYiismataPsDvLAv
                           t   ++ ld f+v+A +  + +++ FG Y+ism+ a s v+ v
  gi|2544341   491 TIQRERLTPATRETLDLFHVMAQMRQEvsprVFGHYVISMTHAASHVMEV 540

                    ELL........qRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYi
                      L+   +  + R  + +  L++ PLFE + DLe     +  L     Y+
  gi|2544341   541 MYLgylaglagRRRGQWHCGLQISPLFETIEDLEHIEPVMTALLDDPSYR 590

                    nridG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                      ++  +++qevm+GYsDs KD G l+  W+LY Aq  +       Gv
  gi|2544341   591 ALLQAagnQQEVMIGYSDSCKDGGILASSWKLYDAQKKVTGLTDSRGVDC 640

                    vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                     +FHGRGGt+GRGGGPt  AiLsqP  t++G ++ t qGEv+   +   +
  gi|2544341   641 RIFHGRGGTIGRGGGPTFDAILSQPQGTVHGQIKFTEQGEVLSSRYSNPE 690

                    LCFrsLqRFtAAtLEHG...mnPPvsPkPEWRkLmeemAvvAtEEYRsvv
                         L       +   +  ++PP   k ++  +++ +       YR
  gi|2544341   691 TAIYELNMGISGLIKAStclVQPPQEEKRDYLGIIDSLVETGEQTYREFT 740

                    vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaW
                     +   F +YF  AtP  E G +niGsRP  Rk + +  +s+RAiPW+F W
  gi|2544341   741 EQTSGFQDYFYEATPVNEIGLLNIGSRPPHRKKGDrSKNSVRAIPWVFGW 790

                    tqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEm
                     q R   P W G+G A           l kL+ mY+eWP+FR  l    m
  gi|2544341   791 AQARHTFPAWYGIGSALEKWRAGAPDRLAKLQTMYEEWPYFRALLSNTQM 840

                    vFAKGDPGiAaLyDkL.LvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDl
                      AK +  iA  y  L L  E  +     L ++Y+ t   +L+i G + l
  gi|2544341   841 SLAKAELHIAQQYAGLcLDPETGQKIFALLSAEYQRTVTQVLHIVGAHTL 890

                    LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                    LE  P L   l  Rd+Y+  Ln +q   LKR RDP  ++t+
  gi|2544341   891 LEENPPLALSLQRRDPYLDPLNHIQLTLLKRTRDP--RITP--------- 929

                    dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     E+  + + L              D L+  +  iAAGm ntG
  gi|2544341   930 -EE--REAWL--------------DPLLRSINAIAAGMRNTG    954

gi|220934054|ref|YP_002512953.1|: domain 1 of 1, from 1 to 947: score 352.5, E = 8e-103
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           +   L P      +k ++    L    L+ +L+ L G     a
  gi|2209340     1    ---MKEDQLMPVNLPPRDKELRARVKLFGNLLgKVLKRLEGRRALAA 44

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v            + D+ K   L a +  Ld     l+ +a++    LAn
  gi|2209340    45 VETLRKGFIALRKQDDPAKRAKLMAFIDKLDADSLELIIRAFSTYFSLAN 94

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AEE +  yR R ++        E+        + tl+ L  ++   P++
  gi|2209340    95 IAEE-DFLYRERRRQVS------EGGPLWVGSFDHTLRELHEQG--IPAD 135

                    vFeALKnqsvDL.vltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
```

```
                  + L  q   ++v+tAHPt + RR ++  + Ri      L  + +  e+
gi|2209340   136 SLQRLLDQLAYVpVFTAHPTEARRRTVMEAQRRIFLAADRLNDRRLGREE 185

                 KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                 ++EL   L   iq  +Rt E+R  +P  qDE+++G+ Y+ E +++ vP
gi|2209340   186 REELTQELETRIQVLWRTNEVRVKKPQVQDEIKYGLFYFEESLFNAVPIT 235

                 LRRvDtALKniGinERl...PYdvP.LikFssWmGGDRDGknPRvtPEvt
                  R  + A++    n+  +++   vP+ ++F sW+GGDRDG nP vtP vt
gi|2209340   236 YRFLEKAIRRTYGNDEAgnpRVRVPsFLRFGSWIGGDRDG-NPNVTPAVT 284

                 RDvCLLaRmmAanlYisqvEDLmFEl..smWRCn.dELRvRAEElyrtaa
                    C La       Y+  v  L  El++s++ C ++E      E  +  a
gi|2209340   285 ELACRLAMEQVLSEYLRRVSALRHELthSLYMCQpSEAFLESLERDSNIA 334

                 rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                    v +   + +     tEPYR  L  +R +L  t    R  L    + +
gi|2209340   335 TA-VFRGSADRFE----TEPYRRKLYIMRYRLTETLNTVRRRLNGENAVL 379

                 sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                 + +  y    e L  L L   sL   GD  +A G L Dl+R   tFG  L
gi|2209340   380 PANSAYASAAEMLNDLRLMHDSLVSHGDANVAAGKLTDLIRLAETFGFHL 429

                 vKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWL..laELkGK
                   LDiRqEs  +   +  i +  ++  +Y   sE  R   L +laE +
gi|2209340   430 FHLDIRQESTVHGQTVAEILKATGLNEdYDALSEPERLALLarLAEAEEL 479

                 RPLlgsDLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDv
                   L g  L  t +++ Ev  v++ +r  AE+  +  G Y+ism+ a s v
gi|2209340   480 PRLDGEALSETAretlEVFHVIGRMR--AEVGPEGIGTYVISMTHAASHV 527

                 LAvELLqRECgvk.........qtLrvvPLFEkLADLeAAPAavekLFsi
                 + v  L R  g+ ++++ ++    +rv PLFE + DL+     +e L
gi|2209340   528 MEVMFLARLAGLAgrneagecfCQIRVSPLFETIEDLRHIEEVLEDLLTQ 577

                 DWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKky
                   Y   +   ++ qevm+GYsDs KD G l+  W LY Aq  i ++   +
gi|2209340   578 PVYARMLKASgnlQEVMLGYSDSCKDGGILASSWNLYEAQQKILRITGAH 627

                 GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF
                  v   lFHGRGGt+GRGGGPtH  iL+qPP t++G ++ t qGEv+ + +
gi|2209340   628 HVACRLFHGRGGTIGRGGGPTHESILAQPPGTVHGQIKFTEQGEVLSYKY 677

                 GEEnLCFrsLqR....FtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEE
                    +     L  + ++   A      nPP+  + ++  +m+e+A    E
gi|2209340   678 SNVETAVYELSMgatgLIKASRCLIDNPPMD-RRDYLGIMDELAALGEEA 726

                 YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGie.sLRAiP
                 YR +  +     +YF   tP  E G++niGsRP+ R+ +   ++s+RAiP
gi|2209340   727 YRDLTDRTEGVLDYFYEITPVQEIGQLNIGSRPSHRRKADRSKsSIRAIP 776

                 WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                 W+F W q R  LP W G+G A     + D   l kL+ mY+eWPFFR  l
gi|2209340   777 WVFGWAQSRHTLPAWYGIGTALERWRQNDPSRLAKLQTMYNEWPFFRSLL 826

                 DLlEmvFAKGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLki
                     m   K D   A  y +L    eL ++ FG+ + ++++ t   +L +
gi|2209340   827 SNCQMALTKADMRTAEEYARLCHDPELakRVFGR-IHEEFERTVTQVLNV 875

                 AGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPh
                 A  + lL+  P L   l  R++Y+  Ln +q   L+R R
gi|2209340   876 ADTQTLLDENPTLALSLMRRNPYMDPLNHIQITLLRRHR----------- 914

                 lsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-
                    E  + +           p  +  P +   L+  +  iAAGm ntG
gi|2209340   915 ---ELHERQ-----------PEAEQDPWIS-PLLRSINAIAAGMRNTG   947

                 *

gi|2209340     -   -
```

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gi|20196764|emb|CAC86386.1|: domain 1 of 1, from 1 to 398: score 352.1, E = 1.1e-102
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2019676     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2019676     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2019676     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                           svDLv+tAHPtqs+RRsLLqKnaRiRnCL+ LsAKDv +eDKk
  gi|2019676     1 -------SVDLVFTAHPTQSARRSLLQKNARIRNCLTLLSAKDVAPEDKK 43

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRRaqPtPqDEmR+GmsYiHEtvWkGvPKFLR
  gi|2019676    44 ELDEALQREIQAAFRTDEIRRAQPTPQDEMRYGMSYIHETVWKGVPKFLR 93

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGinERlPY+vPLikF+sWmGGDRDG nPR tPEvtRDvCLL
  gi|2019676    94 RVDTALKNIGINERLPYNVPLIKFCSWMGGDRDG-NPRATPEVTRDVCLL 142

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    +RmmAanlYi+qvEDLmFElsmWRCn+ELRvRAEEl++t+a++kv+KyYi
  gi|2019676   143 SRMMAANLYIDQVEDLMFELSMWRCNEELRVRAEELHSTPASKKVTKYYI 192

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP+EPYRviLG+vRDKLYntRERaRHLLAtG+seisEe v+t++
  gi|2019676   193 EFWKQIPPNEPYRVILGAVRDKLYNTRERARHLLATGFSEISEESVFTNI 242

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    +eFLEPLELCYksLC+CGDk+iADGsLLDlLRqv+tFGLsLvKLDiRqEs
  gi|2019676   243 DEFLEPLELCYKSLCDCGDKAIADGSLLDLLRQVFTFGLSLVKLDIRQES 292

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+tDvlDAittHL+iGsYR+W+E+KR+EWL+ EL+GKRPLl++DLP+tE
  gi|2019676   293 ERHTDVLDAITTHLGIGSYRSWPEDKRMEWLVMELRGKRPLLPPDLPMTE 342

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dv++a+rv+AELP+DsFG+Yiism+taPsDvLAvELLqRECg++qtL
  gi|2019676   343 EIADVIGAMRVIAELPSDSFGPYIISMCTAPSDVLAVELLQRECGIRQTL 392

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLF
  gi|2019676   393 PVVPLF---------------------------------------------- 398

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|2019676     - ------------------------------------------------- -

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

  gi|2019676     - ------------------------------------------------- -

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|2019676     - ------------------------------------------------- -

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|2019676     - ------------------------------------------------- -

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|2019676     - ------------------------------------------------- -

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
```

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  gi|2019676     - ------------------------------------------------ -

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|2019676     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|2019676     - -------------    -

gi|270502847|ref|ZP_06219747.1|: domain 1 of 1, from 11 to 928: score 351.9, E = 1.2e-102
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        DA LR+ +               Ll +    L    G  L + v
  gi|2705028    11    --DAALRADIRRLGT-----------LLGQ---TLARQEGRPLLDLV 41

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       E+ A+       + +     +L +Ld +    +A+a++    LAn+
  gi|2705028    42 E---EIRAQV-----RSDVPAAAQRLAGLDVTTGTKLARAFSTYFHLANI 83

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    E v+ A   R ++  hG + D a            K +  ++    eE+
  gi|2705028    84 TEQVHRARDLRRRRATHGGWLDQAA-----------KMIAERG-VPAEEI 121

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt..veD
                     A +  +v  v+tAHPt ++RRs+L K   +   L    A  +  +  D
  gi|2705028   122 AAAARRLAVRPVFTAHPTEAARRSILSKLRAVADELDTETANAILygASD 171

                   KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                          L   +   + tDE+R  +P P DE R  + Y+ +   +  P+
  gi|2705028   172 EGPANRRLAELLDLMWQTDELRLDRPDPTDEARNAIYYLRDLYAEAAPQV 221

                   LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   L      L+ +G+ E  P   PL  F  W+GGDRDG nP vtP vtR+v
  gi|2705028   222 LDDLADTLRTLGV-ETSPTSRPL-SFGTWIGGDRDG-NPFVTPVVTREVL 268

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    +            +++L+ E+s+ R     R RA  l   a   k
  gi|2705028   269 RIQHEHGIAATEKAMDELITEVSVSR-----RLRAVSLDLSASLAKDLDA 313

                   YiEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                     E  ++++ v  +EPYR     v+ KL ntRER R    +    ++
  gi|2705028   314 LPEVaprFRRVNAEEPYRLKARCVKAKLANTRERLRADTPH----VPGRD 359

                   vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                    y    e +  LEL   sL     +  A G L   +R vs FGL L  +D
  gi|2705028   360 -YRGSSELIADLELLRASLARNSGQLTAVGRLASAIRTVSAFGLHLATMD 408

                   iRqEseRqtDvlDAittHL.eiGsYReWsEeKRqEWLlaELkGKRPLlgs
                   iR  +e++ +vl  + + ++e+  Y   s   R   L  EL G+RPL
  gi|2705028   409 IREHAEKHHEVLAQLYEAVgEVSDYPALSRLERTKLLADELTGRRPLSTQ 458

                   DLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvEL
                   D P tE  +   d f  + E   D FG++  ++Yiism+    DvLA  +
  gi|2705028   459 DSPLTESARKTFDVFAAIRE-AQDRFGPeviesYIISMTLGVDDVLAAVV 507

                   LqRECgv......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                   L RE g+ + ++++  + +vPL E  A+L+A    ++ L s+  Y+  +
  gi|2705028   508 LAREAGLvdvhsgRARIGIVPLLETPAELNAGGELLDELLSLPAYRALVA 557

                   GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                    +++ qevm+GYsDs K+AG     W + +Aq  +  vA ++Gv L lFH
  gi|2705028   558 ARgdvQEVMLGYSDSNKEAGITTSQWSIHRAQRSLRDVAARHGVHLRLFH 607

                   GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                   GRGGtvGRGGGPtH AiL+qP  t++G+++vt qGEvi   +    L
  gi|2705028   608 GRGGTVGRGGGPTHDAILAQPYGTLDGAIKVTEQGEVISDKYTLPALARE 657

                   sLqRFtAAtLEHGm.....nPPvsPkPEWRkLmeemAvvAtEEYRsvvvK
                    L    AA L   + ++ +  P      W   m+ +   A   YRs+v
  gi|2705028   658 NLELTVAAVLQATLlhtapRQPAEMLERWDAAMDVVSESAFRSYRSLV-E 706
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                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtq
                    +P    YF   tP    G +niGsRPaKR   G G+  LRAiPW+F Wtq
  gi|2705028   707 DPDLPAYFWASTPTELLGALNIGSRPAKRPNTGaGLSGLRAIPWVFGWTQ 756

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                    tR  +P W GvG     A  +       L Em ++W FFR  l  +Em+
  gi|2705028   757 TRQIVPGWFGVGSGL--AAARAAGLADVLAEMNRNWHFFRTFLSNVEMML 804

                    AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                     K D  iA  y + Lv   L+P  +++ ++Y+ tk+ +L +     lL+
  gi|2705028   805 TKTDLTIARRYVETLVPKKLHPIFDKIEQEYELTKQEVLAVTAAPALLDN 854

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                     P L+  l +Rd Y+  L  +q   L+  R+
  gi|2705028   855 SPVLQRTLAVRDTYLEPLHHLQVALLRQYRE------------------- 885

                    skkadeLvkLnptervaP....GLEDtLiLtmKGiAAGmqntG<-*
                    s  a   v   p+ r aP++++ LE  L+ t+ GiAAGm ntG
  gi|2705028   886 SGAAGRAVVTAPGGRRAPndgtALERALLTTVNGIAAGMRNTG    928

gi|238062745|ref|ZP_04607454.1|: domain 1 of 1, from 11 to 928: score 350.9, E = 2.4e-102
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         DA LR+ +                Ll +    L    G  L + v
  gi|2380627    11    --DAALRADIRRLGT----------LLGQ---TLARQEGRPLLDLV 41

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        E+ A+      +        +L +Ld +    +A+a++    LAn+
  gi|2380627    42 E---EIRAQVRSDAPAA-----AQRLGGLDVTTGTKLARAFSTYFHLANI 83

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     E v   +R R  +++         A     ++   K +  ++    eE+
  gi|2380627    84 TEQV---HRARDLRRR--------RAIQGGWLDQAAKMIAERG-VPAEEI 121

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt..veD
                      A +  +v  v+tAHPt ++RRs+L K   +   L    A  +  +  D
  gi|2380627   122 AAAARRLAVRPVFTAHPTEAARRSILSKLRAVADELDAETANAILygASD 171

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                           L   +   + tDE+R  +P P DE R  + Y+ +   +  P+
  gi|2380627   172 EGPANRRLAELLDLMWQTDELRLDRPDPTDEARNAIYYLRDLYAEAAPQV 221

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    L      L+ +G+ E  P   PL  F  W+GGDRDG nP vtP vt +v
  gi|2380627   222 LEDLADTLRTLGV-ETSPTARPL-TFGTWIGGDRDG-NPFVTPQVTGEVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     +            +E L+ E+s+ R    LR    +l    a d
  gi|2380627   269 RIQHEHGIAATEAAMEHLINEVSVSR---RLRGVSLDLSASLAAD--LDA 313

                    YiEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                      E  ++++ v  +EPYR     v+ KL ntRER R     G   ++
  gi|2380627   314 LPEVaprFRRVNAEEPYRLKARCVKAKLANTRERLR----RGTPHVPGRD 359

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                     y    e +  LEL   sL     +  A G L   +R vs FGL L  +D
  gi|2380627   360 -YRGAAELIADLELLRASLARNAGQLTAVGRLATTIRTVSAFGLHLATMD 408

                    iRqEseRqtDvlDAittHL.eiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    +R  +e++ +vl  +   ++e+  Y +     R   L  EL G+RPL
  gi|2380627   409 VREHAEKHHEVLTQLYAAVgEVSDYPSLTRLERTKLLADELTGRRPLSTL 458

                    DLPktEEvkDvldafrvLAELPiDsFG.....aYiismataPsDvLAvEL
                    D P tE  +   d f  + E   D FG++  ++Yiism+    DvLA  +
  gi|2380627   459 DTPLTESARKTFDVFATIRE-AQDRFGsevieSYIISMTLGVDDVLAAVV 507

                    LqRECgv......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                    L RE g+ + ++++  +  vPL E  A+L+A    ++ L s+  Y+  +
  gi|2380627   508 LAREAGLvdvhsgRARIGFVPLLETPAELNAGGELLDELLSLPAYRSLVA 557

                    GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                     +++ qevm+GYsDs K+AG     W + +Aq  +  vA ++Gv L lFH
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  gi|2380627   558 ARgdvQEVMLGYSDSNKEAGITTSQWSIHRAQRALRDVAARHGVHLRLFH 607

                   GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                   GRGGtvGRGGGPtH AiL+qP  t++G+++vt qGEvi   +    L
  gi|2380627   608 GRGGTVGRGGGPTHEAILAQPYGTLDGAIKVTEQGEVISDKYTLPALARE 657

                   sLqRFtAAtLEHGm.....nPPvsPkPEWRkLmeemAvvAtEEYRsvvvK
                    L    AA L   + ++ +  P      W   m+ +   A   YRs+v
  gi|2380627   658 NLELTMAAVLQATLlhtapRQPAEMLERWDASMDVVSDAAFRSYRSLV-E 706

                   EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtq
                   +P   EYF   tP    G +niGsRPaKR   G G+  LRAiPW+F Wtq
  gi|2380627   707 DPDLPEYFWASTPTELLGALNIGSRPAKRPNTGaGLGGLRAIPWVFGWTQ 756

                   tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                   tR  +P W GvG     A  ++      L Em ++W FFR  l  +Em+
  gi|2380627   757 TRQIVPGWFGVGSGL--AAAREAGLAEVLAEMHRNWHFFRTFLSNVEMML 804

                   AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                    K D  iA  y + Lv   L+P   ++ ++Y+ tk+ +L +     lLE
  gi|2380627   805 TKTDLSIARRYVETLVPKKLHPIFAKIEQEYELTKQEVLAVTASPALLEN 854

                   DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                    P L+  l +Rd Y+  L  +q   L+  RD
  gi|2380627   855 SPVLQRTLAVRDTYLEPLHHLQVALLRQYRD------------------- 885

                   skkadeLvkLnptervaP....GLEDtLiLtmKGiAAGmqntG<-*
                   s  a   v   p+ r aP++++ LE  L+ t+ GiAAGm ntG
  gi|2380627   886 SGAAGRAVATAPGGRRAPsdgtALERALLTTVNGIAAGMRNTG    928

gi|283843167|ref|ZP_06360698.1|: domain 1 of 1, from 7 to 936: score 350.3, E = 3.5e-102
                   *->siDAqLRlLvPGKvs..edekLieYDALLlDkFL.DiLqDLHGedLk
                      s  A      P   +  e e  ++ D  Ll + L+D + +  G+++
  gi|2838431     7    SAGAEPVSERPDDAAaiEAETRLRNDIRLLGRILgDTVREQEGQSVF 53

                   EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                   + v      s  +    D     EL a L ++   D++ + +a++    L
  gi|2838431    54 DLVENIRQTSIRFHRDDDKTARAELAAILDGMSIPDTMRIVRAFSYFSHL 103

                   AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                   An+AE+        i++ + G  +  +sA     +  tl +    +  s
  gi|2838431   104 ANIAED-----QNNIRQMRAG--STAGSAPRAGLLAKTLAHARQEG-ISA 145

                   eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                   +E         v  vltAHPt   R+s + ++  i   L q     +t +
  gi|2838431   146 AELRKFFATALVSPVLTAHPTEVRRKSTMDREMQIASLLDQRDRVQLTAD 195

                   DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                   +  + +E L R +   ++t  +RR++ t  DE+  G+s++  t  + vP+
  gi|2838431   196 EWADNEERLRRAVETLWKTNLLRRTKLTVLDEVTNGLSFYDYTFLREVPR 245

                   FLRRvDtALKniGinERlPYd...vPLikFssWmGGDRDGknPRvtPEvt
                        +  L      E +  +++ +  ++  sW+GGDRDG nP vt Ev
  gi|2838431   246 LHSALEDRLADAAKAEGVNSEgelASFLRMGSWIGGDRDG-NPFVTAEVL 294

                   RDvCLLaRmmAanlYisqvEDLmFElsmWR....CndELRvRAEElyrta
                        L        Y++ + +L  Els+  +  +  d +++ AE    t+
  gi|2838431   295 HGTLKLQSTRVLRYYLEELHELGSELSLAShlagITDTVKALAEISPDTS 344

                   ardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi.s
                         Ky           EPYR  +  +  +L  t   a  L    +++
  gi|2838431   345 PHR---KY-----------EPYRLAVSGIYARLAAT---ALALEVENLrA 377

                   eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                    + E A y    +F   L+    sL +    viA G L  l R +  FG
  gi|2838431   378 PVGEAAPYASAQDFKADLDAIHLSLTQHNSGVIARGRLRQLRRAIDCFGF 427

                   sLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK
                    L  LD+Rq s  +   +  +      G+sY    Ee R   L+aEL+
  gi|2838431   428 HLACLDMRQNSAVHERTVGELMDAARPGtSYAVLDEEARIALLIAELRST 477
```

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                    RPLlgsDLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDv
                    RPL    +   +E    l  fr+  +  A     +    iism+   sD
  gi|2838431   478 RPLTSMFVKYSDETVGELSVFReaakAHATYGAAAIPQCIISMTKGVSDL 527

                    LAvELLqRECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYi
                    L v +L +E g+ +++++ ++ vvPLFE + DL+A    +++L +i  Y+
  gi|2838431   528 LEVAVLLKEVGLidpsgRSAINVVPLFETIEDLQACAKIMDRLLAIPEYR 577

                    nridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                      +d +++ qevm+GYsDs KD G +   W LYkA   +i +  ++Gv+L
  gi|2838431   578 RLVDSRgsvQEVMLGYSDSNKDGGFVTSGWELYKAEIGLIEIFEHHGVRL 627

                    vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                     lFHGRGG vGRGGGP   Ai++qP   +nG +R+t qGE+i   +   +
  gi|2838431   628 RLFHGRGGSVGRGGGPSYDAIVAQPGGAVNGQIRITEQGEIITSKYSNVE 677

                    LCFrsLqRFtAAtLEHGmnPP..vsPkPEWRkLmeemAvvAtEEYRsvvv
                    +    L   +AAtLE  +  P++v+P+ ++ + me++   A   YR +v+
  gi|2838431   678 VGRNNLEILAAATLEASLLQPkrVAPHRDYLEAMEQLSALAFKAYRGLVY 727

                    KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                        Fv+YF   t   E   +niGsRPa Rk    ie LRAiPW+F+W q
  gi|2838431   728 ETDGFVDYFWASTVINEISTLNIGSRPASRKKTRAIEDLRAIPWVFSWAQ 777

                    tRFHLPvWLGvGAAF.KhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                     R  LP W G+G A + +      K +  L+ mY+eWPFFR  l  ++mv
  gi|2838431   778 CRLMLPGWYGFGSAVsAWVTAHPDKGIAFLQKMYQEWPFFRTLLSNMDMV 827

                    FAKGDPGiAaLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLkiAGHkDl
                      K   GiA+ y +L+   +++ + FG+ +R+++    ++L  i     l
  gi|2838431   828 LSKSSIGIASRYAELVEDVDVREriFGR-IRAEWHSSIEYLFAIMQQDRL 876

                    LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                    L   P L   +R R +Y+  Ln +q                  +l +E+
  gi|2838431   877 LQSNPLLERSIRHRFPYLDPLNHVQV-----------------QLLREHR 909

                    dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      +           p e+v  G+     Lt+ Gi AG+ n G
  gi|2838431   910 THD-----------PDEQVLRGVQ----LTINGISAGLRNSG    936

gi|145593441|ref|YP_001157738.1|: domain 1 of 1, from 37 to 972: score 350.2, E = 3.9e-102
                    *->siDAqLRlLvPGKvsed.ekLieYDALLlDkFLDiLqDLHGedLkEa
                       s   + R++      + ++  ++ D   l   L   q L  ++ +
  gi|1455934    37    SYSRKERIVTDQHDHDGpDAALRADIRRLGTLLG--QTLARQEGRPL 81

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                         E+ A+      +        +L +Ld a    +A+a++    LAn
  gi|1455934    82 LDLVEEIRAQVRTDAPAA-----AQRLAGLDVATGTRLARAFSTYFHLAN 126

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E v   +R R  +++         A     ++ t K +  ++    eE
  gi|1455934   127 ITEQV---HRARDLRRR--------RAVQGGWLDQTAKMIAERG-VPAEE 164

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt..ve
                    +  A +  ++  v+tAHPt ++RRs+L K   i   L       v  +
  gi|1455934   165 IAAAARRLAIRPVFTAHPTEAARRSILSKLRAIADELDTETTNAVLygAS 214

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    D       L   +   + tDE+R  +P P DE R  + Y+ +   +  P+
  gi|1455934   215 DEGPANRRLAELLDLMWQTDELRLDRPDPTDEARNAIYYLRDLYAEAAPQ 264

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     L      L+ +G+ E  P   PL  F  W+GGDRDG nP vtP vtR+v
  gi|1455934   265 VLDDLADTLRTLGV-ETSPTARPL-TFGTWIGGDRDG-NPFVTPTVTREV 311

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      +a           ++ L+ E+s+ R    LR    +l    a d
  gi|1455934   312 LAIAHEHGLAATEKAMDQLINEVSVSR---RLRGVSLDLSASLATD--LD 356

                    yYiEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                       E  ++++ v  +EPYR     v+ KL ntR R    L +G +  +
```

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  gi|1455934   357 ALPEVaprFRRVNAEEPYRLKARCVKAKLANTRQR----LWQGTAHTPGR 402

                   AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                     y   +e +  LEL   sL     +  A G +   +R vs FGL L  +
  gi|1455934   403 D-YRGSDELIADLELLRASLARNSGQLTAVGRIASTIRTVSAFGLHLATM 451

                   DiRqEseRqtDvlDAittHL.eiGsYReWsEeKRqEWLlaELkGKRPLlg
                   D+R  +e++ +vl  +   ++e+  Y   s   R   L  EL G+RPL
  gi|1455934   452 DVREHAEKHHEVLTQLFGAVgEVSDYPALSRLERTKLLADELTGRRPLST 501

                   sDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvE
                    D P tE  +   d f  + E   D FG +  ++Yiism+    DvLA
  gi|1455934   502 LDTPLTESARRTFDVFGTIRE-AQDRFGTeviesYIISMTLGVDDVLAAV 550

                   LLqRECgv......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                   +L RE g+ + ++++  +  vPL E  A+L+A    ++ L s+  Y+  +
  gi|1455934   551 VLAREAGLvdvhssRARIGFVPLLETPAELNAGGELLDELLSLPAYRALV 600

                   dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                     +++ qevm+GYsDs K+AG     W + +Aq  +  vA ++Gv+L lF
  gi|1455934   601 TARgdvQEVMLGYSDSNKEAGITTSQWSIHRAQRALRDVAARHGVQLRLF 650

                   HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                   HGRGGtvGRGGGPtH AiL+qP  t++G ++vt qGEvi   +    L
  gi|1455934   651 HGRGGTVGRGGGPTHDAILAQPYGTLDGEIKVTEQGEVISDKYTLPALAR 700

                   rsLqRFtAAtLEHGm..nPPvsPkPEWRkLmeemAvvAtEEYRsv..vvK
                     L    AA L   + +  P  P     +    m vv    YRs ++ v
  gi|1455934   701 ENLELTVAAVLQSTLlhTAPRQPAEMLERWDATMDVVSAAAYRSYrdLVE 750

                   EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtq
                   +P    YF   tP    G +niGsRPaKR   G G+  LRAiPW+F Wtq
  gi|1455934   751 DPDLPAYFWASTPTELLGALNIGSRPAKRPNTGaGLAGLRAIPWVFGWTQ 800

                   tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                   tR  +P W GvG     A  +       L Em + W FFR  l  +Em+
  gi|1455934   801 TRQIVPGWFGVGSGL--AAARAAGHGDVLAEMHRSWHFFRTFLSNVEMML 848

                   AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                    K D  iA  y + Lv   L+P  +++ ++Y+ t+  +L +    DlLE
  gi|1455934   849 TKTDLTIARRYVETLVPKKLHPIFHKIEQEYELTRREVLAVTVSPDLLEN 898

                   DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                    P L+  l +Rd Y+  L  +q   L+  RD
  gi|1455934   899 APVLQRTLAVRDTYLEPLHHLQVALLQQYRD------------------- 929

                   skkadeLvkLnptervaP....GLEDtLiLtmKGiAAGmqntG<-*
                   s  +   v   p++r aP++++ LE  L+ t+ GiAAGm ntG
  gi|1455934   930 SGAPGRAVVTAPGSRRAPsdgtALERALLTTVNGIAAGMRNTG    972

gi|280964818|ref|ZP_06239332.1|: domain 1 of 1, from 38 to 968: score 350.0, E = 4.6e-102
                   *->siDAqLRlLvPGKvsedekLieYDALL..lDkFL.DiLqDLHGedLk
                      s+DA     + G  s d +     A +++l + L++ L    G +L
  gi|2809648    38    SLDAG--TFAGGVAS-DVRHAGVRAGVrrLGQLLgESLTRHEGAQLL 81

                   EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                   E v     l+      +D+    +L  +L  +d   ai++A+a+     L
  gi|2809648    82 ELVERVRALA------RDSGDRADLHRVLADVDHPTAIVLARAFTAYFQL 125

                   AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEt...lKkLvlkln
                   An+ E     +R R    +               iEEt++++   v  ++
  gi|2809648   126 ANITEQL---HRARELADR-----------PRGAIEETggrIAAAVAAGQ 161

                   KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                     Pe   + +       v+tAHPt + RRs+L     i   L
  gi|2809648   162 LDPELPAQVVSRLELRPVFTAHPTEASRRSVLDVLRGIAELLDAADDPRA 211

                   tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                    +  +  +D  L   +   + tDE+R  +P P DE R    Y+     +
  gi|2809648   212 QPSRRAVVDRRLAEAVDVLWQTDELRVERPKPTDEARSAAYYLTSIATDV 261
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                    vPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                     P  L   D AL  +G    lP  +  ++F  W GGDRDG nP vtP vt
  gi|2809648   262 LPGLLEELDGALAQVGAG--LPITARPLRFGTWAGGDRDG-NPNVTPTVT 308

                    RDvCLLaRmmAanlYisqvEDLmFEls....mWRCndELRvRAEElyrta
                     Dv  L       + +  v+ L+ +l  ++++    dEL v   +  r a
  gi|2809648   309 LDVLTLQHEFGIRVLLGAVDGLIKDLTastrVVEVSDEL-VASLDADRAA 357

                    ardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGise
                      + v   +i     +   EPYR      R +L  tR+R    LA G +
  gi|2809648   358 HPE-VYDRFI----RLNAAEPYRLKASYLRARLAATRDR----LAAGTAH 398

                    isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                    ++    y  +   L  L +  +sL +   + +ADG L   +R     G+s
  gi|2809648   399 VPGRD-YLSLRGLLADLTVMHRSLMDNRGQLVADGPLRRTIRVAAAVGMS 447

                    LvKLDiRqEseRqtDvlDAittHLei..GsYReWsEeKRqEWLlaELkGK
                    L  LDiR   eR+   l A+   L+  +  Y +     R   L  EL G+
  gi|2809648   448 LATLDIREHGERHHAALGALYDRLDElpRPYADLDRHERIALLSRELAGR 497

                    RPLlgsDLPk.....tEEvkDvldafrv.LAELPiDsFGaYiismataPs
                    RPL g+  P + +++   v +   ++rv L     D   +Yi+sm+
  gi|2809648   498 RPLSGAAAPApadptAAAVLELFATIRVaLDRFGEDVIESYIVSMTRDVD 547

                    DvLAvELLqRECgv.........kqtLrvvPLFEkLADLeAAPAavekLF
                    D+LAv +L RE g+ + +++ + +  +  vPLFE +A+L+AA   ++ +
  gi|2809648   548 DILAVVVLAREAGLleitpgagaRARIGFVPLFETVAELRAAGRLLDGML 597

                    siDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                    +   Y+  +  +++ qe+m+GYsDs KDAG  +  W + +Aq E+  vA+
  gi|2809648   598 ADPSYRAVVAARgdlQEIMLGYSDSSKDAGITASQWEIHRAQRELRDVAR 647

                    kyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf
                    ++Gv L lFHGRGG vGRGGGPt  AiL+qP  t++G ++vt qGEvi
  gi|2809648   648 RHGVVLRLFHGRGGSVGRGGGPTGEAILAQPFGTLDGPIKVTEQGEVISD 697

                    sFGEEnLCFrsLqRFtAAtLEHGm.....nPPvsPkPEWRkLmeemAvvA
                     +   +L  + L    AA LE  + ++++  P+    EW + me +A  A
  gi|2809648   698 KYTLPQLARHNLEIALAAVLEASIlhresRQPLDVLAEWDQTMEAVADSA 747

                    tEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs..GGiesL
                       YR++   +P  v +F  AtP  E G++niGsRP+ R+P++ GG+e L
  gi|2809648   748 RTAYRALTT-DPALVPFFLAATPVDELGHLNIGSRPS-RRPGgvGGLEDL 795

                    RAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFF
                    RAiPW+F Wtq R  LP W G+G     A  +       L EmY+ W FF
  gi|2809648   796 RAIPWVFGWTQSRIILPGWFGLGTGL--AAARAAGAGDTLAEMYRSWHFF 843

                    RvtlDLlEmvFAKGDPGiAaLyDkLLv.aEeLkPFGksLRdkYvEtkdlL
                    R  l  + m  AK D  iA+ y   Lv+aE   PF + +R++ + t   +
  gi|2809648   844 RTFLSNVSMTLAKTDLRIASDYVTTLVpAEKAGPF-EVIRAEHERTVAEV 892

                    LkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtl
                    L + G   lLE  P L+q l +Rd Y+  L  +q   L R R
  gi|2809648   893 LAVTGSATLLEHAPVLRQTLEVRDLYLAPLHALQVSLLARSRA------- 935

                    rPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqnt
                            A+             p+ ++ P L   L+Lt+ GiAAG+ nt
  gi|2809648   936 --------AAQT----------DPGGEIDPRLRRALLLTINGIAAGLRNT 967

                    G<-*
                    G
  gi|2809648   968 G    968

gi|255062470|ref|ZP_05314486.1|: domain 1 of 1, from 3 to 933: score 349.6, E = 6e-102
                    *->siDAqLRlLvPGKvsedekL.ieYDALLlDkFL.DiLqDLHGedLkE
                        +D         K ++d +L+++ D   l + L+D + +  G+   E
  gi|2550624     3    DVDSENYDTNANKLANDKDLpLREDIRFLGRMLgDTVREQEGDKAFE 49

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                     v     ++  +   +D+    EL a L  L   D++ v +a++    L
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gi|2550624    50 LVENIRKIAIRFHREQDPAARHELEAILKQLSDKDSLPVVRAFSYFSLLS 99

                 nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                 n+AE+v+   RRR +++  G     +s t        l ++      +
gi|2550624   100 NIAEDVHHNRRRRAHLRA-GSTPQAGSVTL------ALERVLESSSNART 142

                 EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    +  K   v  vltAHPt   RRs+L  +  i   L      ++t+++
gi|2550624   143 ILADFFKQAIVSPVLTAHPTEVQRRSILDCQLAIERLLKERAWVELTPNE 192

                 KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                  +  +E     iq  + t  +R ++    DE+  G++Y+  t    +P
gi|2550624   193 MRHNEENQRATIQILWQTRMLRPTRLSVYDEIENGLAYYSYTFLSEIPYI 242

                 LRRvDtALKniGinERlPYdvPLi....kFssWmGGDRDGknPRvtPEvt
                   +++  L       Rl  d+PL+++  +  sW+GGDRDG nP vt Ev
gi|2550624   243 YAKIEDLL-----ERRLAGDIPLVtsflRIGSWIGGDRDG-NPFVTHEVM 286

                 RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk
                          +A   Y++ v  +   +s+    + L    +E+++  a
gi|2550624   287 LRAMERQSAVALEYYMDAVQKIGRSMSL---TERLVEVSDEVKKLLATA- 332

                 vvKyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGiseis
                            +P++  EPYR i   +  +L  t  +  H + +   e
gi|2550624   333 ---------PDIPnrSDEPYRRIFLSIGARLVATAKKFGHQVLQLSTEET 373

                 EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                  e  y    eF+  LE   +sL +     +A G+L  l R    FG  L
gi|2550624   374 REP-YAVSAEFVHDLEAIIQSLKQHKSSWVARGALRNLRRAADVFGFHLA 422

                 KLDiRqEseRqtDvlDAittHL.eiGsYReWsEeKRqEWLlaELkGKRPL
                  LD+Rq s  +  v+  + +  ++   Y + sEe R +WLl+E+    PL
gi|2550624   423 PLDMRQHSKIHEQVVSELFEYYtGHKDYLQLSEEERIDWLLSEINRLHPL 472

                 lgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAv
                 l       E  +  l  ++  AE+ ++ +  +   Yiism+t    +L v
gi|2550624   473 LTIPSEFSETTQSELRILQCAAEIHrrfgRAAMPNYIISMTTGVINILEV 522

                 ELLqRECgvkqt.......LrvvPLFEkLADLeAAPAavekLFsiDWYin
                   L R   + qt+++++ +L ++PLFE + DL+     +++LFs+ +Y+
gi|2550624   523 AYLLRQVDLLQTgenpqlhLNIIPLFETISDLQSCGKIMDQLFSLPYYRK 572

                 ridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                  +   ++ qevm+GYsDs KD G ++  W +YkA   + Kv  k+ + L
gi|2550624   573 LLSSMgsvQEVMLGYSDSNKDGGFIASNWEIYKAEIALTKVFAKHQIGLR 622

                 lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                 lFHGRGGtvGRGGGP    iL+qPP  +nG +Rvt qGEvi   + E ++
gi|2550624   623 LFHGRGGTVGRGGGPSYQSILAQPPGSVNGQIRVTEQGEVISSKYAEPEI 672

                 CFrsLqRFtAAtLEHGm..nPPv.sPkPEWRkLmeemAvvAtEEYRsvvv
                   r L    AAt+E  + ++  ++s    +   m+++A +    Y  +v+
gi|2550624   673 GRRNLETLVAATMEATLlgHDSIgSNADQYYPAMNKLAAISFAAYQDLVF 722

                 KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                     F  +F   tP  E   + iGsRP  R  s  ie LRAiPW+F+W q
gi|2550624   723 GTTGFKQFFLESTPIREMAGLHIGSRPPSRTSSDDIEDLRAIPWVFSWSQ 772

                 tRFHLPvWLGvGAAFKhAidKDiKn...lqkLkEmYkeWPFFRvtlDLlE
                  R  LP W G+G A    + +  +n+++l  L+EmY++WPF    l  ++
gi|2550624   773 SRMMLPGWYGFGHAVETFVTQKDQNgqgLALLQEMYQKWPFMQTLLSNMD 822

                 mvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkD
                 mv AK D GiA+ y +L+    L+ +   ++R++    +++L  i G  +
gi|2550624   823 MVLAKTDMGIASRYAELVNDIALREqIFARIREERARSEKWLFAITGNVE 872

                 lLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEy
                 lL   P L   +R R +Yi  Ln +q   L+R R
gi|2550624   873 LLQDNPTLARSIRNRIPYIDPLNHLQVELLRRYR---------------- 906

                 AdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
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                    E+s +    ++L                 + G+ AG+ n G
  gi|2550624   907 SGEDSEEVKRSIHLT----------------INGVTAGLRNSG    933

gi|15827227|ref|NP_301490.1|: domain 1 of 1, from 11 to 934: score 349.3, E = 7.6e-102
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      i A  R  v        + ++ D  Ll   L+D L +  G+++ +
  gi|1582722    11    PIGAVQRTRVGREAT---EPMRADIRLLGTILgDTLREQNGDEVFDL 54

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v      s  +  ++      ++     +Ld   ai + +a++H   LAn
  gi|1582722    55 VERVRVES--FRVRRSEIDRADMARMFSGLDIHLAIPIIRAFSHFALLAN 102

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  +AE+++   RR i++         ++   +s +  t+ kL l      +
  gi|1582722   103 VAEDIHRERRRHIHLDA-------GEPLRDSSLAATYAKLDLAK-LDSAT 144

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt.veD
                  v +AL    v  v+tAHPt   RR +   + Ri   L  L A   t+  D
  gi|1582722   145 VADALTGAVVSPVITAHPTETRRRTVFVTQRRITE-LMRLHAEGHTeTAD 193

                  KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                   + ++  L R i   + t  iR a+    DE+  G+ Y+   +++ +P+
  gi|1582722   194 GRSIERELRRQILTLWQTALIRLARLQISDEIDVGLRYYSAALFHVIPQV 243

                  LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                     v  AL+       l    P+++  sW+GGDRDG nP vt +v R
  gi|1582722   244 NSEVRNALRARWPDAEL-LSGPILQPGSWIGGDRDG-NPNVTADVVRRAT 291

                  LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    a       Y+  +  L  Elsm      L     El   aa+
  gi|1582722   292 GSAAYTVVAHYLAELTHLEQELSM---SARLITVTPELATLAASC----- 333

                  YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                            EPYR  L  +R +L  t        A+ + + + +
  gi|1582722   334 ----QDAACADEPYRRALRVIRGRLSSTA-------AHILDQQPPNQLGL 372

                  kvEeFLEPLELCY......ksLCeCGDkviADGsLLDlLRqvstFGLsLv
                   +  +  P ELC + ++ + sLC  G   +AD  L  l   v  FG  L
  gi|1582722   373 GLPPYSTPAELCAdldtieASLCTHGAALLADDRLALLREGVGVFGFHLC 422

                  KLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPL
                   LD+Rq s+ + +v+  +    ++  +Y + +E++R   L+aEL  +RPL
  gi|1582722   423 GLDMRQNSDVHEEVVAELLAWAGMHQdYSSLPEDQRVKLLVAELGNRRPL 472

                  lg.....sDLPktEEvkDvldafrvLAEL.PiDsFGaYiismataPsDvL
                  +g++ + sDL + E    vl a     EL  + +   Yiism+ + sDvL
  gi|1582722   473 VGdraqlSDLARGE--LAVLAAAAHAVELyGSAAVPNYIISMCQSVSDVL 520

                  AvELLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsiDW
                   v +L +E g+   +++++  ++ + PLFE + DL+   A +  +  +
  gi|1582722   521 EVAILLKETGLLDasgsqpycPVGISPLFETIDDLHNGAAILHAMLELPL 570

                  YinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGv
                  Y+  +  +++ qevm+GYsDs KD G l+A W +Y+A   ++ vA+k G+
  gi|1582722   571 YRTLVAARgnwQEVMLGYSDSNKDGGYLAANWAVYRAELALVDVARKTGI 620

                  KLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGE
                  +L lFHGRGGtvGRGGGP   AiL+qPP  +nGslR t qGEvi   + E
  gi|1582722   621 RLRLFHGRGGTVGRGGGPSYQAILAQPPGAVNGSLRLTEQGEVIAAKYAE 670

                  EnLCFrsLqRFtAAtLEHGm..nPPvsPkPE.WRkLmeemAvvAtEEYRs
                   ++  r L    AAtLE  + +   +    E+   +++e+A  A   Y
  gi|1582722   671 PQIARRNLESLVAATLESTLldVEGLGDAAEsAYAILDEVAGLARRSYAE 720

                  vvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFa
                  +v   P Fv+YF   tP  E G +niG RP+ RkP   i  LRAiPW+ a
  gi|1582722   721 LV-NTPGFVDYFQASTPVSEIGSLNIGNRPTSRKPTTSIADLRAIPWVLA 769

                  WtqtRFHLPvWLGvGAAFKhAi....dKDiKnlqkLkEmYkeWPFFRvtl
                  W q R  LP W G G AF+  +  +++ +++ + +L+++Y+ WPFFR  l
  gi|1582722   770 WSQSRVMLPGWYGTGSAFQQWVaagpESESQRVEMLHDLYQRWPFFRSVL 819
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                    DLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtkdlLLkiA
                      +  v AK D G+Aa y +L+v E L++   +++ d+   t  +   i
  gi|1582722   820 SNMAQVLAKSDLGLAARYAELVVDEALrRRVFDKIADEHRRTIAIHKLIT 869

                    GHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhl
                    GH DlL   P L   +  R +Y+  Ln +q   L+R R
  gi|1582722   870 GHDDLLADNPALARSVFNRFPYLEPLNHLQVELLRRYR------------ 907

                    sKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                            s   de+v+              ++Ltm G+A  + n G
  gi|1582722   908 --------SGHDDEMVQRG------------ILLTMNGLASALRNSG    934

gi|78485862|ref|YP_391787.1|: domain 1 of 1, from 7 to 929: score 346.8, E = 4.2e-101
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         D qLR     +v           LL     +++    G+   +av
  gi|7848586     7    --DKQLRS----RVK----------LLGSLLGEVIETQVGKTTLDAV 37

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                            +   K+ ++   EL a + +  P   il+ +a+     L nL
  gi|7848586    38 EKLRKGYIQLHEKENPELRKELKAFIEAQTPDNLILIIRAFNLYFSLVNL 87

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEE +  + R  ++k  G     +   t s+    +K+  l+     +Ev
  gi|7848586    88 AEEEHQFHERQSQLKSDGPLWMGSVLNTISE----FKQEGLLA----AEV 129

                    FeALKnqsvDL.vltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv..tve
                     e L n+   ++v+tAHPt s RR+++    Ri   L  L   +  + +
  gi|7848586   130 -EKLINKLCYIpVFTAHPTESKRRAVMENLRRIFLTLGELNEAEAynNPY 178

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++E+   L   iq  ++tDE+RR +Pt  DE+R G+ Y+   ++k vP
  gi|7848586   179 AQEEVIKKLQYQIQVLWKTDEVRRMKPTVEDEIRNGIYYFRQSLFKAVPT 228

                    FLRRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRD
                      R ++ AL      + +  + P+ + F sW+GGDRDG nP vt E t
  gi|7848586   229 VYRYMERALARHYPEDNI--QTPnFLNFGSWIGGDRDG-NPFVTHETTIN 275

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                      L+    A   Y   v +L   l   R  +E  ++ E + r    d
  gi|7848586   276 ALLMQSRAAIYEYQKRVYELSSHLTQSRYISE--IKQEVINRATIIDADL 323

                    KyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                    +  + F K   +   EPYR  L  +  +L          L    +e +
  gi|7848586   324 QERV-FHKRSErfRDEPYRRFLYLIHGRLQENLNYIEAQLNAETAEKPKF 372

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y    eFL+ LEL Y sLC  GD+ +AD  L Dl+R v tFG  L++L
  gi|7848586   373 G-YNSEQEFLDDLELIYDSLCSHGDQEVADANLKDLIRLVQTFGFYLMRL 421

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    DiRqEs  +tD +  +  HL+i  Y + sE  R + L   ++    +
  gi|7848586   422 DIRQESTVHTDAVADLLSHLGI-DYLSLSEAERLDLLAQQVSSPTVIDTQ 470

                    DLPktEEvkDvldafrvL....AELPiDsFGaYiismataPsDvLAvELL
                     L   E   +vl+ f+v+++ + E+   +F  Y+ism+   s v+ v  L
  gi|7848586   471 HLDLKEMTLEVLEVFNVMrrmrEEISEKAFNNYVISMTHEASHVMEVLFL 520

                    qRECgvk........qtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                        g+ + + +++   +rv PLFE + DLe        LF    Y   +
  gi|7848586   521 AHQAGLAgynagepyCKIRVSPLFETIQDLEHIVPVTSALFDNPTYHALL 570

                    dG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                      ++++qe+m+GYsDs KD G ls AW LY+Aq  i+K A +y +   lF
  gi|7848586   571 KAsgnQQEIMLGYSDSAKDGGNLSSAWTLYQAQQQIMKLADEYKIDCRLF 620

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGGtvGRGGGPtH AiLsqP  t+ G ++ t qGEv+ + +   +
  gi|7848586   621 HGRGGTVGRGGGPTHSAILSQPTGTVRGEIKFTEQGEVLSYKYSNAETAM 670

                    rsLqRFtAAtLEHG...mnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKE
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                     L       +   +  ++P     P   + m+++A      +R +
  gi|7848586   671 YELSMGITGLMKASkclVKPAQQDNPQHLEAMQKLAKEGEHAFRELTDHT 720

                     PRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqt
                       F  +F  AtP  E G +niGsRP+ Rk +     s+RAiPWiF W q
  gi|7848586   721 EGFFKFFYEATPVNEIGLLNIGSRPSHRKKGNlSKSSIRAIPWIFGWAQA 770

                     RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                     R   P W G G A    ++       +LkEmY++WPFF+  l  + m
  gi|7848586   771 RLTFPAWYGTGSALHNWMKTQTPE--QLKEMYENWPFFKGLLSNIQMALF 818

                     KGDPGiAaLyDkL.LvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                     K D  i   y +L+    + +   + + ++ v   +  L+i G   l+
  gi|7848586   819 KTDLIIGKDYSELgQDQKQAQHIYNMIAEEHVRSVETCLEISGNEYLMAD 868

                     DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                      P +   l  R +Y+  Ln +q   LKR +D          ls E  +E
  gi|7848586   869 TPQVALSLARRTPYLEPLNHIQVAVLKRYKDET--------LSDEEREEW 910

                     skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                              L            L+  +  iAAGm ntG
  gi|7848586   911 ---------LT-----------PLLNSINAIAAGMRNTG    929

gi|192290365|ref|YP_001990970.1|: domain 1 of 1, from 22 to 936: score 346.7, E = 4.4e-101
                     *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +i+A  Rl             + D  Ll + L+D + +  G+++ +
  gi|1922903    22    AIEAETRL-------------RNDIRLLGRILgDTVREQEGQSVFDL 55

                     vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                     v      s  +    D     EL a L ++   D++ + +a++    LAn
  gi|1922903    56 VENIRQTSIRFHRDDDKTARAELAAILDGMSIQDTMRIVRAFSYFSHLAN 105

                     LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     +AE+        i++ + G  +  +sA     +  tl +    +  s +E
  gi|1922903   106 IAED-----QNNIRQMRAG--STAGSAPRAGLLAKTLAHARQEG-ISAAE 147

                     vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                              v  vltAHPt   R+s + ++  i   L q     +t ++
  gi|1922903   148 LRKFFATALVSPVLTAHPTEVRRKSTMDREMQIAGLLDQRDRVQLTADEW 197

                     kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      + +E L R +   ++t  +RR++ t  DE+  G+s++  t  + vP+
  gi|1922903   198 ADNEEWLRRAVETLWKTNLLRRTKLTVLDEVTNGLSFYDYTFLREVPRLH 247

                     R....RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                        ++R   A K  G n      +  ++  sW+GGDRDG nP vt Ev
  gi|1922903   248 SaledRLADAAKAEGANAEGEL-ASFLRMGSWIGGDRDG-NPFVTAEVLH 295

                     DvCLLaRmmAanlYisqvEDLmFElsmWR....CndELRvRAEElyrtaa
                         L        Y++ + +L  Els+  +  +  d +++ AE    t+
  gi|1922903   296 GTLKLQSTRVLRYYLEELHELGSELSLAShlagTTDTVKALAETSPDTSP 345

                     rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGise.
                          Ky           EPYR  +  +  +L  t   a  L    +  +
  gi|1922903   346 HR---KY-----------EPYRLAVSGIYARLAAT---ALKLEVENLRTp 378

                     isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                     + E   y    +F   L+    sL      viA G L  l R +  FG
  gi|1922903   379 VGEAEPYASAQDFKTDLDAIHLSLTTHHSGVIARGRLRQLRRAIDCFGFH 428

                     LvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKR
                     L  LD+Rq s  +   +  +      G+sY    Ee R   L++EL+  R
  gi|1922903   429 LASLDMRQNSAVHERTVGELMDAARPGtSYAVLDEEARIALLISELRSTR 478

                     PLlgsDLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvL
                     PL    +   +E    l  fr+  +  A     +    iism+   sD L
  gi|1922903   479 PLTSMFVKYSDETVGELAVFReaakAHATYGAAAIPQCIISMTKGVSDLL 528

                     AvELLqRECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYin
                      v +L +E g+ +++++ ++ vvPLFE + DL+A    +++L si  Y+
  gi|1922903   529 EVAVLLKEVGLidpsgRSAINVVPLFETIEDLQACAKIMDRLLSIPEYRR 578
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                    ridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                     +d +++ qevm+GYsDs KD G +   W LYkA   +i +  ++Gv+L
  gi|1922903   579 LVDSRgsvQEVMLGYSDSNKDGGFVTSGWELYKAEIGLIEIFEHHGVRLR 628

                    lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                    lFHGRGG vGRGGGP   Ai++qP   +nG +R+t qGE+i   +   ++
  gi|1922903   629 LFHGRGGSVGRGGGPSYDAIVAQPGGAVNGQIRITEQGEIITSKYSNVEV 678

                    CFrsLqRFtAAtLEHGmnPP..vsPkPEWRkLmeemAvvAtEEYRsvvvK
                        L   +AAtLE  +  P++v+P+ ++ + me++   A   YR +v+
  gi|1922903   679 GRNNLEILAAATLEASLLQPkrVAPHRDYLEAMEQLSALAFKAYRGLVYE 728

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                       Fv+YF   t   E   +niGsRPa Rk    ie LRAiPW+F+W q
  gi|1922903   729 TDGFVDYFWASTVINEISTLNIGSRPASRKKTRAIEDLRAIPWVFSWAQC 778

                    RFHLPvWLGvGAAF.KhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                    R  LP W G+G A + +  +   K +  L+ mY+eWPFFR  l  ++mv
  gi|1922903   779 RLMLPGWYGFGSAVsAWVTEHPDKGIAFLQAMYQEWPFFRTLLSNMDMVL 828

                    AKGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlL
                     K   GiA+ y +L+    ++++ FG+ +R+++    d+LL i     lL
  gi|1922903   829 SKSSIGIASRYAELVEDTAIrdRIFGR-IRAEWHSSIDYLLAIMQQDHLL 877

                    EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                       P L   +R R +Y+  Ln +q                  +l +E+
  gi|1922903   878 QSNPLLERSIRHRFPYLDPLNHVQV-----------------QLLREHRT 910

                    EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     +           p e+v  G+     Lt+ Gi AG+ n G
  gi|1922903   911 HD-----------PDEQVLRGVQ----LTINGISAGLRNSG    936

gi|229493485|ref|ZP_04387270.1|: domain 1 of 1, from 3 to 925: score 346.0, E = 7.2e-101
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          A  R   P      e L e   LL      i+ +  G+d+ + v
  gi|2294934     3    TETASHRE-TPREAT--EPLREDIRLLGGILGQIVREQAGDDVFDLV 46

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          s  +  ++      EL +    +   Dai v +a++H   LAnL
  gi|2294934    47 ERARVES--FRVRRSEIDRAELVSLFAEISTDDAIPVIRAFSHFALLANL 94

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+++   RR i+          ++   +s +  t+ kL        + v
  gi|2294934    95 AEDIHRERRRAIHVNA-------GEPPRDSTLAATYTKLDAAD-IDSATV 136

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     eAL    v  v+tAHPt   RR +   ++Ri   +       + v +
  gi|2294934   137 EEALWGALVSPVITAHPTETRRRTVFETQSRITELMRYRERTALSVAETA 186

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ++D  L R i   + t  iR ++   qDE+  G+ Y+   +++ +PK
  gi|2294934   187 DVDLQLRRQILTLWQTALIRLSRLRIQDEIEVGLRYYDAALFEVIPKINA 236

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     v  AL+       l    P+++  sW+GGDRDG nP vt E+
  gi|2294934   237 EVRKALRTRWPDAGL-LPEPILRPGSWIGGDRDG-NPYVTGEIVQRATSR 284

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    a   A    ++ ++ L  Elsm      +    + l +t+  d
  gi|2294934   285 AAATALEHHLEELDHLERELSMSARLVSVTPELDLLASTSGDD------- 327

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaR.HLLAtGiseisEeAvytk
                             EPYR  +  +R +L  t     + L A+G s+   eA yt+
  gi|2294934   328 ---SAFRADEPYRRAIRGIRGRLSATALTVLgELPAHG-SDDGLEA-YTD 372

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      +    L +   sL   GD  iAD  L  l   v  FG  L  LD+Rq
  gi|2294934   373 PAQLQRDLGIIDTSLRRFGDETIADDRLDRLREAVEVFGFHLSGLDMRQN 422

                    seRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgsDLP.
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                    se +  v+  +    ++ + Y + +E  R E L aEL  +RPL  +D
  gi|2294934   423 SEVHESVVAELLAWAGVHpDYASLPEADRVELLSAELTTRRPLTSPDAEf 472

                    ...ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqREC
                    ++  t E++ +    + +  L   +   Yiism+t+ sD+L   +L +E
  gi|2294934   473 selTTKELAIMAAGAKAVRVLGAGAVPNYIISMCTSVSDMLEAAVLLKEV 522

                    gvkq.........tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK
                    gv  ++ +++++ ++ +vPLFE + DL+    ++     i  Y+  +  +
  gi|2294934   523 GVLDpgvgsepscPIGIVPLFETIEDLQGGADTLLATLDIPIYRAIVRSR 572

                    ...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    +++qevm+GYsDs KD G l+A W LY+A  +++  A+k G++L lFHGR
  gi|2294934   573 gdsQEVMLGYSDSNKDGGYLAANWALYRAELDLVDAARKSGIRLRLFHGR 622

                    GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                    GGtvGRGGGP   AiL+qPP  + GslR+t qGEvi   + E  L  r L
  gi|2294934   623 GGTVGRGGGPSYEAILAQPPGAVAGSLRITEQGEVIAAKYAEPRLAHRNL 672

                    qRFtAAtLEHGm...nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                        AAt+E  + + +   s       +++e+A  A   Y  +v   P F
  gi|2294934   673 ETLIAATIESTLldvEGLGSDADAAYAVLDELAALARTAYSELVHDTPGF 722

                    vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                    v YF   tP  E G +niGsRPa Rk    i  LRAiPW+ +W q R  L
  gi|2294934   723 VQYFEASTPVAEIGALNIGSRPASRKQTKAISDLRAIPWVLSWSQSRVML 772

                    PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                    P W G GAAF   id D   l  L  +Y++WPFFR  l  + mv  K D
  gi|2294934   773 PGWYGTGAAFERWIDGDDTRLATLTALYEKWPFFRTVLSNMAMVMSKSDL 822

                    GiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                    G+Aa y +L+   eL+++ FG  + d+ + t  +   i G   l
  gi|2294934   823 GLAARYADLVPDAELrdRVFG-MITDEHERTIRMYKAITGNENLFADNSG 871

                    LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                    L   +  R +Y+  Ln +q   ++R R                 dE
  gi|2294934   872 LERSVHNRFPYLEPLNHLQVELIRRYRS---------------GDES--- 903

                    adeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                              ++v  G+     Ltm G+A  + n G
  gi|2294934   904 ----------DQVRRGIQ----LTMNGLATALRNSG    925

gi|217969857|ref|YP_002355091.1|: domain 1 of 1, from 4 to 920: score 345.8, E = 8.1e-101
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                         DA LR                D  Ll + L+D + D  Ge
  gi|2179698     4    DKDAPLRD---------------DIRLLGRLLgDTVRDQQGEAAFGL 35

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +      s  +    D     EL   L +L    +i v +a++    LAn
  gi|2179698    36 IERIRQNSVRFRRDDDIAARRELEDILDALSREQTIQVVRAFSYFSHLAN 85

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+ +   R R ++         +sA  E  +   l +    +   P+
  gi|2179698    86 IAEDQHHIRRSRAHLIA-------GSAPREGSLAHALERALDSGAADPAA 128

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                             v  vltAHPt   R+s+L  ++ i   L       +t+e+
  gi|2179698   129 LAGFFDGALVSPVLTAHPTEVQRKSILNCETVIARLLDARDRMQLTPEEA 178

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +  DEAL R +   + t  +R a+    DE+  G+sY+  t  +  P+
  gi|2179698   179 EANDEALRRAVLTLWQTRMLRTAKLSVIDEVNNGLSYFETTFLRELPRLY 228

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                       +  L         P  +  ++  sW+GGDRDG nP vt Ev
  gi|2179698   229 ASLEDRLAAADRALGTPELAAFVQVGSWIGGDRDG-NPFVTAEVLERALA 277

                    LaRmmAanlYisqvEDLmFEls....mWRCndELRvRAEEl.yrtaardk
                    +   +A   Y++ +  L   ls + ++    d L + AE  +   + r
  gi|2179698   278 MQCAVALGHYLDELHILGSQLSlgigLVSASDALLALAEASpDHSPHRS- 326
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                    vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                                  EPYR  +  +  +L  t    R LL +     +
  gi|2179698   327 --------------DEPYRRAISGIYARLAATY---RSLLGHDPLRHAVA 359

                    Av..ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                    A ++y       E LE+  +sL   G  ++  G L  l R v  FG  L
  gi|2179698   360 AAqpYPSAAALAEDLEVLHRSLAANGSGALTRGRLRHLRRAVKVFGFHLA 409

                    KLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPL
                     LD+Rq s+ +   +  + +    G++Y +  E+ R   Ll EL   RPL
  gi|2179698   410 PLDLRQNSDVHERTVAELLERACPGtAYASLDEDARCALLLEELATARPL 459

                    lgsDLPktEEvkDvldafrvL..AELP..iDsFGaYiismataPsDvLAv
                      + +  t+E +  l  fr  ++A L  +  +    iis +   sD L
  gi|2179698   460 ASPHVRYTDETEGELAIFRAArqAHLRygTAAIRNCIISKTDDVSDLLEL 509

                    ELLqRECgvkqtLr......vvPLFEkLADLeAAPAavekLFsiDWYinr
                     +L +E g+ ++L +  + ++vPLFE + DLe A   ++++Fsi  Y+
  gi|2179698   510 AVLLKEAGLLRPLEnaldvnIVPLFETIGDLENAAGVMARIFSIPAYRGL 559

                    idGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                    ++ ++++qevm+GYsDs KD G l   W LYkA  E++    ++Gv+L l
  gi|2179698   560 LEARdhtQEVMLGYSDSNKDGGFLTSGWALYKAEGELVETFARHGVRLRL 609

                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                    FHGRGG vGRGGGP   AiL+qP   ++G +R t qGEvi   +G  ++
  gi|2179698   610 FHGRGGSVGRGGGPSYQAILAQPEGAVQGQIRLTEQGEVIGAKYGNPEVG 659

                    FrsLqRFtAAtLEHGmnPP.vsPk.PEWRkLmeemAvvAtEEYRsvvvKE
                     r L    AAtLE  + P + sP +P + + m+ +   A   YR +v+
  gi|2179698   660 RRNLEVLVAATLESSLRPAsASPTpPAFLDAMQALSDAAFAAYRGLVYET 709

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
                      F  YF   t   E   +niGsRPa Rk s  ie LRAiPW+F+W q R
  gi|2179698   710 EGFERYFWESTVISEIAALNIGSRPASRKKSTAIEDLRAIPWVFSWSQCR 759

                    FHLPvWLGvGAAFKhAidKDiKn.lqkLkEmYkeWPFFRvtlDLlEmvFA
                      LP W G+G A +  +      +l  L+ m  eWPFF   l  ++mv
  gi|2179698   760 VMLPGWYGFGSAVRDFLTANPDDgLALLQRMNMEWPFFQTLLSNMDMVLS 809

                    KGDPGiAaLyDkLLvaEeLk..PFGksLRdkYvEtkdlLLkiAGHkDlLE
                    K D  iA+ y +L+    L+++ FG+ +R++ + t   +L+i G  +lL+
  gi|2179698   810 KTDLAIASRYAELVKDAALRdtIFGR-IRAEHQATVGAVLRITGQSELLD 858

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                      P LK  +R R +Y+  Ln +q   L+R RD               A+E
  gi|2179698   859 ANPLLKRSIRNRFPYLDPLNHVQVELLRRHRD---------------AAE 893

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                         de ++L             + + + GiAAG+ n G
  gi|2179698   894 A-GGIDERIRLG------------IHISINGIAAGLRNSG    920

gi|39934841|ref|NP_947117.1|: domain 1 of 1, from 22 to 936: score 345.2, E = 1.3e-100
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +i+A  Rl             + D  Ll + L+D + +  G+++ +
  gi|3993484    22    AIEAETRL-------------RNDIRLLGRILgDTVREQEGQSVFDL 55

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      s  +    D     EL a L ++   D++ + +a++    LAn
  gi|3993484    56 VENIRQTSIRFHRDDDKTARAELAAILDGMSIQDTMRIVRAFSYFSHLAN 105

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+        i++ + G  +  +sA     +  tl +    +  s +E
  gi|3993484   106 IAED-----QNNIRQMRAG--STAGSAPRAGLLAKTLAHARQEG-ISAAE 147

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                             v  vltAHPt   R+s + ++  i   L q     +t ++
  gi|3993484   148 LRKFFATALVSPVLTAHPTEVRRKSTMDREMQIAGLLDQRDRVQLTADEW 197

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
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                    + +E L R +   ++t  +RR++ t  DE+  G+s++  t  + vP+
  gi|3993484   198 TDNEERLRRAVETLWKTNLLRRTKLTVLDEVTNGLSFYDYTFLREVPRLH 247

                    R....RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                       ++R   A K  G n      +  ++  sW+GGDRDG nP vt Ev
  gi|3993484   248 SaledRLADAAKAEGANAEGEL-ASFLRMGSWIGGDRDG-NPFVTAEVLH 295

                    DvCLLaRmmAanlYisqvEDLmFElsmWR....CndELRvRAEElyrtaa
                        L        Y++ + +L  Els+  +  +  d +++ AE    t+
  gi|3993484   296 GTLKLQSTRVLRYYLEELHELGSELSLAShlagTTDTVKALAETSPDTSP 345

                    rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi.se
                         Ky           EPYR  +  +  +L  t   a  L    +++
  gi|3993484   346 HR---KY-----------EPYRLAVSGIYARLAAT---ALKLEVENLrAP 378

                    isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                    + E   y    +F   L+    sL      viA G L  l R +  FG
  gi|3993484   379 VGEAEPYASAQDFKADLDAIHLSLTTHHSGVIARGRLRQLRRAIDCFGFH 428

                    LvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKR
                    L  LD+Rq s  +   +  +      G+sY    E+ R   L++EL+  R
  gi|3993484   429 LASLDMRQNSAVHERTIGELMDAARPGtSYAVLDEDARIALLISELRSTR 478

                    PLlgsDLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvL
                    PL    +   +E    l  fr+  +  A     +    iism+   sD L
  gi|3993484   479 PLTSMFVKYSDETVGELAVFReaakAHATYGAAAIPQCIISMTKGVSDLL 528

                    AvELLqRECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYin
                       +L +E g+ +++++ ++ vvPLFE + DL+A    +++L si  Y+
  gi|3993484   529 ELAVLLKEVGLidpsgRSAINVVPLFETIEDLQACAKIMDRLLSIPEYRR 578

                    ridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                     +d +++ qevm+GYsDs KD G +   W LYkA   +i +  ++Gv+L
  gi|3993484   579 LVDSRgsvQEVMLGYSDSNKDGGFVTSGWELYKAEIGLIEIFEHHGVRLR 628

                    lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                    lFHGRGG vGRGGGP   Ai++qP   +nG +R+t qGE+i   +   ++
  gi|3993484   629 LFHGRGGSVGRGGGPSYDAIVAQPGGAVNGQIRITEQGEIITSKYSNVEV 678

                    CFrsLqRFtAAtLEHGmnPP..vsPkPEWRkLmeemAvvAtEEYRsvvvK
                        L   +AAtLE  +  P++v+P+ ++ + me++   A   YR +v+
  gi|3993484   679 GRNNLEILAAATLEASLLQPkrVAPHRDYLEAMEQLSALAFKAYRGLVYE 728

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                       Fv+YF   t   E   +niGsRPa Rk    ie LRAiPW+F+W q
  gi|3993484   729 TDGFVDYFWASTVINEISTLNIGSRPASRKKTRAIEDLRAIPWVFSWAQC 778

                    RFHLPvWLGvGAAF.KhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                    R  LP W G+G A + +  +   K +  L+ mY+eWPFFR  l  ++mv
  gi|3993484   779 RLMLPGWYGFGSAVsAWVTEHPEKGIAFLQAMYQEWPFFRTLLSNMDMVL 828

                    AKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLE
                     K   GiA+ y +L+    ++ +   ++R+++    d+LL i     lL
  gi|3993484   829 SKSSIGIASRYAELVEDTAIRDrIFSRIRAEWHSSIDYLLAIMQQDHLLQ 878

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                      P L   +R R +Y+  Ln +q                 +l +E+
  gi|3993484   879 SNPLLERSIRHRFPYLDPLNHVQV-----------------QLLREHRTH 911

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +           p e+v  G+     Lt+ Gi AG+ n G
  gi|3993484   912 D-----------PDEQVLRGVQ----LTINGISAGLRNSG    936

gi|85716666|ref|ZP_01047635.1|: domain 1 of 1, from 45 to 973: score 345.0, E = 1.4e-100
                    *->siDAqLRlLvPGKvsed....ekLieYDALLlDkFL.DiLqDLHGed
                       ++   L l   G+   d    ++ ++ D  Ll + L+D + D  G+d
  gi|8571666    45    AMSSLLPLPRAGQLESDaavlDERLRNDIRLLGRILgDTVRDQEGPD 91

                    LkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmL
                    + + v      s  +    D     EL a L ++   +++lv +a++
  gi|8571666    92 MFDLVERIRQTSIRFHRDDDKPARRELEAILDGMSTQETVLVVRAFSYFS 141
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                nLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnK
                 LAn+AE+ +     R + +  G  aD +       +  tl      +
gi|8571666   142 HLANIAEDQNNIRQMRSQTLA-GGVADQGR------LSRTLACAREAG-F 183

                sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt
                s +E         v  vltAHPt   R+s + ++  +   L       +t
gi|8571666   184 SGAELRAFFDSAVVSPVLTAHPTEVRRKSTIDREMEVAALLDRRERMQLT 233

                veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGv
                +++ +  +E L R +   + t  +RR++ t  DE+  G+s++  t  + v
gi|8571666   234 PDEYEASEEQLRRAVLTLWHTNLLRRTKLTVLDEVANGLSFYDYTFLREV 283

                PKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                P+     +  L+           +  ++  sW+GGDRDG nP vt +v R
gi|8571666   284 PRLHCGLEDRLRDASEDGTANELASFLRIGSWIGGDRDG-NPFVTADVMR 332

                DvCLLaRmmAanlYisqvEDLmFElsmWR....CndELRvRAEE.lyrta
                             Y++ + +L  Els+  + ++   ELRv AE +  + +
gi|8571666   333 GTLQRQASRILRYYLDELHELGRELSLAAdltdVSPELRVLAERsADKSP 382

                ardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGise
                 r                EPYR  +  +  +L  t   a  L A  +
gi|8571666   383 HRR---------------GEPYRLAVSGIYARLSAT---AIKLKADTLRP 414

                isEeA.vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                    A+ y    eF   L++   sL      viA G L  l R    FG
gi|8571666   415 PYGAApPYASAAEFSADLDVIHSSLTANNSEVIARGRLRYLRRAADCFGF 464

                sLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK
                 L  LD+Rq s  +   +  +      G+sY    Ee R   Ll EL+
gi|8571666   465 HLACLDLRQNSTVHERTIAELLDAATPGtSYLTLDEEARIVVLLRELRSA 514

                RPLlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDv
                RPL  + +   +E    l  f+  A  ++ L  D+    i+sm+   sD
gi|8571666   515 RPLTSPFITYSDETLGELAVFHAAAAahemLGPDAIPQCIVSMTEGVSDL 564

                LAvELLqRECgvkqt.....LrvvPLFEkLADLeAAPAavekLFsiDWYi
                L v LL +E  +  +++++ + +vPLFE + DL+A    +++L s+  Y+
gi|8571666   565 LEVALLLKEADLVDPtghsaINIVPLFETIEDLQACAGIMDRLLSLPEYR 614

                nrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                  +d+++G qevm+GYsDs KD G +   W LYkA   ++ v  ++ v+L
gi|8571666   615 ALVDsrgGLQEVMLGYSDSNKDGGFVTSGWELYKAEIGLVDVFERHDVRL 664

                vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                 lFHGRGG vGRGGGP   AiL+qP   +nG +R+t qGE+i   +   +
gi|8571666   665 RLFHGRGGSVGRGGGPSYDAILAQPGGAVNGQIRITEQGEIISSKYSNAE 714

                LCFrsLqRFtAAtLEHGmnPP..vsPkPEWRkLmeemAvvAtEEYRsvvv
                +    L   +AAtLE  +  P++ +P  E+ + me +   A   YR +v+
gi|8571666   715 VGRNNLEILAAATLEASLLQPrqSAPSLEYLDAMEALSSRAYTAYRNLVY 764

                KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                  P F +YF   t   E   +niGsRPa Rk    ie LRAiPW+F+W q
gi|8571666   765 ETPGFEDYFWASTVINEISTLNIGSRPASRKKTRKIEDLRAIPWVFSWAQ 814

                tRFHLPvWLGvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                 R  LP W G+G A  ++  d   K +  L+E+Y eWPFFR+ l  ++mv
gi|8571666   815 CRVMLPGWYGFGSATEsWIADHPDKGMGFLQELYAEWPFFRMLLSNMDMV 864

                FAKGDPGiAaLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLkiAGHkDl
                 AK    iA+ y +L+   eL+   FG+ +R ++  t d+LL i G   l
gi|8571666   865 LAKSSIAIASRYADLVPDVELREaiFGR-IRREWHLTIDMLLAIMGQERL 913

                LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                L G P L   +R R +Y+  Ln +q   LK  R               A
gi|8571666   914 LAGNPLLERSIRNRFPYLDPLNHVQVELLKDHR----------------A 947

                dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                + +             e+v  G+     +t+ Gi AG+ n G
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  gi|8571666   948 QCE------------DEQVLRGIQ----ITINGISAGLRNSG    973

gi|2339975|dbj|BAA21835.1|: domain 1 of 1, from 22 to 936: score 344.5, E = 2e-100
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                     +i+A  Rl             + D  Ll + L+D + +  G+ + +
  gi|2339975    22    AIEAETRL------------RNDIRLLGRILgDTVREQEGQTVFDL 55

                     vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                     v      s  +    D     EL a L ++   D++ + +a++    LAn
  gi|2339975    56 VENIRQTSIRFHRDDDKTARAELEAILDGMSIPDTMRIVRAFSYFSHLAN 105

                     LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     +AE+        i++ + G  +  +sA     +  tl +    +  s +E
  gi|2339975   106 IAED-----QNNIRQMRAG--STAGSAPRAGLLAKTLAHARQEG-ISAAE 147

                     vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                              v  vltAHPt   R+s + ++  i   L q     +t ++
  gi|2339975   148 LRKFFATALVSPVLTAHPTEVRRKSTMDREMQIASLLDQRDRVQLTADEW 197

                     kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      + +E L R +   ++t  +RR++ t  DE+  G+s++  t  + vP+
  gi|2339975   198 ADNEERLRRAVETLWKTNLLRRTKLTVLDEVTNGLSFYDYTFLREVPRLH 247

                     RRvDtALKniGinERlPYd...vPLikFssWmGGDRDGknPRvtPEvtRD
                        +  L      E +  d++ +  ++  sW+GGDRDG nP vt Ev
  gi|2339975   248 SALEDRLADAAKAEGVNSDgelASFLRMGSWIGGDRDG-NPFVTAEVLHG 296

                     vCLLaRmmAanlYisqvEDLmFElsmWR....CndELRvRAEElyrtaar
                        L        Y++ + +L  Els+  +  +  d +++ AE    t+
  gi|2339975   297 TLKLQSTRVLRYYLDELHELGSELSLAShlagTTDTVKALAETSPDTSPH 346

                     dkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi.sei
                         Ky           EPYR  +  +  +L  t   a  L    +++ +
  gi|2339975   347 R---KY-----------EPYRLAVSGIYARLAAT---ALKLEVENLrAPV 379

                     sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                      E   y    +F   L+    sL +    viA G L  l R +  FG  L
  gi|2339975   380 GEAEPYASAQDFKADLDAIHLSLTQHNSGVIARGRLRQLRRAIDCFGFHL 429

                     vKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRP
                       LD+Rq s  +   +  +      G+sY    Ee R   L++EL+  RP
  gi|2339975   430 ASLDMRQNSAVHERTITELMDAARPGtSYAMLDEEARIALLISELRSTRP 479

                     LlgsDLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLA
                     L    +   +E    l  fr+  +  A     +    iism+   sD L
  gi|2339975   480 LTSMFVKYSDETVGELAVFReaakAHATYGAAAIPQCIISMTKGVSDLLE 529

                     vELLqRECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                     v +L +E g+ +++++ ++ vvPLFE + DL+A    +++L si  Y+
  gi|2339975   530 VAVLLKEVGLidpsgRSAINVVPLFETIEDLQACAKIMDRLLSIPEYRRL 579

                     idGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                     +d +++ qevm+GYsDs KD G +   W LYkA   +i +  ++Gv+L l
  gi|2339975   580 VDSRgsvQEVMLGYSDSNKDGGFVTSGWELYKAEIGLIEIFEHHGVRLRL 629

                     FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                     FHGRGG vGRGGGP   Ai++qP   +nG +R+t qGE+i   +   ++
  gi|2339975   630 FHGRGGSVGRGGGPSYDAIVAQPGGAVNGQIRITEQGEIITRKYSNVEVG 679

                     FrsLqRFtAAtLEHGmnPP..vsPkPEWRkLmeemAvvAtEEYRsvvvKE
                        L   +AAtLE  +  P++v+P+ ++ + me++   A   YR +v+
  gi|2339975   680 RNNLEILAAATLEASLLQPkrVAPHRDYLEAMEQLSALAFKAYRGLVYET 729

                     PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
                       Fv+YF   t   E   +niGsRPa Rk    ie LRAiPW+F+W q R
  gi|2339975   730 DGFVDYFWASTVINEISTLNIGSRPASRKKTRAIEDLRAIPWVFSWAQCR 779

                     FHLPvWLGvGAAF.KhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                       LP W G+G A + +        +  L+ mY+eWPFFR  l  ++mv
  gi|2339975   780 LMLPGWYGFGSAVsAWVTAHPETGIAFLQKMYQEWPFFRTLLSNMDMVLS 829
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                  KGDPGiAaLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLkiAGHkDlLE
                  K   GiA+ y +L+   +++ + FG+ +R+++    ++L  i     lL
  gi|2339975   830 KSSIGIASRYAELVEDVDVREriFGR-IRAEWHSSIEYLFAIMQQDRLLQ 878

                  GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                    P L   +R R +Y+  Ln +q                  +l +E+
  gi|2339975   879 SNPLLERSIRHRFPYLDPLNHVQV-----------------QLLREHRTH 911

                  nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                  +           p e+v  G+     Lt+ Gi AG+ n G
  gi|2339975   912 D-----------PDEQVLRGVQ----LTINGISAGLRNSG    936

gi|21314564|gb|AAM47007.1|AF512995_1: domain 1 of 1, from 1 to 410: score 344.0, E = 2.9e-100
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2131456     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2131456     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2131456     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2131456     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2131456     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2131456     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2131456     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2131456     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2131456     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|2131456     - ---------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|2131456     - ---------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                      LFEkLADLeAAPAa+++LFs+DWY+nri+GKqevm+GYsDsGKDAG
  gi|2131456      1 ----LFEKLADLEAAPAALARLFSVDWYRNRINGKQEVMIGYSDSGKDAG 46

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  R+sAAWqLYkAqEE+iKvAK+yG+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2131456     47 RFSAAWQLYKAQEELIKVAKQYGIKLTMFHGRGGTVGRGGGPTHLAILSQ 96

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PP+sP
  gi|2131456     97 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPISP 146

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR +m+emAv+AtEEYRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
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  gi|2131456   147 KPEWRAMMDEMAVIATEEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 196

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KDi+nl
  gi|2131456   197 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIQKDIRNL 246

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY++WPFFRvt+DL+EmvFAKG   iAaLyD+LLv+ +L+ FG++
  gi|2131456   247 HMLQEMYNNWPFFRVTIDLVEMVFAKGNHKIAALYDQLLVSKDLWSFGEK 296

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Etk lLL+iAGHkDlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|2131456   297 LRVNYEETKGLLLQIAGHKDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 346

                    KRiRDPsykvtlrPhlsKEyAd.EnskkadeLvkLnptervaPGLEDtLi
                    KRiRDP+y+v +rPh+s+E  ++E  k+adeLvkLn ++++aPGLEDtLi
  gi|2131456   347 KRIRDPNYHVKVRPHISREIMEsESVKPADELVKLNLSSEYAPGLEDTLI 396

                    LtmKGiAAGmqntG<-*
                    LtmKGiAAG+qntG
  gi|2131456   397 LTMKGIAAGLQNTG    410

gi|92118201|ref|YP_577930.1|: domain 1 of 1, from 20 to 929: score 342.8, E = 6.4e-100
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       ++DA LR                D  Ll + L+D + D  G  + +
  gi|9211820    20    ALDARLRD---------------DIRLLGRILgDTVRDQEGAAVFDL 51

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      s  +   +D     EL a L ++   +++lv +a++    LAn
  gi|9211820    52 VERIRQTSIRFHRDEDKPARRELEAILDGMSTDETVLVVRAFSYFSHLAN 101

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+ +     R + +        + A  E  +  tl      +  s +E
  gi|9211820   102 IAEDQNNIRQMRSQSLE-------GGARHEGVLAHTLACAREAG-FSGAE 143

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                             v  vltAHPt   R+s + ++  +   L       +t+++
  gi|9211820   144 LQAFFDSALVSPVLTAHPTEVRRKSTIDREMEVAFLLDRRERMQLTPDEY 193

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +  +E L R +   + t  +RR++ t  DE+  G+s++     + vP+
  gi|9211820   194 EVSEEQLRRAVLTLWQTNLLRRTKLTVLDEVANGLSFYDYAFLREVPRLH 243

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                       +  L+           +  ++  sW+GGDRDG nP vt +v R
  gi|9211820   244 CVLEDRLQDASADGASNEMASFLRIGSWIGGDRDG-NPFVTADVMRGTL- 291

                    LaRmmAanl...YisqvEDLmFElsmWR....CndELRvRAEElyrtaar
                      Rm A+ + + Y++ + +L  Els+  + ++   ELR  AE    t+
  gi|9211820   292 --RMQASRVlryYLDELHELGRELSLAAdltdVSPELRGLAERSADTSPH 339

                    dkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseis
                                    EPYR  +  +  +L  t   a  L A  +
  gi|9211820   340 R--------------RGEPYRLAVSGIYARLSAT---ALKLKADTLRPPY 372

                    EeA.vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                      A+ y    eF   L++  +sL +    viA G L  l R    FG  L
  gi|9211820   373 GKApPYASAAEFSADLDVLHRSLTQNNSEVIARGRLRHLRRAADCFGFHL 422

                    vKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRP
                      LD+Rq s  +   +  +      G+sY   sEe R   Ll EL+  RP
  gi|9211820   423 ACLDLRQNSTVHERTIAELLDAAVPGtSYLALSEEARIVVLLRELRSARP 472

                    LlgsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvL
                    L  + +   +E    l  f+  AE   + FG++  ++ iism+   sD L
  gi|9211820   473 LTSPFITYSDETLGELAVFHAAAE-AHEMFGPgaipqCIISMSEGVSDLL 521

                    AvELLqRECgvkqt.....LrvvPLFEkLADLeAAPAavekLFsiDWYin
                     v LL +E  +  +++++ + +vPLFE + DL+A    +++L s+  Y+
  gi|9211820   522 EVALLLKEADLVDPtghsaINIVPLFETIEDLQACAGIMDRLLSLPEYRA 571
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                    rid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                     +d+++G qevm+GYsDs KD G +   W LYkA   ++ v  ++ v+L
  gi|9211820   572 LVDsrgGLQEVMLGYSDSNKDGGFVTSGWELYKAEIGLVEVFERHQVRLR 621

                    lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                    lFHGRGG vGRGGGP   AiL+qP   +nG +R+t qGE+i   +   ++
  gi|9211820   622 LFHGRGGSVGRGGGPSYDAILAQPGGAVNGQIRITEQGEIISSKYSNAEV 671

                    CFrsLqRFtAAtLEHGmnPP..vsPkPEWRkLmeemAvvAtEEYRsvvvK
                        L   +AAtLE  +  P++ +P  ++ + me +   A   YR +v+
  gi|9211820   672 GRNNLEILAAATLEASLLQPrqSAPSLDYLDAMESLSSRAFAAYRNLVYE 721

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                     P F +YF   t   E   +niGsRPa Rk    ie LRAiPW+F+W q
  gi|9211820   722 TPGFEDYFWASTVINEISTLNIGSRPASRKKTRRIEDLRAIPWVFSWAQC 771

                    RFHLPvWLGvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                    R  LP W G+G A  ++  d   K +  L+E+Y eWPFFR+ l  ++mv
  gi|9211820   772 RVMLPGWYGFGSAVEsWIADHPDKGMAFLQELYGEWPFFRMLLSNMDMVL 821

                    AKGDPGiAaLyDkLL..vaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlL
                    AK    iA+ y +L+++v+     FG+ +R ++  t d LL i G   lL
  gi|9211820   822 AKSSIAIASRYADLVpdVTLRETIFGR-IRSEWHLTIDTLLAIMGQERLL 870

                    EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                     G P L   +R R +Y+  Ln +q   LK  R               A+
  gi|9211820   871 AGNPLLERSIRNRFPYLDPLNHVQVELLKDHR----------------AQ 904

                    EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                  e+v  G+     Lt+ Gi AG+ n G
  gi|9211820   905 GG-----------DEQVLRGIQ----LTINGISAGLRNSG    929

gi|111220081|ref|YP_710875.1|: domain 1 of 1, from 43 to 978: score 342.2, E = 1e-99
                    *->siDAqLRlLvP......GKvsedekLieYDALLlDkFLDiL.qDLHG
                       s    L  L+P+++   G vs d +     A  + +  D+L+q L
  gi|1112200    43    SASTTLDELAPdpgafaGGVSSDARHAAVRA-GVRRLGDLLgQALTR 88

                    edLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailH
                     +          + A     + +    ELG  L  +d   ai++A+a+
  gi|1112200    89 HEGAATLALVEQVRAL---ARRPDNGAELGRLLATVDDRTAIVLARAFTA 135

                    mLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkl
                       LAn+ E     +R R    +               + Et+ ++   l
  gi|1112200   136 YFQLANITEQL---HRSRELSDR----------AKGPLTETFDRMAAAL 171

                    nK.sPeEvFeALKnqsvDL..vltAHPtqsvRRsLLqKnaRiRnCL.aqL
                    + ++ +           +L++v+tAHPt + RRs+L    Ri   L+a
  gi|1112200   172 DAgTLDRSLAESIARRLELrpVFTAHPTEASRRSVLDTLRRIADLLdADS 221

                    sAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHE
                        v   D+      L   +   + tDE+R  +P P DE R    Y+
  gi|1112200   222 PDGAVPAADRDRTQRRLAEMVDVLWQTDELRVERPKPADEARSAAYYLEL 271

                    tvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRv
                       +  P  L   D AL  +G+   lP  +  ++F sW GGDRDG nP v
  gi|1112200   272 IATEVLPDLLEELDLALARVGLT--LPAGAHPVRFGSWAGGDRDG-NPNV 318

                    tPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrt
                    tP vt +v  L       l    vE L+ El        + v  E l +
  gi|1112200   319 TPAVTLEVLTLQHEFGIRLLTASVERLIQELTA--STRVVGVGDELLSSL 366

                    aardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGis
                    aa         + +  +  +EPYR     +  +L  tRER    LA G
  gi|1112200   367 AADREALPEVHDRYIRLNAEEPYRLKCSYILARLAGTRER----LAAGAP 412

                    eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                     ++    y  v e L+ LE+   sL       +ADG LL ++R     GL
  gi|1112200   413 HVPGRD-YGGVAEILDDLEVMRASLNAGDGSLVADGPLLRVIRTARAMGL 461

                    sLvKLDiRqEseRqtDvlDAittHLei..GsYReWsEeKRqEWLlaELkG
                    sL  LDiR  ++++   l A+   ++  +  Y +     R+  L aEL
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  gi|1112200   462 SLATLDIREHADKHHAALAAVYDQVGEldVPYAQLDRPARRTLLSAELAR 511

                   KRPLlgsD.LPktEEvkDvldafrvLAELPiDsFG.....aYiismataP
                   +RPLlg+ + P    v   l+ +r + E   D FG++  ++Yi+sm+
  gi|1112200   512 RRPLLGAVpPPLPPAVLGTLELMRTVRE-ALDRFGgdvieSYIVSMTRDV 560

                   sDvLAvELLqRECgvk.........qtLrvvPLFEkLADLeAAPAavek
                    D+LAv +L RE g+ + +  +++    +  vPLFE +A+L+AA   ++
  gi|1112200   561 DDILAVVVLAREAGLVglgfadrpawARIGFVPLFETVAELRAAGSLLDG 610

                   LFsiDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKv
                   + s   Y+  +  + + qevm+GYsDs KDAG  +  W + kAq E+  v
  gi|1112200   611 MLSDPSYRSLVRARadvQEVMLGYSDSSKDAGITASQWEIHKAQRELRDV 660

                   AKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEvi
                   A+++Gv L lFHGRGG vGRGGGP   Ai++qP  t++Gs++vt qGEvi
  gi|1112200   661 ARRHGVVLRLFHGRGGSVGRGGGPSGEAIMAQPFGTLDGSIKVTEQGEVI 710

                   EfsFGEEnLCFrsLqRFtAAtLEHGm...nPPvsPk..PEWRkLmeemAv
                      +   +L  + L    AA +E  + ++   +sP     W + m+ +A
  gi|1112200   711 SDKYTLPQLARHNLEITLAAVVEASIlhrSSRLSPTvlAGWNETMQAVAD 760

                   vAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs..GGie
                    A   Y + v  +P  v +F  AtP  E G +niGsRP+ R+P+++GG+
  gi|1112200   761 SARVTYQAFV-GDPALVPFFLAATPVEELGNLNIGSRPS-RRPGgtGGLA 808

                   sLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWP
                    LRAiPW+F Wtq R  LP W GvG     A  +       L EmY+ W
  gi|1112200   809 DLRAIPWVFGWTQSRIILPGWFGVGTGL--AAARAAGAGDTLAEMYRSWH 856

                   FFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdl
                   FFR  l  + m  AK D  iA  y   Lv ++     + +R++   t
  gi|1112200   857 FFRTFLGNVQMTLAKSDLTIAQRYVSTLVGDDGGTIFETIRAEHARTVAE 906

                   LLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvt
                   +L + G  +lLE  P L+  l +Rd+Y+  L  +q   L R R
  gi|1112200   907 VLTVTGQAELLENAPTLRHTLEVRDAYLAPLHALQVSLLARARA------ 950

                   lrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqn
                            A E    ad L++              L+Lt+ GiAAG+ n
  gi|1112200   951 ---------AGEG---ADPLLRRA------------LLLTINGIAAGLRN 976

                   tG<-*
                   tG
  gi|1112200   977 TG    978

gi|229541694|ref|ZP_04430754.1|: domain 1 of 1, from 3 to 919: score 339.4, E = 7e-99
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       iD +    +P      +  +++ A LlDk   iL +  Ge L   +
  gi|2295416     3    QIDEK---KAPRMAL--QADMDFLAGLLDKV--ILFE-GGEALLKTI 41

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   q    l+       D      L   +t L+P +   v +a++  L L n+
  gi|2295416    42 QNIRSLAQKARETGDEAFYLQLKKEITDLNPPERQEVIRAFSTYLQLFNI 91

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE.
                    E      RRR  +      +D  +     D  Etl+k     +K P+E
  gi|2295416    92 TEQNFRIKRRREYQSE---DTDQVQPRSLEDGIETLRK-----EKVPAEm 133

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   v e L   s +L++tAHPt + RR +Lq + Ri   L  L     t  +K
  gi|2295416   134 VAELLNSLSLELIITAHPTEATRRTILQIHKRIADLLKALEYAN-TRYEK 182

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   k ++E +  Ei   +   EiR  +P   DE++ G+ Y+   +++  P+
  gi|2295416   183 KVIEETILNEITILWQSSEIREKKPSVLDEVKNGLYYFDNVLFDVLPRIH 232

                   RRvDtALKn.iGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                      +  L  + G   ++P     ++F sW+GGDRDG nP vt ++t
  gi|2295416   233 EDLEDYLHEsYGQRFKVP---SYLHFGSWIGGDRDG-NPNVTADITWKTL 278
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                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     + R +    Y   +  L   ls       + +    l +    +
  gi|2295416   279 EMQRELVLEKYKKSLTTLRELLS--HSSKKISASHALLASVESEE----- 321

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei.sEeAvy
                           +P        L   +D +Y    R   ++ + +  ++  +  y
  gi|2295416   322 -----NTMPAAK-----LWPTKDEIY---RRKLTIMIHKLECVgKNNGGY 358

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                        e L  L +   s+ +          L  ++Rqv  FG  L  LDiR
  gi|2295416   359 QSAKELLADLYMIRDSVNQHHPAGHPIKLLRKVIRQVELFGFHLASLDIR 408

                    qEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgsDL
                      s  +   l  +   ++i + Y++ sE+ +   Ll  L   RP++
  gi|2295416   409 NHSGEHESALAEVLYNVNIAkDYKNLSEDEKVAVLLKALNDPRPMISIYD 458

                    PktEEvkDvldafrvLAELPiDsFG.....aYiismataPsDvLAvELLq
                      t E ++v+++fr++      +FG+++ + Y+isma + sDvL v +L
  gi|2295416   459 TFTPETQEVINTFRMIKR-AHQTFGersiqVYLISMAHSVSDVLEVLVLA 507

                    RECg.........vkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                    +E g  +  +++++   + + PL E +ADL+     +e LF +  Y+n++
  gi|2295416   508 KEAGlyrvypsgdILSEIHIAPLLETIADLRNGAKMLETLFQMPIYRNHL 557

                    dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                      +++ qevm+GYsD  KD G + A WqLYkAq Ei  +  kyG+KL  F
  gi|2295416   558 KVRgnlQEVMLGYSDGSKDGGTMTANWQLYKAQKEIHEMGAKYGIKLKFF 607

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGG  GRGGGP    +LsqPP t+   +++t qGEv+   +   ++ +
  gi|2295416   608 HGRGGSLGRGGGPLYSSLLSQPPVTLGDGVKITEQGEVLSSRYLLRDIAY 657

                    rsLqR.....FtAAt.LEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvv
                    rsL   +++  +A t+     +    P  E  + m+++   A E Y  +v
  gi|2295416   658 RSLEQatstmMCAITeQKQNEKNGKTPNEEAVRAMDKISEYALEKYQELV 707

                    vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWt
                    +++P F  YF+ AtP  E G +niGsRP  Rk s   e LRAiPW+F+Wt
  gi|2295416   708 FRDPDFLSYFKQATPLNEIGELNIGSRPMSRKGSARFEDLRAIPWVFSWT 757

                    qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                    q R  LP W   G      ++ +  n++ L+EmY  WPFF  t+  l m
  gi|2295416   758 QSRQLLPAWYAAGTGLSKYVE-ETGNFKLLQEMYASWPFFHATINNLQMA 806

                    FAKGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDl
                      K +   A  y +L+   e+ ++ FG  ++++Y+ tk+++LkiA  k+l
  gi|2295416   807 LIKAELSTAEEYTRLVKDPEVagRIFG-LIKAEYELTKEMVLKIADQKEL 855

                    LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                    L+  P +K  +RLR++Y+  Ln fq Y +  +R+            +E
  gi|2295416   856 LDYTPNIKESVRLRNPYVDPLNLFQVYLISQLRE-----------RENK 893

                    dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    dE    a  L+               +Lt+ GiAAG+ ntG
  gi|2295416   894 DEK---ARHLLMEV-------------LLTINGIAAGLRNTG    919

gi|159036484|ref|YP_001535737.1|: domain 1 of 1, from 11 to 928: score 338.9, E = 9.6e-99
                    *->siDAqLRlLvPGKvsedekLieYDALLlDk.FLDiLqDLHGedLkEa
                         DA LR+ +         L +  A    ++ LD++     ed++
  gi|1590364    11    --DAALRADIRRLGT---LLGQTLARQEGRpLLDLV-----EDIRAQ 47

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      +A+              +L +Ld a    +A+a++    LAn
  gi|1590364    48 VRTDAPAAAQ---------------RLAGLDVATGTRLARAFSTYFHLAN 82

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E v   +R R  +++         A     ++   K +  ++    eE
  gi|1590364    83 ITEQV---HRARDLRRR--------RAIQGGWLDQAAKMIAERG-VPAEE 120

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt..ve
                    +  A +  ++  v+tAHPt ++RRs+L K   i   L       v  +
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  gi|1590364   121 IAAAARRLAIRPVFTAHPTEAARRSILSKLRAIADELDTETTNAVLygAS 170

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    D       L   +   + tDE+R  +P P DE R  + Y+ +   +  P+
  gi|1590364   171 DEGPANRRLAELLDLMWQTDELRLDRPDPTDEARNAIYYLRDLYAEAAPQ 220

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     L      L+ +G+ E  P   PL  F  W+GGDRDG nP vtP vtR+v
  gi|1590364   221 VLDDLADTLRTLGV-ETSPTARPL-TFGTWIGGDRDG-NPFVTPTVTREV 267

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      +            ++ L+ E+s+ R    LR    +l    a d
  gi|1590364   268 LAIQHEHGLAATERAMDQLINEVSVSR---RLRGVSLDLSASLATD--LD 312

                    yYiEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                       E  ++++ v  +EPYR     v+ KL ntR R R    +G + ++
  gi|1590364   313 ALPEVaprFRRVNAEEPYRLKARCVKAKLANTRQRLR----QGTAHVPGR 358

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y    e +  LEL   sL     +  A G L   +R vs FGL L  +
  gi|1590364   359 D-YRGSGELIADLELLRASLARNSGQLTAVGRLASTIRTVSAFGLHLATM 407

                    DiRqEseRqtDvlDAittHL.eiGsYReWsEeKRqEWLlaELkGKRPLlg
                    D+R  +e++ +vl  +   ++e+  Y   s   R   L  EL G+RPL
  gi|1590364   408 DVREHAEKHHEVLTQLFGAVgEVSDYPALSRLERTKLLADELTGRRPLST 457

                    sDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvE
                     D P tE  +   d f  + E   D FG +  ++Yiism+    DvLA
  gi|1590364   458 VDTPLTESARRTFDVFGTIRE-AQDRFGTeviesYIISMTLGVDDVLAAV 506

                    LLqRECgv......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                    +L RE g+ + ++++  +  vPL E  A+L+A    ++ L s+  Y+  +
  gi|1590364   507 VLAREAGLvdvhssRARIGFVPLLETPAELNAGGDLLDELLSLPAYRALV 556

                    dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                      +++ qevm+GYsDs K+AG     W + +Aq  +  vA ++Gv L lF
  gi|1590364   557 AARgdvQEVMLGYSDSNKEAGITTSQWSIHRAQRALRDVAARHGVHLRLF 606

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGGtvGRGGGPtH AiL+qP  t++G ++vt qGEvi   +    L
  gi|1590364   607 HGRGGTVGRGGGPTHDAILAQPYGTLDGEIKVTEQGEVISDKYTLPALAR 656

                    rsLqRFtAAtLEHGm..nPPvsPkPEWRkLmeemAvvAtEEYRsv..vvK
                      L    AA L   + +  P  P     +    m vv    YRs ++ v
  gi|1590364   657 ENLELTVAAVLQSTLlhTAPRQPAEMLERWDATMDVVSAAAYRSYrdLVE 706

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtq
                    +P    YF   tP    G +niGsRPaKR   G G+  LRAiPW+F Wtq
  gi|1590364   707 DPDLPAYFWASTPTELLGALNIGSRPAKRPNTGaGLAGLRAIPWVFGWTQ 756

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                    tR  +P W GvG     A  +       L Em + W FFR  l  +Em+
  gi|1590364   757 TRQIVPGWFGVGSGL--AAARAAGHADVLAEMHRSWHFFRTFLSNVEMML 804

                    AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                     K D  iA  y + Lv   L+P  +++ ++Y+ t+  +L +    DlLE
  gi|1590364   805 TKTDLAIARRYVETLVPKKLHPIFHKIEQEYELTRREVLAVTVTPDLLEN 854

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                     P L+  l +Rd Y+  L  +q   L+  R+
  gi|1590364   855 APVLQRTLAVRDTYLEPLHHLQVALLRQYRE------------------- 885

                    skkadeLvkLnptervaP....GLEDtLiLtmKGiAAGmqntG<-*
                    s  +   v   p+ r aP++++ LE  L+ t+ GiAAGm ntG
  gi|1590364   886 SGAPGRAVATAPGGRRAPsdgtALERALLTTVNGIAAGMRNTG    928

gi|256677249|ref|ZP_05487560.1|: domain 1 of 1, from 2 to 913: score 337.7, E = 2.3e-98
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s     Rl +P       +L      L D   + L    G++L E v
  gi|2566772     2    SSADDHRLPAPAAAP---ELRADIRRLGDLLGETLVRQEGPELLELV 45
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     l    +G   ++ L+E     t L+ a  ++  +a++    LAn+
gi|2566772    46 ERVRHLTRS-DGEAAARLLGE-----TELETAAQLV--RAFSTYFHLANI 87

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AE v   +R R  + +         A   s +  t  +L       Pe
gi|2566772    88 AEQV---HRGRELRER--------RAEDGSLLARTADRLKDAD---PEHL 123

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                 e +    v  v+tAHPt ++RRs+L K  R+    a L      + D++
gi|2566772   124 RETVAHLNVRPVFTAHPTEAARRSVLNKLRRV----AELLDTPANPADRR 169

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                 +D  L   i   + tDE+R  +P P DE R  + Y+ E   + v   L
gi|2566772   170 RVDTRLAENIDLVWQTDELRVVRPEPADEARNAIYYLDELHADAVGDVLE 219

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     L  iG+  ++P +   + F  W+GGDRDG nP vtP vt Dv +L
gi|2566772   220 DLSAELERIGV--KIPDETRPLTFGTWIGGDRDG-NPNVTPQVTWDVLIL 266

                aRmmAanlYisqvEDLmFElsmWRCnd.ELRvRAEElyrtaardkvvKyY
                      n  ++q++ L    ls    n+       EEl      d    +
gi|2566772   267 QHEHGINDALEQIDYLRGLLS----NSiRYTGVTEELTASLEND--LAHL 310

                iEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                 E ++++K +  +EPYR  +  vR KL nt+ R    LA+G    +
gi|2566772   311 PEIsprYKRLNAEEPYRLKVTCVRQKLENTKNR----LAKGTPHEPGRD- 355

                ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                y    e L  L L   sL        ADG L  ++R    FGL L  +D+
gi|2566772   356 YLGTSELLTDLALVQDSLRAHRGGLFADGRLSRIIRTLAAFGLQLATMDV 405

                RqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLlgs
                R  ++ +   l  +   L+  s+R  + + e R   L  EL+ +RPL +
gi|2566772   406 REHADAHHHALGQLFDRLGEESWRyaDMPREYRAKLLAKELRSRRPLAPT 455

                DLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvEL
                  P     +  l+ f+ +     D FG++  ++Yiism+    Dv A  +
gi|2566772   456 PAPLDAAGEKTLGVFHTIHR-ALDVFGPeviesYIISMCQGADDVFAAAV 504

                LqRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                L RE g+   +++   + +vPL E   +L+AA   ++ + s   Y+  +
gi|2566772   505 LAREAGLMDlhsgwaKIGIVPLLETTDELRAADTILDDMLSDPSYRRLVS 554

                GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                 +++ qevm+GYsDs K  G     W + +Aq  +  vA ++Gv+L lFH
gi|2566772   555 LRgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRHGVRLRLFH 604

                GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                GRGGtvGRGGGP H AiL+qP  t++G ++vt qGEvi   +    L
gi|2566772   605 GRGGTVGRGGGPSHDAILAQPWGTLEGEIKVTEQGEVISDKYLVPSLARE 654

                sLqRFtAAtLEHGm...nPPvsPk..PEWRkLmeemAvvAtEEYRsvvvK
                 L    AAtL     ++ P  s      W   m+ +   A   YR +v
gi|2566772   655 NLELTVAATLQASAlhtAPRQSDEalARWDAAMDLVSEAAHTTYRDLV-S 703

                EPRFvEYFRlAtPElEYGkmniGsRPaKR.kPsGGiesLRAiPWiFaWtq
                +P    YF   tP    G + +GsRP++R+  sGG++ LRAiPW+F Wtq
gi|2566772   704 DPDLSAYFLASTPVDQLGDLHLGSRPSRRpDSSGGLDGLRAIPWVFGWTQ 753

                tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                 R  +P W GvG   K   +     +  L Em + W FFR  l  +Em
gi|2566772   754 SRQIVPGWYGVGSGLKALREAGLDGV--LDEMHEHWHFFRNFLSNVEMTL 801

                AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                AK D  iA  y + Lv +eLk   + ++++   t   +Lki G   lL+
gi|2566772   802 AKTDLRIAQHYVDTLVPDELKHIFDLIKAEHDLTVSEVLKITGGEQLLDS 851

                DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                   L+q   +Rd+Y+  +  +q   L R R               A+E
gi|2566772   852 NKPLQQTFNIRDAYLDPISYLQVTLLARQRA--------------AAEA 886
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                   skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                               +e+  P L   L+Lt+ G+AAG++ntG
  gi|2566772   887 ------------GEEPDPLLARALLLTVNGVAAGLKNTG    913

gi|68304977|gb|AAY89988.1|: domain 1 of 1, from 13 to 933: score 337.5, E = 2.7e-98
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        DAqLR  v  K     kL+            i++   G d+  av
  gi|6830497    13    --DAQLRSAV--KTL--GKLLG----------NIIKTHAGHDVYIAV 43

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                           +        K + L   +  LdP     v ++++    L n+
  gi|6830497    44 EKLRKGFINLRKDNNQIKHDQLIRYIEKLDPKTLKNVIRSFSKYFALVNV 93

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEE    +  R  ++k G  + E+s       + tl+
  gi|6830497    94 AEE-AYQHINRTDRLKSGFDSWEGS------FDQTLRDCNASN-IDDSKL 135

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    e +       v+tAHPt + RRs L    Ri n +  L         ++
  gi|6830497   136 QELINSLHYAPVFTAHPTEAKRRSKLEAMRRIFNTILELQRYKGQSIKRE 185

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   EL E L  Ei   +RtDE+R  +Pt  DE+  G+ Y+   ++k +P   +
  gi|6830497   186 ELIEELQAEILILWRTDEVRLKKPTVIDEVENGLYYFRTSLFKSIPEVYK 235

                   RvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDvCL
                    ++ A+K +   + +   vP+ ikF sW+GGDRDG nP vtP++tR+
  gi|6830497   236 DMEKAIKRVYHTDNI--KVPsFIKFGSWIGGDRDG-NPFVTPDITREAVY 282

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   +    A   Y+     L   l       EL          ++rd    y
  gi|6830497   283 MHAETAIHEYMRRAQNLSTILTH---SLELTRPSNQFLESSKRD--EIYL 327

                   iEFWK...qvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                      +K+++q    EPYR     +R +L   R +    L       +E A
  gi|6830497   328 TNAFKnttQDFAKEPYRRKFKIIRYRL-DQRLKVINQLKNNSQPQAEHA- 375

                   ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                   y    e L+ L +   sL    D ++ D  L D++R v tFG  Lv LDi
  gi|6830497   376 YESEKELLDDLYVIRDSLISDNDLILSDFGLNDFIRLVETFGFHLVNLDI 425

                   RqEseRqtDvl.DAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
                   R Es  +t  ++D +   L+i  Y +  E  R   L   +k    L
  gi|6830497   426 REESTNHTNAIsDVLNVSLQI-DYASMDEKSRINELEKFIKSDINLNQVY 474

                   LPktEEvkDvldafrvLA....ELPiDsFGaYiismataPsDvLAvELLq
                       E  k v+d f v+ + ++E+ + +FG Y+ism+   s v  v  L
  gi|6830497   475 DKLDEASKKVIDVFTVMTrlrnEISVNAFGNYVISMTHHASHVFEVLALA 524

                   RECg........vkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri.
                   + Cg  ++ ++++  +++v PLFE + DL      +e LFs   Y   i+
  gi|6830497   525 KLCGlvnnvngkLESSIQVTPLFETIDDLTRIEEILEDLFSNNTYNSLIg 574

                   ...dGK.qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                   + +d K qevm+GYsDs KD G ls  W LYkAq  +  + Kky +   l
  gi|6830497   575 hykDTKlQEVMLGYSDSCKDGGILSSSWSLYKAQLQVLDISKKYKIECRL 624

                   FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                   FHGRGGtvGRGGGPtH AiL+qP  t+ G +++t qGEv+ + +G  +
  gi|6830497   625 FHGRGGTVGRGGGPTHNAILAQPNGTVRGMIKITEQGEVLSYKYGLPQSA 674

                   FrsLqRFtAAtLEHGmnPPv...sPkPEWRkLmeemAvvAtEEYRsvvvK
                      L       +    +  v++  P   + ++m  m  +    YR +
  gi|6830497   675 SYELELALSGLMKASKHLVVdeaIPINNFEDMMSSMSLMGEKKYRDLTDD 724

                   EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGie.sLRAiPWiFaWtq
                    P  ++YF  AtP  E   +niGsRP+ Rk     + s+RAiPW+F W
  gi|6830497   725 KPGIMDYFYEATPVQELAELNIGSRPSHRKQTNRSKySIRAIPWVFGWSL 774

                   tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
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                    R  LP W G+G A    +     n+  Lk mY eWPFF v lD + m
  gi|6830497   775 SRHTLPAWYGLGTALNKIVSENPSNMDNLKSMYTEWPFFSVLLDNIQMAL 824

                    AKGDPGiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE
                     K D GiA  y +L+  +E  k    ++  +Y  t   LL+i G  +lL
  gi|6830497   825 SKSDIGIAKDYAQLVQNkEAAKDIIADIETEYNSTVSTLLEIVGSDELLA 874

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                        L   l+ R++Y+  Ln +q   L++ R          ++s     E
  gi|6830497   875 ENTKLSLSLKRRQPYLDPLNYIQVMLLQKHR----------KIS----GE 910

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +         +n          D L+ t+  iA Gm+ntG
  gi|6830497   911 D--------TVN---------FDPLLRTIHAIAIGMKNTG    933

gi|254376064|ref|ZP_04991540.1|: domain 1 of 1, from 2 to 913: score 337.1, E = 3.5e-98
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s     Rl +P       +L      L D   + L    G++L E v
  gi|2543760     2    SSADDHRLPAPAAAP---ELRADIRRLGDLLGETLVRQEGPELLELV 45

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         l    +G   ++ L+E     t L+ a  ++  +a++    LAn+
  gi|2543760    46 ERVRHLTRS-DGEAAARLLGE-----TELETAAQLV--RAFSTYFHLANI 87

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE v   +R R  + +         A   s +  t  +L       Pe
  gi|2543760    88 AEQV---HRGRELRER--------RAEDGSLLARTADRLKDAD---PEHL 123

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     e +    v  v+tAHPt ++RRs+L K  R+    a L      + D++
  gi|2543760   124 RETVAHLNVRPVFTAHPTEAARRSVLNKLRRV----AELLDTPASPADRR 169

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +D  L   i   + tDE+R  +P P DE R  + Y+ E   + v   L
  gi|2543760   170 RVDTRLAENIDLVWQTDELRVVRPEPADEARNAIYYLDELHADAVGDVLE 219

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         L  iG+  ++P d   + F  W+GGDRDG nP vtP vt Dv +L
  gi|2543760   220 DLSAELERIGV--KIPDDTRPLTFGTWIGGDRDG-NPNVTPQVTWDVLIL 266

                    aRmmAanlYisqvEDLmFElsmWRCnd.ELRvRAEElyrtaardkvvKyY
                          n  ++q++ L   ls    n+       EEl      d    +
  gi|2543760   267 QHEHGINDALEQIDYLRGLLS----NSiRYTGVTEELTASLEND--LAHL 310

                    iEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                     E ++++K +  +EPYR  +  vR KL nt+ R    LA+G    +
  gi|2543760   311 PEIsprYKRLNAEEPYRLKVTCVRQKLENTKNR----LAKGTPHEPGRD- 355

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y    e L  L L   sL        ADG L  ++R    FGL L  +D+
  gi|2543760   356 YLGTSELLTDLALVQDSLRAHRGGLFADGRLSRIIRTLAAFGLQLATMDV 405

                    RqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLlgs
                    R  ++ +   l  +   L+  s+R  + + e R   L  EL+ +RPL +
  gi|2543760   406 REHADAHHHALGQLFDRLGEESWRyaDMPREYRAKLLAKELRSRRPLAPT 455

                    DLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvEL
                      P     +  l+ f+ +     D FG++  ++Yiism+    Dv A  +
  gi|2543760   456 PAPLDAAGEKTLGVFHTVHR-ALDVFGPeviesYIISMCQGADDVFAAAV 504

                    LqRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                    L RE g+   +++   + +vPL E   +L+AA   ++ + s   Y+  +
  gi|2543760   505 LAREAGLMDlhsgwaKIGIVPLLETTDELRAADTILDDMLSDPSYRRLVS 554

                    GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                     +++ qevm+GYsDs K  G     W + +Aq  +  vA ++Gv+L lFH
  gi|2543760   555 LRgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRHGVRLRLFH 604

                    GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                    GRGGtvGRGGGP H AiL+qP  t++G ++vt qGEvi   +    L
  gi|2543760   605 GRGGTVGRGGGPSHDAILAQPWGTLEGEIKVTEQGEVISDKYLVPSLARE 654
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                    sLqRFtAAtLEHGm...nPPvsPk..PEWRkLmeemAvvAtEEYRsvvvK
                     L    AAtL     ++ P  s      W    m+ +   A   YR +v
  gi|2543760   655 NLELTVAATLQASAlhtAPRQSDEalARWDAAMDLVSEAAHTAYRDLV-S 703

                    EPRFvEYFRlAtPElEYGkmniGsRPaKR.kPsGGiesLRAiPWiFaWtq
                    +P    YF   tP    G + +GsRP++R+  sGG++ LRAiPW+F Wtq
  gi|2543760   704 DPDLSAYFLASTPVDQLGDLHLGSRPSRRpDSSGGLDGLRAIPWVFGWTQ 753

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     R  +P W GvG   K   +     +  L Em + W FFR  l  +Em
  gi|2543760   754 SRQIVPGWYGVGSGLKALREAGLDGV--LDEMHEHWHFFRNFLSNVEMTL 801

                    AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                    AK D  iA  y + Lv +eLk   + ++ +   t   +Lki G   lL+
  gi|2543760   802 AKTDLRIAQHYVDTLVPDELKHIFDLIKTEHDLTVAEVLKITGGEQLLDS 851

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                       L+q   +Rd+Y+  +  +q   L R R               A+E
  gi|2543760   852 NKPLQQTFNIRDAYLDPISYLQVTLLARQRA---------------AAEA 886

                    skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                +e+  P L   L+Lt+ G+AAG++ntG
  gi|2543760   887 ------------GEEPDPLLARALLLTVNGVAAGLKNTG    913

gi|254775781|ref|ZP_05217297.1|: domain 1 of 1, from 11 to 935: score 336.9, E = 4.1e-98
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        i A  R Lv        + ++ D  Ll   L+D + +  G+++ E
  gi|2547757    11    PIGAVQRTLVGREAT---EPMRADIRLLGAILgDTVREQNGQQVFEL 54

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      s  +  ++      EL     ++d   ai v +a++H   LAn
  gi|2547757    55 VERARVES--FRVRRSEIDRAELARMFAGIDIHQAIPVIRAFSHFALLAN 102

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+++   RR i+          ++   +s +  t+ kL        +
  gi|2547757   103 VAEDIHRERRRAIHVAA-------GEPPQDSSLAATYAKLDRAQ-LDSAT 144

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt.veD
                    v eAL+   v  v+tAHPt   RR +   + Ri   L  L A   t+ +D
  gi|2547757   145 VAEALRGAVVSPVITAHPTETRRRTVFVTQHRITE-LMRLHAEGHTeTDD 193

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                     + ++  L R +   + t  iR ++    DE+  G+ Y+    +k +P+
  gi|2547757   194 GRNIELELRRQVLTLWQTALIRLSRLQITDEIEVGLRYYAAAFFKVIPQV 243

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                       v  AL+       l  d P++   sW+GGDRDG nP vt +v R
  gi|2547757   244 NAEVRNALRARWPGADL-LDEPIVAPGSWIGGDRDG-NPNVTADVVRRAT 291

                    LLaRmmAanlYisqvEDLmFElsm....WRCndELRvRAEElyrtaardk
                      a   A   Y+  +     Elsm+ +      EL + AE+    a+ d
  gi|2547757   292 GDAAYTALAHYLAELTACEQELSMsarlVAVTPELAALAEDCAEKARAD- 340

                    vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntR.....ERaRHLLAtGis
                                  EPYR  L  +R +L  t ++  + R  H L  G+
  gi|2547757   341 ---------------EPYRRALRVIRGRLTATAgeildRRPQHELDLGLP 375

                    eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                      +  A      e    L+    sL   G   +AD  L  l   v  FG
  gi|2547757   376 PYATPA------ELRADLDTVDASLRAHGSALLADDRLALLREGVRVFGF 419

                    sLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK
                     L  LD+Rq s+ + +v+  +    ++ + YR+ +E+ R E L aEL  +
  gi|2547757   420 HLCGLDMRQNSDVHEEVVAELLAWAGVHpDYRSLPEDERVELLAAELGTR 469

                    RPLlgsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsD
                    RPL+g      E     l+ +r  A   i  +G+   ++Y+ism+ + sD
  gi|2547757   470 RPLVGDRAELSELADKELGVVRAAAH-AIRRYGPaavpnYVISMCRSVSD 518

                    vLAvELLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsi
```

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                    vL   +L +E g+   +++++  ++ + PLFE + DL+   A +  +  +
  gi|2547757   519 VLEAAILLKEAGLIDasgpepycPVGISPLFETIEDLHNGAAILHAMLEL 568

                    DWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKky
                      Y+  +  ++++qevm+GYsDs KD G l+  W +Y+A   ++ vA+k
  gi|2547757   569 PLYRALVAARgqsQEVMLGYSDSNKDGGYLASSWAVYRAELALVEVARKT 618

                    GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF
                    G++L lFHGRGGtvGRGGGP   AiL+qPP  +nGslR t qGEvi   +
  gi|2547757   619 GIRLRLFHGRGGTVGRGGGPSYEAILAQPPGAVNGSLRLTEQGEVIAAKY 668

                    GEEnLCFrsLqRFtAAtLEHGm..nPPvsPkPE.WRkLmeemAvvAtEEY
                     E ++  r L    AAtLE  + +   +    E+   +++e+Av A   Y
  gi|2547757   669 AEPQVAQRNLESLVAATLESTLldVEGLGDTAEpAYAVLDEVAVLAQRAY 718

                    RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWi
                      +v   P Fv+YF   tP  E G +niGsRP+ RkP   i  LRAiPW+
  gi|2547757   719 AELVHETPGFVDYFMASTPVSEIGSLNIGSRPTSRKPTESIADLRAIPWV 768

                    FaWtqtRFHLPvWLGvGAAFKhAi....dKDiKnlqkLkEmYkeWPFFRv
                     aW q R  LP W G G AF   i  +++     +  L+++Y+ WPFFR
  gi|2547757   769 LAWSQSRVMLPGWYGTGSAFEQWIaagpQSRAERVDILHDLYRRWPFFRS 818

                    tlDLlEmvFAKGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLL
                     l  l  v AK D G+Aa y +L+    L+++ FGk + d+   t  +
  gi|2547757   819 VLSNLAQVLAKSDLGLAAQYAELVDDAALrqRVFGK-IADEHRRTIAMHK 867

                    kiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlr
                     i G   lL   P L   +  R +Y+  Ln +q   L+R R
  gi|2547757   868 LITGQDNLLADNPALARSVFNRFPYLEPLNHLQVELLRRYR--------- 908

                    PhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG
                               s   deLv+             ++Ltm G+A  + n G
  gi|2547757   909 -----------SGDDDELVQRG------------ILLTMNGLASALRNSG 935

                    <-*

  gi|2547757     -     -

gi|134094240|ref|YP_001099315.1|: domain 1 of 1, from 4 to 944: score 336.7, E = 4.6e-98
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +    R L        +  ++ D  Ll + L+D+L D  G+ + E+
  gi|1340942     4    QLKTPTRTLTSSADK--DAPLKEDIRLLGRLLgDVLRDQQGDAVFEI 48

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      +  +    D +   EL   L  L    +i v +a++    LAn
  gi|1340942    49 VETIRQTAVRFRRESDVQAGAELNKLLKKLTREQTISVVRAFSYFSHLAN 98

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+ +   RRR +++        +s   +  +   l kL   +  s +
  gi|1340942    99 IAEDQHHNRRRRAHLLA-------GSQPQDGSVACALEKLHDAG-VSGAT 140

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKD..vtve
                    v    K   +  vltAHPt   R+s+L  +  i   La   A+D ++t
  gi|1340942   141 VRKFFKDALISPVLTAHPTEVQRKSILDAEHDIASLLA---ARDlpMTAK 187

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++ E  E +H  +   + t  +R ++ t  DE+   +sY+  t  +  P
  gi|1340942   188 ERAENTERIHSRVTTLWQTRLLRYTKLTVEDEINNALSYYRMTFLRELPA 237

                    FLRRvDtALKniGinERlPYdv.......PL.ikFssWmGGDRDGknPRv
                        ++       i ER P  +++ ++++PL i+  sW+GGDRDG nP v
  gi|1340942   238 LYEDIESE-----IAERFPQRAssasreqPLyIQMGSWIGGDRDG-NPNV 281

                    tPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrt
                      +               +Y++ v  L  Els+      L     E++
  gi|1340942   282 NGDTMQLALARQSTTILEFYLEEVHALGAELSI---STFLAGVSPEVQAL 328

                    aardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi.
                    a +   +            E YR  L  +  +L  t   aR   At ++
  gi|1340942   329 ADKSPDTSEH-------RTDEQYRRALIGMYARLAAT---ARAQGATVLr 368
```

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                    seisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFG
                     ei     y +  eF   L     sL      ++    L  lLR    FG
  gi|1340942   369 KEIGSAPAYENAAEFSSDLQALADSLKARHGAALIKPRLASLLRAAEIFG 418

                    LsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkG
                      L  LD+Rq s+ +  vl  + +  ++ s Y   +EeK+   LlaEL
  gi|1340942   419 FHLATLDMRQSSDVHERVLSELFKCAQVESaYAALPEEKKVALLLAELDH 468

                    KRPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsD
                     R L+ + +   EE    l  +r   ++ ++ +  +   Yiis + + sD
  gi|1340942   469 PRLLYSPYVDYSEETNSELSILRAASDIRkrygARAIRNYIISHTETVSD 518

                    vLAvELLqRECgv...........kqtLrvvPLFEkLADLeAAPAavekL
                    +L v LLqRE g+ + ++++++ ++  L v+PLFE + DL+ A   +e++
  gi|1340942   519 MLEVLLLQRETGLlrldtdkdsvgQLELMVIPLFETIPDLRLAATIMEQV 568

                    FsiDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvA
                     +i   +  i  +++ qevm+GYsDs KD G l   W LYkA   ++ v
  gi|1340942   569 MAIPQVRKLIAKQghlQEVMLGYSDSNKDGGFLTSNWELYKAETQLVEVF 618

                    KkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviE
                     + GvKL lFHGRGGtvGRGGGP   AiL+qPP t+nG +R t qGE+i
  gi|1340942   619 NNAGVKLRLFHGRGGTVGRGGGPSYEAILAQPPGTVNGQIRLTEQGEIIA 668

                    fsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPk......PEWRkLmeemAv
                      F   ++  r L    AAtLE  + P  s  ++ ++  E+  +m e+
  gi|1340942   669 SKFSNPEIGRRNLALLVAATLEASLIPAPSETrhakklAEFESVMGELSE 718

                    vAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesL
                     A   YR +v+  P F +YF  AtP  E   +niGsRPa Rk    ie L
  gi|1340942   719 LAYKAYRNLVYETPGFTDYFFAATPIAEIAELNIGSRPASRKATRRIEDL 768

                    RAiPWiFaWtqtRFHLPvWLGvGAAFKhAi...dKDiKnlqkLkEmYkeW
                    RAiPW F+W q R  LP W G+G A    ++++d   K +  L+ m keW
  gi|1340942   769 RAIPWGFSWGQCRLLLPGWYGFGSAIELWLtqgDNKAKRVATLRAMLKEW 818

                    PFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk.PFGksLRdkYvEtk
                    PFF   l  ++mv  K D  +A+ y +L+    L++   k++ ++ + t
  gi|1340942   819 PFFATLLSNMDMVLSKTDLAVASRYAELVSDKKLRnSIFKRIVNEHERTS 868

                    dlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsyk
                      L  i G k+ L   P L   ++ R +Y+  Ln +q   +KR R
  gi|1340942   869 ASLTLITGKKERLANNPLLARSIKNRFAYLDPLNHLQVELIKRHR----- 913

                    vtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGm
                               A  n   ad+ v+              + L + GiAAG+
  gi|1340942   914 -----------ATMNGGDADDRVRRG-----------IHLSINGIAAGL 940

                    qntG<-*
                     ntG
  gi|1340942   941 RNTG    944

gi|282887782|ref|ZP_06296361.1|: domain 1 of 1, from 107 to 1055: score 336.2, E = 6.5e-98
                    *->siDAqLRl.LvPGKvsed.ekLieYDALLlDkFL.DiLqDLHGedLk
                       s D  + ++   G+  +d+++ +  D   l + L+D+L +  G+ +
  gi|2828877   107    SEDTVMAApKTNGRTRDDkDHPLFQDIRYLGRLLgDVLREQEGDAVF 153

                    EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    ++v      +  +    D    + L  kL sL P  ++ v +a++    L
  gi|2828877   154 DVVETIRQTAVRFRREDDNAAAQTLDKKLRSLSPEQTVSVVRAFSYFSHL 203

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                    An+AE+ +   R Ri+ +        +sA     i   l +Lv  +  +
  gi|2828877   204 ANIAEDRHRNRRHRIHALA-------GSAAQPGSIAYALERLVEAG-AAA 245

                    eEvFeALKnqsvDL.vltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                      v +   n +  ++vltAHPt   R+s+L  +  +   La    + +t
  gi|2828877   246 TPVLQQFFNDALIVpVLTAHPTEVQRKSILDAEHDVARLLAE-RDQQLTD 294

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
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                    ++   +  L   +   + t  +R ++ t  DE+   +sY+  t  + +P
  gi|2828877   295 RERAQNERMLRARVTSLWQTRMLRDSRLTVADEIENALSYYRATFLEEIP 344

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                         ++ ALK  G+  RlP   P  +  sW+GGDRDG nP vt E
  gi|2828877   345 ALYADIEEALKEHGLEARLP---PFFQMGSWIGGDRDG-NPNVTAETLEH 390

                    vCLLaRmmAanlYisqvEDLmFEls....mWRCndELRvRAEEl.yrtaa
                           +    Y++qv  L  Els ++ +    dEL++ AE  + r +
  gi|2828877   391 AIARQAEVIFEHYLEQVHKLGAELSvsnlLAGASDELKALAEISpDRSPH 440

                    rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYn.tRER....aRHLLAt
                    r                EPYR  L  +  +L  + R R +++a  L
  gi|2828877   441 RT---------------DEPYRRALIGMYTRLAAsARVRlgegAVPLRSA 475

                    GiseisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvs
                    G    +  A +y +  eF+  L +   sL       +A   L  l R
  gi|2828877   476 GRGAAPIRATpYDDASEFVRDLHVLMDSLAAHHGAPLAAPRLAPLARAAE 525

                    tFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaE
                     FG  L  +D+Rq s+ +  v+  + +  +++  Y    E  + E LlaE
  gi|2828877   526 VFGFHLASIDLRQSSDIHEAVIAELLKRAGVhDDYAALDESAKLEVLLAE 575

                    LkGKRPLlgsDLPktEEvkDvldafrvL..AELPiDsFGa.....Yiism
                    L   RPL    LP  E    v   + vL++A +  + FGa+  ++Yiis
  gi|2828877   576 LAQPRPL---RLPYAEYSDLVKSELGVLeqARVTREKFGAravrnYIISH 622

                    ataPsDvLAvELLqRECgv............kqtLrvvPLFEkLADLeAA
                    + + sD + v LLq+E g+ +++ ++ +++ k +L v+PLFE + DL+ A
  gi|2828877   623 TETVSDLVEVMLLQKETGLlqgrlgnadnpaKAALMVIPLFETIPDLRNA 672

                    PAavekLFsi...DWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAq
                    P  +  L ++++ D  i +    qevm+GYsDs KD G l   W LY+A
  gi|2828877   673 PHIMRDLLALpgaDSIIEHQGNEQEVMLGYSDSNKDGGFLTSNWELYRAE 722

                    EEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvt
                      ++    + G+ L lFHGRGGtvGRGGGPt  AiLsqPP t++G +R t
  gi|2828877   723 LALVSLFNERGITLRLFHGRGGTVGRGGGPTYQAILSQPPGTVDGQIRLT 772

                    vqGEviEfsFGEEnLCFrsLqRFtAAtLE.....HGmnPPvsPkPEWRkL
                     qGEvi   FG  ++  r L    AAtLE +  +HG  P  +  P + +
  gi|2828877   773 EQGEVIASKFGNPEIGRRNLETVVAATLEasllpHGNAP--ADLPAFEET 820

                    meemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs
                    m+++   A   YR++v+  P F EYF   tP  E   +niGsRPa Rk
  gi|2828877   821 MQQLSDAAMASYRALVYETPGFKEYFFESTPISEIAELNIGSRPASRKLQ 870

                    G....GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDi
                     ++++ ie LRAiPW F+W q R  L  W G+G A    +d+ +++
  gi|2828877   871 DpkhrKIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVAAYLDsapsdaERG 920

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kP
                    + l  Lk m k WPFF   l  ++mv AK D  +A+ y  L+    L+k
  gi|2828877   921 RRLSLLKKMHKSWPFFSTLLSNMDMVLAKTDLAVASRYAALVSDKKLrKH 970

                    FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfq
                      +++ ++++ t + L +i G ++ L   P L   ++ R +Y+  Ln +q
  gi|2828877   971 VFERIVAEWERTSKVLSEITGKRERLAENPLLARSIKNRFPYLDPLNHLQ 1020

                    AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                       LKR R                A +           n   rv  G+
  gi|2828877  1021 VELLKRHR----------------AGDT----------N--ARVRRGIH- 1041

                    tLiLtmKGiAAGmqntG<-*
                       Lt+ GiAAG+ ntG
  gi|2828877  1042 ---LTINGIAAGLRNTG    1055

gi|466887|gb|AAA17132.1|: domain 1 of 1, from 1 to 907: score 335.4, E = 1.1e-97
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        + A +RlL  G +   + L e      D   D++  +  e+ +
  gi|466887|     1    -MRADIRLL--GTIL-GDTLREQNG---DEVFDLVERVRVESFRV-- 38
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                            ++      ++     +Ld   ai + +a++H   LAn+
gi|466887|    39 ------------RRSEIDRADMARMFSGLDIHLAIPIIRAFSHFALLANV 76

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AE+++   RR i++         ++   +s +  t+ kL l      + v
gi|466887|    77 AEDIHRERRRHIHLDA-------GEPLRDSSLAATYAKLDLAK-LDSATV 118

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt.veDK
                 +AL    v  v+tAHPt   RR +   + Ri   L  L A   t+  D
gi|466887|   119 ADALTGAVVSPVITAHPTETRRRTVFVTQRRITE-LMRLHAEGHTeTADG 167

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                + ++  L R i   + t  iR a+    DE+  G+ Y+   +++ +P+
gi|466887|   168 RSIERELRRQILTLWQTALIRLARLQISDEIDVGLRYYSAALFHVIPQVN 217

                RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                  v  AL+       l    P+++  sW+GGDRDG nP vt +v R
gi|466887|   218 SEVRNALRARWPDAEL-LSGPILQPGSWIGGDRDG-NPNVTADVVRRATG 265

                LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                 a       Y+  +  L  Elsm      L     El   aa+
gi|466887|   266 SAAYTVVAHYLAELTHLEQELSM---SARLITVTPELATLAASC------ 306

                iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                          EPYR  L  +R +L  t        A+ + + + +
gi|466887|   307 ---QDAACADEPYRRALRVIRGRLSSTA-------AHILDQQPPNQLGLG 346

                vEeFLEPLELCY......ksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                +  +  P ELC + ++ + sLC  G   +AD  L  l   v  FG  L
gi|466887|   347 LPPYSTPAELCAdldtieASLCTHGAALLADDRLALLREGVGVFGFHLCG 396

                LDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLl
                LD+Rq s+ + +v+  +    ++  +Y + +E++R   L+aEL  +RPL+
gi|466887|   397 LDMRQNSDVHEEVVAELLAWAGMHQdYSSLPEDQRVKLLVAELGNRRPLV 446

                g.....sDLPktEEvkDvldafrvLAEL.PiDsFGaYiismataPsDvLA
                g++ + sDL + E    vl a     EL  + +   Yiism+ + sDvL
gi|466887|   447 GdraqlSDLARGE--LAVLAAAAHAVELyGSAAVPNYIISMCQSVSDVLE 494

                vELLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsiDWY
                v +L +E g+   +++++  ++ + PLFE + DL+   A +  +  +  Y
gi|466887|   495 VAILLKETGLLDasgsqpycPVGISPLFETIDDLHNGAAILHAMLELPLY 544

                inridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvK
                +  +  +++ qevm+GYsDs KD G l+A W +Y+A   ++ vA+k G++
gi|466887|   545 RTLVAARgnwQEVMLGYSDSNKDGGYLAANWAVYRAELALVDVARKTGIR 594

                LvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEE
                L lFHGRGGtvGRGGGP   AiL+qPP  +nGslR t qGEvi   + E
gi|466887|   595 LRLFHGRGGTVGRGGGPSYQAILAQPPGAVNGSLRLTEQGEVIAAKYAEP 644

                nLCFrsLqRFtAAtLEHGm..nPPvsPkPE.WRkLmeemAvvAtEEYRsv
                ++  r L    AAtLE  + +   +    E+   +++e+A  A   Y  +
gi|466887|   645 QIARRNLESLVAATLESTLldVEGLGDAAEsAYAILDEVAGLARRSYAEL 694

                vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaW
                v   P Fv+YF   tP  E G +niG RP+ RkP   i  LRAiPW+ aW
gi|466887|   695 V-NTPGFVDYFQASTPVSEIGSLNIGNRPTSRKPTTSIADLRAIPWVLAW 743

                tqtRFHLPvWLGvGAAFKhAi....dKDiKnlqkLkEmYkeWPFFRvtlD
                 q R  LP W G G AF+  +  +++ +++ + +L+++Y+ WPFFR  l
gi|466887|   744 SQSRVMLPGWYGTGSAFQQWVaagpESESQRVEMLHDLYQRWPFFRSVLS 793

                LlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtkdlLLkiAG
                 +  v AK D G+Aa y +L+v E L++   +++ d+   t  +   i G
gi|466887|   794 NMAQVLAKSDLGLAARYAELVVDEALrRRVFDKIADEHRRTIAIHKLITG 843

                HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                H DlL   P L   +  R +Y+  Ln +q   L+R R
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  gi|466887|   844 HDDLLADNPALARSVFNRFPYLEPLNHLQVELLRRYR------------ 880

                   KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                         s   de+v+             ++Ltm G+A  + n G
  gi|466887|   881 -------SGHDDEMVQRG-----------ILLTMNGLASALRNSG    907

gi|2499464|sp|Q59757.1|CAPP_RHOMR: domain 1 of 1, from 6 to 936: score 335.2, E = 1.3e-97
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         q+ +   G +s    L e   LL      ++q++ G+++ E v
  gi|2499464     6    ----QIEIEGTG-IS--RPLSEHVNLLGGLLGQVIQEMAGPEMLELV 45

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        l  +      ++  e   +++ s    + + + +a+     L n
  gi|2499464    46 ETLRRLCKQAAQENRPEFREQAYTRIHSATYDELLWLLRAYTAFFHLVNQ 95

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AE  e+    R + ++    +       Es i+E +  L  ++ ++ ++v
  gi|2499464    96 AEQQEIIRINRERAQQ----STPERPRPES-IDEAILALKQQG-RTLDDV 139

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      L    +   +tAHPt + RRs+L K+  i   L+q     +t+e+++
  gi|2499464   140 LTLLERLDIQPTVTAHPTEARRRSILYKQQHIAQMLSQQRRCQLTPEEQE 189

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    L   LH  i     t E+R  +Pt  DE+  G+ +i  t+W+ vP+
  gi|2499464   190 TLLLDLHNQITLLLGTAEVREERPTVRDEVEQGLYFIQSTIWEAVPRIYE 239

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    v  AL+       + +  P +++ sW+G DRDG nP vtPE+tR   L
  gi|2499464   240 DVRRALRRY-YGADVDFR-PFLRYRSWIGSDRDG-NPYVTPEITRWTALT 286

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    R +A   Y++ +  L   ls+    d   +  EEl r  ard
  gi|2499464   287 QRRLALQRYMEELRQLRRRLSL---SDRYVAPPEELRRSLARD------- 326

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                        +PP           R K+     R   LL + + +    A   +
  gi|2499464   327 AREVSLPPHVLRQFRHESFRLKISYIMGRLHGLL-QALDDPTQPAPDYDA 375

                   EeFLEPLELCYksLCeCGDkviA.DGsLLDlLRqvstFGLsLvKLDiRqE
                   + F+E L L  + L  CG   iA+   L  lL    tFG  Lv LD+Rq
  gi|2499464   376 DAFVEDLRLLQRCLEACGLERIArHDQLTRLLVLAQTFGFHLVTLDVRQH 425

                   seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   s  +   +  + +  ++  +YR  +E +RqE L  EL+  RPLl++
  gi|2499464   426 SSVHEAAVAELLRLAGVENdYRALPESRRQELLAEELSNPRPLLPPGARV 475

                   tEEvkDvldafrvLAELPi...DsFGaYiismataPsDvLAvELLqREC.
                    E  + vl++f v+ EL   ++   G+Yi+sm+ + sD L   LL +E +
  gi|2499464   476 SEATRQVLETFAVIRELVQldpRLVGSYIVSMTHTVSDLLEPMLLAKEVg 525

                   ..............gvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYin
                     + ++++++++++v+ ++  vPLFE + DLeAA   +e + s   Y+
  gi|2499464   526 lwhyerdprtgkpgHVRCPIDFVPLFETIEDLEAAASRMEAILSHPVYRM 575

                   rid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                   ++  ++G qe+m+GYsDs KD G   A W L +AqE ++ v  ++Gv
  gi|2499464   576 QVAargGFQEIMLGYSDSTKDGGYWMANWALHRAQEQLAEVCLRHGVDFR 625

                   lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                   lFHGRGGtvGRGGG    AiL+ PP   nG +R t qGEvi f +   ++
  gi|2499464   626 LFHGRGGTVGRGGGRANQAILAMPPVVHNGRIRFTEQGEVISFRYALPEI 675

                   CFrsLqRFtAAtLEHGmnPPvsPk....PEWR.kLmeemAvvAtEEYRsv
                     r L     A L     P  s  ++++P  R++Lm+e+A      YR +
  gi|2499464   676 AHRHLEQIVNAMLRVVGLPAASGTdgtdPATRnRLMDELAARSMRAYRRL 725

                   vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiF
                   +   P F  ++   tP     ++ i sRP  R  +  ++ esLRAiPW+F
  gi|2499464   726 I-DAPDFWSWYTRITPIDQISRLPIASRPVSRSSAREVdfESLRAIPWVF 774
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                    aWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLl
                    aWtq R+ +P W G+G A    ++     l  L+  Y+ WPFFR  l
  gi|2499464   775 AWTQVRYLIPGWFGIGQALDELLQTSPEHLETLRTWYRSWPFFRTVLQNA 824

                    ..EmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGH
                    ++Emv A+ +  iAa yD+LL  +    F + + ++Y   +  +L+i
  gi|2499464   825 qrEMVRARLE--IAAYYDRLL-GDGPTAFHQMIEEDYHRARTAILRITDQ 871

                    kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                      lL+ DP +++ + LR++Y   Ln +q   ++RiR
  gi|2499464   872 ESLLDHDPIIRKSVQLRNPYTDVLNLVQLELMRRIRSGA----------- 910

                    EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    E   E+                   L   L L + GiAA mq tG
  gi|2499464   911 EADREP-------------------LRRALFLSINGIAAAMQSTG    936

gi|118465776|ref|YP_882518.1|: domain 1 of 1, from 11 to 935: score 334.0, E = 3e-97
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        i A  R Lv        + ++ D  Ll   L+D + +  G+++ E
  gi|1184657    11    PIGAVQRTLVGREAT---EPMRADIGLLGAILgDTVREQNGQQVFEL 54

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      s  +  ++      EL     ++d   ai v +a++H   LAn
  gi|1184657    55 VERARVES--FRVRRSEIDRAELARMFAGIDIHQAIPVIRAFSHFALLAN 102

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+++   RR i+          ++   +s +  t+ kL        +
  gi|1184657   103 VAEDIHRERRRAIHVAA-------GEPPQDSSLAATYAKLDRAQ-LDSAT 144

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK.DvtveD
                    v eAL+   v  v+tAHPt   RR +   + Ri   L  L A + +  +D
  gi|1184657   145 VAEALRGAVVSPVITAHPTETRRRTVFVTQHRITE-LMRLHAEgHIETDD 193

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                     + ++  L R +   + t  iR ++    DE+  G+ Y+    +k +P+
  gi|1184657   194 GRNIELELRRQVLTLWQTALIRLSRLQITDEIEVGLRYYAAAFFKVIPRV 243

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                       v  AL+       l  d P++   sW+GGDRDG nP vt +v R
  gi|1184657   244 NAEVRNALRARWPGADL-LDEPIVAPGSWIGGDRDG-NPNVTADVVRRAT 291

                    LLaRmmAanlYisqvEDLmFElsm....WRCndELRvRAEElyrtaardk
                      a   A   Y+  +     Elsm+ +      EL + AE+    a+ d
  gi|1184657   292 GDAAYTALAHYLAELTACEQELSMsarlVAVTPELAALAEDCAEKARAD- 340

                    vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRE.....RaRHLLAtGis
                                  EPYR  L  +R +L  t  +  ++R  H L  G+
  gi|1184657   341 --------------EPYRRALRVIRGRLTATAAeildrRPQHELDLGLP 375

                    eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                      +  A      e    L+    sL   G   +AD  L  l   v  FG
  gi|1184657   376 PYATPA------ELRGDLDTVDASLRAHGSALLADDRLALLREGVRVFGF 419

                    sLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK
                     L  LD+Rq s+ + +v+  +    ++ + YR+ +E+ R E L aEL  +
  gi|1184657   420 HLCGLDMRQNSDVHEEVVAELLAWAGVHpDYRSLPEDERVELLAAELGTR 469

                    RPLlgsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsD
                    RPL+g      E     l+ +r  A   i  +G+   ++Y+ism+ + sD
  gi|1184657   470 RPLVGDRAELSELADKELGVVRAAAH-AIRRYGPaavpnYVISMCRSVSD 518

                    vLAvELLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsi
                    vL   +L +E g+   +++++  ++ + PLFE + DL+   A +  +  +
  gi|1184657   519 VLEAAILLKEAGLIDasgpepycPVGISPLFETIEDLHNGAAILHAMLEL 568

                    DWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKky
                      Y+  +  ++++qevm+GYsDs KD G l+  W +Y+A   ++ vA+k
  gi|1184657   569 PLYRALVAARgqsQEVMLGYSDSNKDGGYLASSWAVYRAELALVEVARKT 618

                    GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF
                    G++L lFHGRGGtvGRGGGP   AiL+qPP  +nGslR t qGEvi   +
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  gi|1184657   619 GIRLRLFHGRGGTVGRGGGPSYEAILAQPPGAVNGSLRLTEQGEVIAAKY 668

                   GEEnLCFrsLqRFtAAtLEHGm..nPPvsPkPE.WRkLmeemAvvAtEEY
                    E ++  r L    AAtLE  + +   +    E+   +++e+Av A   Y
  gi|1184657   669 AEPQVAQRNLESLVAATLESTLldVEGLGDTAEpAYAVLDEVAVLAQRAY 718

                   RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWi
                     +v   P Fv+YF   tP  E G +niGsRP+ RkP   i  LRAiPW+
  gi|1184657   719 AELVHETPGFVDYFMASTPVSEIGSLNIGSRPTSRKPTESIADLRAIPWV 768

                   FaWtqtRFHLPvWLGvGAAFKhAi....dKDiKnlqkLkEmYkeWPFFRv
                    aW q R  LP W G G AF   i  +++     +  L+++Y+ WPFFR
  gi|1184657   769 LAWSQSRVMLPGWYGTGSAFEQWIaagpQSRAERVDILHDLYRRWPFFRS 818

                   tlDLlEmvFAKGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLL
                    l  l  v AK D G+Aa y +L+    L+++ FGk + d+   t  +
  gi|1184657   819 VLSNLAQVLAKSDLGLAAQYAELVDDAALrrRVFGK-IADEHRRTIAMHK 867

                   kiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlr
                    i G   lL   P L   +  R +Y+  Ln +q   L+R R
  gi|1184657   868 LITGQDNLLADNPALARSVFNRFPYLEPLNHLQVELLRRYR--------- 908

                   PhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG
                              s   deLv+              ++Ltm G+   + n G
  gi|1184657   909 -----------SGDDDELVQRG-----------ILLTMNGLTSALRNSG 935

                   <-*

  gi|1184657     -     -

gi|82703804|ref|YP_413370.1|: domain 1 of 1, from 10 to 937: score 333.9, E = 3.2e-97
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      siD      +  K  +d+ L e D  Ll + L+D L +  Ge   +
  gi|8270380    10    SIDTN-PNYIHDKEPKDDPLRE-DIRLLGRMLgDTLREQEGEPTFDL 54

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v      +  +   +D+k  +EL   L  L    +  v +a++    L n
  gi|8270380    55 VENIRQTAIRFRRDQDPKARQELDRLLNQLSNKATEAVVRAFSQFSQLSN 104

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE+++   RRR  ++         s      +   l  + +k   s +
  gi|8270380   105 IAEDMHHNRRRRSYLLA-------RSQPQAGSVARALDLVFSKE-TSSAA 146

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                            v  vltAHPt   RRs+L  +  i   L       +t+++
  gi|8270380   147 LGRFFDKALVSPVLTAHPTEVQRRSILDCQLAIARLLNERDRVQLTPDEL 196

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +E L   iq  + t  +R a+    DE++ G++Y+H t    vP
  gi|8270380   197 SKNEEGLRTNIQILWQTRMLRSARLSVYDEIKNGLAYYHYTFLTEVPHLY 246

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                     ++  L    + ++ P   P ++  sW+GGDRDG nP vt Ev
  gi|8270380   247 AEIEDLLER-RMGDKAPRIPPFLRIGSWIGGDRDG-NPFVTHEVLLHAAE 294

                   LaRmmAanlYisqvEDLmFEls....mWRCndELRvRAEElyrtaardkv
                       +A  +Y+  v  +   ls ++++    + L + AE     a +
  gi|8270380   295 RQSALALDFYMGEVHRIGRRLSltdrLVDVDEALAALAEASPDRAPSR-- 342

                   vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                                EPYR  L  +  +L  t     H + +     + e
  gi|8270380   343 ------------ADEPYRRALIGIYARLAATSMGLGHAIRQRRPVGPAEP 380

                   vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                    yt+  e +  L++  +sL +     +A G L  + R    FG  L  LD
  gi|8270380   381 -YTDSLELVRDLDIVIHSLEQHKSELLARGDLRRVRRAAEVFGFHLAPLD 429

                   iRqEseRqtDvlDAittH.LeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                   +Rq s  +  v+  + + + ++  Y + +E  R   Ll+E++  R L  +
  gi|8270380   430 MRQHSHIHEQVVAELFERgANLKGYSDLPEAERVRCLLTEVSSPRLLRSP 479
```

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                    DLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvEL
                     L   E  +  l  ++  AE+    FG+   ++Y+is a   sD+L v L
  gi|8270380   480 YLDYSELAQSELHIVETAAEI-HRRFGPaalpnYVISKADGISDILEVAL 528

                    LqRECgvkqt.......LrvvPLFEkLADLeAAPAavekLFsiDWYinri
                    L +E g+ ++++++  ++ +vPLFE +ADL+     ++ LFsi +Y+  +
  gi|8270380   529 LLKEVGLLRAgekpclhINIVPLFETIADLRGCARIMDELFSIPYYRKLV 578

                    dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                    d +++ qevm+GYsDs KD G l+A W LYkA  E+ Kv  k+ v L lF
  gi|8270380   579 DSRndvQEVMLGYSDSNKDGGFLAANWELYKAETELTKVFAKHKVELRLF 628

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGGtvGRGGGP   AiL+qPP  +nG +R+t qGEvi   + + ++
  gi|8270380   629 HGRGGTVGRGGGPSYQAILAQPPGSVNGQIRITEQGEVIGSKYSDPEIGR 678

                    rsLqRFtAAtLEHGm..nPPv.sPkPEWRkLmeemAvvAtEEYRsvvvKE
                    r L    AAt+E  + ++  ++    E+  +me +A  A   YRs+v+
  gi|8270380   679 RNLETLVAATIEATLlsHDTLgQCADEYYGVMEVLAGDALRAYRSLVYET 728

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
                    P F  YF   tP  E   +niGsRP  Rk s  ie LRAiPW F+W   R
  gi|8270380   729 PGFNRYFQESTPIKEIAGLNIGSRPPSRKKSDLIEDLRAIPWTFSWGVNR 778

                    FHLPvWLGvGAAFKhAidKDiK...nlqkLkEmYkeWPFFRvtlDLlEmv
                      +  W G+G A    ++++ K+++ l  L+ mY+ WPF    l  ++mv
  gi|8270380   779 AMITGWYGFGTAVEMFVQREGKgdnGLGLLQKMYQAWPFLQTLLSNMDMV 828

                    FAKGDPGiAaLyDkLLvaEeLk..PFGksLRdkYvEtkdlLLkiAGHkDl
                     AK D GiA+ y +L+   eL+++ FG+ +  +++   ++L  + G  +l
  gi|8270380   829 LAKTDMGIASRYAELVTDVELRreVFGR-IQKEWELSVKWLFAVTGRTEL 877

                    LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                    L   P L   +R R +Yi  Ln +q   L+R R
  gi|8270380   878 LQDNPTLARSIRNRTPYIDPLNHLQVELLRRYR---------------- 910

                    dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       s  a + v              + Lt+ G+AAG+ n G
  gi|8270380   911 ---SGDATDAVTRA-----------IQLTINGVAAGLRNSG    937

gi|289635970|ref|ZP_06468254.1|: domain 1 of 1, from 142 to 1090: score 333.6, E = 3.9e-97
                    *->siDAqLRl.LvPGKvsed.ekLieYDALLlDkFL.DiLqDLHGedLk
                       s DA   ++   G+  +d+++ +  D   l + L+D+L +  G+++
  gi|2896359   142    SADAPPPApKTNGRTRDDkDHPLFQDIRYLGRLLgDVLREQEGDEVF 188

                    EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    ++v      +  +    D    + L  kL sL P  ++ v +a++    L
  gi|2896359   189 DVVETIRQTAVRFRREDDNAAAQTLDKKLRSLSPEQTVSVVRAFSYFSHL 238

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                    An+AE+ +   R Ri+ +        +sA     i   l +Lv  +  +
  gi|2896359   239 ANIAEDRHRNRRHRIHALA-------GSAAQPGSIAYALERLVEAG-AAA 280

                    eEvFeALKnqsvDL.vltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                      v +   n +  ++vltAHPt   R+s+L  +  +   La    + +t
  gi|2896359   281 TPVLQQFFNDALIVpVLTAHPTEVQRKSILDAEHDVARLLAE-RDQQLTE 329

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                     ++   +  L   +   + t  +R ++ t  DE+   +sY+  t  + +P
  gi|2896359   330 RERAHNETMLRARVTSLWQTRMLRDSRLTVADEIENALSYYRATFLEEIP 379

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                         ++ ALK  G+  RlP   P  +  sW+GGDRDG nP vt E
  gi|2896359   380 ALYADIEEALKEHGLEARLP---PFFQMGSWIGGDRDG-NPNVTAETLEH 425

                    vCLLaRmmAanlYisqvEDLmFEls....mWRCndELRvRAEEl.yrtaa
                           +    Y++qv  L  Els ++ +    dEL++ A+  + r +
  gi|2896359   426 AIARQAEVIFEHYLEQVHKLGAELSvsnlLAGASDELKALADISpDRSPH 475

                    rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYn.tRER....aRHLLAt
                    r                 EPYR  L  +  +L  + R R ++++  L
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  gi|2896359   476 RT---------------DEPYRRALIGMYTRLAAsARVRlgegSVPLRSA 510

                   GiseisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvs
                   G    +  A +y +  eF+  L +   sL       +A   L  l R
  gi|2896359   511 GRGAAPIRATpYDDASEFVRDLHVLIDSLAAHHGAPLAAPRLAPLARAAE 560

                   tFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaE
                    FG  L  +D+Rq s+ +  v+  + +  +++  Y   sE  +   LlaE
  gi|2896359   561 VFGFHLASIDLRQSSDIHEAVIAELLKRAGVhDDYAALSESEKLAVLLAE 610

                   LkGKRPLlgsDLPktEEvkDvldafrvL..AELPiDsFGa.....Yiism
                   L   RPL    LP  E    v   + vL++A +  + FGa+  ++Yiis
  gi|2896359   611 LAQPRPL---RLPYAEYSDLVKSELGVLeqARVTREKFGAravrnYIISH 657

                   ataPsDvLAvELLqRECgv............kqtLrvvPLFEkLADLeAA
                   + + sD + v LLq+E g+ +++ ++++++ k +L v+PLFE + DL+ A
  gi|2896359   658 TETVSDLVEVMLLQKETGLlqgqlgnpndpaKAALMVIPLFETIPDLRNA 707

                   PAavekLFsi...DWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAq
                   P  +  L ++++ D  i +    qevm+GYsDs KD G l   W LY+A
  gi|2896359   708 PHIMRDLLALpgaDSIIEHQGNEQEVMLGYSDSNKDGGFLTSNWELYRAE 757

                   EEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvt
                     ++    + G+ L lFHGRGGtvGRGGGPt  AiLsqPP t++G +R t
  gi|2896359   758 LALVSLFNERGITLRLFHGRGGTVGRGGGPTYQAILSQPPGTVDGQIRLT 807

                   vqGEviEfsFGEEnLCFrsLqRFtAAtLE.....HGmnPPvsPkPEWRkL
                    qGEvi   FG  ++  r L    AAtLE +  +HG  P  +  P + +
  gi|2896359   808 EQGEVIASKFGNPEIGRRNLETVVAATLEasllpHGNAP--AELPAFEET 855

                   meemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs
                   m+++   A   YR++v+  P F EYF   tP  E   +niGsRPa Rk
  gi|2896359   856 MQQLSDAAMASYRALVYETPGFKEYFFESTPISEIAELNIGSRPASRKLQ 905

                   G....GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDi
                    ++++ ie LRAiPW F+W q R  L  W G+G A    +d+ ++++
  gi|2896359   906 DpkhrKIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVGAYLDgapsdtERA 955

                   KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kP
                   + l  Lk m k WPFF   l  ++mv AK D  +A+ y  L+    L+k
  gi|2896359   956 RRLALLKKMHKSWPFFSTLLSNMDMVLAKTDLAVASRYAALVSDKKLrKH 1005

                   FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfq
                     +++ ++++ t + L +i G  + L   P L   ++ R +Y+  Ln +q
  gi|2896359  1006 VFERIVAEWERTSKVLSEISGKSERLAENPLLARSIKNRFPYLDPLNHLQ 1055

                   AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                      LKR R               A +           n   rv  G+
  gi|2896359  1056 VELLKRHR----------------AGDT----------N--ARVRRGIH- 1076

                   tLiLtmKGiAAGmqntG<-*
                      Lt+ GiAAG+ ntG
  gi|2896359  1077 ---LTINGIAAGLRNTG    1090

gi|152980037|ref|YP_001352831.1|: domain 1 of 1, from 16 to 959: score 332.9, E = 6.4e-97
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      +  A  ++  P      +  ++ D  Ll + L+D+L D  G+ + E+
  gi|1529800    16    AKKAVNKAANPATNK--DAPLKEDIRLLGRILgDVLRDQEGDAVFEV 60

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v      +  +    D +   +L   L  L    +i v +a++    LAn
  gi|1529800    61 VETIRQTAVRFRREADVQAGADLNKLLKKLTREQTISVVRAFSYFSHLAN 110

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE+ +   RRR +++        +sA  E  +   l kL   +    +
  gi|1529800   111 IAEDQHHNRRRRAHLLA-------GSAPQEGSVAFALEKLANAG-VNGAT 152

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKD..vtve
                   v    K   +  vltAHPt   R+s+L  +  i   La   A+D ++t
  gi|1529800   153 VRKFFKDALISPVLTAHPTEVQRKSILDAEHDIARLLA---ARDlpMTAR 199
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                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++    E L   +   + t  +R ++    DE+   +sY+  t  +  P
  gi|1529800   200 ERAANTELLRSLVTTLWQTRLLRYSKLSVEDEINNALSYYRITFLRELPA 249

                    FLRRvDtALKniGinERlPYdv..........PLikFssWmGGDRDGknP
                        ++       i E  P  +++ + +++++  ++  sW+GGDRDG nP
  gi|1529800   250 LYEDIESE-----IAEQFPQRAssananrdqhSYVQMGSWIGGDRDG-NP 293

                    RvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEly
                     v  +                +Y++ v  L  El +      L     E++
  gi|1529800   294 NVNGDTMQLALARQSTTILEFYLEEVHALGAELPV---STFLAGVSPEVQ 340

                    rtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtG
                      a +   +             E YR  L  +  +L  t   aR   At
  gi|1529800   341 ALADKSPDTSEH-------RADEQYRRALIGIYARLAAT---ARAHGATN 380

                    i..seisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvs
                    i + e+   A y    eF   L L   sL e    v+    L  lLR
  gi|1529800   381 IlrKEVGPGAPYESAVEFSADLQLLVDSLKERHGAVLIKPRLAPLLRAAE 430

                    tFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaE
                     FG  L  LD+Rq s+ +  vl  + +  e++ sY + +E+K+ E Ll+E
  gi|1529800   431 IFGFHLATLDMRQSSDVHERVLSELFKRAEVeTSYADLPEQKKVELLLTE 480

                    LkGKRPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismata
                    L   R L+ + +   +E    l+ +r    + ++ ++ +   Yiis + +
  gi|1529800   481 LDKPRLLYSPYIDYSDETNSELNILRAAHHIRqrygSRAIRNYIISHTET 530

                    PsDvLAvELLqRECgvkqt...........LrvvPLFEkLADLeAAPAav
                     sD L v LLqRE g+ +++++  + ++ +L v+PLFE + DL+ A   +
  gi|1529800   531 VSDLLEVLLLQRETGLLRPdtdvasvgeveLMVIPLFETIPDLRLAASIM 580

                    ekLFsiDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEii
                    e++ +i   +  i  +++ qevm+GYsDs KD G l   W LYkA  E++
  gi|1529800   581 EQVMAIPKVRRLIAKQghlQEVMLGYSDSNKDGGFLTSNWELYKAETELV 630

                    KvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGE
                     v  + GvKL lFHGRGGtvGRGGGP   AiL+qPP t+nG +R t qGE
  gi|1529800   631 NVFNRAGVKLRLFHGRGGTVGRGGGPSYEAILAQPPGTVNGQIRLTEQGE 680

                    viEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPk......PEWRkLmee
                    +i   F   ++  r L    AAtLE  + PP + ++  ++  E+  +m e
  gi|1529800   681 IIASKFSNPEIGRRNLALLVAATLEASLTPPPADRkaakklAEFESVMAE 730

                    mAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi
                    +   A   YR +v+  P F +YF +AtP  E   +niGsRPa Rk    i
  gi|1529800   731 LSELAYKGYRNLVYETPGFTDYFFSATPIAEIAELNIGSRPASRKATRRI 780

                    esLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidK...DiKnlqkLkEmY
                    e LRAiPW F+W q R  LP W G+G A    ++++++  K +  L+ m+
  gi|1529800   781 EDLRAIPWGFSWGQCRLLLPGWYGFGSAIEQWLEQgenKAKRVATLRAMF 830

                    keWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk.PFGksLRdkYv
                    keWPFF   l  ++mv  K D  +A+ y +++v   L++   k++ ++ +
  gi|1529800   831 KEWPFFVTLLSNMDMVLSKTDLAVASRYSEMVVDRKLRnSIFKRIVAEHE 880

                    EtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDP
                     t   L  i G k+ L   P L   ++ R +Y+  Ln +q   +KR R
  gi|1529800   881 RTSSCLTLITGKKERLANNPLLARSIKNRFAYLDPLNHLQVELIKRHR-- 928

                    sykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiA
                                 A+    k d+ v+              + L + GiA
  gi|1529800   929 --------------AAMRDGKIDDRVRRG-----------IHLSINGIA 952

                    AGmqntG<-*
                    AG+ ntG
  gi|1529800   953 AGLRNTG    959

gi|120403691|ref|YP_953520.1|: domain 1 of 1, from 14 to 936: score 332.6, E = 7.7e-97
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        i A  R  v G+ +   + ++ D  Ll   L+D + +  G+++ +
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gi|1204036    14    PIGAVHRTQV-GRDA--TEPMREDIRLLGAILgDTVREQNGDEVFDL 57

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    + E   + A +  ++      ++     ++d   a+ v +a+ H   LAn
gi|1204036    58 I-ERARVEA-FRVRRSEIDRADIAKLFDGVDVHLALPVIRAFTHFALLAN 105

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+++   RR ++          ++   +s +  t+ kL +
gi|1204036   106 VAEDIHRERRRAVHEAA-------GEPPQDSSLAATYLKLDSAE-LDAVA 147

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v +AL    v  v+tAHPt   RR +   + Ri   L  L     t  D
gi|1204036   148 VADALAGALVSPVITAHPTETRRRTVFDTQHRITE-LMRLRLHGHTTADG 196

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +++D  L R i   + t  iR ++   qDE+  G+ Y+    ++ +P+
gi|1204036   197 RDIDRELRRHILTLWQTALIRLSRLKIQDEIETGLRYYAAAFFEVIPQVN 246

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                      v tAL+       l  + P+++  sW+GGDRDG nP vt +v R
gi|1204036   247 AEVRTALQARWPEGGL-LEEPIVRPGSWIGGDRDG-NPNVTADVVRLATG 294

                    LaRmmAanlYisqvEDLmFElsm....WRCndELRvRAEElyrtaardkv
                     a   A   Y+  +  L  Elsm+ +     d L + A+  +  a+ d
gi|1204036   295 SAAHTAFAHYFAELTALEQELSMsarlVHISDQLGALADACHEPARAD-- 342

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                                 EPYR  L  v  +L  t   aR +L        +
gi|1204036   343 --------------EPYRRALRVVHARLTAT---ARQILDRQPEHELDLG 375

                    v..ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                    +++y    e L+ L++   sL   G  v+AD  L  l   v  FG  L
gi|1204036   376 MdpYSAPGELLDDLDVIDASLRANGSAVLADDRLARLREAVRVFGFHLSG 425

                    LDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLl
                    LD+Rq s+ + +v+  +    ++ + Y +  E  R E L aEL  +RPL+
gi|1204036   426 LDMRQNSDVHEEVVAELLAWAGVHpDYASLGESERVEILAAELGTRRPLI 475

                    gsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAv
                    g D    E  +  ld +   A   +  FG++  ++Y+ism+ + sD+L
gi|1204036   476 GQDAELSELARKELDIVAAAAR-AVHVFGPeavpnYVISMCQSVSDMLEA 524

                    ELLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsiDWYi
                     +L +E g+   ++ ++  ++ +vPLFE + DL+     +e    +  Y+
gi|1204036   525 AILLKEAGLLDatsahpyaPVGIVPLFETIDDLQHGASILEAALDLPLYR 574

                    nrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                      +  ++G qevm+GYsDs KD G  l+A W LY+A  +++  A++ G++L
gi|1204036   575 AVVTargGSQEVMLGYSDSNKDGGYLAANWALYRAELDLVESARRTGIRL 624

                    vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                     lFHGRGGtvGRGGGP   AiL+qPP  ++GslR t qGEvi   + E
gi|1204036   625 RLFHGRGGTVGRGGGPSYDAILAQPPGAVQGSLRLTEQGEVIAAKYAEPR 674

                    LCFrsLqRFtAAtLE......HGmnPPvsPkPEWRkLmeemAvvAtEEYR
                    +  r L    AAtLE +  +  G+     P  E   +++++A  A   Y
gi|1204036   675 IARRNLETLLAATLEatlldvEGLGDAANPAYE---VLDDLAARAQRAYA 721

                    svvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiF
                     +v   P FvEYF+  tP  E G +niGsRP+ RkP   i  LRAiPW+
gi|1204036   722 ELVHETPGFVEYFKASTPVSEIGALNIGSRPTSRKPTTSISDLRAIPWVL 771

                    aWtqtRFHLPvWLGvGAAFKhAidK...DiKnlqkLkEmYkeWPFFRvtl
                    aW q R  LP W G G AF   +  +++    l  L+++Y+ WPFF   l
gi|1204036   772 AWSQSRVMLPGWYGTGTAFEEYVGEgpgSAERLAVLQDLYRRWPFFATVL 821

                    DLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtkdlLLkiA
                      +  v AK D G+A  y +L+  E L++   +++ d+ + t  +   i
gi|1204036   822 SNMAQVLAKSDLGLAYRYAELVEDEALrRRVFDKIADEHQRTIRMHELIT 871

                    GHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhl
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                    GH DlL   P L   +  R +Y+  Ln +q   L+R R
  gi|1204036   872 GHDDLLADNPALARSVFNRFPYLEPLNHLQVELLRRYR------------ 909

                    sKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                            s   deLv+              ++Ltm G+A  + n G
  gi|1204036   910 --------SGDQDELVQRG------------ILLTMSGLATALRNSG    936

gi|256815765|ref|ZP_05540780.1|: domain 1 of 1, from 3 to 913: score 332.2, E = 1.1e-96
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s D q   +     s   +L      L D   + L    G++L + v
  gi|2568157     3    SADDQ--TVSTATTS--SELRADIRRLGDLLGETLVRQEGPELLDLV 45

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         l  e     D +   EL   L + +   a  + +a++    LAn+
  gi|2568157    46 EKVRRLTRE-----DGEAAAEL---LRGTELQTAAKLVRAFSTYFHLANV 87

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     E v   +R R  + +         A     +  t  +L       Pe
  gi|2568157    88 TEQV---HRGRELRAR--------RAAEGGLLSRTADRLKDAD---PEHL 123

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     + ++n  +  v+tAHPt ++RRs+L K  Ri    a L    v   D++
  gi|2568157   124 RDTVRNLNIRPVFTAHPTEAARRSVLNKLRRI----AALLDTPVIESDRR 169

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     LD  L   i   + tDE+R  +P P DE R  + Y+ E     v   L
  gi|2568157   170 RLDTRLAENIDLVWQTDELRVVRPEPADEARNAIYYLDELHAGAVGDVLE 219

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         L  +G+   lP d   + F  W+GGDRDG nP vtP vt Dv +L
  gi|2568157   220 DLTAELERVGV--HLPDDTRPLTFGTWIGGDRDG-NPNVTPQVTWDVLIL 266

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkvvKyY
                          n  ++ +++L   ls    n+     A+EEl    + d
  gi|2568157   267 QHEHGINDALEMIDELRGFLS----NSIRYTGAtEELLTSLRAD--LDAL 310

                    iEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                     E ++++K +  +EPYR     +R KL nt+ R    LA+G    +
  gi|2568157   311 PEIsprYKRLNAEEPYRLKATCIRQKLENTKLR----LAKGTTHEPGRD- 355

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y    e L  L +   sL e      ADG L   +R    FGL L  +D+
  gi|2568157   356 YLGTGELLADLRIIQASLREHRGGLFADGRLARTIRTLAAFGLQLATMDV 405

                    RqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLlgs
                    R  ++ +   l  +   L+  s+R  + + + R   L  EL+ +RPL +
  gi|2568157   406 REHADAHHHALGQLFDRLGEESWRyaDMPRDYRGKLLAKELRSRRPLAPT 455

                    DLPk...tEEvkDvldaf.rvLAELPiDsFGaYiismataPsDvLAvELL
                      P +   E    v ++++r LA    +   +Yiism+    Dv A  +L
  gi|2568157   456 PAPVdaaGEKTLGVFQTVkRALAVFGPEVIESYIISMCQGADDVFAATVL 505

                    qRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                     RE g+   + +   + +vPL E   +L+AA   +e + +   Y+  +
  gi|2568157   506 AREAGLIDlhagwaKIGIVPLLETTDELKAADTILEDMLADPSYRRLVAL 555

                    K...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                    +++ qevm+GYsDs K  G     W + +Aq  +  vA +yGv+L lFHG
  gi|2568157   556 RgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRYGVRLRLFHG 605

                    RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                    RGGtvGRGGGPtH AiL+qP  t++G ++vt qGEvi   +    L
  gi|2568157   606 RGGTVGRGGGPTHDAILAQPWGTLEGEIKVTEQGEVISDKYLIPALAREN 655

                    LqRFtAAtLEH.GmnPP....vsPkPEWRkLmeemAvvAtEEYRsvvvKE
                    L    AAtL  + ++  ++++v     W   m+ +   A   YR +v  +
  gi|2568157   656 LELSVAATLQAsALHTAprqsVEALARWDAAMDVVSDAAHTAYRKLV-ED 704

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWtq
                    P    YF   tP      + +GsRP+ R+P+ G++ + LRAiPW+F Wtq
  gi|2568157   705 PDLPTYFLASTPVDQLADLHLGSRPS-RRPGSGVslDGLRAIPWVFGWTQ 753
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                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     R  +P W GvG   K   +     +  L Em ++W FFR  +  +Em
  gi|2568157   754 SRQIVPGWYGVGSGLKALREAGLDTV--LDEMHQQWHFFRNFISNVEMTL 801

                    AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                    AK D  iA  y + Lv +eL+   + ++++ + t   +L++ G ++lL+
  gi|2568157   802 AKTDLRIAEHYVDTLVPDELQHVFDAIKAEHELTVAEVLRVTGEQELLDA 851

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                    DP LKq   +Rd+Y+  +  +q   LKR RD               A+
  gi|2568157   852 DPVLKQTFSIRDAYLDPISYLQVALLKRQRD---------------AAAA 886

                    skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                +e+  P L   L+Lt+ G+AAG+ ntG
  gi|2568157   887 ------------GEQPDPLLARALLLTVNGVAAGLRNTG    913

gi|41407267|ref|NP_960103.1|: domain 1 of 1, from 11 to 935: score 331.7, E = 1.5e-96
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        i A  R Lv        + ++ D  Ll   L+D + +  G+++ E
  gi|4140726    11    PIGAVQRTLVGREAT---EPMRADIRLLGAILgDTVREQNGQQVFEL 54

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      s  +  ++      EL     ++d   ai v +a++H   LAn
  gi|4140726    55 VERARVES--FRVRRSEIDRAELARMFAGIDIHQAIPVIRAFSHFALLAN 102

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+++   RR i+          ++   +s +  t+ kL        +
  gi|4140726   103 VAEDIHRERRRAIHVAA-------GEPPQDSSLAATYAKLDRAQ-LDSAM 144

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt.veD
                    v eAL+   v  v+tAHPt   RR +   + Ri   L  L A   t+ +D
  gi|4140726   145 VAEALRGAVVSPVITAHPTETRRRTVFVTQHRITE-LMRLHAEGHTeTDD 193

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                     + ++  L R +   + t  iR ++    DE+  G+ Y+    +k +P+
  gi|4140726   194 GRNIELELRRQVLTLWQTALIRLSRLQITDEIEVGLRYYAAAFFKVIPQV 243

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                       v  AL+       l  d P++   sW+GGDRDG nP vt +v R
  gi|4140726   244 NAEVRNALRARWPGADL-LDEPIVAPGSWIGGDRDG-NPNVTADVVRRAT 291

                    LLaRmmAanlYisqvEDLmFElsm....WRCndELRvRAEElyrtaardk
                      a   A   Y+  +     Elsm+ +      EL + AE+    a+ d
  gi|4140726   292 GDAAYTALAHYLAELTACEQELSMsarlVAVTPELAALAEDCAEKARAD- 340

                    vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRE.....RaRHLLAtGis
                                   EPYR  L  +R +L  t  +  ++R  H L  G+
  gi|4140726   341 ---------------EPYRRALRVIRGRLTATAAeildrRPQHELDLGLP 375

                    eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                      +  A      e    L+    sL   G   +AD  L  l   v  FG
  gi|4140726   376 PYATPA------ELRADLDTVDASLRAHGSALLADDRLALLREGVRVFGF 419

                    sLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK
                     L  LD+Rq s+ + +v+  +    ++ + YR+ +E+ R E L aEL  +
  gi|4140726   420 HLCGLDMRQNSDVHEEVVAELLAWAGVHpDYRSLPEDERVELLAAELGTR 469

                    RPLlgsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsD
                    RPL+g      E     l+ +r  A   i  +G+   ++Y+ism+ + sD
  gi|4140726   470 RPLVGDRAELSELADKELGVVRAAAH-AIRRYGPaavpnYVISMCRSVSD 518

                    vLAvELLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsi
                    vL   +L +E g+   +++++  ++ + PL E + DL+   A +  +  +
  gi|4140726   519 VLEAAILLKEAGLIDasgpepycPVGISPLLETIEDLHNGAAILHAMLEL 568

                    DWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKky
                      Y+  +  ++++qevm+GYsDs KD G l+  W +Y+A   ++ vA+k
  gi|4140726   569 PLYRALVAARgqsQEVMLGYSDSNKDGGYLASSWAVYRAELALVEVARKI 618

                    GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF
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                    G++L lFHGRGGtvGRGGGP   AiL+qPP  +nGslR t qGEvi   +
  gi|4140726   619 GIRLRLFHGRGGTVGRGGGPSYEAILAQPPGAVNGSLRLTEQGEVIAAKY 668

                    GEEnLCFrsLqRFtAAtLEHGm..nPPvsPkPE.WRkLmeemAvvAtEEY
                     E ++  r L    AAtLE  + +   +    E+   +++e+Av A   Y
  gi|4140726   669 AEPQVAQRNLESLVAATLESTLldVEGLGDTAEpAYAVLDEVAVLAQRAY 718

                    RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWi
                      +v   P Fv+YF   tP  E G +niGsRP+ RkP   i  LRAiPW+
  gi|4140726   719 AELVHETPGFVDYFMASTPVSEIGSLNIGSRPTSRKPTESIADLRAIPWV 768

                    FaWtqtRFHLPvWLGvGAAFKhAi....dKDiKnlqkLkEmYkeWPFFRv
                     aW q R  LP W G G AF   i  +++     +  L+++Y+ WPFFR
  gi|4140726   769 LAWSQSRVMLPGWYGTGSAFEQWIaagpQSRAERVDILHDLYRRWPFFRS 818

                    tlDLlEmvFAKGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLL
                     l  l  v AK D G+Aa y +L+    L+++ FGk + d+   t  +
  gi|4140726   819 VLSNLAQVLAKSDLGLAAQYAELVDDAALrrRVFGK-IADEHRRTIAMHK 867

                    kiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlr
                     i G   lL   P L   +  R +Y+  Ln +q   L+R R
  gi|4140726   868 LITGQDNLLADNPALARSVFNRFPYLEPLNHLQVELLRRYR--------- 908

                    PhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG
                               s   deLv+              ++Ltm G+A  + n G
  gi|4140726   909 ----------SGDDDELVQRG-----------ILLTMNGLASALRNSG 935

                    <-*

  gi|4140726     -     -

gi|268317216|ref|YP_003290935.1|: domain 1 of 1, from 2 to 938: score 331.6, E = 1.5e-96
                    *->siDAqLRlLvPGK.vsedekLieYDALLlDkFLDiLqDLHGedLkEa
                       s+   L + + G ++s    L e   LL      ++q++ G+++ E
  gi|2683172     2    SVLPPLQIEIEGTgIS--RPLSEHVNLLGGLLGQVIQEMAGPEMLEL 46

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     l  +      ++  e   +++ s    + + + +a+     L n
  gi|2683172    47 VETLRRLCKQAAQENRPELREQAYTRIHSATYDELLWLLRAYTAFFHLVN 96

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AE  e+    R + ++    +       Es i+E +  L  ++ ++ ++
  gi|2683172    97 QAEQQEIIRINRERAQQ----STPEHPRPES-IDEAILALKQQG-RTLDD 140

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v   L    +   ltAHPt + RRs+L K+  i   L+q     +t+e++
  gi|2683172   141 VLALLERLDIQPTLTAHPTEARRRSILYKQQHIARLLSQQRRCRLTPEEQ 190

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + L   LH  i     t E+R  +Pt  DE+  G+ +i  t+W+ vP+
  gi|2683172   191 EALLVDLHNQITLLLGTAEVREERPTVRDEVEQGLYFIQSTIWEAVPRIH 240

                    RRvDtALKn.iGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                      v  AL+   G         P +++ sW+G DRDG nP vtPE+tR
  gi|2683172   241 EDVRRALRRyYGTDADF---RPFLRYRSWIGSDRDG-NPYVTPEITRWTA 286

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    L  R +    Y++ +  L   ls+    d      EEl r  ard
  gi|2683172   287 LTQRRLVLQRYMEELRQLRRRLSL---SDRYVPPPEELRRSLARD----- 328

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                           +PP           R K+     R   LL + + +    A
  gi|2683172   329 --AREVSLPPHVLRQFRHESFRLKISYIMGRLHGLL-QALDDPTQPAPDY 375

                    kvEeFLEPLELCYksLCeCGDkviA.DGsLLDlLRqvstFGLsLvKLDiR
                    + + F+E L L  + L  CG   iA+   L  lL  v tFG  Lv LD+R
  gi|2683172   376 DADAFVEDLRLLQRCLEACGLERIArHDQLSRLLVLVQTFGFHLVTLDVR 425

                    qEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgsDL
                    q s  +   +  + +  ++  +YR  +E +RqE L  EL+  RPLl++
  gi|2683172   426 QHSSVHEAAVAELLRLAGVENdYRALPESRRQELLAEELSNPRPLLPPGA 475
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                    PktEEvkDvldafrvLAELPi...DsFGaYiismataPsDvLAvELLqRE
                       E  + vl++f  + EL   ++   G+Yi+sm+ + sD L   LL +E
  gi|2683172   476 RVSEATRQVLETFAAIRELVQldpRLVGSYIVSMTHTVSDLLEPMLLAKE 525

                    C..............gvkqtLrvvPLFEkLADLeAAPAavekLFsiDWY
                     +  + ++++++++++v+ ++  vPLFE + DLeAA   +e + s   Y
  gi|2683172   526 VglwhyerdprtgkpgHVRCPIDFVPLFETIEDLEAAASRMEAILSHPVY 575

                    inrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvK
                    + ++  ++G qe+m+GYsDs KD G   A W L +AqE ++ v  ++Gv
  gi|2683172   576 RMQVAargGFQEIMLGYSDSTKDGGYWMANWALHRAQEQLAEVCLRHGVD 625

                    LvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEE
                      lFHGRGGtvGRGGG    AiL+ PP   nG +R t qGEvi f +
  gi|2683172   626 FRLFHGRGGTVGRGGGRANQAILAMPPVVHNGRIRFTEQGEVISFRYALP 675

                    nLCFrsLqRFtAAtLEHGmnPPvsPk....PEWR.kLmeemAvvAtEEYR
                    ++  r L     A L     P  s  ++++P  R++Lm+e+A      YR
  gi|2683172   676 EIAHRHLEQIVNAMLRVVGLPAASGTdgtdPATRnRLMDELATRSMRAYR 725

                    svvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPW
                     ++   P F  ++   tP     ++ i sRP  R  +  ++ esLRAiPW
  gi|2683172   726 RLI-DAPDFWSWYTRITPIDQISRLPIASRPVSRSSAREVdfESLRAIPW 774

                    iFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlD
                    +FaWtq R+ +P W G+G A    ++     l  L+  Y+ WPFFR  l
  gi|2683172   775 VFAWTQVRYLIPGWFGIGQALDELLQTSPEHLETLRTWYRSWPFFRTVLQ 824

                    Ll..EmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiA
                      ++Emv A+ +  iAa yD+LL  +    F + + ++Y   +  +L+i
  gi|2683172   825 NAqrEMVRARLE--IAAYYDRLL-GDGPTAFHQMIEEDYHRARTAILRIT 871

                    GHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhl
                       +lL+ DP +++ + LR++Y   Ln +q   ++R R
  gi|2683172   872 DQEELLDHDPIIRKSVQLRNPYTDVLNLVQLELMRRYRQ----------- 910

                    sKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    + E   E+                   L   L L + GiAA mq tG
  gi|2683172   911 APEADREP-------------------LRRALFLSINGIAAAMQSTG    938

gi|186476931|ref|YP_001858401.1|: domain 1 of 1, from 81 to 1030: score 331.6, E = 1.6e-96
                    *->siDAqLRlLv.PGKvsed.ekLieYDALLlDkFL.DiLqDLHGedLk
                         DA   ++ + G+  ed+++ +  D   l + L+D++ +  G+++
  gi|1864769    81    RHDAPASAVKdDGRTREDkDQPLFEDIRYLGRLLgDVVREQEGDEVF 127

                    EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    ++v      +  +    D+   + L  kL +L P  ++ v +a++    L
  gi|1864769   128 DVVETIRQTAVRFRREDDSVAAQALDKKLRALSPEQTVSVVRAFSYFSHL 177

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                    An+AE+     R R+++ +  D a  +s      i   l +Lv     +
  gi|1864769   178 ANIAED-----RHRNRRHRIHDLA--GSTSQPGTIAHALDRLVEAN-AAA 219

                    eEvFeALKnqsvDL.vltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                      v +   n +  ++vltAHPt   R+s+L  +  i   La    + +t
  gi|1864769   220 TPVLQQFFNDALIVpVLTAHPTEVQRKSILDAQHDIARLLAE-RDQPLTA 268

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                     +    D  L   +   + t  +R ++ t  DE+   +sY+  t  + +P
  gi|1864769   269 REHLQNDSLLRARVTSLWQTRMLRDSRLTVADEIENALSYYRATFLEEIP 318

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                    +    ++ AL   G+  RlP   P  +  sW+GGDRDG nP vt E
  gi|1864769   319 QLYADIEEALVEHGLDARLP---PFFQMGSWIGGDRDG-NPNVTGETLEN 364

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkv
                           +    Y++qv  L  Els+    + L + A++El+  a+
  gi|1864769   365 AITRQAAVIFEHYLEQVHKLGAELSV----SNLLAGAsDELKALAQAS-- 408

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei....
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                              EPYR  L  +  +L      aR  L  G+  +++ +
  gi|1864769   409 -----PDHSPHRTDEPYRRALIGMYTRLAAS---ARVRLGEGVVPVrsag 450

                  ....sEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvst
                  ++ ++  Av+y +  eF+  L +   sL e     +A   L  l R
  gi|1864769   451 pgipPIRAVpYGDSSEFVRDLHVLIDSLAEHHGASLATPRLSPLTRAAEV 500

                  FGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaEL
                  FG  L  +D+Rq s+ +  v+  + +  ++ s+Y   sE  +   LlaEL
  gi|1864769   501 FGFHLASIDLRQSSDIHEAVIAELFKRAGVESdYAALSEAEKLRVLLAEL 550

                  kGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGa.....Yiismata
                     R L  + +     vk  l+ ++  A +  + FGa+  ++Yiis + +
  gi|1864769   551 AQPRLLRSPYVDYSNLVKSELGVLE-QARVTREKFGAravrnYIISHTET 599

                  PsDvLAvELLqRECgv............kqtLrvvPLFEkLADLeAAPAa
                   sD + v LLq+E g+ +++ ++ +++ +  L v+PLFE + DL+ AP
  gi|1864769   600 VSDLVEVMLLQKEAGLlqgtlgsathpaRAGLMVIPLFETIPDLRNAPHI 649

                  vekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEi
                  +  L + ++iD  i      qevm+GYsDs KD G l   W LY+A   +
  gi|1864769   650 MRDLLAlpgIDAIIENQGNEQEVMLGYSDSNKDGGFLTSNWELYRAELAL 699

                  iKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqG
                  +    + G+ + lFHGRGGtvGRGGGPt  AiLsqPP t++G +R t qG
  gi|1864769   700 VSLFNERGITMRLFHGRGGTVGRGGGPTYQAILSQPPGTVDGQIRLTEQG 749

                  EviEfsFGEEnLCFrsLqRFtAAtLEHGmnP....PvsPkPEWRkLmeem
                  Evi   FG  ++  r L    AAtLE  + P+++ P s  PE+ + m+ +
  gi|1864769   750 EVIASKFGNPDIGRRNLETVVAATLEASLLPhgsaPKSQLPEFEETMQVL 799

                  AvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG...
                     A   YR++v+  P F +YF + tP  E   +niGsRPa Rk   +++
  gi|1864769   800 SDAAMASYRALVYETPGFTDYFFSSTPIAEIAELNIGSRPASRKLQDpkq 849

                  .GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn......lq
                  + ie LRAiPW F+W q R  L  W G+G A    +d    n +++++l
  gi|1864769   850 rKIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVAGWLDAAGANmererrLN 899

                  kLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGks
                  +L+ m k WPFF   l  ++mv AK D  +A+ y  L+    L+k   ++
  gi|1864769   900 QLRKMHKVWPFFSNLLSNMDMVLAKTDLAVASRYAALVTDKKLrKHVFER 949

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  + ++++ t + L +i G k+ L   P L   ++ R +Y+  Ln +q   L
  gi|1864769   950 IVAEWERTSNVLSEITGQKERLSDNPLLARSIKNRFPYLDPLNHLQVELL 999

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KR R               A +           n   rv  G+     L
  gi|1864769  1000 KRHR----------------AGDT----------N--VRVRRGIH----L 1017

                  tmKGiAAGmqntG<-*
                  t+ GiAAG+ ntG
  gi|1864769  1018 TINGIAAGLRNTG    1030

gi|227980965|ref|ZP_04028227.1|: domain 1 of 1, from 1 to 921: score 331.2, E = 2.1e-96
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                              P + +   + ++ D  Ll   L+D + +  Ge + +
  gi|2279809     1    ------MTSEPARAA--TEPLRDDIRLLGGILgDTVREQAGERIFDL 39

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v      s  +  ++     e L a  t L  a+a+ v +a++H   LAn
  gi|2279809    40 VENARQES--FRVRRSEIDREQLAAMFTDLPTAEAVPVIRALSHFALLAN 87

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  LAE+ +   RR i+ +        ++A   s +  t+  L   +    +
  gi|2279809    88 LAEDLHRERRRAIHVRA-------GEAPQASSLAHTYTLLEDAG-LDGDA 129

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  v  AL+   v  v+tAHPt   RR +   + Ri   +       + + +
  gi|2279809   130 VRAALRHALVVPVITAHPTETRRRTVFDTQHRITELMRYRDRTQLDPREE 179
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                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + +   L R i   + t  +R  +   qDE+  G+ Y+     + +P+
  gi|2279809   180 EQVQVNLRRQILTLWDTALVRLERLRIQDEVVNGLRYFDAAFLEVMPQIN 229

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                      + t L+ +     l    P+++  sW+GGDRDG nP vt Ev
  gi|2279809   230 HEIRTRLRELYPGTGL-LSEPILRPGSWIGGDRDG-NPYVTGEVVTMASR 277

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                     a   A   Y+ q+ +L  El++      L    +El   a  d
  gi|2279809   278 RAAATALEHYLRQLLELEKELAL---SLRLTTVSDELLALAEWD------ 318

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi.seisEeA.vy
                        Kq    EPYR  L  +R +L  t   a  LL   +++ i  +A+ y
  gi|2279809   319 -TSPKQA--DEPYRRALRWIRGRLSTT---AADLLDEPLdAGIDIDApRY 362

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                        e L  L +   sL   GD  iAD  L Dl     tFG  L  LD+R
  gi|2279809   363 GGPSELLADLAVVDASLRTAGDGLIADARLQDLREALNTFGFHLSGLDMR 412

                    qEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgsDL
                    q s+ + + +  +    ++ + Y +  E  R   L  EL+ +RPL+g+
  gi|2279809   413 QNSDVHEETISELFAWAGVHpDYASLDESDRVRLLTDELRLRRPLVGPGA 462

                    PktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAvELLqR
                      tE  +  l+ ++   + +A L   +   Yiism+t+ sD L   +L +
  gi|2279809   463 EFTEQTAKELGVLHaaadAVANLGPGAVPNYIISMCTSVSDLLEAAVLLK 512

                    ECgvkqt.............LrvvPLFEkLADLeAAPAavekLFsiDWYi
                    E g+ ++++++  +   + ++ +vPLFE + DL+   A++   F +  Y+
  gi|2279809   513 EAGLLRPgdgsaadavatcsVNIVPLFETIEDLQQGAATMRAAFEVPVYR 562

                    nridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                      +dGK++ qe+m+GYsDs KD G l+A W LY+A  +++ +A++ Gv L
  gi|2279809   563 SLVDGKgglQEIMLGYSDSNKDGGYLAANWALYRAELDLVAMARDAGVTL 612

                    vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                     lFHGRGGtvGRGGGP   AiL+qPP  + G lR t qGE+i   + E
  gi|2279809   613 RLFHGRGGTVGRGGGPSYDAILAQPPGAVRGTLRLTEQGEIIAAKYAEPA 662

                    LCFrsLqRFtAAtLEHGm...nPPvsPkPEWRkLmeemAvvAtEEYRsvv
                    L  r L    AAtLE  + + +       E   +++e+A  A E Y  +v
  gi|2279809   663 LATRNLESLLAATLESTLldvEGLGDDAEEAYAVLDELAALAREAYGDLV 712

                    vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWt
                     +   FvEYF   tP  E G +niGsRP+ Rk    i  LRAiPW+ aW
  gi|2279809   713 HRTDGFVEYFTTSTPVEEIGSLNIGSRPSSRKQTSKISDLRAIPWVMAWS 762

                    qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                      R  LP + G GAA    id     l +L+ +Y+ WPFF   l  +  v
  gi|2279809   763 LSRVMLPGFYGTGAAIEKWIDGGPSRLEQLRALYRRWPFFQTVLSNMAQV 812

                    FAKGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDl
                     AK D G+Aa y +L+    L+++ FGk + d+   t ++   iA   Dl
  gi|2279809   813 LAKSDLGLAARYAELVPDAALreRVFGK-IADEHRRTIEMYYAIAETDDL 861

                    LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                    L   P LK  +  R +Y+  Ln +q   L+R R                A
  gi|2279809   862 LADNPALKRSVFNRFPYLEPLNHLQVELLRRYR----------------A 895

                    dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     +                P +   ++Ltm G+A  + n G
  gi|2279809   896 GDT----------------DPQVQRGILLTMNGLATALRNSG    921

gi|254818408|ref|ZP_05223409.1|: domain 1 of 1, from 14 to 938: score 330.3, E = 3.8e-96
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        i A  R  v G+ +   + ++ D  Ll   L+D + +  G ++ E
  gi|2548184    14    PIGAVQRTPV-GRAA--TEPMRADIRLLGAILgDTVREQNGREVFEL 57

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
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                v      s  +  ++      EL      +d   ai v +a++H   LAn
gi|2548184     58 VERARVES--FRVRRSEIDRAELARMFYRIDIHQAIPVIRAFSHFALLAN 105

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                +AE+++   RR ++          ++   +s +  t+ kL        +
gi|2548184    106 VAEDIHRERRRAVHVAA-------GEPPPDSTLAATYAKLDEAQ-LDSDT 147

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK.DvtveD
                v +ALK   v  v+tAHPt   RR +   + Ri n L  L A +    +D
gi|2548184    148 VADALKGAVVAPVITAHPTETRRRTVFVTQHRI-NELMRLHAEgHAETDD 196

                KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                 + ++  L R +   + t  iR ++    DE+  G+ Y+    +k +P+
gi|2548184    197 GRNIELELRRQVLTLWQTALIRLSRLQITDEIEVGLRYYAAAFFKVIPQV 246

                LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   v   L+       l +d P+++  sW+GGDRDG nP vt +v R
gi|2548184    247 NAEVRDTLRARWPDADL-FDEPMLQPGSWIGGDRDG-NPNVTADVVRQAT 294

                LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                  a   A   Y+  +  L  Elsm      +     El    a +
gi|2548184    295 GSAAFTALAHYLAELTALEQELSMSARLVSVTPALTELAGGCAEK----- 339

                YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv..
                           EPYR  +  +R +L  t   +  +L     ++ +   ++
gi|2548184    340 -------ARADEPYRRAVRVIRARLSAT---SAAILDRTPQQVLDLGLpp 379

                ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                y    e    L+    sL   G   +AD  L  l   v  FG  L  LD+
gi|2548184    380 YETPAELGADLDTMDESLRGHGSALLADDRLALLREGVRVFGFHLCGLDM 429

                RqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgsD
                Rq s+ + +v+  +    ++ + YR+ +E+ R E L aEL  +RPL+  D
gi|2548184    430 RQNSDAHEEVICELLAWAGVHpDYRSLPEDERVELLAAELGTRRPLVADD 479

                LPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvELL
                    +  +  l+ +r  A   i  +G++  ++Y+ism+ + sDvL   +L
gi|2548184    480 AQLSDLARGELGVVRAAAH-AIKRYGPsavpnYVISMCRSVSDVLEAAIL 528

                qRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                 +E g+   +++++  ++ + PLFE + DL+     +  +  +  Y+  +
gi|2548184    529 LKEAGLIDasgpepycPVGISPLFETIDDLHNGATILHAMLELPIYRALV 578

                dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                  ++++qevm+GYsDs KD G l+  W +Y+A   ++ vA+k G++L lF
gi|2548184    579 AARgetQEVMLGYSDSNKDGGYLASSWAVYRAELALVEVARKTGIRLRLF 628

                HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                HGRGGtvGRGGGP   AiL+qPP  +nGslR t qGEvi   + E +
gi|2548184    629 HGRGGTVGRGGGPSYEAILAQPPGAVNGSLRLTEQGEVIAAKYAEPQAAQ 678

                rsLqRFtAAtLE......HGmnPPvsPkPEWRkLmeemAvvAtEEYRsvv
                r L    AAtLE++  +  G+     P      +++e+Av A   Y  +v
gi|2548184    679 RNLESLLAATLEstlldvEGLGDAAEPA---YAVLDEVAVQAQRAYAELV 725

                vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWt
                   P Fv+YF   tP  E G +niGsRP+ RkP   i  LRAiPW+ aW
gi|2548184    726 HDTPGFVDYFMASTPVSEIGSLNIGSRPTSRKPTESISDLRAIPWVLAWS 775

                qtRFHLPvWLGvGAAFKhAi....dKDiKnlqkLkEmYkeWPFFRvtlDL
                q R  LP W G G AF   i  +++ +   +  L+++Y+ WPFFR  l
gi|2548184    776 QSRVMLPGWYGTGSAFEQWIaagpQSEAERVSILHDLYQRWPFFRSVLSN 825

                lEmvFAKGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAG
                l  v AK D G+Aa y +L+  EeL+++ FGk + d+   t  +   i G
gi|2548184    826 LAQVLAKSDLGLAARYAELVGDEELrrRVFGK-IVDEHGRTIAMHKLITG 874

                HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                   lL   P L   +  R +Y+  Ln +q   L+R R
gi|2548184    875 QDNLLADNPALARSVFNRFPYLEPLNHLQVELLRRYR------------- 911
```

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                    KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                           s   deLv+              ++Ltm G+A  + n G
  gi|2548184   912 -------SGDDDELVQRG------------ILLTMNGLASALRNSG    938

gi|292492252|ref|YP_003527691.1|: domain 1 of 1, from 20 to 962: score 330.3, E = 4e-96
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s D q +   P +   d +L     L       ++q    e +  av
  gi|2924922    20    SPD-QTKNATPWR---DKELRARVKLFGNLLGQVIQAQSREKVFAAV 62

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                            +   K+ + K   L   +  Ld      v +a++    LAn+
  gi|2924922    63 EALRKGYINLRKKENPDKRIQLLRLISKLDVETLTQVVRAFSIYFSLANI 112

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEE   Ay  R ++++     D +        EEtl+ +   +   P
  gi|2924922   113 AEE---AYQHRQRQRR----IDAGGPLWRGSFEETLQEVRNGG-VGPGQL 154

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L   +   v+tAHPt + RR ++    +i      L    +   + +
  gi|2924922   155 QILLDSLAYIPVITAHPTEAKRRTVMEHLRKIFLTSKLLDEARLSQREEE 204

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     L   L R iq  ++tDE+R  +P   DE+  G+ Y+   +++ vP   R
  gi|2924922   205 ALHRQLERQIQVLWKTDEVRAHRPQVRDEIINGLFYFKVSLFQAVPETYR 254

                    RvDtALKni...GinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRD
                      + A+  + ++ + E     vP+ ++F sW+GGDRDG nP v PE+t
  gi|2924922   255 QLEEAIHKVygdDLPENTTIRVPsFLHFGSWIGGDRDG-NPNVKPEITAM 303

                    vCLLaRmmAanlYisqvEDLmFEls.............mWRCndELRvRAE
                       L   mA   Y++ + +Lm  l ++ +  ++++  m   n++L    E
  gi|2924922   304 AVRLQMRMALRHYLERIGELMRILThsipliqpstalMDSINQDLNDCPE 353

                    Elyrtaardkvv KyYiEFWKqvPPtEPYRviLGdvRDKLY.ntRERaRHL
                     l   + r                 EPYR  L  +R +L +n R    HL
  gi|2924922   354 ALLGNPTRF--------------SHEPYRRKLYLMRYRLLdNLRAVELHL 389

                    LAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                            +    y   +eFL  L L   sL + GD  iA G L Dl+R
  gi|2924922   390 KPESGLSPPSGVGYPSEDEFLQDLYLIRDSLINHGDGNIAAGELQDLIRL 439

                    vstFGLsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLl
                    v  FG  L KLDiRqEs  +t+ +  + +  ++ ++Y + sE  Rq  L
  gi|2924922   440 VESFGFYLLKLDIRQESSCHTEAVAELVKQAGLHpAYLDLSETERQQLLS 489

                    aELkGK......RPLlgsDLPktEEvkDvldafrvLAELPiDsFGaYiis
                      L   ++ + +R  l +    t E+ Dv+  +r   E+    FG Y+is
  gi|2924922   490 EQLAREegvpidREQLTPPTRETLEIFDVMAQMR--REVSPRVFGTYVIS 537

                    mataPsDvLAvELLqRECgvkqt........LrvvPLFEkLADLeAAPAa
                    m+ a s vL v  L    g+ + ++++ + +L++ PLFE + DLe
  gi|2924922   538 MTHAASHVLEVMFLGHLAGLAKHqqgqwhcdLQISPLFETIEDLEHIEPV 587

                    vekLFsiDWYinridG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEi
                    +  L     Y   ++ ++++qevm+GYsDs KD G l+  W+LY Aq  +
  gi|2924922   588 MTALLDDPSYQALLQAsgnQQEVMIGYSDSCKDGGILASSWKLYEAQKKV 637

                    iKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqG
                         + Gv   +FHGRGGt+GRGGGPt  AiLsqP  t++G ++ t qG
  gi|2924922   638 TALTGDRGVDCRIFHGRGGTIGRGGGPTFDAILSQPRGTVHGQIKFTEQG 687

                    EviEfsFGEEnLCFrsLqRFtAAtLEHG...mnPPvsPkPEWRkLmeemA
                    Ev+   +   +     L       +      ++PP   k ++  +m+ +A
  gi|2924922   688 EVLSSRYSNTETAIYELDMGISGLIKASaclVQPPQEEKRDYLGVMDFLA 737

                    vvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.Gie
                          YR +    P F +YF  AtP  E G +niGsRP+ Rk + +
  gi|2924922   738 EAGERAYRELTEETPGFQDYFYEATPVNEIGLLNIGSRPSHRKKGDrSKA 787

                    sLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWP
                    s+RAi W+F W q R   P W G+G A           l kL+ mY+eWP
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  gi|2924922   788 SVRAIAWVFGWAQARHTFPAWYGIGSALEQWRAGAPDRLAKLQAMYQEWP 837

                   FFRvtlDLlEmvFAKGDPGiAaLyDkL.LvaEeLkPFGksLRdkYvEtkd
                   +FR  l  + m  AK +  iA  y +L L  E        L ++Y+ t
  gi|2924922   838 YFRAMLSNIQMSLAKAELRIAQQYAELcLDPETGERIFAMLSAEYQRTVT 887

                   lLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykv
                    +L+i G + lLE  P L   lR Rd+Y+  Ln +q   ++R RDP
  gi|2924922   888 QVLHIVGAHTLLEENPSLALSLRRRDPYLDPLNHIQLTLIQRTRDP---- 933

                   tlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmq
                                         L p er a    D L+  +  iAAGm
  gi|2924922   934 ----------------------LLTPVERQA--WIDPLLRSINAIAAGMR 959

                   ntG<-*
                   ntG
  gi|2924922   960 NTG    962

gi|20196768|emb|CAC86356.1|: domain 1 of 1, from 1 to 398: score 330.2, E = 4.1e-96
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2019676     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2019676     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2019676     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                          svDLv+tAHPtqs+RRsLLqKnaRiRnCL+qL A D+t +DK+
  gi|2019676     1 -------SVDLVFTAHPTQSARRSLLQKNARIRNCLTQLKAPDITEDDKQ 43

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL REiqAAFRtDEiRRaqPtPqDEmR+GmsYiHEtvWkGvPKFLR
  gi|2019676    44 ELDEALQREIQAAFRTDEIRRAQPTPQDEMRYGMSYIHETVWKGVPKFLR 93

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALKniGi ERlPYdvPLikF+sWmGGDRDG nPRvtPEvtRDvCLL
  gi|2019676    94 RVDTALKNIGITERLPYDVPLIKFCSWMGGDRDG-NPRVTPEVTRDVCLL 142

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   +RmmAanlYi+q+EDLmFElsmWRCndELR+RAEEl +t+  +kv+KyYi
  gi|2019676   143 SRMMAANLYIDQIEDLMFELSMWRCNDELRARAEELLKTPDAKKVTKYYI 192

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWKq+PP+EPYRviLG+vRDKLYntRERaRHLLAtG+s+i+E+A++tkv
  gi|2019676   193 EFWKQIPPNEPYRVILGAVRDKLYNTRERARHLLATGYSDIPEDAIFTKV 242

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   E+ LEPLELCYksL +CGDkviA+GsLLD+LRqv+tFGLsLvKLDiRqEs
  gi|2019676   243 EQILEPLELCYKSLIDCGDKVIAEGSLLDVLRQVYTFGLSLVKLDIRQES 292

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   eR+tDv+DAittHL+iGsYR+W+EeKR EWL+ ELkGKRPLl++DLP+tE
  gi|2019676   293 ERHTDVIDAITTHLGIGSYRSWPEEKRVEWLVGELKGKRPLLPPDLPMTE 342

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dv++a++vLAELP+DsFG+Yiism+taPsDvLAvELLqRECg+kqtL
  gi|2019676   343 EIADVVGAMHVLAELPSDSFGPYIISMCTAPSDVLAVELLQRECGIKQTL 392

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLF
  gi|2019676   393 PVVPLF---------------------------------------- 398

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|2019676     - ---------------------------------------------- -
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                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

  gi|2019676     - ------------------------------------------------- -

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|2019676     - ------------------------------------------------- -

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|2019676     - ------------------------------------------------- -

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|2019676     - ------------------------------------------------- -

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|2019676     - ------------------------------------------------- -

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|2019676     - ------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|2019676     - -------------    -

gi|56476048|ref|YP_157637.1|: domain 1 of 1, from 65 to 990: score 330.2, E = 4.2e-96
                  *->siDAqLRlLvPGKvsedekL..ieYDALLlDkFL.DiLqDLHGedLk
                         q     P +   ++k  +++ D  Ll + L+D + D HGe
  gi|5647604    65    ----QRSHPHPEQTMTEDKDapLREDIRLLGRVLgDTVRDQHGEAAF 107

                  EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    +       s  +    D     EL   L +L    +i v +a++    L
  gi|5647604   108 ALIERIRQTSVRFRRDDDNAARLELEGILDALSREQTIEVVRAFSYFSHL 157

                  AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                   n+AE+ +   R R ++         +sA  E  +   l +    +   P
  gi|5647604   158 SNIAEDQHHIRRSRAHLIA-------GSAPREGSVAHALVRALASG-LPP 199

                  eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                  +          +  vltAHPt   R+s+L  ++ i   L       +t+e
  gi|5647604   200 ARLAAFFDTALISPVLTAHPTEVQRKSILNCETDIAHLLDARDRMTLTPE 249

                  DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                  +++E DEAL R +   + t  +R a+    DE+  G+sY+  t  +  P
  gi|5647604   250 ERQESDEALRRTVLTLWQTRMLRPAKLSVVDEVANGLSYFDATFLRELPH 299

                  FLRRvDtALKniGinERlP.YdvP.LikFssWmGGDRDGknPRvtPEvtR
                       +  L  +     l + + P  ++  sW+GGDRDG nP vt +v
  gi|5647604   300 LYANLEDQL--VSRDPALAgLELPaFLQVGSWIGGDRDG-NPFVTADVLE 346

                  DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                      +       +Y++ +  L   ls+      L    + l   aar
  gi|5647604   347 RTLAMQAGAVLGFYLDELHALGARLSL---ALGLVTASDALLALAARS-- 391

                  vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                                EPYR  +  +  +L  t      LL t     +
  gi|5647604   392 -----PDHSPHRNDEPYRRAISGIYARLAATH---HALLGTEPPRHPVAV 433

                  v..ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                   ++y  v e  + L++  +sL   G  ++A G L  l R v  FG  L
  gi|5647604   434 AepYAAVAELADDLDVIHRSLVANGSAALARGQLRRLRRAVRVFGFHLAP 483

                  LDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLl
                  +D+Rq se +  v+  +      G +Y    E  R E L+ EL   RPL
  gi|5647604   484 IDLRQNSEVHERVVAELLATARTGTdYATLDEAARVELLIEELATPRPLA 533

                  gsDLPktEEvkDvldafrvLAELPiDsFGa....YiismataPsDvLAvE
                   + +   +E +  l  fr          G+  ++ iis +   sD L
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```
  gi|5647604   534 SPHVRYSDETEGELAIFRTARAAHRRYGGPaipnCIISKTDDVSDLLELA 583

                   LLqRECgvkqt......LrvvPLFEkLADLeAAPAavekLFsiDWYinri
                   LL +E g+ +++++  ++ +vPLFE + DL  AP  +++LF++  Y+n +
  gi|5647604   584 LLLKEAGLLRPheraldVNIVPLFETIEDLANAPSVMDRLFALPGYMNLL 633

                   ....dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                     ++d   evm+GYsDs KD G l   W LYkA   +i v  ++G++L l
  gi|5647604   634 aasrDRTHEVMLGYSDSNKDGGFLTSGWALYKAEIGLIEVFARHGIRLRL 683

                   FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                   FHGRGG vGRGGGP   AiL+qP   ++G +R t qGEvi   +G  ++
  gi|5647604   684 FHGRGGSVGRGGGPSYEAILAQPGGAVQGQIRLTEQGEVIAAKYGNPEVG 733

                   FrsLqRFtAAtLEHGmnPPvsPkP..EWRkLmeemAvvAtEEYRsvvvKE
                    r L    AAtLE  +    +P P+ E+ + m+ +  vA   YR +v+
  gi|5647604   734 RRNLEVIVAATLEASLLADRAPAPrvEFLDTMQALSDVAFAAYRGLVYDT 783

                   PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
                     F  YF   t   E   +niGsRPa Rk +  ie LRAiPW+F+W q R
  gi|5647604   784 EGFERYFWESTVISEIAELNIGSRPASRKKGTRIEDLRAIPWVFSWSQCR 833

                   FHLPvWLGvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                     LP W G+G A K++        + +L+ m +eW FF   l  ++mv A
  gi|5647604   834 LMLPGWFGFGSAVKtWLAAHADDGIARLQAMHREWSFFAALLSNMDMVLA 883

                   KGDPGiAaLyDkLLvaEeLk.PFGksLRdkYvEtkdlLLkiAGHkDlLEG
                   K D  iA+ y  L+   +L++   +++R+++ +t d LL i G ++lL+G
  gi|5647604   884 KTDLAIASRYAGLVKDVNLRdAIFERIRNEWHDTVDALLAITGQRELLDG 933

                   DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                    P LK  +R R +Y+  Ln +q   L+R R                E
  gi|5647604   934 NPLLKRSIRNRFPYLDPLNHVQVELLRRHR------------------ET 965

                   skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       d  ++L             + + + GiAAG+ n G
  gi|5647604   966 --HDDARIRLG------------IHISINGIAAGLRNSG    990

gi|256802423|ref|ZP_05532047.1|: domain 1 of 1, from 3 to 910: score 329.2, E = 8.4e-96
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      s D q         s   +L      L D   + L    G++L + v
  gi|2568024     3    SADDQTTT-----TS--SELRADIRRLGDLLGETLVRQEGPELLDLV 42

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        l  e     D +   EL  + t Ld a  ++  +a++    LAn+
  gi|2568024    43 EKVRRLTRE-----DGEAAAEL-LRGTELDTAAKLV--RAFSTYFHLANV 84

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    E v   +R R  + +         A     +  t  +L       Pe
  gi|2568024    85 TEQV---HRGRELRAR--------RAAEGGLLARTADRLKDAD---PEHL 120

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    e ++   v  v+tAHPt ++RRs+L K  R+    a L    v   D++
  gi|2568024   121 RETVRHLNVRPVFTAHPTEAARRSVLNKLRRV----AALLDTPVIESDRR 166

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    LD  L   i   + tDE+R  +P P DE R  + Y+ E   + v   L
  gi|2568024   167 RLDIRLAENIDLVWQTDELRVVRPEPADEARNAIYYLDELHANAVGDVLE 216

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                        L   G+  +lP d   + F  W+GGDRDG nP vtP vt D+ +L
  gi|2568024   217 DLTAELERAGV--KLPDDTRPLTFGTWIGGDRDG-NPNVTPQVTWDILIL 263

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkvvKyY
                         n  ++ +++L   ls    n+   + A+EEl    + d
  gi|2568024   264 QHEHGINDALETIDELRGFLS----NSIRYAGAtEELLTSLQAD--LENL 307

                   iEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                    E ++++K +  +EPYR     +R KL nt+ R    LA+G +   +
  gi|2568024   308 PEIsprYKRLNAEEPYRLKATCIRQKLENTKKR----LAKGTAH-RDGRD 352
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                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y    e L+ L +  +sL e      ADG L   +R    FGL L  +D+
  gi|2568024   353 YLGTAELLDDLRIIQRSLREHRGGLFADGRLARTIRTLAAFGLQLATMDV 402

                    RqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLlgs
                    R  ++ +   l  +   L+  s+R  + + + R   L  EL+ +RPL +
  gi|2568024   403 REHADAHHHALGQLFDRLGEESWRyaDMPRDYRAKLLAKELRSRRPLAPT 452

                    DLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvEL
                      P     +  l+ f+ +     + FG++  ++Yiism+    Dv A  +
  gi|2568024   453 PAPVDAPGEKTLGVFQTVKK-ALEVFGPeviesYIISMCQGADDVFAAAV 501

                    LqRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                    L RE g+   + +   + +vPL E   +L+AA   +e + s   Y+  +
  gi|2568024   502 LAREAGLIDlhagwaKIGIVPLLETTDELKAADTILEDMLSDPSYRRLVA 551

                    GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                     +++ qevm+GYsDs K  G     W + +Aq  +  vA +yGv+L lFH
  gi|2568024   552 LRgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRYGVRLRLFH 601

                    GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                    GRGGtvGRGGGPtH AiL+qP  t++G ++vt qGEvi   +    L
  gi|2568024   602 GRGGTVGRGGGPTHDAILAQPWGTLEGEIKVTEQGEVISDKYLIPALARE 651

                    sLqRFtAAtLEH.GmnPP....vsPkPEWRkLmeemAvvAtEEYRsvvvK
                     L    AAtL  + ++  ++++v     W   m+ +   A   YR +v
  gi|2568024   652 NLELTVAATLQAsALHTAprqsVEALSRWDAAMDVVSEAAHAAYRRLV-E 700

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWt
                    +P    YF   tP      + +GsRP+ R+P+ G++ + LRAiPW+F Wt
  gi|2568024   701 DPDLPTYFLASTPVDQLADLHLGSRPS-RRPGSGVslDGLRAIPWVFGWT 749

                    qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                    q R  +P W GvG   K   +     +  L Em +eW FFR  +  +Em
  gi|2568024   750 QSRQIVPGWFGVGSGLKALREAGLDTV--LDEMHQEWHFFRNFISNVEMT 797

                    FAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE
                     AK D  iA  y + Lv +eLk   + ++++ + t   +L++ G ++lL+
  gi|2568024   798 LAKTDLRIAQHYVDTLVPDELKHVFDTIKAEHELTVREVLRVTGEQELLD 847

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                      P LKq   +Rd+Y+  +  +q   LKR RD               A+
  gi|2568024   848 AAPVLKQTFAIRDAYLDPISYLQVALLKRQRD---------------AAG 882

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                +e+  P L   L+Lt+ G+AAG+ ntG
  gi|2568024   883 A------------GEQPDPLLARALLLTVNGVAAGLRNTG    910

gi|91782419|ref|YP_557625.1|: domain 1 of 1, from 46 to 994: score 328.4, E = 1.4e-95
                    *->siDAqLRl.LvPGKvsed.ekLieYDALLlDkFL.DiLqDLHGedLk
                          Aq  ++ + G+  ed+++ +  D   l + L+D+L +  G+ +
  gi|9178241    46    PASAQAPApKANGRTREDkDHPLFQDIRYLGRLLgDVLREQEGDAVF 92

                    EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    ++v      +  +    D+   + L  kL sL P  ++ v +a++    L
  gi|9178241    93 DVVETIRQTAVRFRREDDSAAAQTLDKKLRSLSPEQTVSVVRAFSYFSHL 142

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                    An+AE+ +   R Ri+ +        +s      i   l +Lv  +  +
  gi|9178241   143 ANIAEDRHRNRRHRIHELA-------GSTSQPGTIAHSLERLVEAGAAAT 185

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                        e   n  +  vltAHPt   R+s+L  +  +   La    + +t
  gi|9178241   186 PVLQEFFNNALIVPVLTAHPTEVQRKSILDAQHDVARLLAE-RDQQLTDR 234

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++   +  L   +   + t  +R ++    DE+   +sY+  t  + +P
  gi|9178241   235 ERAHNEAMLRARVTSLWQTRMLRDSRLSVADEIENALSYYRATFLEEIPA 284

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                        ++ AL   G+  RlP   P  +  sW+GGDRDG nP vt E
```

```
  gi|9178241   285 LYADIEEALAEHGLEARLP---PFFQMGSWIGGDRDG-NPNVTAETLENA 330

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkvv
                          +    Y++qv  L  Els+    + L + A++ l+  aa
  gi|9178241   331 ITRQAAVIFEHYMEQVHKLGAELSV----SNLLAGAsDALKELAAVS--- 373

                    KyYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER....aRHLLAtGis
                           q P++  EPYR  L  +  +L  + R R ++++  +   G
  gi|9178241   374 ------PDQSPhrTDEPYRRALIGMYTRLAAsARVRlgegSVPVRSAGRG 417

                    eisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFG
                      +  A +y +  eF+  L +   sL e     +A   L  l R    FG
  gi|9178241   418 AAPVRAKpYADSAEFVRDLHVLIDSLAEHHGAPLAAPRLSPLARAAEVFG 467

                    LsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaELkG
                      L  +D+Rq s+ +  v+  + +  +++  Y e +E  +   Ll+EL
  gi|9178241   468 FHLASIDLRQSSDVHEAVITELLRRAGVeENYAELPEADKLNVLLSELAQ 517

                    KRPLlgsDLPktEEvkDvldafrvL..AELPiDsFGa.....Yiismata
                     RPL    LP  E    v   + vL++A +  + FGa+  ++Yiis + +
  gi|9178241   518 PRPL---RLPFAEYSDLVKSELGVLeeARVTREKFGAravrnYIISHTET 564

                    PsDvLAvELLqRECgv.............kqtLrvvPLFEkLADLeAAPAa
                     sD + v LLq+E g+ ++  ++ +++ +  L v+PLFE + DL+ AP
  gi|9178241   565 VSDLVEVMLLQKETGLlrgclgnandpaQAGLMVIPLFETIPDLRNAPHI 614

                    vekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEi
                    +  L + +++D  i +    qevm+GYsDs KD G l   W LY+A   +
  gi|9178241   615 MRDLIAlpgVDALIEHQGNEQEVMLGYSDSNKDGGFLTSNWELYRAELAL 664

                    iKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqG
                    +    + Gv L lFHGRGGtvGRGGGPt  AiLsqPP t++G +R t qG
  gi|9178241   665 VSLFNERGVTLRLFHGRGGTVGRGGGPTYQAILSQPPGTVDGQIRLTEQG 714

                    EviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP.vsPk..PEWRkLmeemA
                    Evi   FG  ++  r L    AAtLE  + P +++P + P + + m+++
  gi|9178241   715 EVIASKFGNPEIGRRNLETVVAATLEASLLPHgIAPAqlPAFEETMQQLS 764

                    vvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....
                      A   YR++v+  P F EYF   tP  E   +niGsRPa Rk   ++++
  gi|9178241   765 DAAMASYRALVYETPGFKEYFFESTPISEIAELNIGSRPASRKLQDpkqr 814

                    GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiKnlqk
                     ie LRAiPW F+W q R  L  W G+G A    +d+ +++    + l
  gi|9178241   815 KIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVAAHLDsapsdaERTRRLAL 864

                    LkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksL
                    Lk m k+WPFF   l  ++mv AK D  +A+ y  L+    L+k   +++
  gi|9178241   865 LKKMHKTWPFFANLLSNMDMVLAKTDLAVASRYAALVSDKKLrKHVFERI 914

                    RdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLK
                     ++++ t + L +i G  + L   P L   ++ R +Y+  Ln +q   LK
  gi|9178241   915 VAEWERTSKVLSEITGKSERLAENPLLARSIKNRFPYLDPLNHLQVELLK 964

                    RiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLt
                    R R                A +           n   rv  G+     L
  gi|9178241   965 RHR----------------AGDT----------N--ARVRRGIH----LS 982

                    mKGiAAGmqntG<-*
                    + GiAAG+ ntG
  gi|9178241   983 INGIAAGLRNTG    994

gi|239930781|ref|ZP_04687734.1|: domain 1 of 1, from 3 to 910: score 328.3, E = 1.5e-95
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s D q         s   +L      L D   + L    G++L + v
  gi|2399307     3    SADDQTTT-----TS--SELRADIRRLGDLLGETLVRQEGPELLDLV 42

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         l  e     D +   EL   L + +   a  + +a++    LAn+
  gi|2399307    43 EKVRRLTRE-----DGEAAAEL---LRGTELQTAAKLVRAFSTYFHLANV 84
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                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                 E v   +R R  + +         A     +  t  +L       P+
gi|2399307    85 TEQV---HRGRELRAR--------RAAEGGLLARTADRLKDAD---PDHL 120

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                 e ++   v  v+tAHPt ++RRs+L K  Ri    a L    v   D++
gi|2399307   121 RETVRHLNVRPVFTAHPTEAARRSVLNKLRRI----AALLDTPVIESDRR 166

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                 LD  L   i   + tDE+R  +P P DE R  + Y+ E     v   L
gi|2399307   167 RLDTRLAENIDLVWQTDELRVVRPEPTDEARNAIYYLDELHAGAVGDVLE 216

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     L   Gi  RlP d   + F  W+GGDRDG nP vtP vt Dv +L
gi|2399307   217 DLTAELERAGI--RLPDDTRPLTFGTWIGGDRDG-NPNVTPQVTWDVLIL 263

                aRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkvvKyY
                      n  ++ +++L   ls    n+     A+EEl    + d    +
gi|2399307   264 QHEHGINDALEMIDELRGFLS----NSIRYTGAtEELLTSLQAD--LDHL 307

                iEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                 E ++++K +  +EPYR     +R KL nt+ R    LA+G    +
gi|2399307   308 PEIsprYKRLNAEEPYRLKATCIRQKLENTKLR----LAKGTPHEPGRD- 352

                ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                y    e L  L +   sL e      ADG L   +R    FGL L  +D+
gi|2399307   353 YLGTGELLTDLRIVQASLREHRGGLFADGRLARTIRTLAAFGLQLATMDV 402

                RqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLlgs
                R  ++ +   l  +   L+  s+R  + + + R   L  EL+ +RPL +
gi|2399307   403 REHADAHHHALGQLFDRLGEESWRyaDMPRDYRTKLLAKELRSRRPLAPT 452

                DLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvEL
                  P     +  l+ f+ +     + FG++  ++Yiism+    Dv A  +
gi|2399307   453 PAPVDAAGEKTLGVFQTVKR-ALEVFGPeviesYIISMCQGADDVFAAAV 501

                LqRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                L RE g+   + +   + +vPL E   +L+AA   +e + +   Y+  +
gi|2399307   502 LAREAGLIDlhagwaKIGIVPLLETTDELKAADTILEDMLADPSYRRLVA 551

                GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                 +++ qevm+GYsDs K  G     W + +Aq  +  vA +yGv+L lFH
gi|2399307   552 LRgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRYGVRLRLFH 601

                GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                GRGGtvGRGGGPtH AiL+qP  t++G ++vt qGEvi   +    L
gi|2399307   602 GRGGTVGRGGGPTHDAILAQPWGTLEGEIKVTEQGEVISDKYLIPALARE 651

                sLqRFtAAtLEH.GmnPP....vsPkPEWRkLmeemAvvAtEEYRsvvvK
                 L    AAtL  + ++  ++++v     W   m+ +   A   YR +v
gi|2399307   652 NLELSVAATLQAsALHTAprqsVEALARWDAAMDVVSDAAHAAYRRLV-E 700

                EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtq
                +P    YF   tP      + +GsRP++R  sG G++ LRAiPW+F Wtq
gi|2399307   701 DPDLPAYFFASTPVDQLADLHLGSRPSRRPDSGaGLDGLRAIPWVFGWTQ 750

                tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                 R  +P W GvG   K   +     +  L Em ++W FFR  +  +Em
gi|2399307   751 SRQIVPGWFGVGSGLKALREAGLDTV--LDEMHQQWHFFRNFISNVEMTL 798

                AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                AK D  iA  y + Lv + Lk   + + ++ + t   +L++ G ++lL+
gi|2399307   799 AKTDLRIARHYVDTLVPDHLKHVFDTIEAEHELTVAEVLRVTGEQELLDA 848

                DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                DP LKq   +Rd+Y+  +  +q   LKR RD               A+
gi|2399307   849 DPVLKQTFTIRDAYLDPISYLQVALLKRQRD---------------AAAA 883

                skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                           +e+  P L   L+Lt+ G+AAG+ ntG
gi|2399307   884 ------------GEQPDPLLSRALLLTVNGVAAGLRNTG    910
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gi|288962822|ref|YP_003453116.1|: domain 1 of 1, from 1 to 923: score 328.1, E = 1.8e-95
                  *->siDAqLRlLvPGKvse.dekLieYDALLlDkFL.DiLqDLHGedLkE
                         + ++     se+ ++ ++ D  Ll + L+D +    Ge + +
  gi|2889628     1    -----MSAILLQESSEtKDQPLREDIRLLGRILgDTVRSQEGEAVFD 42

                  avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                  +v      s  +   +D     EL a L sL P  +  v +a++    LA
  gi|2889628    43 IVERIRQTSIRFHRDEDEGARKELEAILNSLSPPQTARVVRAYSFFSHLA 92

                  nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                  n+AE+ +   R R + +  G  a ++  t   D  E  K  v       +
  gi|2889628    93 NIAEDQHHIRRTRAHALA-GSAARDGTMTHALD--EATKAGVTTQ--QLK 137

                  EvFe.ALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                  E F++AL    v  vltAHPt   R+s+L  +  i   La      +t+e
  gi|2889628   138 EFFDgAL----VSPVLTAHPTEVQRKSILTVQMAIAKLLAERDHGPMTPE 183

                  DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                  + +   E L R +   + t  +R ++    DE+  G+ ++  t  + +P+
  gi|2889628   184 EEETNLESLQRAVLTLWQTAILRATKLAVTDEVSNGLTFYDYTFLREMPR 233

                  FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                  F    +  L+ +            ++  sW+GGDRDG nP vt  v R
  gi|2889628   234 FYAQLEDHLRKMDPSWTTTELPSFLRMGSWIGGDRDG-NPFVTAPVLRQA 282

                  CLLaRmmAanlYisqvEDLmFElsm....WRCndELRvRAEEl.yrtaar
                    +    A  +Y++ +  L  Els++++     + LR  AE  +   + r
  gi|2889628   283 MRMQSTRALQFYLDELHSLGAELSLstrvIDVSEPLRQLAERSpDPSPHR 332

                  dkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseis
                  +                EPYR  +  +  +L  t  R+   L   +  +
  gi|2889628   333 K---------------LEPYRRAISGIYARLAATM-RTLDGLEAPLHAVG 366

                  EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                  +   y    eF   L++  +sL   G  ++A G L  l R v  FG  L
  gi|2889628   367 DAPPYLSPAEFGADLDIIDRSLTVNGSAALAKGRLRHLRRAVDLFGFHLA 416

                  KLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPL
                   +D+Rq s+ +   +  +    + G++Y   sE+ R   L+ EL+  RPL
  gi|2889628   417 SIDLRQNSDVHERSVAELLSFADTGAdYTALSEDERIALLVRELETNRPL 466

                  lgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAv
                         EE    l+ +r  A+ + +   D+    +is +   sD+L v
  gi|2889628   467 ASRYADYSEETSSELEILRTAADararFGADAVVNCVISKTDGVSDILEV 516

                  ELLqRECgvkqt......LrvvPLFEkLADLeAAPAavekLFsiDWYinr
                   +L +E g+ ++++++ +L + PLFE + DL+    ++++L si  Y+
  gi|2889628   517 AVLLKEAGLLRPkdqtldLNIAPLFETIGDLRNCATTMDRLLSIPTYRRF 566

                  idGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                  ++ +++ qevm+GYsDs KD G +   W LYkA   ++ v  ++Gv+L l
  gi|2889628   567 LESRgnlQEVMLGYSDSNKDGGFMTSGWELYKAEIALVEVFARHGVRLRL 616

                  FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                  FHGRGG vGRGGGP   AiL+qP   ++G++R+t qGEvi   +   ++
  gi|2889628   617 FHGRGGSVGRGGGPSYQAILAQPAGAVQGAIRITEQGEVIAGKYSNPEVG 666

                  FrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEEYRsvvvK
                   r L   +AAtLE  +  P s  P ++ + + mee+   A   YR +v+
  gi|2889628   667 RRNLETLAAATLEATLLHPESAAPCsdlFLQTMEELSEHAFKAYRGLVYE 716

                  EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                     F  YF   t   E   +niGsRPa Rk s  ie LRAiPW+F+W q
  gi|2889628   717 TEGFERYFWESTVIGEIANLNIGSRPASRKKSTSIEDLRAIPWVFSWAQC 766

                  RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                  R  LP W G+G A K  +      + +L+ m ++W FF   l  ++mv
  gi|2889628   767 RLMLPGWFGFGSAVKAYLAEHPDGMERLRAMHRDWGFFSTLLSNMDMVLS 816

                  KGDPGiAaLyDkLLvaEeLk.PFGksLRdkYvEtkdlLLkiAGHkDlLEG
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                  K    iA+ y  L+    L++    ++R+++++  d LL i     lLE
  gi|2889628   817 KSNIAIASRYAGLVSDPALRdAIFTRIRAEWQDSIDALLAITEQSALLEK 866

                  DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                   P L   +R R +Y+  Ln +q   LKR R                 +
  gi|2889628   867 NPLLARSIRNRFPYLDPLNHVQVELLKRHR----------------TSDS 900

                  skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                             +e++a G+     Lt+ GiAAG+ n G
  gi|2889628   901 ------------GEQIARGIH----LTINGIAAGLRNSG    923

gi|73917654|sp|Q5P7H5.2|CAPP_AZOSE: domain 1 of 1, from 4 to 916: score 326.5, E = 5.2e-95
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       DA LR               D  Ll + L+D + D HGe
  gi|7391765     4    DKDAPLRE--------------DIRLLGRVLgDTVRDQHGEAAFAL 35

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  +      s  +    D     EL   L +L    +i v +a++    L n
  gi|7391765    36 IERIRQTSVRFRRDDDNAARLELEGILDALSREQTIEVVRAFSYFSHLSN 85

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  +AE+ +   R R ++         +sA  E  +   l +    +   P+
  gi|7391765    86 IAEDQHHIRRSRAHLIA-------GSAPREGSVAHALVRALASG-LPPAR 127

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                           +  vltAHPt   R+s+L  ++ i   L       +t+e++
  gi|7391765   128 LAAFFDTALISPVLTAHPTEVQRKSILNCETDIAHLLDARDRMTLTPEER 177

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  +E DEAL R +   + t  +R a+    DE+  G+sY+  t  +  P
  gi|7391765   178 QESDEALRRTVLTLWQTRMLRPAKLSVVDEVANGLSYFDATFLRELPHLY 227

                  RRvDtALKniGinERlP.YdvP.LikFssWmGGDRDGknPRvtPEvtRDv
                     +  L  +     l + + P  ++  sW+GGDRDG nP vt +v
  gi|7391765   228 ANLEDQL--VSRDPALAgLELPaFLQVGSWIGGDRDG-NPFVTADVLERT 274

                  CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                    +       +Y++ +  L   ls+      L    + l   aar
  gi|7391765   275 LAMQAGAVLGFYLDELHALGARLSL---ALGLVTASDALLALAARS---- 317

                  yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv.
                              EPYR  +  +  +L  t      LL t     +    +
  gi|7391765   318 ---PDHSPHRNDEPYRRAISGIYARLAATH---HALLGTEPPRHPVAVAe 361

                  .ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                  +y  v e  + L++  +sL   G  ++A G L  l R v  FG  L  +D
  gi|7391765   362 pYAAVAELADDLDVIHRSLVANGSAALARGQLRRLRRAVRVFGFHLAPID 411

                  iRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgs
                  +Rq se +  v+  +      G +Y    E  R E L+ EL   RPL  +
  gi|7391765   412 LRQNSEVHERVVAELLATARTGTdYATLDEAARVELLIEELATPRPLASP 461

                  DLPktEEvkDvldafrvLAELPiDsFGa....YiismataPsDvLAvELL
                   +   +E +  l  fr          G+  ++ iis +   sD L   LL
  gi|7391765   462 HVRYSDETEGELAIFRTARAAHRRYGGPaipnCIISKTDDVSDLLELALL 511

                  qRECgvkqt......LrvvPLFEkLADLeAAPAavekLFsiDWYinri..
                   +E g+ +++++  ++ +vPLFE + DL  AP  +++LF++  Y+n +
  gi|7391765   512 LKEAGLLRPheraldVNIVPLFETIEDLANAPSVMDRLFALPGYMNLLaa 561

                  ..dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                  ++d   evm+GYsDs KD G l   W LYkA   +i v  ++G++L lFH
  gi|7391765   562 srDRTHEVMLGYSDSNKDGGFLTSGWALYKAEIGLIEVFARHGIRLRLFH 611

                  GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                  GRGG vGRGGGP   AiL+qP   ++G +R t qGEvi   +G  ++  r
  gi|7391765   612 GRGGSVGRGGGPSYEAILAQPGGAVQGQIRLTEQGEVIAAKYGNPEVGRR 661

                  sLqRFtAAtLEHGmnPPvsPkP..EWRkLmeemAvvAtEEYRsvvvKEPR
                   L    AAtLE  +    +P P+ E+ + m+ +  vA   YR +v+
  gi|7391765   662 NLEVIVAATLEASLLADRAPAPrvEFLDTMQALSDVAFAAYRGLVYDTEG 711
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                    FvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFH
                    F  YF   t   E   +niGsRPa Rk +  ie LRAiPW+F+W q R
  gi|7391765   712 FERYFWESTVISEIAELNIGSRPASRKKGTRIEDLRAIPWVFSWSQCRLM 761

                    LPvWLGvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                    LP W G+G A K++        + +L+ m +eW FF   l  ++mv AK
  gi|7391765   762 LPGWFGFGSAVKtWLAAHADDGIARLQAMHREWSFFAALLSNMDMVLAKT 811

                    DPGiAaLyDkLLvaEeLk.PFGksLRdkYvEtkdlLLkiAGHkDlLEGDP
                    D  iA+ y  L+   +L++   +++R+++ +t d LL i G ++lL+G P
  gi|7391765   812 DLAIASRYAGLVKDVNLRdAIFERIRNEWHDTVDALLAITGQRELLDGNP 861

                    YLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnsk
                     LK  +R R +Y+  Ln +q   L+R R                  E
  gi|7391765   862 LLKRSIRNRFPYLDPLNHVQVELLRRHR------------------ET-- 891

                    kadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      d  ++L             + + + GiAAG+ n G
  gi|7391765   892 HDDARIRLG------------IHISINGIAAGLRNSG    916

gi|290580816|ref|YP_003485208.1|: domain 1 of 1, from 1 to 907: score 326.3, E = 6.3e-95
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                               +      +d + i  +  +l k L+D  + + G    +
  gi|2905808     1    ------MTINKLESRNDKEAIAEEITILTKLLdDATKTMVGSASFDK 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls e       +K +EL   +  L   + ++v + ++ +  L n
  gi|2905808    42 ITLFKKLSIE-------EKHQELEREIEQLTNEEMVVVSRYFSILPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+    sAt E         Lv+   K  +E
  gi|2905808    85 ISEDVNLAYEINYQNNNDIDYLGKLSATIE---------LVSSQ-KNAQE 124

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +   L n  v  vltAHPtq  R+ +L     i   L +          K
  gi|2905808   125 I---LENVNVVPVLTAHPTQVQRKTMLDLTNHIHELLRKYRDVKAGSINK 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +   + + R +     tD iR  +     E+   m Y+   + kGv K +
  gi|2905808   172 QKWYDDMRRYVELIMQTDIIREKKLKVTNEITNVMEYYNSSLIKGVTKLI 221

                    RRvDtALKniGinERlPY.dvPLikFssWmGGDRDGknPRvtPEvtRDvC
                        t  K +        +++  i    W+GGDRDG nP vt E  +
  gi|2905808   222 ----TEYKHLSQQKGFDLgNAKPITMGMWIGGDRDG-NPFVTAETLKISA 266

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    L+   +  n Yi++v DL   +s+      L      ++  a r   v
  gi|2905808   267 LVQNEVILNYYIDKVSDLYRTFSL---STSLSTISNAVKEMADRSTDVSI 313

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRE..RaRHLLAtGiseisEeAv
                    Y E        EPYR     +  +L  t    +  HL      + +
  gi|2905808   314 YRE-------KEPYRKAFHYIQSRLQETLIylKNNHLEELESEDSAQILP 356

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y    eF   L L   sL e    +   G L +lL  v  FG  L  +D+
  gi|2905808   357 YQSAQEFRNDLQLIKDSLLENNGSAFITGDLTELLQAVDVFGFFLASIDM 406

                    RqEseRq.tDvlDAittHLeiGsYReWsEeKRqEWLlaELkGK.RPLlgs
                    Rq+s  ++t v + +     +  Y + +Ee +   Ll EL   +R L
  gi|2905808   407 RQDSSVHeTCVAELLASANIVANYSDLPEEEKIAILLKELTEDpRILSAT 456

                    DLPktEEvkDvldaf....rvLAELPiDsFGaYiismataPsDvLAvELL
                     + k E ++  l  f++ ++    L  D     iis + + sD+    ++
  gi|2905808   457 HVEKSEILQKELAIFktarKLKDALGEDVIKQHIISHTESISDMFELAIM 506

                    qRECgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK.
                     +E g+ +++k  +++vPLFE + DL+     + +    D  +  i   +
  gi|2905808   507 LKEVGLvdtdKARVQIVPLFETIEDLDNSREIMRQYLNYDIVKKWIAANh 556

                    ..qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRG
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                    + qe+m+GYsDs KD G ls  W LYkAq E+  +  + GvK++ FHGRG
  gi|2905808   557 nyQEIMLGYSDSNKDGGYLSSGWALYKAQNELTEIGSDNGVKITFFHGRG 606

                    GtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLq
                    GtvGRGGGP   Ai sqP   i+  +R t qGEvi   +G  ++ +  L
  gi|2905808   607 GTVGRGGGPSYEAITSQPFGSIKDRIRLTEQGEVIGNKYGNKDVAYYNLE 656

                    RFtAAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFv
                        AtL+  +   +   ++   +R +m+e+       YR +v+    F
  gi|2905808   657 MLVSATLDRMVTRRIVNSdnlVNYRLIMDEIVADSNLIYRDLVFGNEHFY 706

                    EYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLP
                    +YF  A P  E   +niGsRPa Rk    i  LRAiPW+F+W q R   P
  gi|2905808   707 DYFFAASPIREVSSLNIGSRPAARKTITEISGLRAIPWVFSWSQNRIMFP 756

                    vWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPG
                     W GvG AFKh idKD Knl kL+EmY+ WPFF   l  ++mv  K
  gi|2905808   757 GWYGVGSAFKHFIDKDEKNLTKLQEMYQSWPFFHSLLSNVDMVLSKSNMN 806

                    iAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                    iA  y kL   Ee k     + d+++ tk+ +L i  Hk lLE   YLK
  gi|2905808   807 IAFEYAKLCQDEETKEVFATILDEWQLTKNVILAIESHKQLLEDNSYLKA 856

                    rlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkade
                     l  R +Y   Ln +q   +KR R  +               En
  gi|2905808   857 SLDYRLPYFNVLNYIQIELIKRQRRGEL-------------GEN------ 887

                    LvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                LE  + +t+ G+A G+ n G
  gi|2905808   888 -------------LENLIHITINGVATGLRNSG    907

gi|24379180|ref|NP_721135.1|: domain 1 of 1, from 1 to 907: score 325.8, E = 8.5e-95
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                              +      +d + i  +  +l k L+D  + + G    +
  gi|2437918     1    ------MTINKLESRNDKEAIAEEITILTKLLdDATKTMVGSASFDK 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls e       +K +EL   +  L   + ++v + ++ +  L n
  gi|2437918    42 ITLFKKLSIE-------EKHQELEREIEQLTNEEMVVVSRYFSILPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+    sAt E         Lv+   K  +E
  gi|2437918    85 ISEDVNLAYEINYQNNNDIDYLGKLSATIE---------LVSSQ-KNAQE 124

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +   L n  v  vltAHPtq  R+ +L     i   L +          K
  gi|2437918   125 I---LENVNVVPVLTAHPTQVQRKTMLDLTNHIHELLRKYRDVKAGSINK 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +   + + R +     tD iR  +     E+   m Y+   + kGv K +
  gi|2437918   172 QKWYDDMRRYVELIMQTDIIREKKLKVTNEITNVMEYYNSSLIKGVTKLI 221

                    RRvDtALKniGinERlPY.dvPLikFssWmGGDRDGknPRvtPEvtRDvC
                        t  K +        +++  i    W+GGDRDG nP vt E  +
  gi|2437918   222 ----TEYKHLSHQKGFDLgNAKPITMGMWIGGDRDG-NPFVTAETLKISA 266

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    L+   +  n Yi++v DL   +s+      L      ++  a r   v
  gi|2437918   267 LVQNEVILNYYIDKVSDLYRTFSL---STSLSTISNAVKEMADRSTDVSI 313

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRE..RaRHLLAtGiseisEeAv
                    Y E        EPYR     +  +L  t    +  HL      + +
  gi|2437918   314 YRE-------KEPYRKAFHYIQSRLQETLIylKNNHLEELESEDSAQILP 356

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y    eF   L L   sL e    +   G L +lL  v  FG  L  +D+
  gi|2437918   357 YQSAQEFRNDLQLIKDSLLENNGSAFITGDLTELLQAVDVFGFFLASIDM 406

                    RqEseRq.tDvlDAittHLeiGsYReWsEeKRqEWLlaELkGK.RPLlgs
                    Rq+s  ++t v + +     +  Y + +Ee +   Ll EL   +R L
  gi|2437918   407 RQDSSVHeTCVAELLASANIVANYSDLPEEEKIAILLKELTEDpRILSAT 456
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                    DLPktEEvkDvldaf....rvLAELPiDsFGaYiismataPsDvLAvELL
                     + k E ++  l  f++ ++    L  D     iis + + sD+    ++
  gi|2437918   457 HVEKSEILQKELAIFktarKLKDALGEDVIKQHIISHTESISDMFELAIM 506

                    qRECgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK.
                     +E g+ +++k  +++vPLFE + DL+     + +    D  +  i   +
  gi|2437918   507 LKEVGLvdtdKARVQIVPLFETIEDLDNSREIMRQYLNYDIVKKWIAANh 556

                    ..qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRG
                    + qe+m+GYsDs KD G ls  W LYkAq E+  +  + GvK++ FHGRG
  gi|2437918   557 nyQEIMLGYSDSNKDGGYLSSGWALYKAQNELTEIGYDNGVKITFFHGRG 606

                    GtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLq
                    GtvGRGGGP   Ai sqP   i+  +R t qGEvi   +G  ++ +  L
  gi|2437918   607 GTVGRGGGPSYEAITSQPFGSIKDRIRLTEQGEVIGNKYGNKDVAYYNLE 656

                    RFtAAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFv
                        AtL+  +   +   ++   +R +m+e+       YR +v+    F
  gi|2437918   657 MLVSATLDRMVTRRIVNSdnlVNYRLIMDEIVADSNLIYRDLVFGNEHFY 706

                    EYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLP
                    +YF  A P  E   +niGsRPa Rk    i  LRAiPW+F+W q R   P
  gi|2437918   707 DYFFAASPIREVSSLNIGSRPAARKTITEISGLRAIPWVFSWSQNRIMFP 756

                    vWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPG
                     W GvG AFKh idKD Knl kL+EmY+ WPFF   l  ++mv  K
  gi|2437918   757 GWYGVGSAFKHFIDKDEKNLTKLQEMYQSWPFFHSLLSNVDMVLSKSNMN 806

                    iAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                    iA  y kL   Ee k     + d+++ tk+ +L i  Hk lLE   YLK
  gi|2437918   807 IAFEYAKLCQDEETKEVFATILDEWQLTKNVILAIESHKQLLEDNSYLKA 856

                    rlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkade
                     l  R +Y   Ln +q   +KR R  +              En
  gi|2437918   857 SLDYRLPYFNVLNYIQIELIKRQRRGEL-------------GEN------ 887

                    LvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                LE  + +t+ G+A G+ n G
  gi|2437918   888 -------------LENLIHITINGVATGLRNSG    907

gi|25008189|sp|Q93MH3.1|CAPP_CORCT: domain 1 of 1, from 1 to 919: score 325.7, E = 9.4e-95
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                   +    + ++ D   l + L++++ +  G+++ E
  gi|2500818     1    -------------MT---DFLRDDIRFLGRILgEVIAEQEGQEVYEL 31

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      s +    k    ++ L  +  ++ Pa a  +A+a++H   LAn
  gi|2500818    32 VEQARLTSFDIA--KGNAEMDSLVQVFDGITPAKATPIARAFSHFALLAN 79

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAE+ +       + ++     D ++   +s ++ t  kL   +n   e
  gi|2500818    80 LAEDLH------DEELR-EQALDAGDTPPDSTLDATWLKL-NEGNVGAEA 121

                    vFeALKnqsvDLvltAHPtqsvRRsLL..qK....naRiRnCLaqLsAKD
                    v + L+n  v  vltAHPt   RR + + qK  +++ R R  L
  gi|2500818   122 VADVLRNAEVAPVLTAHPTETRRRTVFdaQKwittHMRERHALQSAEPTA 171

                    vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWk
                     t     E++  + R i   + t  iR a+P   DE+  G+ Y+   + +
  gi|2500818   172 RTQSKLDEIEKNIRRRITILWQTALIRVARPRIEDEIEVGLRYYKLSLLE 221

                    GvPKFLRRvDtALKniGinERlPYdvPL...ikFssWmGGDRDGknPRvt
                     +P+  R v   L+     ER   dvPL++ +k  sW+GGD DG nP vt
  gi|2500818   222 EIPRINRDVAVELR-----ERFGEDVPLkpvVKPGSWIGGDHDG-NPYVT 265

                    PEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrta
                              a       Y  q+  L  Els+    +E+     El
  gi|2500818   266 AGTVEYSTRRAAETVLKYYARQLHSLEHELSLSDRMNEVTPQLLELADAG 315

                    ardkvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGi
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                    d            vP++  EPYR  +  vR ++  t        A  i
  gi|2500818   316 HND------------VPsrVDEPYRRAVHGVRGRILATT-------AELI 346

                    seisEeAvytkv.......EeFLEPLELCYksLCeCGDkviADGsLLDlL
                     e + e v+ kv ++  ++EeFL       +sL e  D  iAD  L  l+
  gi|2500818   347 GEDAVEGVWFKVftpyaspEEFLNDALTIDHSLRESNDVLIADDRLSVLI 396

                    RqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEW
                      +  FG  L  LD+Rq se   Dvl  + +  ++ ++YRe sEe + E
  gi|2500818   397 SAIESFGFNLYSLDLRQNSESYEDVLTELFERAQVTAnYRELSEEEKLEV 446

                    LlaELkGKRPLlgsDLPktEEvkDv.ldafrvLAELPiDsFGa.....Yi
                    Ll EL+  RPL++       Ev D +l+ fr   E  +  FG++  ++ i
  gi|2500818   447 LLKELRSPRPLIPHGSDEYSEVTDReLGIFRTASE-AVKKFGPrmvphCI 495

                    ismataPsDvLAvELLqRECgv........kqtLrvvPLFEkLADLeAAP
                    isma +  DvL   +L +E g+   ++++++ t+ v+PLFE + DL+A
  gi|2500818   496 ISMASSVTDVLEPMVLLKEFGLiaangdnpRGTVDVIPLFETIEDLRAGA 545

                    AavekLFsiDWYinri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqE
                      +  L+ iD Y+n + ++d  qevm+GYsDs KD G +sA W LY A
  gi|2500818   546 GILGELWKIDLYRNYLlqrDNVQEVMLGYSDSNKDGGYFSANWALYDAEL 595

                    EiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtv
                     ++   +  GvKL lFHGRGGtvGRGGGP   AiL+qP   ++Gs+R+t
  gi|2500818   596 QLVELCRSAGVKLRLFHGRGGTVGRGGGPSYDAILAQPKGAVQGSVRITE 645

                    qGEviEfsFGEEnLCFrsLqRFtAAtLEHGm..nPPvsPkPEWRkLmeem
                    qGE+i   +G  +   r L     AtLE  + +   +  +    ++m e+
  gi|2500818   646 QGEIISAKYGNPETARRNLEALVSATLEASLldVSELTDHQRAYDIMSEI 695

                    AvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGie
                           Y s+v  +  F++YF   tP  E G +niGsRP+ Rk    +e
  gi|2500818   696 SELSLKKYTSLVHEDQGFIDYFTQSTPLQEIGSLNIGSRPSSRKQTSSVE 745

                    sLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAi...dKDiKnlqkLkEmYk
                     LRAiPW+ +W q R  LP W GvG A    i+++++  + +  L+ + +
  gi|2500818   746 DLRAIPWVLSWSQSRVMLPGWFGVGTALEQWIgegEQATQRIAELQTLNE 795

                    eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL....vaEeLkPFGksLRdk
                     WPFF   lD +  v  K +  +A Ly +L+++++vaE +      + ++
  gi|2500818   796 SWPFFTSVLDNMAQVMSKAELRLAKLYADLIpdreVAERVY---SVIHEE 842

                    YvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiR
                    Y  tk++   i G  DlL+  P L   +  R +Y+  Lnv+q   ++R R
  gi|2500818   843 YFLTKKMFCVITGSDDLLDDNPLLARSVQRRYPYLLPLNVIQVEMMRRYR 892

                    DPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKG
                                K    E+       v  n            + Ltm G
  gi|2500818   893 -------------KGDQSEQ-------VSRN------------IQLTMNG 910

                    iAAGmqntG<-*
                    +   + n G
  gi|2500818   911 LSTALRNSG    919

gi|262039622|ref|ZP_06012916.1|: domain 1 of 1, from 7 to 929: score 325.6, E = 1e-94
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            L  +   K    e L+e   LL     + +    G  +  +
  gi|2620396     7    ---TPLPTVKLDKQQ--ETLLEHNRLLGTLLGETIFTYAGLHIFKVT 48

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        E s  Y      +   +L      L  ++ + v + +     LAn+
  gi|2620396    49 ESLREASISYYKTNKQESRKDLSLFCSELGDSEILRVIRGFTYFSVLANI 98

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v   y  R  k          + t    +E  l  L  k+  s e +
  gi|2620396    99 AEDVYQVYQHRSMKFS--------NKTEMGTLEKSLENLKKKG-ISIEKI 139

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     eA+K  sv  vltAHPtq  R+s+L    +i   L++     +   D
  gi|2620396   140 LEAMKKVSVVPVLTAHPTQVQRKSILDLMRKITDTLSKYENVQIHQIDES 189
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                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    E  + L   i+  + t  +R +q    DE+   +sY+  t ++ +P
  gi|2620396   190 EWIDELNSKIKILWQTSMLRTSQLRVTDEISNALSYYNITFFNEIPELTN 239

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    +       +G n         +    W+GGDRDG nP vt +
  gi|2620396   240 KFQEISEKLGENKFEAEKLIPLTMGMWIGGDRDG-NPYVTVDTLETSAQA 288

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                      +    +Y++ +E +  +lsm     E+    E l    a+ kv  + +
  gi|2620396   289 QALTLFQFYLDEIESIYRDLSMSNTMTEVSKDLEKLSE--ASGKVSPHRV 336

                    EFWKqvPPtEPYRviLGdvRDKLYntRER...aRHLLAtGiseisEeAvy
                           +EPYR  L ++ D+L  t  +  + + +L     + s +  y
  gi|2620396   337 --------NEPYRRALTAINDRLLATAYKlceNKEVLPPKRKD-SLDIPY 377

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                       EeF   LE+   sL e    ++  G L  l+     FG  L  +D+R
  gi|2620396   378 SSPEEFTKDLEIVANSLIENNSEALVKGKLRNLISGTKIFGFHLATIDLR 427

                    qEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK.RPLlgsD
                    q+s  +   +  + +  +i  +Y + +E+ R E Ll EL+  +R L  +
  gi|2620396   428 QDSSIHELCVAELLKSANIMEdYLSLPENARCEMLLRELEHDpRILSDPT 477

                    LPktEEvkDvldafrvLAELPiDsFGaYi.....ismataPsDvLAvELL
                    + + E +k  l  fr +  L  D F + i +++ is at+ sD+L + +L
  gi|2620396   478 ISQSELLKGELAIFRKVKSL-RDRFDSRIiekhlISHATSVSDMLEIAIL 526

                    qRECgvkq.......tLrvvPLFEkLADLeAAPAavekLFs...iDWYin
                     +E  + ++++++   +++vPLFE + DLeA    +ek Fs + +  ++
  gi|2620396   527 LKEANLAKgdknsfcDIQIVPLFETVEDLEASSEILEKWFSlplVQKWME 576

                    ridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                    +   Kqevm+GYsDs KD G ls  W LYkAq  +     k+ v++  FH
  gi|2620396   577 KSGRKQEVMLGYSDSNKDGGYLSSSWSLYKAQKKLTALGNKFDVQISFFH 626

                    GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                    GRGGtvGRGGGP   AiL+qP    +G +R t qGEvi   +G  +L F+
  gi|2620396   627 GRGGTVGRGGGPSYEAILAQPEGGADGTIRLTEQGEVIGAKYGNPDLGFK 676

                    sLqRFtAAtLEHGmnPPvsPk.PEWRkLmeemAvvAtEEYRsvvvKEPRF
                     L     A LE G       k  E+ k++ee+       YR +v+    F
  gi|2620396   677 NLEALVSAALESGALTVEDAKwDEYEKIIEEISESSYKVYRELVYNTEGF 726

                    vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                     ++F   tP      +niGsRP+ Rk    +esLRAiPW+F+W q R  L
  gi|2620396   727 TDFFFEITPINAIAGLNIGSRPSSRKKKQSLESLRAIPWVFSWSQSRIML 776

                    PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                    P W G+GA F   i+K   nl  L+ mY+eWPFFR  +   +mv  K D
  gi|2620396   777 PGWYGLGASFTEWINKNPDNLSILQKMYREWPFFRSVISNADMVLSKSDL 826

                    GiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                     iA+ y kL    e+ +k F + +++ ++ t d L ki G   lL   P
  gi|2620396   827 RIASEYVKLAQNQEVaqKIFSEIVKE-WELTLDVLKKITGNDVLLADNPE 875

                    LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                    L   lR R +Y   +n +q   LKR+R+                dE
  gi|2620396   876 LASSLRNRLAYFDSMNYLQIELLKRLRE---------------GDES--- 907

                    adeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                  L   L + + G+A G+ n G
  gi|2620396   908 -------E-------DLRKALHISINGLATGLRNSG    929

gi|257126840|ref|YP_003164954.1|: domain 1 of 1, from 5 to 933: score 325.5, E = 1e-94
                    *->siDAqLRlLvPGKvse.dekLieYDALLlDkFLDiLqDLHGedLkEa
                           +  L   K  e++e+L+    L      + +    G  + E+
  gi|2571268     5    --NLPITPLSSVKLDErQENLLSHNRLFANLLGETIFRYAGLHIYEV 49

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
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                    E s  Y   k  +    L +    L   + + v ++++    LAn
gi|2571268    50 TEKLKEASIKYYETKNQEARKNLSSFCSDLTDVEILRVIRSFSIFAALAN 99

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE+v   +  R  k          +      +E  l+ L  k+  s e
gi|2571268   100 IAEDVYQTHEQRYAKIS--------NKLQIGTLEKSLQNLKEKG-ISQEK 140

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLs.AKDvtveD
                   +  A+   s+  vltAHPtq  R+s+L    ++   L +  + K   +++
gi|2571268   141 ILKAMEKVSIVPVLTAHPTQVQRKSILDLTKKLTDILDKYEnVKSNQIDE 190

                   KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    k L + L R iq  + t  +R ++    DE+   +sY+  t ++ +P
gi|2571268   191 NKWLND-LSRGIQIWWQTAMLRATKLRVTDEISNALSYYNITFFNEIPAL 239

                   LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   + +     K +G  E        +    W+GGDRDG nP vt +
gi|2571268   240 MNKFQEISKALGYSEMKSQALVPLTMGMWIGGDRDG-NPYVTVDTLEQSA 288

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                       +     Y++ v ++  Elsm      L     El++ a
gi|2571268   289 QDQAIKLFQHYFNEVQEIYRELSM---SVSLSNVTQELQKLAEAA----- 330

                   YiEFWKqvPPt...EPYRviLGdvRDKL....YntRERaRHLLAtGisei
                          v P +++EPYR  L  +RD+L  + Yn  +  R LL     e
gi|2571268   331 -----GEVSPHrtrEPYRRALTTIRDRLlataYNLCDYYRDLLPPK-REN 374

                   sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                     +  y  v eF + L     sL       +A G L  l+     FG  L
gi|2571268   375 GLDIPYKLVSEFTDDLVTVAESLKKNNSEFLAKGKLTNLISATKIFGFHL 424

                   vKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaELkGK.R
                     +D+Rq+s  +   +  + + +  +i   Y + sE+ R E Ll EL+  +R
gi|2571268   425 ATIDLRQDSSVHEVCVAELLKSANIlEDYLSLSENARCEILLRELEYDpR 474

                   PLlgsDLPktEEvkDvldafrvLAELPiDsFGaYi.....ismataPsDv
                    L  s +P+ E ++  l  fr    L  D FG  i +++ is +t+ sD+
gi|2571268   475 ILSDSTIPQSETLASELAIFRKTKSL-RDRFGNKIieknlISHTTSVSDM 523

                   LAvELLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFs..
                   L + +L +E  + ++ ++++   L++vPLFE + DL AAP  + k F  +
gi|2571268   524 LEIAILLKEANLAKgyngnefcDLQIVPLFETVEDLIAAPDILRKWFNlp 573

                   .iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyG
                    +  ++ +   Kqevm+GYsDs KD G ls  W LYkAq E+  + +++
gi|2571268   574 lVQKWMEKNGRKQEVMLGYSDSNKDGGYLSSSWSLYKAQKELTAIGREFD 623

                   vKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFG
                   v +  FHGRGGtvGRGGGP   AiL+qP    +G +R t qGEvi   +G
gi|2571268   624 VEISFFHGRGGTVGRGGGPSYEAILAQPEGSTHGTIRLTEQGEVIGAKYG 673

                   EEnLCFrsLqRFtAAtLE.HGmnPPvsPkPEWRkLmeemAvvAtEEYRsv
                     +L F+ L     A LE+  +    +   E+ +++ee+       YR +
gi|2571268   674 NPDLGFKNLEALVSAALEsCALTTEDANWEEYEQIIEEVSNLSYYAYRDL 723

                   vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaW
                   v+    F  +F   tP      +niGsRP+ Rk    +esLRAiPW+F+W
gi|2571268   724 VYNTEGFSNFFFEVTPINFIAGLNIGSRPSSRKKTQTLESLRAIPWVFSW 773

                   tqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEm
                    q R  LP W GvG AF   id     l  L+EmY+eWPFF+ t+  +Em
gi|2571268   774 SQARIMLPGWYGVGTAFTKWIDNNDEKLEILQEMYNEWPFFKSTISNVEM 823

                   vFAKGDPGiAaLyDkLLv.aEeLkPFGksLRdkYvEtkdlLLkiAGHkDl
                   v  K D  i   y kL  + E  +   k++  ++  t d+L ki   kD+
gi|2571268   824 VLSKSDLSIFREYVKLASdQETAQRIFKEIEKEWILTIDILKKIT-KKDV 872

                   LEGDPY.LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEy
                   L  D  +L   lR R +Y   +n +q   +KR R
gi|2571268   873 LLADNLeLVSSLRNRLPYFDSMNYLQIELIKRSR---------------- 906
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                    AdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    A +ns +    +++                + G+A G+ n G
  gi|2571268   907 AGDNSEELRKAIHIS----------------INGLATGLRNSG    933

gi|21221565|ref|NP_627344.1|: domain 1 of 1, from 3 to 911: score 325.4, E = 1.2e-94
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s D q         s   +L      L D   + L    G++L E v
  gi|2122156     3    SADDQ----TTTTTS--SELRADIRRLGDLLGETLVRQEGPELLELV 43

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         l  e     D +   EL   L + +   a  + +a++    LAn+
  gi|2122156    44 EKVRRLLTRE-----DGEAAAEL---LRGTELETAAKLVRAFSTYFHLANV 85

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     E v   +R R    k         A     +  t  +L       Pe
  gi|2122156    86 TEQV---HRGRELGAK--------RAAEGGLLARTADRLKDAD---PEHL 121

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     e ++n  v  v+tAHPt ++RRs+L K  Ri    a L    v   D++
  gi|2122156   122 RETVRNLNVRPVFTAHPTEAARRSVLNKLRRI----AALLDTPVNESDRR 167

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     LD  L   i   + tDE+R  +P P DE R  + Y+ E     v   L
  gi|2122156   168 RLDTRLAENIDLVWQTDELRVVRPEPADEARNAIYYLDELHLGAVGDVLE 217

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         L   G+  +lP d   + F  W+GGDRDG nP vtP vt Dv +L
  gi|2122156   218 DLTAELERAGV--KLPDDTRPLTFGTWIGGDRDG-NPNVTPQVTWDVLIL 264

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkvvKyY
                          n  ++ +++L   ls    n+   + A+EEl    + d
  gi|2122156   265 QHEHGINDALEMIDELRGFLS----NSIRYAGAtEELLASLQAD--LERL 308

                    iEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                     E ++++K +  +EPYR     +R KL nt+ R    LA+G     +
  gi|2122156   309 PEIsprYKRLNAEEPYRLKATCIRQKLENTKQR----LAKGTPH-EDGRD 353

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y    + ++ L +   sL e      ADG L   +R    FGL L  +D+
  gi|2122156   354 YLGTAQLIDDLRIVQTSLREHRGGLFADGRLARTIRTLAAFGLQLATMDV 403

                    RqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLlgs
                    R  ++ +   l  +   L+  s+R  + + e R   L  EL+ +RPL +s
  gi|2122156   404 REHADAHHHALGQLFDRLGEESWRyaDMPREYRTKLLAKELRSRRPLAPS 453

                    DLPk...tEEvkDvldaf.rvLAELPiDsFGaYiismataPsDvLAvELL
                      P + + E    v ++++r L     +   +Yiism+    Dv A  +L
  gi|2122156   454 PAPVdapGEKTLGVFQTVrRALEVFGPEVIESYIISMCQGADDVFAAAVL 503

                    qRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                     RE g+   + +   + +vPL E   +L+AA   +e L +   Y+  +
  gi|2122156   504 AREAGLIDlhagwaKIGIVPLLETTDELKAADTILEDLLADPSYRRLVAL 553

                    K...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                    +++ qevm+GYsDs K  G     W + +Aq  +  vA +yGv+L lFHG
  gi|2122156   554 RgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRYGVRLRLFHG 603

                    RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                    RGGtvGRGGGPtH AiL+qP  t++G ++vt qGEvi   +    L
  gi|2122156   604 RGGTVGRGGGPTHDAILAQPWGTLEGEIKVTEQGEVISDKYLIPALAREN 653

                    LqRFtAAtLEHGm...nPPvsPk..PEWRkLmeemAvvAtEEYRsvvvKE
                    L    AAtL     ++ P  s      W   m+ +   A   YR +v  +
  gi|2122156   654 LELTVAATLQASAlhtAPRQSDEalARWDAAMDVVSDAAHTAYRHLV-ED 702

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWtq
                    P    YF   tP      + +GsRP+ R+P+ G++ + LRAiPW+F Wtq
  gi|2122156   703 PDLPTYFLASTPVDQLADLHLGSRPS-RRPGSGVslDGLRAIPWVFGWTQ 751

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     R  +P W GvG   K   +     +  L Em ++W FFR  +  +Em
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  gi|2122156   752 SRQIVPGWYGVGSGLKALREAGLDTV--LDEMHQQWHFFRNFISNVEMTL 799

                   AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                   AK D  iA  y + Lv +eLk   + ++++ + t   +L++ G  +lL+
  gi|2122156   800 AKTDLRIAQHYVDTLVPDELKHVFDTIKAEHELTVAEVLRVTGESELLDA 849

                   DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                   DP LKq   +Rd+Y+  +  +q   L R R              E A+ n
  gi|2122156   850 DPVLKQTFTIRDAYLDPISYLQVALLGRQR--------------EAAAAN 885

                   skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      +d L+               L+Lt+ G+AAG+ ntG
  gi|2122156   886 -EDPDPLLARA------------LLLTVNGVAAGLRNTG    911

gi|20196770|emb|CAC86357.1|: domain 1 of 1, from 1 to 398: score 324.4, E = 2.3e-94
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2019677     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2019677     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2019677     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                          svDLv+tAHPtqs+RRsLLqKnaRiRnCL+qLsAKD t+eDKk
  gi|2019677     1 -------SVDLVFTAHPTQSARRSLLQKNARIRNCLTQLSAKDTTPEDKK 43

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL REiqAAFRtDEiRRaqPtPqDEmR+GmsYiHEtvWkGvPKFLR
  gi|2019677    44 ELDEALAREIQAAFRTDEIRRAQPTPQDEMRYGMSYIHETVWKGVPKFLR 93

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALK iGinERlPY+vPLikF+sWmGGDRDG nPRvtPEvtRDvCLL
  gi|2019677    94 RVDTALKDIGINERLPYNVPLIKFCSWMGGDRDG-NPRVTPEVTRDVCLL 142

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   +RmmAanlYi+qvEDLmFElsmWR n ELR+RA+El +t+a++kv+KyYi
  gi|2019677   143 SRMMAANLYIDQVEDLMFELSMWRSNAELRARADELLSTPASKKVTKYYI 192

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWKq+PP+EPYRviLG+vRDKLYntRERaRH+LAtG+sei+Ee v+t +
  gi|2019677   193 EFWKQIPPNEPYRVILGAVRDKLYNTRERARHILATGVSEIPEESVFTSI 242

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   E+ +EPLELCYksL +CGDk+iA+GsLLDlLRqv+ FGLsLvKLDiRqEs
  gi|2019677   243 EQIIEPLELCYKSLVDCGDKAIAEGSLLDLLRQVFIFGLSLVKLDIRQES 292

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   eR+tDv+DAittHL+iGsYR+W+E+KR EWL++ELkGKRPLl++DLP+tE
  gi|2019677   293 ERHTDVIDAITTHLGIGSYRSWPEDKRVEWLVSELKGKRPLLPADLPMTE 342

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dv++a++v+AELP+DsFG+Yiism+taPsDvLAvELLqRECg+kqtL
  gi|2019677   343 EIADVIGAMKVIAELPSDSFGPYIISMCTAPSDVLAVELLQRECGIKQTL 392

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLF
  gi|2019677   393 PVVPLF---------------------------------------------- 398

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|2019677     - ---------------------------------------------- -

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

  gi|2019677     - ---------------------------------------------- -
```

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                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|2019677     - ------------------------------------------------- -

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|2019677     - ------------------------------------------------- -

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|2019677     - ------------------------------------------------- -

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|2019677     - ------------------------------------------------- -

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|2019677     - ------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|2019677     - -------------    -

gi|239981711|ref|ZP_04704235.1|: domain 1 of 1, from 3 to 928: score 324.3, E = 2.4e-94
                  *->siDAqLRlLv....PGKvsedekLieYDALLlDkFLDiLqDLHGedL
                     s DAq      +++PG      +  +     l   +  L DL Ge L
  gi|2399817     3    SADAQATTTSatgrPGPTE-TPEPARTTSPELRADIRRLGDLLGEAL 48

                  kEavqECYElsAeYEGKkD.tkKLeELGakLt.sLdPaDailvAkailHm
                    + qE  El    E  +  t+  +E  a L ++L+   a  + +a++
  gi|2399817    49 --VRQEGHELLDLVERVRAlTRTDGEAAAELLgGLELEIAAKLVRAFSTY 96

                  LnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkln
                    LAn+ E v   +R R  + +    a+E+       +  t  +L
  gi|2399817    97 FHLANVTEQV---HRGRELRAR---RAEEGGL-----LARTADRLKDAD- 134

                  KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                    Pe     ++n  v  v+tAHPt ++RRs+L K  Ri    a L    v
  gi|2399817   135 --PEHLRATVQNLNVRPVFTAHPTEAARRSVLGKLRRI----AELLETPV 178

                  tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                     D++  D  L   i   + tDE+R  +P P DE R  + Y+ E
  gi|2399817   179 IEADRRRHDTRLAENIDLVWQTDELRVVRPEPADEARNAVYYLDELHAGA 228

                  vPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                  v   L      L  +G    lP +   + F  W+GGDRDG nP vtPEvt
  gi|2399817   229 VGDVLEDLTAELARVGFE--LPENSRPLTFGTWIGGDRDG-NPNVTPEVT 275

                  RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaard
                   Dv +L      n  ++ v++L   ls    n+     A+EEl    + d
  gi|2399817   276 WDVLILQHEHGINDALEVVDELRGFLS----NSIRYTGAtEELLASLQAD 321

                  kvvKyYiEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGise
                      +  E ++++K +  +EPYR     vR KL nt+ER    LA+G +
  gi|2399817   322 --LDHLPEIsprYKRLNAEEPYRLKATCVRQKLENTKER----LAQGTAH 365

                  isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                   +    y    e L  L L   sL e      ADG +   +R    FGL
  gi|2399817   366 QPGRD-YLGTAELLTDLTLIQDSLREHRGGLFADGRMNRTIRTLAAFGLQ 414

                  LvKLDiRqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGK
                  L  +D+R  ++ +   l  +   L+  s+R  + + + R   L  EL+ +
  gi|2399817   415 LATMDVREHADAHHHALGQLFDRLGEESWRyaDMPRDYRTRLLAKELRSR 464

                  RPLlgsDLPk...tEEvkDvldaf.rvLAELPiDsFGaYiismataPsDv
                  RPL +s  P +   E    v  +++r LA    +   +Yiism+    Dv
  gi|2399817   465 RPLAPSPAPLdaaGEKTLNVFHTVrRALAVFGPEVVESYIISMCQGADDV 514

                  LAvELLqRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWY
                   A  +L RE g+   + +   + +vPL E   +L+AA   ++ + +   Y
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  gi|2399817   515 FAAAVLAREAGLIDlhagwaKIGIVPLLETTDELRAADVILDEMLADPSY 564

                   inridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvK
                   +  +  +++ qevm+GYsDs K  G     W + +Aq  +  vA +yGv+
  gi|2399817   565 RLLVSLRgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRYGVR 614

                   LvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEE
                   L lFHGRGGtvGRGGGP H AiL+qP  t++G ++vt qGEvi   +
  gi|2399817   615 LRLFHGRGGTVGRGGGPSHDAILAQPWGTLEGEIKVTEQGEVISDKYLVP 664

                   nLCFrsLqRFtAAtLEH.GmnPP....vsPkPEWRkLmeemAvvAtEEYR
                    L    L    AAtL  + ++  ++++v     W   m+ +   A   YR
  gi|2399817   665 SLARENLELTVAATLQAsALHTAprqsVEALARWDAAMDTVSEAAHTAYR 714

                   svvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPW
                    +v  +P    YF   tP      + +GsRP+ R+P+ G++ + LRAiPW
  gi|2399817   715 KLV-EDPDLPSYFLASTPVDQLAELHLGSRPS-RRPGSGVslDGLRAIPW 762

                   iFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlD
                   +F Wtq R  +P W GvG   K   +     +  L EmY+ W FFR  +
  gi|2399817   763 VFGWTQSRQIVPGWFGVGSGLKALREAGLDGV--LSEMYEHWHFFRNFVS 810

                   LlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGH
                    +Em  AK D  iA  y + Lv +eL+   + + ++   t   +L++ G
  gi|2399817   811 NVEMTLAKTDLRIARHYVDTLVPDELRHVFDLIEAEHALTVAEILRVTGG 860

                   kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                    +lL+  P L+q   +Rd+Y+  +  +q   L R R
  gi|2399817   861 EELLDSNPVLQQTFAIRDAYLDPISYLQVSLLARQRA------------- 897

                   EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     A+E             +e   P L   L+Lt+ G+AAG+ ntG
  gi|2399817   898 --AAER------------GEDPDPLLSRALLLTVNGVAAGLRNTG    928

gi|225165040|ref|ZP_03727237.1|: domain 1 of 1, from 24 to 966: score 323.4, E = 4.7e-94
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       + A +   +      + k ++ +   l   L+ ++  + Ge
  gi|2251650    24    PVSARVAKGAGSSAIGELKRLRGEIHFLSTSLgRVIRAVEGETTLAT 70

                   vqECYEls.AeYEGKkDtkKLeELGakL....tsLdPaDailvAkailHm
                   v     l++A   G   +       a+L+++  sL Pa+a   A a+
  gi|2251650    71 VEKLRTLAkARRTGAGNPASAANADARLsetvASLMPAEAFNQAMAFTLY 120

                   LnLAnLAEE...velAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvl
                     L nLAEE+ +v+l  RR   ++     a  +    Es ++  l  L
  gi|2251650   121 FELVNLAEEnfrVQLLRRRSAARLA----APGGPPVRES-LDAALAELKA 165

                   klnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsA
                   ++   P+E  e L    ++Lv+tAHPt s RR LL K  R+   L q
  gi|2251650   166 RG-VGPDELQELLDRVGIELVFTAHPTESKRRTLLTKLQRLAFILRQ--- 211

                   KDvt......veDKkELDEA.LHREiqAAFRtDEiRRaqPtPqDEmRaGm
                   +D t++  ++v       EA++ REi   + tD  R a+P   DE R G+
  gi|2251650   212 RDTTggvaggVAGAAVPAEAeIEREIASLWLTDRSRVARPGVNDEARTGL 261

                   sYiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDG
                    Y+   +++  P+    ++ AL+      R P     + F sW+GGDRDG
  gi|2251650   262 WYFSTALFDVLPRLQADMERALRLHYPGVRAP--SRWLTFGSWIGGDRDG 309

                   knPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE
                    nP vt  vt  + +L R +A          +L   l +    d +
  gi|2251650   310 -NPNVTASVTAGILVLHRRLAVEKLAAATRELSRALTISDRRDNV---TP 355

                   Elyrtaardkvv KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLL
                   El r  + ++ +   +E      P EPYR +      +L    E  R
  gi|2251650   356 ELRRLLRENRHISAHVEELADRYPHEPYRLLFASLCARLARASEENRDGS 405

                   AtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqv
                         + +e    + +   E      +sL       +A+G   D
  gi|2251650   406 TLLGGPVVDETCL-HADTLREVFAAIRRSLLAGRGALLAEGEFKDTAHAL 454
```

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                    stFGLsLvKLDiRqEseRq.tDvlDAittHLeiGsYReWsEeKRqEWLla
                      FGL    LDiRq s  ++  v + + +  +i  Y +  E+ R++ L
  gi|2251650   455 EVFGLHTASLDIRQHSSHHeAAVAELLRQLYQIDDYMKLGEQARRDALAR 504

                    EL.kGKRPL.lgsDLPktEEvkDvldafrvLAELPi.....DsFGaYiis
                     L++   PL+           + v+d + vLA L   + ++D+ G Yiis
  gi|2251650   505 ALdRATSPLdAEQRAALSAATRNVIDPL-VLAGLAAakfgpDALGIYIIS 553

                    mataPsDvLAvELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiD
                    m+   sDvL v LL R  g   ++++ PLFE L DL  AP  + +LFs
  gi|2251650   554 MTDDVSDVLEVALLMRLAG--AAMPIAPLFETLDDLTRAPDVLSQLFSHP 601

                    WY...inridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyG
                     +++     dG+q+vm+GYsDs KD G l A W LY+AqE i+   +++G
  gi|2251650   602 AFpglPVARDGRQHVMLGYSDSNKDCGYLTANWALYRAQETIVVACRRHG 651

                    vKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFG
                    v+++lFHGRGG + RGGGP   AiL+qP    +G +R+t qGEv+   +
  gi|2251650   652 VRVMLFHGRGGSIARGGGPAARAILAQPAGLADGGIRITEQGEVLSTRYH 701

                    EEnLCFrsLqRFtAAtL..EHGmnPPvsPkPEWRkLmeemAvvAtEEYRs
                    + +L  r L   t   + + H      +P   W + me m       Y++
  gi|2251650   702 DRDLAHRILEQMTYGVIlgAHAARHVQAPPAAWTEAMETMSAAGFAAYKA 751

                    vvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFa
                    +v  +P F  +++ AtP  E   + +GsRP+ R+    +  LRAiPW+F+
  gi|2251650   752 LVHDDPEFLQFWKQATPIDEISNLKLGSRPTYRRATQSVADLRAIPWVFS 801

                    WtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlE
                    W q RF  P W G+G A    +++     + L+ m  eWPFF   +D  E
  gi|2251650   802 WMQSRFNFPGWYGLGSALEAVLKRGAAGKKLLRTMHAEWPFFQTLIDNAE 851

                    mvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkD
                    +   K D GiA Ly  L+    ++ +    L  ++   +  +L i G +
  gi|2251650   852 LTMRKADMGIARLYASLVTDSRIRErILSALTGEFARAERAILAITGRRR 901

                    lLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEy
                    lL G+P L + + LR++Yi  Ln +q   L+R+R           lsK
  gi|2251650   902 LLAGEPVLLKSVELRNPYIDPLNYLQVDMLRRLR--------AGGLSK-- 941

                    AdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    AdE+     ++v+L                 + Gi  G++ntG
  gi|2251650   942 ADED--AVRGVVELT----------------INGISGGLKNTG    966

gi|19552797|ref|NP_600799.1|: domain 1 of 1, from 1 to 919: score 323.1, E = 5.8e-94
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                  +    + ++ D   l + L++++ +  G+++ E
  gi|1955279     1    -------------MT---DFLRDDIRFLGQILgEVIAEQEGQEVYEL 31

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      s +    k    ++ L  +  ++ Pa a  +A+a++H   LAn
  gi|1955279    32 VEQARLTSFDIA--KGNAEMDSLVQVFDGITPAKATPIARAFSHFALLAN 79

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAE+    y    + +      D ++   +s ++ t  kL   +n   e
  gi|1955279    80 LAEDL---YDEELREQA----LDAGDTPPDSTLDATWLKL-NEGNVGAEA 121

                    vFeALKnqsvDLvltAHPtqsvRRsLL..qK....naRiRnCLaqLsAKD
                    v + L+n  v  vltAHPt   RR + + qK  +++ R R  L
  gi|1955279   122 VADVLRNAEVAPVLTAHPTETRRRTVFdaQKwittHMRERHALQSAEPTA 171

                    vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWk
                     t     E++  + R i   + t  iR a+P   DE+  G+ Y+   + +
  gi|1955279   172 RTQSKLDEIEKNIRRRITILWQTALIRVARPRIEDEIEVGLRYYKLSLLE 221

                    GvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEv
                     +P+  R v   L+     E +P   P++k  sW+GGD DG nP vt E
  gi|1955279   222 EIPRINRDVAVELRE-RFGEGVPLK-PVVKPGSWIGGDHDG-NPYVTAET 268

                    tRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaard
                           a       Y  q+  L  Els+    + +      l      d
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  gi|1955279   269 VEYSTHRAAETVLKYYARQLHSLEHELSLSDRMNKVTPQLLALADAGHND 318

                   kvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                                  vP++  EPYR  +  vR ++  t        A  i e
  gi|1955279   319 ------------VPsrVDEPYRRAVHGVRGRILATT-------AELIGED 349

                   sEeAvytkv.......EeFLEPLELCYksLCeCGDkviADGsLLDlLRqv
                   + e v+ kv ++  ++EeFL       +sL e  D  iAD  L  l+  +
  gi|1955279   350 AVEGVWFKVftpyaspEEFLNDALTIDHSLRESKDVLIADDRLSVLISAI 399

                   stFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLla
                     FG  L  LD+Rq se   Dvl  + +  ++ ++YRe sE  + E Ll
  gi|1955279   400 ESFGFNLYALDLRQNSESYEDVLTELFERAQVTAnYRELSEAEKLEVLLK 449

                   ELkGKRPLlgsDLPktEEvkDv.ldafrvLAELPiDsFGa.....Yiism
                   EL+  RPL++       Ev D +l+ fr   E  +  FG++  ++ iism
  gi|1955279   450 ELRSPRPLIPHGSDEYSEVTDReLGIFRTASE-AVKKFGPrmvphCIISM 498

                   ataPsDvLAvELLqRECgv........kqtLrvvPLFEkLADLeAAPAav
                   a +  DvL   +L +E g+   ++++++ t+ v+PLFE + DL+A    +
  gi|1955279   499 ASSVTDVLEPMVLLKEFGLiaangdnpRGTVDVIPLFETIEDLQAGAGIL 548

                   ekLFsiDWYinri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEii
                   + L+ iD Y+n + ++d  qevm+GYsDs KD G +sA W LY A   ++
  gi|1955279   549 DELWKIDLYRNYLlqrDNVQEVMLGYSDSNKDGGYFSANWALYDAELQLV 598

                   KvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGE
                      +  GvKL lFHGRGGtvGRGGGP   AiL+qP   ++Gs+R+t qGE
  gi|1955279   599 ELCRSAGVKLRLFHGRGGTVGRGGGPSYDAILAQPRGAVQGSVRITEQGE 648

                   viEfsFGEEnLCFrsLqRFtAAtLEHGm..nPPvsPkPEWRkLmeemAvv
                   +i   +G  +   r L     AtLE  + +   +  +    ++m e+
  gi|1955279   649 IISAKYGNPETARRNLEALVSATLEASLldVSELTDHQRAYDIMSEISEL 698

                   AtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLR
                       Y s+v  +  F++YF   tP  E G +niGsRP+ Rk    +e LR
  gi|1955279   699 SLKKYASLVHEDQGFIDYFTQSTPLQEIGSLNIGSRPSSRKQTSSVEDLR 748

                   AiPWiFaWtqtRFHLPvWLGvGAAFKhAi...dKDiKnlqkLkEmYkeWP
                   AiPW+ +W q R  LP W GvG A    i+++++  + +  L+ + + WP
  gi|1955279   749 AIPWVLSWSQSRVMLPGWFGVGTALEQWIgegEQATQRIAELQTLNESWP 798

                   FFRvtlDLlEmvFAKGDPGiAaLyDkLL....vaEeLkPFGksLRdkYvE
                   FF   lD +  v  K +  +A Ly +L+++++vaE +      +R++Y
  gi|1955279   799 FFTSVLDNMAQVMSKAELRLAKLYADLIpdteVAERVY---SVIREEYFL 845

                   tkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPs
                   tk++   i G  DlL+  P L   +  R +Y+  Lnv+q   ++R R
  gi|1955279   846 TKKMFCVITGSDDLLDDNPLLARSVQRRYPYLLPLNVIQVEMMRRYR--- 892

                   ykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAA
                             K    E+       v  n            + Ltm G+
  gi|1955279   893 ----------KGDQSEQ-------VSRN------------IQLTMNGLST 913

                   GmqntG<-*
                    + n G
  gi|1955279   914 ALRNSG    919

gi|291303250|ref|YP_003514528.1|: domain 1 of 1, from 1 to 914: score 322.8, E = 6.9e-94
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +D  L         +d+  ++ D   l   L+D L    G++L +
  gi|2913032     1    -MDTTLE--------DDDAGLRADIRRLGSLLgDSLVRQEGQQLLDL 38

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v E   l    + K  +++L EL ++ t+++      +A+a+     LAn
  gi|2913032    39 VEEIRHLVRT-DAKAAAQRLAEL-SVDTGMN------LARAFALYFHLAN 80

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   + E v+ A   R ++ + G + +E  A tE      +K   l      +
  gi|2913032    81 ITEQVHRARELRRRRVRRGGWLEE--AATE------IKAEGLDA----DR 118
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                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv..e
                    +  A +   v  v+tAHPt ++RRs+L K   +   L    A     ++
  gi|2913032   119 IAKAARGLEVSPVFTAHPTEAARRSILTKLRQLADVLDSEAAEAALAgqA 168

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    D    D  L   i   + tDE+R  +P P DE R  + Y+ +   +  P+
  gi|2913032   169 DTAATDLRLAELIDLLWQTDEVRINRPEPTDEARNAVYYLTDLYADAAPR 218

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     LR     L  +G    l  d PL +F  W+GGDRDG nP vtPEvtR v
  gi|2913032   219 VLRDLAQVLTELGAEPSLS-DSPL-RFGTWIGGDRDG-NPNVTPEVTRRV 265

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      L          s vE ++ Els+    + LR    E       d
  gi|2913032   266 LTLQHEHGIRAAESMVESMISELSV---SQQLRPATPEFMASLEAD--LA 310

                    yYiEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                       E +++++ v   EPYR     vR KL  t  RaRH  A G + ++
  gi|2913032   311 ALPELpprFRRVNSAEPYRLKARCVRAKLAAT--RARH--ASGTAHVPGR 356

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y +  e    LE  Y sL        A+G L D +R v  FGL L  +
  gi|2913032   357 D-YADGTELYTDLETFYDSLTASTGGLAAEGRLADSMRVVAAFGLHLATM 405

                    DiRqEseRqtDvlDAittHLeiGs.....YReWsEeKRqEWLlaELkGKR
                    DiR  + ++   l  +   L    + +++Y + s   R   L aEL  +R
  gi|2913032   406 DIREHAAKHHAALAELFDRLRPDDdldkpYGDLSRAERFALLAAELDSRR 455

                    PLlgsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDv
                    PLl +      E +  ld fr +       FG++   +Yi+sm+  P D
  gi|2913032   456 PLLTPAAALSPETRKTLDVFRCIVS-AQRRFGPqvaatYIVSMTQGPDDL 504

                    LAvELLqRECgv......kqtLrvvPLFEkLADLeAAPAavekLFsiDWY
                    LA  +L RE g+ + + ++  +  vPL E + +LeA     + L  +  Y
  gi|2913032   505 LAAAVLAREAGLvdihagRADIGFVPLLEGVPELEAGRQIWNDLLNTPAY 554

                    inrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvK
                    +  +d ++G qevm+GYsDs K+ G  +  W +  Aq E+   A ++Gv+
  gi|2913032   555 RRIVDargGIQEVMLGYSDSNKESGIAASQWAIQSAQRELRDAAAEHGVR 604

                    LvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEE
                    L lFHGRGGtvGRGGGPtH AiL+qP  t++G ++vt qGEv+   +
  gi|2913032   605 LRLFHGRGGTVGRGGGPTHEAILAQPYGTLDGTIKVTEQGEVLSDKYTLP 654

                    nLCFrsLqRFtAAtLEHGm.....nPPvsPkPEWRkLmeemAvvAtEEYR
                     L    L    AA L   + ++++    s    W   m+++   A   YR
  gi|2913032   655 VLARENLELTVAAVLKATLlhdtpRHDASTLDVWYGTMDRLSGSARTAYR 704

                    svvvKEPRFvEYFRlAtPElEYGkmniGsRPaKR.kPsGGiesLRAiPWi
                    s++   P   EYF    P    G +niGsRPaKR+  s G++ LRAiPW+
  gi|2913032   705 SLI-DHPGLPEYFWAVSPTELLGALNIGSRPAKRpDASAGLDGLRAIPWV 753

                    FaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDL
                    F Wtq R  +P W GvG     A +  +  +  L  mY+ W FF   +
  gi|2913032   754 FGWTQSRQIVPGWFGVGTGLATAREAVSDEV--LSAMYERWQFFSTFISN 801

                    lEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHk
                    +Em   K D  iA  y + Lv   L+P  + +R++   t   +L++ G
  gi|2913032   802 VEMTLVKTDMDIAERYVDTLVPPRLRPLFDTIRAEHARTVTEVLRLTGKS 851

                    DlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKE
                    +lL   P L+  l +Rd Y+  L  +q   L R R              E
  gi|2913032   852 ELLADNPQLRRTLAVRDRYLAPLHHLQIALLHRHR--------------E 887

                    yAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     A ++                 P L   L+ t+ GiAAGm ntG
  gi|2913032   888 SATDD-----------------PSLTRALLTTVNGIAAGMRNTG    914

gi|183982260|ref|YP_001850551.1|: domain 1 of 1, from 11 to 935: score 322.3, E = 1e-93
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        i    R  +        + ++ D  Ll   L+D + +  G+++ E
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gi|1839822    11    PIGDVHRTRIGREAT---EPMRADIRLLGAILgDTVREQNGDEVFEL 54

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v E   + A +  ++      E+     ++d   ai + +a++H   LAn
gi|1839822    55 V-ERARVEA-FRVRHSEIDRAEMARMFEGIDIHHAIPIIRAFSHFALLAN 102

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+++   RR i+          ++   +s +  t+ kL        +
gi|1839822   103 VAEDIHRERRRSIHVAA-------GEPPQDSSLAATYMKLDAAQ-LDSAT 144

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt.veD
                    + eALK   v  v+tAHPt   RR +   + Ri   L  L A   t+ +D
gi|1839822   145 IAEALKGALVSPVITAHPTETRRRTIFETQHRITQ-LMRLHAEGHTeTDD 193

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                     + ++  L R +   + t  iR  +    DE+  G+ Y+   +++ +P+
gi|1839822   194 GRGIEVELRRQVLRLWQTALIRLFRLQISDEIEVGLRYYPAALFEVIPQV 243

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                       v  AL+       l    P+++  sW+GGDRDG nP vt Ev R
gi|1839822   244 NAEVRDALRARWPDADL-LSEPILRPGSWIGGDRDG-NPNVTAEVVRLAT 291

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                      a   A   Y+  +  L  Elsm      L     El   a
gi|1839822   292 GSAAFTALAHYLAELTALAQELSM---SARLITVTPELATLADAC----- 333

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv..
                             P EPYR  L  vR +L  t   a  +L +      E   ++
gi|1839822   334 ----PAGARPDEPYRRALQVVRGRLSAT---AAEILDQQPQHTLELGLpp 376

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y    e    L+    sL + G   +AD  L  l   v  FG  L  LD+
gi|1839822   377 YATAAELRADLDTIDASLHNHGAGLLADDRLARLREAVRVFGFHLSGLDM 426

                    RqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgsD
                    Rq s+ +  v+  +    ++ + Y + +E  R E L aEL+ +RPL+
gi|1839822   427 RQNSDVHEQVVGELLAWAGVHpDYTSLAEAERVELLAAELSTRRPLIRDG 476

                    LPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvELL
                        +  +  l+ +   A   + +FG+   ++Yiism+ + sD+L   +L
gi|1839822   477 AQLSDLARSELGVLAAAAH-AVWTFGPaavpnYIISMCRSVSDMLEAAVL 525

                    qRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                     +E g+   +++++  ++ + PLFE + DL+   A ++ +  +  Y+  +
gi|1839822   526 LKEVGLLDasesepycPVGISPLFETIEDLHNGAAILQAMLDLPLYRALV 575

                    d...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                      ++G qevm+GYsDs KD G l+A W +Y+A   ++  A+k G++L lF
gi|1839822   576 TargGCQEVMLGYSDSNKDGGYLAANWAVYRAELALVETARKTGIRLRLF 625

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGGtvGRGGGP   AiL+qPP  + GslR t qGEvi   + E ++
gi|1839822   626 HGRGGTVGRGGGPSYQAILAQPPGAVSGSLRLTEQGEVIAAKYAEPQMAR 675

                    rsLqRFtAAtLE......HGmnPPvsPkPEWRkLmeemAvvAtEEYRsvv
                    r L    AAtLE++  +  G+    +P      +++e+A  A   Y  +v
gi|1839822   676 RNLESLLAATLEstlldvEGLGDTAAPA---YAVLDEVAALAQRAYAELV 722

                    vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWt
                       P FvEYF+  tP  E G +niGsRP+ RkP   i  LRAiPW+ aW
gi|1839822   723 HETPGFVEYFKASTPVSEIGALNIGSRPTSRKPTASIADLRAIPWVLAWS 772

                    qtRFHLPvWLGvGAAFKhAi....dKDiKnlqkLkEmYkeWPFFRvtlDL
                    q R  LP W G G AF   +  +++ +   lq L+++Y+ WPFFR  l
gi|1839822   773 QSRVMLPGWYGTGSAFEQWLaagpESEADRLQVLHDLYQRWPFFRSVLSN 822

                    lEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtkdlLLkiAGH
                    +  v AK D  +Aa y +L+  E L++   +++ d+   t  +  +i G
gi|1839822   823 MAQVMAKSDLELAARYSELVADETLrRRVFDKIADEHHRTIAMYKRITGQ 872

                    kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
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                   DlL   P L   +  R +Y+  Ln +q   L+R R
  gi|1839822   873 DDLLADNPALARSVFNRFPYLEPLNHLQVELLRRYR-------------- 908

                   EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       E+    de v+              ++Ltm G+A  + n G
  gi|1839822   909 --SGED----DESVQRG------------ILLTMNGLASALRNSG    935

gi|20196772|emb|CAC86358.1|: domain 1 of 1, from 1 to 398: score 322.1, E = 1.2e-93
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2019677     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2019677     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2019677     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                          svDLv+tAHPtqs+RRsLLq naRiRnCL+ LsAKD t+eDKk
  gi|2019677     1 -------SVDLVFTAHPTQSARRSLLQNNARIRNCLTLLSAKDTTPEDKK 43

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL REiq AFRtDEiRRaqPtPqDEmR+GmsYiHEtvWkGvPKFLR
  gi|2019677    44 ELDEALQREIQSAFRTDEIRRAQPTPQDEMRYGMSYIHETVWKGVPKFLR 93

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALKniGinERlPYdvPLikF+sWmGGDRDG nPRvtPEvtRDvCLL
  gi|2019677    94 RVDTALKNIGINERLPYDVPLIKFCSWMGGDRDG-NPRVTPEVTRDVCLL 142

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   +RmmAanlYi+qvEDLmFElsmWR n+ELRvRAEEl +t+a++kv+KyYi
  gi|2019677   143 SRMMAANLYIDQVEDLMFELSMWRSNEELRVRAEELLSTPASKKVTKYYI 192

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWKq+PP+EPYRviLG+vRDKLYntRERaRHLLAtG+s+isE+A++t++
  gi|2019677   193 EFWKQIPPNEPYRVILGAVRDKLYNTRERARHLLATGFSDISEDAIFTNI 242

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   Ee LEPLELCYksL + GDk iADGsLLDlLRqv+ FGLsLvKLDiRqEs
  gi|2019677   243 EEILEPLELCYKSLVDVGDKTIADGSLLDLLRQVFIFGLSLVKLDIRQES 292

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   eR+tDvlDAittHL+iGsYR+W+E+KR EWL++EL+GKRPLl++DLP+tE
  gi|2019677   293 ERHTDVLDAITTHLGIGSYRSWPEDKRVEWLVSELSGKRPLLPPDLPMTE 342

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dv++a++v+AELP+DsFG+Yiism+taPsDv AvELLqRECg+k+tL
  gi|2019677   343 EIADVIGAMKVIAELPSDSFGPYIISMCTAPSDVFAVELLQRECGIKKTL 392

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLF
  gi|2019677   393 PVVPLF---------------------------------------------- 398

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|2019677     - ---------------------------------------------- -

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

  gi|2019677     - ---------------------------------------------- -

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|2019677     - ---------------------------------------------- -

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|2019677     - ---------------------------------------------- -
```

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                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|2019677     - ------------------------------------------------ -

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|2019677     - ------------------------------------------------ -

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|2019677     - ------------------------------------------------ -

                  tmKGiAAGmqntG<-*

  gi|2019677     - -------------    -

gi|225874618|ref|YP_002756077.1|: domain 1 of 1, from 26 to 947: score 322.0, E = 1.2e-93
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       +A LR  v        ++++  A   D F   + DL  + ++
  gi|2258746    26    --EAPLRRDVRSLGMLLGEVLREQAG--DAFFQRVEDLRLNAIRRR- 67

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                      E  Ae   ++    ++   a + sL   +a  + +a+     L nL
  gi|2258746    68 ----ETQAEGQQQQADALMQSTVAGVHSLPVDEAYYLTRAFAFYFDLINL 113

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AE  +   RRR  +++        s      +  tl+ +   +  + eE
  gi|2258746   114 AETNHRKRRRRSLQLH-------NSEAQRGSLRGTLRAMREAG-ITAEEA 155

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     L    v  v+tAHPt  +RRs+L K  Ri   La L    +  e+ +
  gi|2258746   156 LAYLSRIFVVPVFTAHPTEVARRSVLFKRRRIGEFLAHLDSIPLPDEEMQ 205

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                  +L+ A+  Ei A +  DE+R  +P   DE+++G+ Y+   +++  P+
  gi|2258746   206 DLENAVTAEITALWQSDEVRSRRPEVADEIKMGLDYYEVSIFETLPRLYE 255

                  RvDtALK.niGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   v  AL +  G+         ++ F sW+GGDRDG nP vtP vtR+
  gi|2258746   256 EVSAALAsEYGLTLDAASLPLMLGFGSWIGGDRDG-NPFVTPQVTREAIH 304

                  LaRmmAanlYisqvEDLmFElsm....WRCndELRvRAEElyrtaardkv
                   aR     +Y+  v  L+  l  + ++    dELR R +      +
  gi|2258746   305 EARTRLLDFYLTRVQQLIDLLTTsaqqLPVSDELRTRLDNYLAEIRVGED 354

                  vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                  v +   F       E YR  L  vR +L  t   a        + ++
  gi|2258746   355 VLFGPRF-----QFELYRRYLACVRARLLRTAGHAAPNADSLEASLAALP 399

                  vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                   y    + +E L +  +sL       iA+  +  +L  v tFGL L  LD
  gi|2258746   400 PYCSAHDLMEDLSVLRRSLAAHRGERIAETLVDPFLLLVRTFGLHLHTLD 449

                  iRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
                  +Rq +  +   l+      e  ++   s e   E            ++
  gi|2258746   450 VRQHARIHRKALE------ECSAWQAGSNENAVE------------IPQH 481

                  L.PktEEvkDvldafrvLAELPiDs....FGaYiismataPsDvLAvELL
                  L+P t    Dvld++r + E+   ++++    Y+is a + sDv Av  L
  gi|2258746   482 LsPST---LDVLDTMRAIQEVKASCspeaIRQYVISGAASASDVTAVLWL 528

                  qRECgvkqt.......LrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                   R  g+  ++++++++L  vPLFE + DL+ AP     L+    Y+  +
  gi|2258746   529 ARLAGINPAgrdgdpgLMPVPLFESIEDLRNAPEVCRELWTNPAYRELLA 578

                  G...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                    ++ qe+m+GYsDs KD G l   W +++A   + +vA + G+ L lFH
  gi|2258746   579 SwgnTQEIMLGYSDSNKDGGMLTSTWEIFRAHRALHQVAHECGITLRLFH 628

                  GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
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                    GRGGtvGRGGGPtH  i +qP D  +G +R+t qGEv+ f + +  L  r
  gi|2258746   629 GRGGTVGRGGGPTHRSIYAQPVDAFDGQIRITEQGEVLNFKYSDVVLAER 678

                    sLqRFtAAtLEHGmnPPv.........sPkPEWRkLmeemAvvAtEEYRs
                     L    AA L+    P  +++++++++   P W    +e+   A + YR
  gi|2258746   679 NLELMIAASLDALARPNArqpdghqtgVLEPAWESAFDELSSLAYDFYRE 728

                    vvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFa
                     ++ +P    YF  AtP  E  +  iGsRP++R      +sLRAiPW+F
  gi|2258746   729 QILHDPEVLQYFEQATPVSELEHAKIGSRPSRRGGKMSFDSLRAIPWVFG 778

                    WtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlE
                    Wtq R  +P W GvG AF   ++K       L+Em  e+P F   +  +E
  gi|2258746   779 WTQSRLLIPAWFGVGHAFTAFLQKPGGA-ELLREMLTEFPLFIDLVRNVE 827

                    mvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkD
                    m  AK D GiA+Ly  L+    L+ +   +L+++++ t++ LL iA   D
  gi|2258746   828 MALAKADLGIASLYSSLVPDAGLRErVFTKLKAEFERTREALLTIAQQDD 877

                    lLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEy
                    lL   P L   +RLR++Y+  +  +q   L+R R            s
  gi|2258746   878 LLQNNPVLARSIRLRNPYVDPMSLIQVDLLRRKR--------ALVASSNG 919

                    AdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    A+ +        +L    r   G       t+ Gi AG+ ntG
  gi|2258746   920 AASP--------ELDAIHRAIAG-------TINGISAGLRNTG    947

gi|145295706|ref|YP_001138527.1|: domain 1 of 1, from 1 to 920: score 322.0, E = 1.2e-93
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                   +    + ++ D   l + L++++ +  G+++ E
  gi|1452957     1    -------------MT---DFLRDDIRFLGRILgEVIAEQEGQEVYEL 31

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      s +    k    ++ L  +  ++ Pa a  +A+a++H   LAn
  gi|1452957    32 VEQARLTSFDIA--KGNAEMDSLVQVFDGITPAKATPIARAFSHFALLAN 79

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAE+ +       + ++     D ++   +s ++ t  kL   +n   e
  gi|1452957    80 LAEDLH------DEELR-EQALDAGDTPPDSTLDATWLKL-NEGNVGAEA 121

                    vFeALKnqsvDLvltAHPtqsvRRsLL..qK....naRiRnCLaqLsAKD
                    v + L+n  v  vltAHPt   RR + + qK  +++ R R  L
  gi|1452957   122 VADVLRNAEVAPVLTAHPTETRRRTVFdaQKwittHMRERHALQSAEPTA 171

                    vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWk
                     t     E++  + R i   + t  iR a+P   DE+  G+ Y+   + +
  gi|1452957   172 RTQSKLDEIEKNIRRRITILWQTALIRVARPRIEDEIEVGLRYYKLSLLE 221

                    GvPKFLRRvDtALKniGinERlPYdvPL...ikFssWmGGDRDGknPRvt
                     +P+  R v   L+     ER   dvPL++ +k  sW+GGD DG nP vt
  gi|1452957   222 EIPRINRDVAVELR-----ERFGEDVPLkpvVKPGSWIGGDHDG-NPYVT 265

                    PEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrta
                     E        a       Y  q+  L  Els+    + +      l
  gi|1452957   266 AETVEYSTHRAAETVLKYYARQLHSLEHELSLSDRMNKVTPQLLALADAG 315

                    ardkvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGi
                      d           vP++  EPYR  +  vR ++  t        A  i
  gi|1452957   316 HND------------VPsrVDEPYRRAVHGVRGRILATT-------AELI 346

                    seisEeAvytkv.......EeFLEPLELCYksLCeCGDkviADGsLLDlL
                     e + e v+ kv ++  ++EeFL       +sL e  D  iAD  L  l+
  gi|1452957   347 GEDAVEGVWFKVftpyaspEEFLNDALTIDHSLRESNDTLIADDRLSVLI 396

                    RqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEW
                      +  FG  L  LD+Rq se   Dvl  + +  ++ ++YRe sEe + E
  gi|1452957   397 SAIESFGFNLYSLDLRQNSESYEDVLTELFERAQVTAnYRELSEEEKLEV 446

                    LlaELkGKRPLlgsDLPktEEvkDv.ldafrvLAELPiDsFGa.....Yi
                    Ll EL+  RPL++       Ev D +l+ fr   E  +  FG++  ++ i
  gi|1452957   447 LLKELRSPRPLIPHGSDEYSEVTDReLGIFRTASE-AVKKFGPrmvphCI 495
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                    ismataPsDvLA.vELLqRECgv........kqtLrvvPLFEkLADLeAA
                    isma +  DvL ++ LL +E g+   ++++++ t+ v+PLFE + DL+A
  gi|1452957   496 ISMASSVTDVLEpMVLLLKEFGLiaangdnpRGTVDVIPLFETIEDLRAG 545

                    PAavekLFsiDWYinri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAq
                       +  L+ iD Y+n + ++d  qevm+GYsDs KD G +sA W LY A
  gi|1452957   546 AGILGELWKIDLYRNYLlqrDNVQEVMLGYSDSNKDGGYFSANWALYDAE 595

                    EEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvt
                      ++   +  GvKL lFHGRGGtvGRGGGP   AiL+qP   ++Gs+R+t
  gi|1452957   596 LQLVELCRSAGVKLRLFHGRGGTVGRGGGPSYDAILAQPKGAVQGSVRIT 645

                    vqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm..nPPvsPkPEWRkLmee
                     qGE+i   +G  +   r L     AtLE  + +   +  +    ++m e
  gi|1452957   646 EQGEIISAKYGNPETARRNLEALVSATLEASLldVSELTDHQRAYDIMSE 695

                    mAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi
                    +       Y s+v  +  F++YF   tP  E G +niGsRP+ Rk    +
  gi|1452957   696 ISELSLKKYTSLVHEDQGFIDYFTQSTPLQEIGSLNIGSRPSSRKQTSSV 745

                    esLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAi...dKDiKnlqkLkEmY
                    e LRAiPW+ +W q R  LP W GvG A    i+++++  + +  L+ +
  gi|1452957   746 EDLRAIPWVLSWSQSRVMLPGWFGVGTALEQWIgegEQATQRIAELQTLN 795

                    keWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL....vaEeLkPFGksLRd
                    + WPFF   lD +  v  K +  +A Ly +L+++++vaE +      + +
  gi|1452957   796 ESWPFFTSVLDNMAQVMSKAELRLAKLYADLIpdreVAERVY---SVIHE 842

                    kYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRi
                    +Y  tk++   i G  DlL+  P L   +  R +Y+  Lnv+q   ++R
  gi|1452957   843 EYFLTKKMFCVITGSDDLLDDNPLLARSVQRRYPYLLPLNVIQVEMMRRY 892

                    RDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmK
                    R             K    E+       v  n            + Ltm
  gi|1452957   893 R-------------KGDQSEQ-------VSRN------------IQLTMN 910

                    GiAAGmqntG<-*
                    G+   + n G
  gi|1452957   911 GLSTALRNSG    920

gi|170691942|ref|ZP_02883106.1|: domain 1 of 1, from 136 to 1081: score 321.7, E = 1.5e-93
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        + A  +     +  +d  L + D   l + L+D+L +  G+ + ++
  gi|1706919   136    IVIAAPKTNGRTRDDKDHPLFQ-DIRYLGRLLgDVLREQEGDAVFDV 181

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      +  +    D    + L  kL sL P  ++ v +a++    LAn
  gi|1706919   182 VETIRQTAVRFRREDDNAAAQTLDKKLRSLSPEQTVSVVRAFSYFSHLAN 231

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+ +   R Ri+ +        +sA     i   l +Lv  +  +
  gi|1706919   232 IAEDRHRNRRHRIHALA-------GSAPQPGSIAYALERLVEAG-AAATP 273

                    vFeALKnqsvDL.vltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    v +   n +  ++vltAHPt   R+s+L  +  +   La    + +t  +
  gi|1706919   274 VLQQFFNNALIVpVLTAHPTEVQRKSILDAEHDVARLLAE-RDQQLTDRE 322

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    +   +  L   +   + t  +R ++ t  DE+   +sY+  t  + +P
  gi|1706919   323 RAHNETMLRARVTSLWQTRMLRDSRLTVADEIENALSYYRATFLEEIPAL 372

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                       v+ ALK  G+  RlP   P  +  sW+GGDRDG nP vt E
  gi|1706919   373 YADVEEALKEHGLEARLP---PFFQMGSWIGGDRDG-NPNVTAETLEHAI 418

                    LLaRmmAanlYisqvEDLmFEls....mWRCndELRvRAEEl.yrtaard
                         +    Y++qv  L  Els ++ +    dEL++ AE  + r + r
  gi|1706919   419 SRQAEVIFEHYLEQVHKLGAELSvsnlLAGASDELKALAESSpDRSPHRT 468

                    kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYn.tRER....aRHLLAtGi
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                                EPYR  L  +  +L  + R R ++++  L   G
  gi|1706919   469 ---------------DEPYRRALIGMYTRLAAsARVRlgegSVPLRSAGR 503

                   seisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstF
                      +  A +y +  eF   L +   sL e     +A   L  l R    F
  gi|1706919   504 GAAPIRATpYDDAAEFARDLHVLIDSLAEHHGAPLAAPRLAPLARAAEVF 553

                   GLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaELk
                   G  L  +D+Rq s+ +  v+  + +  +++  Y    E  + + Ll+EL
  gi|1706919   554 GFHLASIDLRQSSDIHEAVIAELFKRAGVhDDYAALEESEKLDVLLTELA 603

                   GKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataP
                     RPL  +     + vk  l+ ++  A +  + FGa+  ++Yiis + +
  gi|1706919   604 QPRPLRLPYADYSDLVKSELGVLE-QARVTREKFGAravrnYIISHTETV 652

                   sDvLAvELLqRECgv............kqtLrvvPLFEkLADLeAAPAav
                   sD + v LLq+E g+ +++ ++ +++ k +L v+PLFE + DL+ AP  +
  gi|1706919   653 SDLVEVMLLQKETGLlqgrlgdandpaKAALMVIPLFETIPDLRNAPHIM 702

                   ekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEii
                     L + +++D  i +    qevm+GYsDs KD G l   W LY+A   ++
  gi|1706919   703 RDLLAlpgVDSIIEHQGNEQEVMLGYSDSNKDGGFLTSNWELYRAELALV 752

                   KvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGE
                       +  + L lFHGRGGtvGRGGGPt  AiLsqPP t++G +R t qGE
  gi|1706919   753 SLFNERAITLRLFHGRGGTVGRGGGPTYQAILSQPPGTVDGQIRLTEQGE 802

                   viEfsFGEEnLCFrsLqRFtAAtLE.....HGmnPPvsPkPEWRkLmeem
                   vi   FG  ++  r L    AAtLE +  +HG  P  +  P + + m+++
  gi|1706919   803 VIASKFGNPDIGRRNLETVVAATLEasllpHGNAP--AELPAFEQTMQQL 850

                   AvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG...
                      A   YR++v+  P F EYF   tP  E   +niGsRPa Rk   +++
  gi|1706919   851 SDAAMASYRALVYETPGFKEYFFESTPISEIAELNIGSRPASRKLQDpkq 900

                   .GiesLRAiPWiFaWtqtRFHLPvWLGvG...AAFKhAidKDi...Knlq
                   + ie LRAiPW F+W q R  L  W G+G+  AAF      D ++++ l
  gi|1706919   901 rKIEDLRAIPWGFSWGQCRLLLTGWYGFGsavAAFLDGAPSDAergRRLA 950

                   kLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGks
                    Lk m k WPFF   l  ++mv AK D  +A+ y  L+    L+k   ++
  gi|1706919   951 LLKKMHKSWPFFSTLLSNMDMVLAKTDLAVASRYAALVSDKKLrKHVFER 1000

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   + ++++ t + L +i G  + L   P L   ++ R +Y+  Ln +q   L
  gi|1706919  1001 IVAEWERTSKVLSEITGKSERLAENPLLARSIKNRFPYLDPLNHLQVELL 1050

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KR R                 d n              rv  G+     L
  gi|1706919  1051 KRHRS---------------GDTN-------------ARVRRGIH----L 1068

                   tmKGiAAGmqntG<-*
                   t+ GiAAG+ ntG
  gi|1706919  1069 TINGIAAGLRNTG    1081

gi|290959806|ref|YP_003490988.1|: domain 1 of 1, from 3 to 910: score 321.4, E = 1.9e-93
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      s D q        vs   +L      L D   + L    G+dL E v
  gi|2909598     3    SADDQTTT-----VS--SELRADIRRLGDLLGETLVRQEGPDLLELV 42

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        l  e +G   +  L       t L+ a  ++  +a++    LAn+
  gi|2909598    43 ERVRSLTRE-DGEAAADLLRG-----TELETAAKLV--RAFSTYFHLANV 84

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    E v   +R R  + +         A     +  t  +L       Pe v
  gi|2909598    85 TEQV---HRGRELRAR--------RAAEGGLLARTADRLKDAD---PEHV 120

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    e + n  v  v+tAHPt ++RRs+L K  Ri    a L    v   D++
  gi|2909598   121 RETVGNLNVRPVFTAHPTEAARRSVLNKLRRI----AALLETPVIDSDRR 166
```

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                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                      D  L   i   + tDE+R  +P P DE R  + Y+ E     v   L
  gi|2909598   167 RHDTRLAENIDLVWQTDELRVVRPEPADEARNAIYYLDELHAGAVGDVLE 216

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         L  +G+   +P     + F  W+GGDRDG nP vtP vt Dv +L
  gi|2909598   217 DLTAELERVGVT--IPDATRPLTFGTWIGGDRDG-NPNVTPQVTWDVLIL 263

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkvvKyY
                          n  ++ +++L   ls    n+     A+E+l    + d
  gi|2909598   264 QHEHGINDALELIDELRGFLS----NSIRYTGAtEDLLTSLRAD--LEAL 307

                    iEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                     E ++++K +  +EPYR     +R KL nt+ R    LA+Gi    +
  gi|2909598   308 PEIsprYKRLNAEEPYRLKATCIRQKLENTKQR----LAKGIPH-EDGRD 352

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y    e L  L L   sL e      ADG +   +R    FGL L  +D+
  gi|2909598   353 YLGTGELLKDLTLIQTSLREHRGGLFADGRMNRTIRTLAAFGLQLATMDV 402

                    RqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLlgs
                    R  ++ +   l  +   L+  s+R ++ + e R   L  EL+ +RPL +
  gi|2909598   403 REHADAHHHALGQLFDRLGEESWRyeDMPREYRHKLLARELRSRRPLGPT 452

                    DLPktEEvkDvldaf....rvLAELPiDsFGaYiismataPsDvLAvELL
                      P     +  l+ f++ ++ LA    +   +Yiism+    Dv A  +L
  gi|2909598   453 PAPLDAAGAKTLGVFetvkKALAVFGPEVIESYIISMCQGADDVFAATVL 502

                    qRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                     RE g+   + +   + +vPL E   +L+ A   +e + +   Y+  +
  gi|2909598   503 AREAGLVDlhagwaRIGIVPLLETTDELKSADTILEEMLADPSYRRLVAL 552

                    K...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                    +++ qevm+GYsDs K  G     W + +Aq  +  vA +yGv+L lFHG
  gi|2909598   553 RgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRYGVRLRLFHG 602

                    RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                    RGGtvGRGGGP H AiL+qP  t++G ++vt qGEvi   +    L
  gi|2909598   603 RGGTVGRGGGPSHDAILAQPWGTLEGEIKVTEQGEVISDKYLVPSLAREN 652

                    LqRFtAAtLEHGm.....nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKE
                    L    AAtL     ++++   v     W   m+ +   A   YR +v  +
  gi|2909598   653 LELTVAATLQASAlhtspRQSVEALARWDAAMDLVSDAAHAAYRRLV-ED 701

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWtq
                    P    YF   tP      + +GsRP+ R+P+ G++ + LRAiPW+F Wtq
  gi|2909598   702 PDLPTYFLASTPVDQLADLHLGSRPS-RRPGSGVslDGLRAIPWVFGWTQ 750

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     R  +P W GvG   K   +     +  L Em ++W FFR  l  +Em
  gi|2909598   751 SRQIVPGWFGVGSGLKALREAGLDTV--LDEMHEQWHFFRNFLSNVEMTL 798

                    AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                    AK D  iA  y + Lv +eLk   + +R + + t   +L++ G   lL+
  gi|2909598   799 AKTDLRIAQHYVDTLVPDELKHVFDTIRTEHELTVREVLRVTGEEKLLDA 848

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                     P L+q   +Rd+Y+  +  +q   LKR RD               A+
  gi|2909598   849 NPVLQQTFSIRDAYLDPISYLQVALLKRQRD---------------AAAA 883

                    skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                +e+  P L   L+Lt+ G+AAG+ ntG
  gi|2909598   884 ------------GEEADPLLARALLLTVNGVAAGLRNTG    910

gi|217977979|ref|YP_002362126.1|: domain 1 of 1, from 1 to 923: score 321.0, E = 2.4e-93
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        +   L  +     s  e+ +  D  Ll + L+D + +  Ged
  gi|2179779     1    -MTKVLDPISANSASTIERPLIDDIRLLGQILgDTIREQEGEDTFGL 46

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
```

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                v     ls e+E   D+     L   L sL P  a+ v +a++    LAn
gi|2179779    47 VEQARRLSVEFERHADPDAELKLNELLRSLTPQQAMAVIRAFSYFAHLAN 96

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                +AE+ +   RRR  +    +  DE +  t   ++ t+  L      +Pe
gi|2179779    97 IAED-RHNIRRRAAQAA--ERPDEHDGGT---LDKTFELLAAAS-ITPEA 139

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                v eA+    v  vltAHPt   RRsLL  +  i   L  L    +  e
gi|2179779   140 VAEAIAQARVSPVLTAHPTEVQRRSLLDAERAIAQLL--LARETLSGERP 187

                kELDEALHRE.iqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                +   E + R +i   + t  +R a+    DE+   ++++  t  k +P+
gi|2179779   188 RKQNEMMLRArIAQLWQTRLLRYARLSVRDEIENSLAFYQMTFLKQIPQL 237

                LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                  R++  L  + +       +   +  sW+GGDRDG nP v    t +
gi|2179779   238 YARIEERLGSLPV-------ASFFRMGSWIGGDRDG-NPNVNAG-TLELA 278

                LLaRm.mAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                L    + A   Y+  + +L  Els+      L   AE l+  a +
gi|2179779   279 LRRQCdTALRHYLREIHELGAELSI---SGRLFGCAEALQELAEKS---- 321

                yYiEFWKqvPPtEPYRviLGdvRDKLYntR......ERaRHLLAtGisei
                            EPYR  L  v  +L  t +  +++E  RH +A G
gi|2179779   322 ---GDENPFRDDEPYRRALIGVYSRLSSTLtlltggEALRHAVAPG---- 364

                sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                     y +  e    L +   sL      ++  G L  l R v  FG  L
gi|2179779   365 ---EPYANAGELQADLGVIEDSLRANHGAALVPGRLGPLRRAVDVFGFHL 411

                vKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRP
                  +D+Rq s+R+ + l  +     i + Y    E+ Rq  L+  L+  RP
gi|2179779   412 ASVDLRQSSDRHEETLKELMSVARIVpDYSALDEDARQNLLIDLLRDPRP 461

                LlgsDL...PktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLA
                L  + ++ +P+tEE  ++ +a r+        +   Yiis + + sD L
gi|2179779   462 LRVPGVtysPRTEEELEIFEAARdARRTFGEPAVVHYIISHTETVSDLLE 511

                vELLqRECgvkq..........tLrvvPLFEkLADLeAAPAavekLFsiD
                v  Lq+ECg+ ++  ++++++  L vvPLFE + DL+ A   +   +++
gi|2179779   512 VLALQKECGMVHgvlgepgtsaELMVVPLFETIEDLRNAATIMRGFYALP 561

                WYin..ridG.KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKky.
                     +r  G  qe+m+GYsDs KD G +   W LY+    ++   K+++
gi|2179779   562 GVAEltRASGaEQEIMLGYSDSNKDGGFFTSNWELYRSSTALAALFKEHd 611

                GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF
                G+ L lFHGRGGtvGRGGGP   AiL+qPP t+ G +R t qGEvi   +
gi|2179779   612 GIALRLFHGRGGTVGRGGGPSYQAILAQPPGTVAGQIRLTEQGEVISSKY 661

                GEEnLCFrsLqRFtAAtLEHGmnPPvsPkP.EWRkLmeemAvvAtEEYRs
                   ++    L    AAt+E  + P     P+E+ +  ee+       +R+
gi|2179779   662 ANPEIGLLNLEALVAATIEATLLPSAGAAPkEFLDAAEELSQASMKAFRA 711

                vvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFa
                v++  PRFv+YF  AtP  E   +niGsRPa Rk    ie LRAiPW F+
gi|2179779   712 VIYDNPRFVDYFFTATPIAEIAELNIGSRPASRKSTRRIEDLRAIPWSFS 761

                WtqtRFHLPvWLGvGAAFKhAidKD.iKnlqkLkEmYkeWPFFRvtlDLl
                W q R  LP W G+G A    + K +   +  L+ m  eWPFFR  l  +
gi|2179779   762 WGQARINLPGWFGFGSAVEQFVAKApAERMALLRRMGAEWPFFRALLSNM 811

                EmvFAKGDPGiAaLyDkLLvaEeLk..PFGksLRdkYvEtkdlLLkiAGH
                +mv AK D G+A+ y +L+   eL ++ FG s+ +++  t + L +i G
gi|2179779   812 DMVLAKADMGLAGRYAELVPDQELAksVFG-SIEAEWARTTKALNEITGV 860

                kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                   L   P L   ++ R +Yi  Ln +q   L+R R            s
gi|2179779   861 STRLSDNPALAGAIKHRFPYISPLNHLQVELLRRWR-----------SG 898
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                    EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    E+ d           L             +++t+ G+AAG+ ntG
  gi|2179779   899 EHDDKT---------LR-----------SILITINGVAAGLRNTG    923

gi|29830109|ref|NP_824743.1|: domain 1 of 1, from 3 to 910: score 320.0, E = 4.8e-93
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s D q         s   +L      L D   + L    G++L + v
  gi|2983010     3    SADDQTTT-----TS--SELRADIRRLGDLLGETLVRQEGPELLDLV 42

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         l  e     D +   EL   L + +   a  + +a++    LAn+
  gi|2983010    43 EKVRRLTRE-----DGEAAAEL---LRGTELETAAKLVRAFSTYFHLANV 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     E v   +R R  + k         A     +  t  +L       Pe
  gi|2983010    85 TEQV---HRGRELRTK--------RAAEGGLLARTADRLKDAD---PEHL 120

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       +Kn  v  v+tAHPt ++RRs+L K  Ri    a L    v   D++
  gi|2983010   121 RATVKNLNVRPVFTAHPTEAARRSVLNKLRRI----AALLETPVIEADRR 166

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                      D  L   i   + tDE+R  +P P DE R  + Y+ E     v   L
  gi|2983010   167 RYDTRLAENIDLVWQTDELRVVRPEPADEARNAIYYLDELHAGAVGDVLE 216

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         L  +G+   lP d   + F  W+GGDRDG nP vtPEvt Dv +L
  gi|2983010   217 DLTAELERVGV--QLPDDTRPLTFGTWIGGDRDG-NPNVTPEVTWDVLIL 263

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkvvKyY
                          n  ++ +++L   ls    n+     A+EEl      d
  gi|2983010   264 QHEHGINDALELIDELRGFLS----NSIRYTGAtEELLTSLGTD--LERL 307

                    iEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                     E ++++K +  +EPYR     +R KL nt+ R    LA+G +  +
  gi|2983010   308 PEIsprYKRLNAEEPYRLKATCIRQKLENTKQR----LAKGTAHQPGRD- 352

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y    e L  L L   sL e      ADG +   +R    FGL L  +D+
  gi|2983010   353 YLGTGELLHDLKLIQTSLREHRGGLFADGRMDRTIRTLAAFGLQLATMDV 402

                    RqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLlgs
                    R  ++ +   l  +   L+  s+R  + + + R   L  EL+ +RPL +s
  gi|2983010   403 REHADAHHYALGQLFDRLGEESWRyaDMPRDYRGKLLAKELRSRRPLAPS 452

                    DLPktEEvkDvldaf....rvLAELPiDsFGaYiismataPsDvLAvELL
                      P     +  l+ f++ +r LA    +   +Yiism+    Dv A  +L
  gi|2983010   453 PAPLDAAGAKTLGVFhtvkRALAVFGPEVIESYIISMCQGADDVFAAAVL 502

                    qRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                     RE g+   + +   + +vPL E   +L+AA   +e + s   Y+  +
  gi|2983010   503 AREAGLLDlhagwaKIGIVPLLETTDELKAADTILEDMLSDPSYRRLVAL 552

                    K...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                    +++ qevm+GYsDs K  G     W + +Aq  +  vA +yGv+L lFHG
  gi|2983010   553 RgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRYGVRLRLFHG 602

                    RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                    RGGtvGRGGGP H AiL+qP  t++G ++vt qGEvi   +    L
  gi|2983010   603 RGGTVGRGGGPSHDAILAQPWGTLEGEIKVTEQGEVISDKYLVPSLAREN 652

                    LqRFtAAtLEHGm...nPPvsPk..PEWRkLmeemAvvAtEEYRsvvvKE
                    L    AAtL     ++ P  s      W   m+ +   A   YR +v  +
  gi|2983010   653 LELTVAATLQASAlhtAPRQSDEalARWDAAMDVVSDAAHSAYRRLV-ED 701

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWtq
                    P    YF   tP      + +GsRP+ R+P+ G++ + LRAiPW+F Wtq
  gi|2983010   702 PDLPTYFLASTPVDQLADLHLGSRPS-RRPGSGVslDGLRAIPWVFGWTQ 750

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     R  +P W GvG   K   +     +  L Em ++W FFR  l  +Em
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  gi|2983010   751 SRQIVPGWFGVGSGLKALREAGLDTV--LDEMHEQWHFFRNFLSNVEMTL 798

                   AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                   AK D  iA  y + Lv + Lk     + ++ + t   +L+i G   lL+
  gi|2983010   799 AKTDLRIARHYVDTLVPDHLKHVFATIEAEHELTVREVLRITGGEKLLDT 848

                   DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                    P L+q   +Rd+Y+  +  +q   LKR RD               A++
  gi|2983010   849 HPVLQQTFAIRDAYLDPISYLQVALLKRQRDAA-------------AADT 885

                   skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     ++d L+               L+Lt+ G+AAG+ ntG
  gi|2983010   886 --PPDPLLARA-----------LLLTVNGVAAGLRNTG    910

gi|118617446|ref|YP_905778.1|: domain 1 of 1, from 11 to 935: score 319.9, E = 5.2e-93
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       i    R  +        + ++ D  Ll   L+D + +  G+++ E
  gi|1186174    11    PIGDVHRTRIGREAT---EPMRADIRLLGAILgDTVREQNGDEVFEL 54

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v E   + A +  ++      E+     ++d   ai + +a++H   LAn
  gi|1186174    55 V-ERARVEA-FRVRHSEIDRAEMARMFEGIDIHHAIPIIRAFSHFALLAN 102

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE+++   RR i+          ++   +s +  t+ kL        +
  gi|1186174   103 VAEDIHRERRRSIHVAA-------GEPPRDSSLTATYMKLYAAQ-LDSAT 144

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt.veD
                   + eALK   v  v+tAHPt   RR +   + Ri   L  L A   t+ +D
  gi|1186174   145 IAEALKGALVSPVITAHPTETRRRTIFETQHRITQ-LMRLHAEGHTeTDD 193

                   KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    + ++  L R +   + t  iR  +    DE+  G+ Y+   +++ + +
  gi|1186174   194 GRGIEVELRRQVLRLWQTALIRLFRLQISDEIEVGLRYYPAALFEVISQV 243

                   LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                      v  AL+       l    P+++  sW+GGDRDG nP vt Ev R
  gi|1186174   244 NAEVRDALRARWPDADL-LSEPILRPGSWIGGDRDG-NPNVTAEVVRLAT 291

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     a   A   Y+  +  L  Elsm      L     El   a
  gi|1186174   292 GSAAFTALAHYLAELTALAQELSM---SARLITVTPELATLADAC----- 333

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv..
                            P EPYR  L  vR +L  t   a  +L +      E   ++
  gi|1186174   334 ----PAGARPDEPYRRALQVVRGRLSAT---AAEILDQQPQHTLELGLpp 376

                   ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                   y    e    L+    sL + G   +AD  L  l   v  FG  L  LD+
  gi|1186174   377 YATAAELRADLDTIDASLHNHGAGLLADDRLARLREAVRVFGFHLSGLDM 426

                   RqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgsD
                   Rq s+ +  v+  +    ++ + Y + +E  R E L aEL+ +RPL+
  gi|1186174   427 RQNSDVHEQVVGELLAWAGVHpDYTSLAEAERVELLAAELSTRRPLIRDG 476

                   LPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvELL
                       +  +  l+ +   A   + +FG+   ++Yiism+ + sD+L   +L
  gi|1186174   477 AQLSDLARSELGVLAAAAH-AVWTFGPaavpnYIISMCWSVSDMLEAAVL 525

                   qRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                    +E g+   +++++  ++ + PLFE + DL+   A ++ +  +  Y+  +
  gi|1186174   526 LKEVGLLDasesepycPVGISPLFETIEDLHNGAAILQAMLDLPLYRALV 575

                   d...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                     ++G qevm+GYsDs KD G l+A W +Y+A   ++  A+k G++L lF
  gi|1186174   576 TargGCQEVMLGYSDSNKDGGYLAANWAVYRAELALVETARKTGIRLRLF 625

                   HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                   HGRGGtvGRGGGP   AiL+qPP  + GslR t qGEvi   + E ++
  gi|1186174   626 HGRGGTVGRGGGPSYQAILAQPPGAVSGSLRLTEQGEVIAAKYAEPQMAR 675
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                    rsLqRFtAAtLE......HGmnPPvsPkPEWRkLmeemAvvAtEEYRsvv
                    r L    AAtLE++     G+    +P      +++e+A  A   Y  +v
  gi|1186174   676 RNLESLLAATLEstllavEGLGDTAAPA---YAVLDEVAALAQRAYAELV 722

                    vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWt
                       P FvEYF+  tP  E+G +niGsRP+ RkP   i  LRAiPW+ aW
  gi|1186174   723 HETPGFVEYFKASTPVSEFGALNIGSRPTSRKPTASIADLRAIPWVLAWS 772

                    qtRFHLPvWLGvGAAFKhAi....dKDiKnlqkLkEmYkeWPFFRvtlDL
                    q R  LP W G G AF   +  +++ +   lq L+++Y+ WPFFR  l
  gi|1186174   773 QSRVMLPGWYGTGSAFEQWLaagpESEADRLQVLHDLYQRWPFFRSVLSN 822

                    lEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtkdlLLkiAGH
                    +  v AK D  +Aa y +L+  E L++   +++ d+   t  +  +i G
  gi|1186174   823 MAQVMAKSDLELAARYSELVADETLrRRVFDKIADEHHRTIAMYKRITGQ 872

                    kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                     DlL   P L   +  R +Y+  Ln +q   L+R R
  gi|1186174   873 DDLLADNPALARSVFNRFPYLEPLNHLQVELLRRYR-------------- 908

                    EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        E+    de v+              ++Ltm G+A  + n G
  gi|1186174   909 --SGED----DESVQRG-----------ILLTMNGLASALRNSG    935

gi|253755158|ref|YP_003028298.1|: domain 1 of 1, from 1 to 898: score 318.1, E = 1.8e-92
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedL.kEa
                              ++      ++ + i+ +  +l     iL ++  + ++ E
  gi|2537551     1    ------MAIQKLENYNNKEAIREEVTILTS---ILEEVAAQMMpAET 38

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                         Els            + L a +  L+  +  ++ + +  +  L n
  gi|2537551    39 FAKIVELSQ----LSRQDDYQALIAIISQLNNDELAVISRYFAVLPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+    s t +         +v+k     +E
  gi|2537551    85 ISEDVDLAYEINHQNNIDQDYLGKISTTID---------MVSKQ-ENAAE 124

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + e L    v  vltAHPtq  R s+L     i   L       +    K
  gi|2537551   125 ILEKL---NVVPVLTAHPTQVQRQSMLDLTKHIHELLRRYRDVKLGLLNK 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                       ++ L   i     tD iR  +     E+   m Y+     k v K
  gi|2537551   172 NKWEDELRYYIEIIMQTDMIREKKLKVTNEITNVMEYYNSSFIKAVTKLQ 221

                    RRvD..tALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    R   +  A K i +n   P     i    W+GGDRDG nP vt E  +
  gi|2537551   222 REYKrlAAEKGIVLNNPRP-----ITMGMWIGGDRDG-NPFVTAETLKLS 265

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                     L    +  n Y +q+  L   +s+      +      l   +
  gi|2537551   266 ALTQCEVIMNYYDEQLYKLYRNFSLSTSIVNVSTAVKMLADLSEDS---S 312

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                     Y E       +EPYR     +  KL ntR+   H       + + +  y
  gi|2537551   313 VYRE-------NEPYRRAFHYIQMKLANTRDYLVH-------NKPSDVRY 348

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     +v eF   L    +sL e    ++  G   +lL  v  FG  L  +D+R
  gi|2537551   349 SNVAEFKADLLAIKQSLVENKSMALLKGDFTELLEAVEAFGFYLASIDMR 398

                    qEseRq.tDvlDAittHLeiGsYReWsEeKRqEWLlaELkGK.RPLlgsD
                    q+s  ++  v + +     +  Y + sEe +   Ll  L+  +R L
  gi|2537551   399 QDSSIHeASVAELLASARIVEDYSSLSEEAKCHVLLKQLETDpRILSATH 448

                    LPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvELLq
                    +Pk E ++  l  f    EL ++ + +     iis + + sD L   +L
  gi|2537551   449 MPKSEQLEKELAIFAAARELKdklgEEIIKQHIISHSESVSDLLELAVLL 498

                    RECgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK..
                    +E g+ + +k  +++vPLFE + DL+ AP ++ +   +D  +  i G +
```

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  gi|2537551   499 KEVGLvdvdKARVQIVPLFETIEDLDNAPDTMRQYLQLDLAKRWIAGNky 548

                   .qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                    qe+m+GYsDs KD G ls  W LYkAq E+ ++ ++yGv ++ FHGRGG
  gi|2537551   549 yQEIMLGYSDSNKDGGYLSSGWTLYKAQNELTQIGQDYGVNITFFHGRGG 598

                   tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                   tvGRGGGP   Ai sqP   i+  lR t qGEvi   +G  +  +  L
  gi|2537551   599 TVGRGGGPSYDAITSQPFGSIKDRLRLTEQGEVIGNKYGNKDAAYYNLEM 648

                   FtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEEYRsvvvKEPRFvE
                      AtL+  +   +    E +++R+ m+e+       YR +v+  P F +
  gi|2537551   649 LVSATLDRMVTQMITDPNEidgYRETMDEIVSDSYRIYRDLVFNNPHFYD 698

                   YFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPv
                   YF  A P  E   +niGsRPa Rk    i  LRAiPW+F+W q R  LP
  gi|2537551   699 YFFAASPIREVSSLNIGSRPAARKTITEIGGLRAIPWVFSWSQNRVMLPG 748

                   WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                   W GvG  FK  idK   nl kL+ mY+ WPFFR  l  ++mv  K    i
  gi|2537551   749 WYGVGSSFKRFIDKHPDNLSKLQKMYESWPFFRSLLSNVDMVLSKSNMNI 798

                   AaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                   A  y k+  +Ee++   + + d+++ tk+++L i    +lL   P+LK
  gi|2537551   799 AFEYAKMCESEEVRNIFHVILDEWQLTKEIILSIEQNDELLAELPFLKAS 848

                   lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                   l  R +Y   Ln +q   + R+R        r +lsKE  +En      L
  gi|2537551   849 LDYRMPYFNVLNYIQIELIHRLR--------RGELSKE--QEN------L 882

                   vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   +++                 + G+A G+ n G
  gi|2537551   883 IHIT----------------INGVATGLRNSG    898

gi|146318181|ref|YP_001197893.1|: domain 1 of 1, from 1 to 898: score 318.0, E = 2e-92
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedL.kEa
                             ++      ++ + i+ +  +l     iL ++  + ++ E
  gi|1463181     1    ------MAIQKLENYNNKEAIREEVTILTS---ILEEVAAQMMpAET 38

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                        Els            + L a +  L+  +  ++ + +  +  L n
  gi|1463181    39 FAKIVELSQ----LSRQDDYQALIAIISQLNNDELAVISRYFAVLPLLIN 84

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   + E+v+lAy    +     D+    s t +         +v+k     +E
  gi|1463181    85 ISEDVDLAYEINHQNNIDQDYLGKISTTID---------MVSKQ-ENAAE 124

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   + e L    v  vltAHPtq  R s+L     i   L       +    K
  gi|1463181   125 ILEKL---NVVPVLTAHPTQVQRQSMLDLTKHIHELLRRYRDVKLGLLNK 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      ++ L   i     tD iR  +     E+   m Y+     k v K
  gi|1463181   172 NKWEDELRCYIEIIMQTDMIREKKLKVTNEITNVMEYYNSSFIKAVTKLQ 221

                   RRvD..tALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                   R   +  A K i +n   P     i    W+GGDRDG nP vt E  +
  gi|1463181   222 REYKrlAAEKGIVLNNPRP-----ITMGMWIGGDRDG-NPFVTAETLKLS 265

                   CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                    L    +  n Y +q+  L   +s+      +      l   +
  gi|1463181   266 ALTQCEVIMNYYDEQLYKLYRNFSLSTSIVNVSTAVKMLADLSEDS---S 312

                   yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                    Y E       +EPYR     +  KL ntR+   H       + + +  y
  gi|1463181   313 VYRE-------NEPYRRAFHYIQMKLANTRDYLVH-------NKPSDVRY 348

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                    +v eF   L    +sL e    ++  G   +lL  v  FG  L  +D+R
  gi|1463181   349 SNVAEFKADLLAIKQSLVENKSMALLKGDFTELLEAVEAFGFYLASIDMR 398
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                    qEseRq.tDvlDAittHLeiGsYReWsEeKRqEWLlaELkGK.RPLlgsD
                    q+s  ++  v + +     +  Y + sEe +   Ll  L+  +R L
  gi|1463181   399 QDSSIHeASVAELLASARIVEDYSSLSEEAKCHVLLKQLETDpRILSATH 448

                    LPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvELLq
                    +Pk E ++  l  f    EL ++ + +     iis + + sD L   +L
  gi|1463181   449 MPKSEQLEKELAIFAAARELKdklgEEIIKQHIISHSESVSDLLELAVLL 498

                    RECgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK..
                    +E g+ + +k  +++vPLFE + DL+ AP ++ +   +D  +  i G +
  gi|1463181   499 KEVGLvdvdKARVQIVPLFETIEDLDNAPDTMRQYLQLDLAKRWIAGNky 548

                    .qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                     qe+m+GYsDs KD G ls  W LYkAq E+ ++ ++yGv ++ FHGRGG
  gi|1463181   549 yQEIMLGYSDSNKDGGYLSSGWTLYKAQNELTQIGQDYGVNITFFHGRGG 598

                    tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                    tvGRGGGP   Ai sqP   i+  lR t qGEvi   +G  +  +  L
  gi|1463181   599 TVGRGGGPSYDAITSQPFGSIKDRLRLTEQGEVIGNKYGNKDAAYYNLEM 648

                    FtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEEYRsvvvKEPRFvE
                       AtL+  +   +    E +++R+ m+e+       YR +v+  P F +
  gi|1463181   649 LVSATLDRMVTQMITDPNEidgYRETMDEIVSDSYRIYRDLVFNNPHFYD 698

                    YFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPv
                    YF  A P  E   +niGsRPa Rk    i  LRAiPW+F+W q R  LP
  gi|1463181   699 YFFAASPIREVSSLNIGSRPAARKTITEIGGLRAIPWVFSWSQNRVMLPG 748

                    WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                    W GvG  FK  idK   nl kL+ mY+ WPFFR  l  ++mv  K    i
  gi|1463181   749 WYGVGSSFKRFIDKHPDNLSKLQKMYESWPFFRSLLSNVDMVLSKSNMNI 798

                    AaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                    A  y k+  +Ee++   + + d+++ tk+++L i    +lL   P+LK
  gi|1463181   799 AFEYAKMCESEEVRNIFHVILDEWQLTKEIILSIEQNDELLAELPFLKAS 848

                    lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                    l  R +Y   Ln +q   + R+R        r +lsKE  +En      L
  gi|1463181   849 LDYRMPYFNVLNYIQIELIHRLR--------RGELSKE--QEN------L 882

                    vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +++                 + G+A G+ n G
  gi|1463181   883 IHIT----------------INGVATGLRNSG    898

gi|223933776|ref|ZP_03625747.1|: domain 1 of 1, from 1 to 898: score 317.6, E = 2.5e-92
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                              ++      ++ + i+ +  +l   L+ +     +   E
  gi|2239337     1    ------MAIQKLENYNNKEAIREEVTILTSILEKVAAQMMPA--ETF 39

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        Els +   + D + L    a +  L+  +  ++ + +  +  L n+
  gi|2239337    40 AKIVELS-QLSRQDDYRALI---AIISQLNNDELAVISRYFAVLPLLINI 85

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     E+v+lAy    +     D+    s t +         +v+k     +E+
  gi|2239337    86 SEDVDLAYEINHQNNIDQDYLGKISTTID---------MVSKQ-ENAAEI 125

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     e L     v  vltAHPtq  R s+L     i   L       +    K
  gi|2239337   126 LEKL---NVVPVLTAHPTQVQRQSMLDLTKHIHELLRRYRDVKLGLLNKN 172

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                      ++ L   i     tD iR  +     E+   m Y+     k v K  R
  gi|2239337   173 KWEDELRCYIEIIMQTDMIREKKLKVTNEITNVMEYYNSSFIKAVTKLQR 222

                    RvD..tALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                       +  A K i +n   P     i    W+GGDRDG nP vt E  +
  gi|2239337   223 EYKrlAAEKGIVLNNPRP-----ITMGMWIGGDRDG-NPFVTAETLKLSA 266

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    L    +  n Y +q+  L   +s+      +      l   +
```

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  gi|2239337   267 LTQCEVIMNYYDDQLYKLYRNFSLSTSIVNVSTAVKMLADLSEDS---SI 313

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                   Y E       +EPYR     +  KL ntR+   H       + + +  y
  gi|2239337   314 YRE-------NEPYRRAFHYIQMKLANTRDYLVH-------NKPSDVRYS 349

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   +v eF   L    +sL e    ++  G   +lL  v  FG  L  +D+Rq
  gi|2239337   350 NVAEFKADLLAIKQSLVENKSMALLKGDFTELLEAVEAFGFYLASIDMRQ 399

                   EseRq.tDvlDAittHLeiGsYReWsEeKRqEWLlaELkGK.RPLlgsDL
                   +s  ++  v + +     +  Y + sEe +   Ll  L+  +R L    +
  gi|2239337   400 DSSIHeASVAELLASARIVEDYSSLSEEAKCHVLLKQLETDpRILSATHM 449

                   PktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvELLqR
                   Pk E ++  l  f    EL ++ + +     iis + + sD L   +L +
  gi|2239337   450 PKSEQLEKELAIFAAARELKdklgEEIIKQHIISHSESVSDLLELAVLLK 499

                   ECgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...
                   E g+ + +k  +++vPLFE + DL+ AP ++ +   +D  +  i G +
  gi|2239337   500 EVGLvdvdKARVQIVPLFETIEDLDNAPDTMRQYLQLDLAKRWIAGNkyy 549

                   qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                   qe+m+GYsDs KD G ls  W LYkAq E+ ++ ++yGv ++ FHGRGGt
  gi|2239337   550 QEIMLGYSDSNKDGGYLSSGWTLYKAQNELTQIGQDYGVNITFFHGRGGT 599

                   vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                   vGRGGGP   Ai sqP   i+  lR t qGEvi   +G  +  +  L
  gi|2239337   600 VGRGGGPSYDAITSQPFGSIKDRLRLTEQGEVIGNKYGNKDAAYYNLEML 649

                   tAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEEYRsvvvKEPRFvEY
                     AtL+  +   +    E +++R+ m+e+       YR +v+  P F +Y
  gi|2239337   650 VSATLDRMVTQMITDPNEidgYRETMDEIVSDSYRIYRDLVFNNPHFYDY 699

                   FRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvW
                   F  A P  E   +niGsRPa Rk    i  LRAiPW+F+W q R  LP W
  gi|2239337   700 FFAASPIREVSSLNIGSRPAARKTITEIGGLRAIPWVFSWSQNRVMLPGW 749

                   LGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiA
                    GvG  FK  idK   nl kL+ mY+ WPFFR  l  ++mv  K    iA
  gi|2239337   750 YGVGSSFKRFIDKHPDNLSKLQKMYESWPFFRSLLSNVDMVLSKSNMNIA 799

                   aLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrl
                     y k+  +Ee++   + + d+++ tk+++L i    +lL   P+LK  l
  gi|2239337   800 FEYAKMCESEEVRNIFHVILDEWQLTKEIILSIEQNDELLAELPFLKASL 849

                   RLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLv
                     R +Y   Ln +q   + R+R        r +lsKE  +En      L+
  gi|2239337   850 DYRMPYFNVLNYIQIELIHRLR--------RGELSKE--QEN------LI 883

                   kLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   ++                + G+A G+ n G
  gi|2239337   884 HIT----------------INGVATGLRNSG    898

gi|158318318|ref|YP_001510826.1|: domain 1 of 1, from 34 to 981: score 317.5, E = 2.7e-92
                   *->siDAqLRlLvPGKvsedekLieYDALL..lDkFL.DiLqDLHGedLk
                         Aq      G vs d +     A +++l   L++ L    G++L
  gi|1583183    34    DQQAQDPGGFSGGVSSDARHAAVRAGVrrLGALLgEALTRHEGPELL 80

                   EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                     v     l+   +G        EL a+L ++d   ail+A+a+     L
  gi|1583183    81 ALVERVRMLARGEDGGT------ELAAVLDGVDARQAILLARAFTAYFQL 124

                   AnLAEEvelAyR...RRikkkkhGDFaDEasAttEsDiEEtlKkLvlkln
                   An+ E  + A   ++R  ++++  D aD         i E +   v+
  gi|1583183   125 ANITEQLHRAREisdRPRSRLR--DLADR--------IAEAVDEGVVDP- 163

                   KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                     P+Ev   L+      v+tAHPt + RRs+L     i   L
  gi|1583183   164 GLPAEVMRRLQLRP---VFTAHPTEASRRSVLETLRGIADLLDATDDPRR 210
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                    tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                       D + L   L   +   + tDE+R  +P P DE R    Y+     +
  gi|1583183   211 PGADDERLARRLAELVDVLWQTDELRVERPKPADEARSAAYYLTSIATEV 260

                    vPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                     P  L   DtA   iG+   lP  +  + F sW GGDRDG nP vtPEvt
  gi|1583183   261 LPDLLEELDTAFAGIGVE--LPVTARPLAFGSWAGGDRDG-NPNVTPEVT 307

                    RDvCLLaRmmAanlYisqvEDLmFElsm.WRCndELRvRAEElyrtaard
                     +v  L       +    v+ L+ El  + R   E  v  + l   aa
  gi|1583183   308 LEVLNLQYEFGIRVLTALVDRLVRELTAsTRVVGE--VSGDLLAALAADR 355

                    kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                           + +  +  +EPYR     +  +L  tR R    LA G   ++
  gi|1583183   356 AALPEVYDRFIRLNAEEPYRLKCSYILARLAGTRAR----LAAGAPHVPG 401

                    eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                       y +  + ++ LEL   sL       +A G L   +R  s  GLsL
  gi|1583183   402 KD-YLRPTDLVDELELMRVSLAASHGELVANGPLRRAIRTASAVGLSLAT 450

                    LDiRqEseRqtDvlDAittHL.eiGs.YReWsEeKRqEWLlaELkGKRPL
                    LDiR  ++ +   l Ai   L e+  +YR+     R   L aEL G+RPL
  gi|1583183   451 LDIREHADAHHAALGAIYDQLaELDVpYRDLDRPARLALLSAELAGRRPL 500

                    lgsDLPkt.EEvkDvldafrvLAELPiDsFG.....aYiismataPsDvL
                    lg+  P+ +E v+  l+ +  +     D +G++  ++Yi+sm+    D+L
  gi|1583183   501 LGAVPPRLpERVARTLELLTTVRH-ALDQYGdgvieSYIVSMTRDADDIL 549

                    AvELLqRECgvk.........................qtLrvvPLFE
                    Av +L RE g+ + ++++++++++ +++++++  +      +  vPLFE
  gi|1583183   550 AVAVLAREAGLVglgrppgtssgpgigterdgpavpavawARIGFVPLFE 599

                    kLADLeAAPAavekLFsiDWYinridGK...qevmvGYsDsGKDAGRlsA
                     +A+L+AA   +++L +   Y+  +  +++ qevm+GYsDs KDAG  +
  gi|1583183   600 TVAELRAAGTLLDRLLADPSYRALVAARgdvQEVMLGYSDSSKDAGITAS 649

                    AWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDt
                     W + kAq E+   A+ +Gv L lFHGRGG vGRGGGP   AiL+qP  t
  gi|1583183   650 QWEIHKAQRELRDTARAHGVVLRLFHGRGGSVGRGGGPSGEAILAQPFGT 699

                    inGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs.....
                    ++G ++vt qGEvi   +   +L  + L     A +E  +    s+ +++
  gi|1583183   700 LDGPIKVTEQGEVISDKYTLPQLARQNLEITLSAVVEASVLHRTSrltgq 749

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                        W   m  +A  A + YRs+v  +P  v +F  AtP  E G +niGs
  gi|1583183   750 ALAGWNGTMTAVADAAKDAYRSLVA-DPALVPFFLAATPVEELGNLNIGS 798

                    RPaKRkP..sGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi
                    RP+ R+P++sGG+  LRAiPW+F Wtq R  LP W GvG     A  ++
  gi|1583183   799 RPS-RRPggSGGLADLRAIPWVFGWTQARIILPGWFGVGSGL--AAAREA 845

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                         L EmY+ W FFR  l  + m  AK D  iA  y   Lv
  gi|1583183   846 GAGGELAEMYRSWHFFRTFLGNVQMTLAKSDLAIAQRYVSALVDPATAAL 895

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                     + +Rd+ + t   +L + G   lLE  P L+  l +Rd+Y+  L  +q
  gi|1583183   896 FDVIRDEHERTVREVLAVTGQAGLLETAPVLRHTLLVRDAYLAPLHALQV 945

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      L R R                A+ +         +       P L
  gi|1583183   946 SLLARTR----------------AAGD---------IA-----DPQLRRG 965

                    LiLtmKGiAAGmqntG<-*
                    L+Lt+ GiAAG+ ntG
  gi|1583183   966 LLLTINGIAAGLRNTG    981

gi|254407576|ref|ZP_05022466.1|: domain 1 of 1, from 3 to 913: score 317.4, E = 2.9e-92
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s D     L    +s   +L      L D   + L    G++L E v
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gi|2544075     3    SADD----LTTSAMSTSTELRADIRRLGDLLGETLVRQEGPELLELV 45

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         l  e     D +   EL   L +++   a  + +a++    LAn+
gi|2544075    46 EKVRRLLTRE-----DGEAAAEL---LRGIELETAAKLVRAFSTYFHLANV 87

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     E v   +R R  + +         A     +  t  +L       Pe
gi|2544075    88 TEQV---HRGRELRAR--------RAAEGGLLARTADRLKDAD---PEHL 123

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     + + n  v  v+tAHPt ++RRs+L K  Ri    a L    v   D++
gi|2544075   124 RQTVANLNVRPVFTAHPTEAARRSVLNKLRRI----AALLETPVIETDRR 169

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                      D  L   i   + tDE+R  +P P DE R  + Y+ E     v   L
gi|2544075   170 RYDTRLAENIDLVWQTDELRVVRPEPADEARNAIYYLDELHAGAVGDVLE 219

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         L  +G+  ++P     + F  W+GGDRDG nP vtP vt Dv +L
gi|2544075   220 DLTAELERVGV--KIPDATRPLTFGTWIGGDRDG-NPNVTPQVTWDVLIL 266

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkvvKyY
                          n  ++ +++L   ls    n+     A+EEl    + d
gi|2544075   267 QHEHGINDALELIDELRGFLS----NSIRYTGAtEELLESLQAD--LERL 310

                    iEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                     E ++++K +  +EPYR     +R KL nt+ R    LA+Gi    +
gi|2544075   311 PEIsprYKRLNAEEPYRLKATCIRQKLENTKTR----LAKGIPH-EDGRD 355

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y    e L  L L   sL e      ADG +   +R    FGL L  +D+
gi|2544075   356 YLGTSELLSDLTLIQTSLREHRGGLFADGRMDRTIRTLAAFGLQLATMDV 405

                    RqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLlgs
                    R  ++ +   l  +   L+  s+R  + + e R   L  EL+ +RPL +
gi|2544075   406 REHADAHHHALGQLFDRLGEESWRyaDMPREYRAKLLAKELRSRRPLAPT 455

                    DLPk...tEEvkDvldaf.rvLAELPiDsFGaYiismataPsDvLAvELL
                      P +   E    v ++++r LA    +   +Yiism+    Dv A  +L
gi|2544075   456 PAPVdaaGEKTLGVFQTVkRALAVFGPEVIESYIISMCQGADDVFAAAVL 505

                    qRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                     RE g+   + +   + +vPL E   +L+AA   +e + s   Y+  +
gi|2544075   506 AREAGLLDlhagwaKIGIVPLLETTDELKAADTILEDMLSDPSYRRLVAL 555

                    K...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                    +++ qevm+GYsDs K  G     W + +Aq  +  vA +yGv+L lFHG
gi|2544075   556 RgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRYGVRLRLFHG 605

                    RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                    RGGtvGRGGGP H AiL+qP  t++G ++vt qGEvi   +    L
gi|2544075   606 RGGTVGRGGGPSHDAILAQPWGTLEGEIKVTEQGEVISDKYLVPSLAREN 655

                    LqRFtAAtLEHGm...nPPvsPk..PEWRkLmeemAvvAtEEYRsvvvKE
                    L    AAtL     ++ P  s      W   m+ +   A   YR +v  +
gi|2544075   656 LELTVAATLQASAlhtAPRQSDEalARWDAAMDVVSDAAHAAYRRLV-ED 704

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWtq
                    P    YF   tP      + +GsRP+ R+P+ G++ + LRAiPW+F Wtq
gi|2544075   705 PDLPTYFLASTPVDQLADLHLGSRPS-RRPGSGVslDGLRAIPWVFGWTQ 753

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     R  +P W GvG   K   +     +  L Em ++W FFR  +  +Em
gi|2544075   754 SRQIVPGWFGVGSGLKALREAGLDTV--LDEMHEQWHFFRNFISNVEMTL 801

                    AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                    AK D  iA  y + Lv  eL+    ++ ++ + t   +L++ G  +lL+
gi|2544075   802 AKTDLRIARHYVETLVPAELQHVFADIEAEHELTVREVLRVTGEDELLDA 851

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
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                    P LKq   +Rd+Y+  +  +q   LKR RD               A+
  gi|2544075   852 TPVLKQTFAIRDAYLDPISYLQVTLLKRQRD---------------AAAA 886

                    skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                +e+  P L   L+Lt+ G+AAG+ ntG
  gi|2544075   887 ------------GEEPDPLLARALLLTVNGVAAGLRNTG    913

gi|272527540|ref|ZP_06223827.1|: domain 1 of 1, from 125 to 1072: score 316.6, E = 5.3e-92
                    *->siDAqLRlLvPGKvsed.ekLieYDALLlDkFL.DiLqDLHGedLkE
                       s  A       G+  ed+++ +  D   l + L+D+L +  G+ + +
  gi|2725275   125    SAAAPTVKNGGGRTREDkDHPLFQDIRYLGRLLgDVLREQEGDAVFD 171

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    +v      +  +    D+   + L  kL sL P  ++ v +a++    LA
  gi|2725275   172 VVETIRQNAVRFRREDDSAAAQTLDKKLRSLTPEQTVSVVRAFSYFSHLA 221

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE+ +   R Ri+ +        +sA     i   l +Lv  +  +
  gi|2725275   222 NIAEDRHRNRRHRIHALA-------GSASQPGTIAHALERLVAAG-AAAT 263

                    EvFeALKnqsvDL.vltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                     v +     +  ++vltAHPt   R+s+L  +  i   La    + +t
  gi|2725275   264 PVLQRFFDDALIMpVLTAHPTEVQRKSILDAQHDIARLLAE-RDQPLTNR 312

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++   +  L   +   + t  +R a+ t  DE+   +sY+  t  +  P
  gi|2725275   313 ERAHNEAMLRARVTSLWQTRMLRDARLTVADEIENALSYYRSTFLEELPA 362

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                        ++ ALK  G+  RlP   P  +  sW+GGDRDG nP vt E
  gi|2725275   363 LYADIEEALKEHGLEARLP---PFFQMGSWIGGDRDG-NPNVTAETLENA 408

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                          +    Y+ qv  L  Elsm      +     El   +  +
  gi|2725275   409 ITRQAAVIFEHYLVQVHKLGEELSMSNVLVGVSDALNELADISPDH--SP 456

                    yYiEFWKqvPPtEPYRviLGdvRDKLYn.tRER....aRHLLAtGiseis
                    +  +        EPYR  L  +  +L  + R R ++++  L   G    +
  gi|2725275   457 HRTD--------EPYRRALIGIYTRLAAsARVRlgegSVPLRSAGRGVAP 498

                    EeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                      A +y +  +F+  L +   sL e     +A   L  l R    FG  L
  gi|2725275   499 IRATpYDDAADFVRDLHVLIDSLAEHHGAPLAAPRLAPLARAAEVFGFHL 548

                    vKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRP
                      +D+Rq s+ +  v+  + +  ++ + Y   sE  +   LlaEL   R
  gi|2725275   549 ASIDLRQSSDIHEAVIAELLKRAGVEdDYAGLSEANKLKVLLAELAQPRA 598

                    LlgsDLPktEEvkDvldafrvLAELPi..DsFGa.....YiismataPsD
                    L    +P  E    v   + vL E  i+++ FGa+  ++Yiis + + sD
  gi|2725275   599 L---RVPYAEYSDLVKSELAVLEEARItrEKFGAravrnYIISHTETVSD 645

                    vLAvELLqRECgv.............kqtLrvvPLFEkLADLeAAPAavek
                     + v LLq+E g+  ++ ++++++ + +L v+PLFE + DL+ AP  +
  gi|2725275   646 LVEVMLLQKETGLllghlgdehdpaRASLMVIPLFETIPDLRNAPHIMRD 695

                    LFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKv
                    L + ++i   i +    qevm+GYsDs KD G l   W LY+A   ++
  gi|2725275   696 LIAlpgIGALIEHQGNEQEVMLGYSDSNKDGGFLTSNWELYRAELALVSL 745

                    AKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEvi
                      + Gv L lFHGRGGtvGRGGGPt  AiLsqPP t+ G +R t qGEvi
  gi|2725275   746 FNERGVTLRLFHGRGGTVGRGGGPTYQAILSQPPGTVAGQIRLTEQGEVI 795

                    EfsFGEEnLCFrsLqRFtAAtLEHGmnP...PvsPkPEWRkLmeemAvvA
                       F   ++  r L    AAtLE  + P+++ ++  P + + m+++   A
  gi|2725275   796 ASKFANPEIGRRNLETVVAATLEASLLPhdhTLAELPVYEETMQQLSDTA 845

                    tEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....Gie
                       YR++v+  P F EYF   tP  E   +niGsRPa Rk   ++++ ie
  gi|2725275   846 MAAYRALVYETPGFKEYFFESTPIAEIAELNIGSRPASRKLQDpkqrKIE 895
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                    sLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiKnlqkLkE
                     LRAiPW F+W q R  L  W G+G A    +d+ +++    + l  Lk
  gi|2725275   896 DLRAIPWGFSWGQCRLLLTGWYGFGSAVTEHLDsapsdaERARRLALLKK 945

                    mYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdk
                    m k WPFF   +  ++mv AK D  +A+ y  L+    L+k   +++ ++
  gi|2725275   946 MHKSWPFFANLMSNMDMVIAKTDLAVASRYAALVTDKKLrKHVFERIVAE 995

                    YvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiR
                    ++ t + L +i G  + L   P L   ++ R +Y+  Ln +q   LKR R
  gi|2725275   996 WERTSKVLSEITGKSERLAENPLLARSIKNRFPYLDPLNHLQVELLKRYR 1045

                    DPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKG
                                   A +           n   rv  G+     L + G
  gi|2725275  1046 ----------------AGDT----------N--ARVRRGIH----LCING 1063

                    iAAGmqntG<-*
                    iAAG+ ntG
  gi|2725275  1064 IAAGLRNTG    1072

gi|260891421|ref|ZP_05902684.1|: domain 1 of 1, from 9 to 933: score 316.0, E = 7.9e-92
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            L  +   K    e+L+    L      + +    G  + E+
  gi|2608914     9    ---TPLPSVKLDKHQ--EDLLVHNELFATLLGETIFRYAGLHIYEVT 50

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        E s  Y   +  +    L +    L  a+ + v + ++    LAn+
  gi|2608914    51 EKLKEASSKYYKTQKQEARKNLSSFCSDLTDAEILRVIRGFSIFSALANI 100

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v   +  R  k          +      +E  lK L  k+  s + +
  gi|2608914   101 AEDVYQTHEQRYAKIS--------NKPQIGSLEKSLKNLKKKG-ISQDKI 141

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      A+   s+  vltAHPtq  R+s+L    ++   L +         D
  gi|2608914   142 LKAMEKVSIVPVLTAHPTQVQRKSILDLTKKLTDILDKYENVKSHQIDEN 191

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    E    L R iq  + t  +R ++    DE+   +sY+  t ++ +P+ +
  gi|2608914   192 EWLNDLSRGIQIWWQTSMLRASKLRVTDEISNALSYYNITFFNEIPRLMN 241

                    RvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRDvCL
                    +     K +G n  +  ++ L++    W+GGDRDG nP vt
  gi|2608914   242 KFQEISKTLG-NSEVKSQALLpLTMGMWIGGDRDG-NPYVTVNTLEQSAQ 289

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                       +     Y++ v ++  +lsm      +    EEl+  a
  gi|2608914   290 EQAIKLFQHYLDVVREIYRDLSM---SISMTNVTEELQNLAEAS------ 330

                    iEFWKqvPP...tEPYRviLGdvRDKL....YntRERaRHLLAtGiseis
                          v P+++ EPYR  L  + D+L  + Y   +  R LL     +
  gi|2608914   331 ----GEVSPhrtHEPYRRALTTITDRLlataYKLCDYNRDLLPPKRKN-G 375

                    EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                     +  y    eF   L +   sL       +  G L  l+     FG  L
  gi|2608914   376 IDLPYKSANEFTYDLVIVAESLKKNNSEFLTQGKLNNLISATKIFGFHLA 425

                    KLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaELkGK.RP
                     +D+Rq+s  +   +  + +  +i G Y + sE+ R E Ll EL+  +R
  gi|2608914   426 TIDLRQDSSVHEICVAELLKSANIlGDYLSLSEDARCEILLRELEHDpRI 475

                    LlgsDLPktEEvkDvldafrvLAELPiDsFGaYi.....ismataPsDvL
                    L  + +P+ E ++  l  +r    L  + FG+ i +++ is at+ sD+L
  gi|2608914   476 LSDPTIPQSETLASELAIYRKAKSL-RERFGSKIieknlISHATSVSDML 524

                    AvELLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsiDW
                     + +L +E  + +++++++   L++vPLFE + DL AAP  + k F +
  gi|2608914   525 EIAILLKEANLAKgnegnefcDLQIVPLFETVEDLIAAPDILRKWFNLPL 574

                    Yinrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGv
```

```
                    +  +d+++ Kqevm+GYsDs KD G ls  W LYkAq E+  + +++ v
  gi|2608914   575 VKKWMDkkgRKQEVMLGYSDSNKDGGYLSSSWSLYKAQKELTAIGREFDV 624

                    KLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGE
                     +  FHGRGGtvGRGGGP   AiL+qP    +G +R t qGEvi   +G
  gi|2608914   625 EISFFHGRGGTVGRGGGPSYEAILAQPEGSTDGTIRLTEQGEVIGAKYGN 674

                    EnLCFrsLqRFtAAtLE.HGmnPPvsPkPEWRkLmeemAvvAtEEYRsvv
                     +L  + L     A LE+  +    +   E+ k++e++       YR +v
  gi|2608914   675 PDLGLKNLEALVSAALEsSALTEEDADWEEYEKIIENVSDLSYYAYRDLV 724

                    vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWt
                    +    F ++F   tP      +niGsRP+ Rk    ++sLRAiPW+F+W
  gi|2608914   725 YNTDGFSDFFFEVTPINFIAGLNIGSRPSSRKKTQSLDSLRAIPWVFSWS 774

                    qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                    q R  LP W GvG AF   id D K l  L+ mYkeWPFFR t+  ++mv
  gi|2608914   775 QARIMLPGWYGVGTAFTKWIDNDDKKLEILQKMYKEWPFFRSTISNVDMV 824

                    FAKGDPGiAaLyDkLLv.aEeLkPFGksLRdkYvEtkdlLLkiAGHkDlL
                      K D  i a y kL  + E  +   k++  ++v t d+L ki G   lL
  gi|2608914   825 LSKTDLSIFAEYVKLASdQETAQKIFKEIEKEWVLTIDILKKITGNDVLL 874

                    EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                       P L   lR R sY   +n +q   +KR R               A
  gi|2608914   875 ADNPELVSSLRNRLSYFDSMNYLQIELIKRSR----------------AG 908

                    EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    ++s +    +++                 + G+A G+ n G
  gi|2608914   909 DDSEELRKAIHIS----------------INGLATGLRNSG    933

gi|115352520|ref|YP_774359.1|: domain 1 of 1, from 50 to 998: score 315.9, E = 8.1e-92
                    *->siDA...qLRlLvPGKvsedek...LieYDALLlDkFL.DiLqDLHG
                        i A+++  R   PG    ++k+++L e D   l + L+D++ +  G
  gi|1153525    50    TIKAsgpAARTAKPGVRTREDKdgpLFE-DIRFLGRLLgDVVREQEG 95

                    edLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailH
                    + + ++v      +  +    D++  + L  kL  L P  ++ v +a++
  gi|1153525    96 DTVFDVVETIRQTAVKFRREDDSEAAQTLEKKLRKLTPEQTVSVVRAFSY 145

                    mLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkl
                       LAn+AE+ +   RRRi+ +        +sA     +   l +L   +
  gi|1153525   146 FSHLANIAEDRHHNRRRRIHALA-------GSAPQPGTVAYALEQLKTTG 188

                    nKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKD
                    n s            +  vltAHPt   R+s+L  +  i   La    +
  gi|1153525   189 NASKRLLQRFFDDALIVPVLTAHPTEVQRKSILDAQHDIARLLAE-RDQP 237

                    vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWk
                    +t  ++   +  L   + A + t  +R ++ t  DE+   +sY+  t  +
  gi|1153525   238 LTARERSYNESMLRARVTALWQTRMLRDSRLTVGDEIENALSYYRATFLD 287

                    GvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEv
                      P     ++ AL   G+  R+P     ++  sW+GGDRDG nP vt
  gi|1153525   288 ELPALYGDIEAALAEHGLPARVP---AFLQMGSWIGGDRDG-NPNVTGPT 333

                    tRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaard
                      +       +    Y++qv  L  Els+    + L v A +  +  a
  gi|1153525   334 LDEAINRQAAVILEHYLEQVHKLGAELSV----SNLLVGANDAVKALAAA 379

                    kvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                               q P++  EPYR  L  +  +L      aR  L  G   +
  gi|1153525   380 --------SPDQSPhrVDEPYRRALIGIYTRLAAS---ARVRLGEGTVPV 418

                    ........sEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLR
                    ++ +++ ++  A++y + E F+  L +   sL e     +A   L  l+R
  gi|1153525   419 rsagrgapPVRAIpYADSEAFVADLKVLTASLEEHHGASLAAPRLTPLVR 468

                    qvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWL
                        FG  L  +D+Rq s+ +  v+  +    ++ ++Y   +Ee +   L
  gi|1153525   469 AAEVFGFHLASIDLRQSSDIHEAVVAELFARAGVEAdYAALAEEDKLRVL 518
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                    laELkGKRPLlgsDLPktEEvkDvldaf....rvLAELPiDsFGaYiism
                    la L   RPL  + L      +  l+ f++ ++v A     +   Yiis
  gi|1153525   519 LAALADPRPLRSPYLEYSALAQSELGVFekarEVRAQFGARAVRNYIISH 568

                    ataPsDvLAvELLqREC.........gvkqtLrvvPLFEkLADLeAAPAa
                    + + sD + v LLq+E +  +++ +++ k+ L v+PLFE + DL+ A
  gi|1153525   569 TETVSDLVEVLLLQKETgllegplgsHAKNGLMVIPLFETIPDLRDAARI 618

                    vekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEi
                    +   F+ ++iD  i +    qevm+GYsDs KD G l   W LY+A   +
  gi|1153525   619 MREYFAlpgIDALIAHQGAEQEVMLGYSDSNKDGGFLTSNWELYRAELAL 668

                    iKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqG
                    + v ++  + L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qG
  gi|1153525   669 VDVFRERKITLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQG 718

                    EviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv...sPkPEWRkLmeemA
                    Evi   F   ++  r L    AAtLE  + P  + ++  P +   m+ +
  gi|1153525   719 EVIASKFANPEIGRRNLETVVAATLEASLLPQSnapAQLPAFEAAMQTLS 768

                    vvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....
                      A   YR++v+  P F +YF + tP +E   +niGsRPa Rk   ++++
  gi|1153525   769 DAAMASYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASRKLQDpknr 818

                    GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiKnlqk
                     ie LRAiPW F+W q R  L  W G+G A    +d+ +++    K l
  gi|1153525   819 KIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVSAYLDgapdeaERTKRLTL 868

                    LkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksL
                    Lk m k+WPFF   l  ++mv AK D  +A+ y +L+    L+k   +++
  gi|1153525   869 LKKMNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVADRKLrKHVFERI 918

                    RdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLK
                     ++++ t + L +i GH   L   P L   ++ R +Y+  Ln +q   +K
  gi|1153525   919 VAEWERTSQALAEITGHEGRLATNPLLARSIKNRFPYLDPLNHLQVELIK 968

                    RiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLt
                    R R               A +           n   r   G+     Lt
  gi|1153525   969 RHR----------------AGDT----------N--ARLRRGIH----LT 986

                    mKGiAAGmqntG<-*
                    + GiAAG+ ntG
  gi|1153525   987 INGIAAGLRNTG    998

gi|187923069|ref|YP_001894711.1|: domain 1 of 1, from 125 to 1075: score 315.8, E = 8.9e-92
                    *->siDAqLRlLvP...GKvsed.ekLieYDALLlDkFL.DiLqDLHGed
                          A     +P+++G+  ed+++ +  D   l + L+D+L +  G+
  gi|1879230   125    QSPASANTSAPkgnGRTREDkDHPLFQDIRYLGRLLgDVLREQEGDA 171

                    LkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmL
                    + ++v      +  +     D+   + L  kL sL P  ++ v +a++
  gi|1879230   172 VFDVVETIRQNAVRFRREDDSAAAQTLDKKLRSLSPEQTVSVVRAFSYFS 221

                    nLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnK
                     LAn+AE+ +   R Ri+ +        +s      i   l +Lv
  gi|1879230   222 HLANIAEDRHRNRRHRIHALA-------GSTSQPGTIAHALERLVEAN-A 263

                    sPeEvFeALKnqsvDL.vltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                    +   v +   n +  ++vltAHPt   R+s+L  +  +   La    + +
  gi|1879230   264 AATPVLQQFFNDALIVpVLTAHPTEVQRKSILDAQHDVARLLAE-RDQQL 312

                    tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                    t  ++   +  L   +   + t  +R ++    DE+   +sY+  t
  gi|1879230   313 TERERAHNEAMLRARVTSLWQTRMLRDSRLSVADEIENALSYYRATFLTE 362

                    vPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                    +P     ++ AL   Gi  RlP   P  +  sW+GGDRDG nP vt E
  gi|1879230   363 IPALYADIEEALTEHGIDARLP---PFFQMGSWIGGDRDG-NPNVTAETL 408

                    RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaard
```

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                          +    Y++qv  L  Els+    + L + A+E l+  aa
  gi|1879230   409 ENAITRQAAVIFEHYMEQVHKLGAELSV----SNLLAGAsEALKELAAIS 454

                    kvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER....aRHLLAt
                               q P++  EPYR  L  +  +L  + R R ++++  +
  gi|1879230   455 ---------PDQSPhrTDEPYRRALIGMYTRLAAsARVRlgegSVPVRSA 495

                    GiseisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvs
                    G    +  A +y +  eF+  L +   sL e     +A   L  l R
  gi|1879230   496 GRGVAPIRAKpYDDSSEFVRDLHVLIDSLAEHHGAPLAAPRLSPLARAAE 545

                    tFGLsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaE
                     FG  L  +D+Rq s+ +  v+  + +  ++ + Y    Ee +   LlaE
  gi|1879230   546 VFGFHLASIDLRQSSDIHEAVIAELLKRAGVEdDYAALTEEDKLKVLLAE 595

                    LkGKRPLlgsDLPktEEvkDvldafrvLAELPi..DsFGa.....Yiism
                    L   R L    LP  E    v   + vL E  i+++ FGa+  ++Yiis
  gi|1879230   596 LAQPRSL---RLPYAEYSDLVKSELGVLEEARItrEKFGAravrnYIISH 642

                    ataPsDvLAvELLqRECgv............kqtLrvvPLFEkLADLeAA
                    + + sD + v LLq+E g+ +++ ++ +++ +  L v+PLFE + DL+ A
  gi|1879230   643 TETVSDLVEVMLLQKETGLlrgrlgdandpaQAGLMVIPLFETIPDLRNA 692

                    PAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAq
                    P  +  L + +++D  i +    qevm+GYsDs KD G l   W LY+A
  gi|1879230   693 PHIMRDLIAlpgVDALIEHQGNEQEVMLGYSDSNKDGGFLTSNWELYRAE 742

                    EEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvt
                      ++    + Gv L lFHGRGGtvGRGGGPt  AiLsqPP t++G +R t
  gi|1879230   743 LALVSLFNERGVTLRLFHGRGGTVGRGGGPTYQAILSQPPGTVDGQIRLT 792

                    vqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP.vsPk..PEWRkLme
                     qGEvi   FG  ++  r L    AAtLE  + P +++P + P + + m+
  gi|1879230   793 EQGEVIASKFGNPEIGRRNLETVVAATLEASLLPHdIAPAqlPAFEETMQ 842

                    emAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.
                    ++   A   YR++v+  P F EYF   tP  E   +niGsRPa Rk   +
  gi|1879230   843 QLSDAAMASYRALVYETPGFKEYFFESTPIAEIAELNIGSRPASRKLQDp 892

                    ...GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid...KDiK...n
                    +++ ie LRAiPW F+W q R  L  W G+G A    +d+ + D  +++
  gi|1879230   893 kqrKIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVATYLDsapTDAErksR 942

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFG
                    l  Lk m k+WPFF   l  ++mv AK D  +A+ y  L+    L+k
  gi|1879230   943 LALLKKMHKTWPFFANLLSNMDMVLAKTDLAVASRYAALVSDKKLrKHVF 992

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    +++ ++++ t + L +i G  + L   P L   ++ R +Y+  Ln +q
  gi|1879230   993 ERIVAEWERTSKVLSEITGKSERLAENPLLARSIKNRFPYLDPLNHLQVE 1042

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     LKR R                A +           n   rv  G+
  gi|1879230  1043 LLKRHR----------------AGDT----------N--ARVRRGIH--- 1061

                    iLtmKGiAAGmqntG<-*
                     L + GiAAG+ ntG
  gi|1879230  1062 -LSINGIAAGLRNTG    1075

gi|119962288|ref|YP_946565.1|: domain 1 of 1, from 10 to 932: score 315.0, E = 1.6e-91
                    *->siDAqLRlLvPGKvse..dekLieYDALLlDkFLDiLqDLHGedLkE
                        + A LR+ v  +vs    e L++     l + ++ +  L  e+ kE
  gi|1199622    10    DLAAELRADVR-RVSTllGESLVRQHGPELLQLVEQVRLLTKES-KE 54

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    a     +    +       ++ EL   L sL    a  + +a+     L
  gi|1199622    55 AARGGADATGPWSAHDVVAQVREL---LASLPLDQATDLVRAFAFYFHLS 101

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n AE v+     R ++ k     D   A   s+i          ++  P+
  gi|1199622   102 NAAEQVHRVRGLRTRQEK-----DGWLAKAVSEI---------AGQAGPQ 137
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                  EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                     + +    v  ++tAHPt + RRs+L K  ++   La   A
  gi|1199622   138 VLQDVINGLDVRPIFTAHPTEASRRSVLDKVRKLSDVLAEPTAEGTSARR 187

                  KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                  ++  D  L   i   + tDE+R  +PtP DE R  + Y+   + + +P
  gi|1199622   188 RQ--DQQLAEIIDQMWQTDELRQVRPTPVDEARNAIYYLNSILTDAMPEM 235

                  LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                  L      L   G+   lP  +  +kF sW+GGDRDG nP vt  vt+++
  gi|1199622   236 LTDLSELLAEHGVT--LPAAAAPLKFGSWIGGDRDG-NPNVTAAVTKEIL 282

                  LLaRmmAanlYisqvEDLmFEls....mWRCndELR.vRAEElyrtaard
                   L    A  + i  +++L+  ls+++ ++   +EL +    +l+  +  d
  gi|1199622   283 QLQNQNAVRISIALIDELISVLSnstaLFGADQELLdSITADLKNLPGLD 332

                  kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                     K  +E   q    EPYR  L  ++ KL nt    R + A  + e
  gi|1199622   333 ---KRILELNAQ----EPYRLKLTCIKAKLINT---GRRISASTYHEPGR 372

                  eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                  +  y    e L    L   sL +     +ADG+L  + R +  FGL L
  gi|1199622   373 D--YATTPELLAEFGLLEASLRNHSAGLVADGALARVRRAIAAFGLHLAT 420

                  LDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPL.
                  LDiR  ++ + D +  +   L+  ++Y e   e R  +L aEL  +RPL+
  gi|1199622   421 LDIREHADYHHDAVGQLVDRLGTEkAYGELTREERFTFLGAELASRRPLs 470

                  .lgsDLPktEE.vkDvldafr.vLAELPiDsFGaYiismataPsDvLAvE
                  + +  L  t ++  Dv  ++r+ L     D    Yiism+    DvLA
  gi|1199622   471 gHPIKLEGTADgTYDVFRSIRqALHTYGPDVVETYIISMTRGADDVLAAA 520

                  LLqRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYin
                  +L RE g+ +  +++++  +   PL E + +L+A    v++L s   Y+
  gi|1199622   521 VLAREAGLidlfsgkpHAKIGFAPLLETVEELRASAEIVDQLLSDPSYRE 570

                  ..ridGK.qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                    r+ G  qevm+GYsDs K+ G +   W + k q  +  vA k+Gv++
  gi|1199622   571 lvRLRGDiQEVMLGYSDSNKESGVMTSQWEIHKTQRKLRDVAAKHGVRVR 620

                  lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                  lFHGRGG vGRGGGPt  Ai++qP   ++G ++ t qGEvi   +   +L
  gi|1199622   621 LFHGRGGSVGRGGGPTYDAIMAQPNGVLEGEIKFTEQGEVISDKYSLPEL 670

                  CFrsLqRFtAAtLE.HGmn..PPvs..PkPEWRkLmeemAvvAtEEYRsv
                      L    AA + +  ++++P  s++ +  + ++me +   A   YR +
  gi|1199622   671 ARENLELSLAAVMQgSALHrtPRTSddERERYANVMETISDAAFARYRTL 720

                  vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFa
                  +  +P    YF   tP    G +niGsRP+KR  sG G+  LRAiPW+F
  gi|1199622   721 I-DDPQLPAYFLASTPVEQLGSLNIGSRPSKRPDSGaGLGGLRAIPWVFG 769

                  WtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlE
                  Wtq R  +P W GvG   K A  ++     +L Em + W FFR  +  +E
  gi|1199622   770 WTQSRQIVPGWFGVGSGLKAA--REAGDTDQLLEMMDRWHFFRSVISNVE 817

                  mvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDl
                  m  AK D  iA+ y   Lv EeL+   + +Rd+Y+ t   + ++ G  +l
  gi|1199622   818 MTLAKTDMEIAGHYVSSLVPEELHRLFHMIRDEYELTVAEIERLTGEMEL 867

                  LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                  L+  P LK  l +Rd Y+  +  +q   L+R+R
  gi|1199622   868 LDAQPTLKRSLEIRDQYLDPISYLQVELLRRVR----------------- 900

                  dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   E+        +L  + ++   L   +++t+ G+AAG+ ntG
  gi|1199622   901 -EE--------QLS-GGEIDERLQRAMLITVNGVAAGLRNTG    932

gi|152967316|ref|YP_001363100.1|: domain 1 of 1, from 28 to 954: score 313.7, E = 3.8e-91
                  *->siDAqLRlLvPGKvsedekLieYDALL..lDkFLDi.LqDLHGedLk
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                    A   +L    vs de      A +++l   L  +L    G +L
gi|1529673    28    ---ASQDVLTVDGVSSDEGHAALRASVrrLGELLGAsLTRHEGAELL 71

                  EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                  + v     l+      +++    EL   L ++d   ai++A+a+     L
gi|1529673    72 DLVERVRALA------READDGAELARLLSGVDDRTAIVLARAFTAYFQL 115

                  AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                  An  E     +R     k+       +   t   + E l    l    +
gi|1529673   116 ANASEQL---HRGLELSKQ----PGGGLSATLGRVREALESGDLDR-DTA 157

                  eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                  + +   L+      v+tAHPt s RRs+L    Ri   +
gi|1529673   158 QQILGRLQLRP---VFTAHPTESSRRSILDLLLRITGIVEASEDPAQRAT 204

                  DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                  D +     L   +   + tDE+R  +P P DE R  + Y+        P
gi|1529673   205 DAERGQRRLAELVDLLWQTDELRVLRPRPADEARSALHYLRNLTSTVLPD 254

                  FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                   L      L  +G+   lP d+  ++F sW+GGDRDG nP vtPEvt +v
gi|1529673   255 LLEDLAVGLDELGLD--LPVDAQPLRFGSWVGGDRDG-NPNVTPEVTMEV 301

                  CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                    L    A  +      DL+ El+     + +    E l + aa
gi|1529673   302 LGLQHDAALDVLTAVTRDLLTELAA--STQVVGFSPELLASLAADAEALP 349

                  yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                           +  +EPYR  L  v  +L  tR R    L tG   ++    y
gi|1529673   350 EVHAARVHLNGEEPYRFKLSYVLARLEGTRTR----LHTGAEHVPGRD-Y 394

                  tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                    v eF   L L   sL     + +ADG++   LR v   G  L  LD+R
gi|1529673   395 AGVGEFTADLLLIQDSLRRNDGQMVADGAVARALRVVRAVGFGLATLDVR 444

                  qEseRqtDvlDAittHLe..iGsYReWsEeKRqEWLlaELkGKRPLlgsD
                    + R+ + l Ai   L++ i  Y       R   L  E+ G RPL+g+
gi|1529673   445 EHAGRHHEALAAIYDRLGelITPYAALDRSARTKLLSKEMTGHRPLIGAA 494

                  L.PktEEvkDvldafrvLAELPiDsFG.....aYiismataPsDvLAvEL
                  ++  t   + v++ f  +     D FG+++ + Yi+sm+    D  Av +
gi|1529673   495 VrTLTGTPAQVVQLFTTI-RTALDRFGeetieTYIVSMTQGIDDLFAVVV 543

                  LqRECgvkq...........tLrvvPLFEkLADLeAAPAavekLFsiDWY
                  L RE g+    ++++ ++   +   PLFE + +LeAA   +e L s   Y
gi|1529673   544 LAREVGLVDlaetpgandvaRIGFAPLFETVTELEAAEELLEGLLSDPSY 593

                  inridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvK
                  +  +  +++ qe+m+GYsDs KDAG  +  Wq+ +Aq  +  vA ++Gv
gi|1529673   594 RRVVAARgdvQEIMLGYSDSSKDAGIAASRWQIHRAQRALRDVAARHGVT 643

                  LvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEE
                  L lFHGRGG vGRGGGPt  AiL+qP  t++G ++vt qGEvi   +
gi|1529673   644 LRLFHGRGGSVGRGGGPTGEAILAQPYGTLDGPIKVTEQGEVISDKYVQP 693

                  nLCFrsLqRFtAAtLEHGmnPPvsPkP.....EWRkLmeemAvvAtEEYR
                   L  + L     A LE       s +P++  + W   m  +A    E YR
gi|1529673   694 RLARHNLEVALSAALEASTLHRTSLQPgevldGWDTTMGLVAAKGQEAYR 743

                  svvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs..GGiesLRAiPW
                  ++v  +P  v +F  AtP  E G +niGsRP+ R+P+++GG+e LRAiPW
gi|1529673   744 ALV-GDPGLVPFFLAATPVEELGNLNIGSRPS-RRPGgtGGLEDLRAIPW 791

                  iFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlD
                  +F Wtq R  +P W GvG   + A  ++      L+ m+  W FFR  +
gi|1529673   792 VFGWTQSRINVPGWFGVGSGLRAA--REAGRGEDLRAMFAGWSFFRSFVS 839

                  LlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGH
                   + m  AK D GiAa y + Lva + +   + +R++   t + +L +
gi|1529673   840 NVQMTLAKTDLGIAAHYVEELVAPDQRGAFDVIRAEHARTLEEVLLLTEQ 889
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                    kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                     +lL   P L+  l LRd+Y+  L  +q   L R R
  gi|1529673   890 DELLQSAPVLRRTLELRDAYLAPLHALQVSLLGRAR-------------- 925

                    EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                    ++ v P L   L+Lt+ GiAAGm ntG
  gi|1529673   926 ----------------ASGDAVDPALRRALLLTINGIAAGMRNTG    954

gi|172061377|ref|YP_001809029.1|: domain 1 of 1, from 53 to 998: score 313.6, E = 4e-91
                    *->siDAqLRlLvPGKvsedek...LieYDALLlDkFL.DiLqDLHGedL
                             R   PG    ++k+++L e D   l + L+D++ +  G+ +
  gi|1720613    53    TSGPAARTAKPGVRTREDKdgpLFE-DIRFLGRLLgDVVREQEGDTV 98

                    kEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLn
                     ++v      +  +    D++  + L  kL  L P  ++ v +a++
  gi|1720613    99 FDVVETIRQTAVKFRREDDSEAAQTLEKKLRKLTPEQTVSVVRAFSYFSH 148

                    LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                    LAn+AE+ +   RRRi+ +        +sA     +   l +L   +n s
  gi|1720613   149 LANIAEDRHHNRRRRIHALA-------GSAPQPGTVAYALEQLKTTGNAS 191

                    PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                                +  vltAHPt   R+s+L  +  i   La    + +t
  gi|1720613   192 KRLLQRFFDDALIVPVLTAHPTEVQRKSILDAQHDIARLLAE-RDQPLTA 240

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                     ++   +  L   + A + t  +R ++ t  DE+   +sY+  t  +  P
  gi|1720613   241 RERSYNESMLRARVTALWQTRMLRDSRLTVGDEIENALSYYRATFLDELP 290

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                         ++ AL   G+  R+P      +  sW+GGDRDG nP vt     +
  gi|1720613   291 ALYGDIEAALAEHGLPARVP---AFFQMGSWIGGDRDG-NPNVTGPTLDE 336

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                           +    Y++qv  L  Els+    + L v A +  +  a
  gi|1720613   337 AINRQAAVILEHYLEQVHKLGAELSV----SNLLVGANDAVKALAAA--- 379

                    KyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGisei...
                            q P++  EPYR  L  +  +L      aR  L  G   +++
  gi|1720613   380 -----SPDQSPhrVDEPYRRALIGIYTRLAAS---ARVRLGEGTVPVrsa 421

                    .....sEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvs
                    +++ ++  A++y + E F+  L +   sL e     +A   L  l+R
  gi|1720613   422 grgapPVRAIpYADSEAFVADLKVLTASLEEHHGASLAAPRLTPLVRAAE 471

                    tFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaE
                     FG  L  +D+Rq s+ +  v+  +    ++ ++Y   +Ee +   Lla
  gi|1720613   472 VFGFHLASIDLRQSSDIHEAVVAELFARAGVEAdYAALAEEDKLRVLLAA 521

                    LkGKRPLlgsDLPktEEvkDvldaf....rvLAELPiDsFGaYiismata
                    L   RPL  + L      +  l+ f++ ++v A     +   Yiis + +
  gi|1720613   522 LADPRPLRSPYLEYSALAQSELGVFekarEVRAQFGARAVRNYIISHTET 571

                    PsDvLAvELLqREC.........gvkqtLrvvPLFEkLADLeAAPAavek
                     sD + v LLq+E +  +++ +++ k+ L v+PLFE + DL+ A   +
  gi|1720613   572 VSDLVEVLLLQKETgllegplgsHAKNGLMVIPLFETIPDLRDAARIMRE 621

                    LFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKv
                     F+ ++iD  i +    qevm+GYsDs KD G l   W LY+A   ++ v
  gi|1720613   622 YFAlpgIDALIAHQGAEQEVMLGYSDSNKDGGFLTSNWELYRAELALVDV 671

                    AKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEvi
                     ++  + L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGEvi
  gi|1720613   672 FRERKITLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEVI 721

                    EfsFGEEnLCFrsLqRFtAAtLEHGmnPPv...sPkPEWRkLmeemAvvA
                       F   ++  r L    AAtLE  + P  + ++  P +   m+ +   A
  gi|1720613   722 ASKFANPEIGRRNLETVVAATLEASLLPQSnapAQLPAFEAAMQTLSDAA 771

                    tEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....Gie
                       YR++v+  P F +YF + tP +E   +niGsRPa Rk   ++++ ie
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  gi|1720613   772 MASYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASRKLQDpknrKIE 821

                   sLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiKnlqkLkE
                    LRAiPW F+W q R  L  W G+G A    +d+ ++     K l  Lk
  gi|1720613   822 DLRAIPWGFSWGQCRLLLTGWYGFGSAVSAYLDgapdaaERTKRLTLLKK 871

                   mYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdk
                   m k+WPFF   l  ++mv AK D  +A+ y +L+    L+k   +++ ++
  gi|1720613   872 MNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVADRKLrKHVFERIVAE 921

                   YvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiR
                   ++ t + L +i GH   L   P L   ++ R +Y+  Ln +q   +KR R
  gi|1720613   922 WERTSQALAEITGHEGRLATNPLLARSIKNRFPYLDPLNHLQVELIKRHR 971

                   DPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKG
                                A +           n   r   G+     Lt+ G
  gi|1720613   972 ----------------AGDT----------N--ARLRRGIH----LTING 989

                   iAAGmqntG<-*
                   iAAG+ ntG
  gi|1720613   990 IAAGLRNTG    998

gi|170703457|ref|ZP_02894226.1|: domain 1 of 1, from 53 to 998: score 313.5, E = 4.3e-91
                   *->siDAqLRlLvPGKvsedek...LieYDALLlDkFL.DiLqDLHGedL
                            R   PG    ++k+++L e D   l + L+D++ +  G+ +
  gi|1707034    53    TSGPAARTAKPGVRTREDKdgpLFE-DIRFLGRLLgDVVREQEGDTV 98

                   kEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLn
                    ++v      +  +    D++  + L  kL  L P  ++ v +a++
  gi|1707034    99 FDVVETIRQTAVKFRREDDSEAAQTLEKKLRKLTPEQTVSVVRAFSYFSH 148

                   LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                   LAn+AE+ +   RRRi+ +        +sA     +   l +L   +n s
  gi|1707034   149 LANIAEDRHHNRRRRIHALA-------GSAPQPGTVAYALEQLKTTGNAS 191

                   PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                              +  vltAHPt   R+s+L  +  i   La    + +t
  gi|1707034   192 KRLLQRFFDDALIVPVLTAHPTEVQRKSILDAQHDIARLLAE-RDQPLTA 240

                   eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                    ++   +  L   + A + t  +R ++ t  DE+   +sY+  t  +  P
  gi|1707034   241 RERSYNESMLRARVTALWQTRMLRDSRLTVGDEIENALSYYRATFLDELP 290

                   KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                        ++ AL   G+  R+P      +  sW+GGDRDG nP vt     +
  gi|1707034   291 ALYGDIEAALAEHGLPARVP---AFFQMGSWIGGDRDG-NPNVTGPTLDE 336

                   vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                          +    Y++qv  L  Els+    + L v A +  +  a
  gi|1707034   337 AINRQAAVILEHYLEQVHKLGAELSV----SNLLVGANDAVKALAAA--- 379

                   KyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGisei...
                          q P++  EPYR  L  +  +L      aR  L  G   +++
  gi|1707034   380 -----SPDQSPhrVDEPYRRALIGIYTRLAAS---ARVRLGEGTVPVrsa 421

                   .....sEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvs
                   +++ ++  A++y + E F+  L +   sL e     +A   L  l+R
  gi|1707034   422 grgapPVRAIpYADSEAFVADLKVLTASLEEHHGASLAAPRLAPLVRAAE 471

                   tFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaE
                    FG  L  +D+Rq s+ +  v+  +    ++ ++Y   +Ee +   Lla
  gi|1707034   472 VFGFHLASIDLRQSSDIHETVVAELFARAGVEAdYAALAEEDKLRVLLAA 521

                   LkGKRPLlgsDLPktEEvkDvldaf....rvLAELPiDsFGaYiismata
                   L   RPL  + L      +  l+ f++ ++v A     +   Yiis + +
  gi|1707034   522 LADPRPLRSPYLEYSALAQSELGVFekarEVRAQFGARAVRNYIISHTET 571

                   PsDvLAvELLqREC.........gvkqtLrvvPLFEkLADLeAAPAavek
                    sD + v LLq+E +  +++ +++ k+ L v+PLFE + DL+ A   +
  gi|1707034   572 VSDLVEVLLLQKETgllegplgsHAKNGLMVIPLFETIPDLRDAARIMRE 621
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                    LFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKv
                     F+ ++iD  i +    qevm+GYsDs KD G l   W LY+A   ++ v
  gi|1707034   622 YFAlpgIDALIAHQGAEQEVMLGYSDSNKDGGFLTSNWELYRAELALVDV 671

                    AKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEvi
                     ++  + L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGEvi
  gi|1707034   672 FRERKITLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEVI 721

                    EfsFGEEnLCFrsLqRFtAAtLEHGmnPPv...sPkPEWRkLmeemAvvA
                       F   ++  r L    AAtLE  + P  + ++  P +   m+ +   A
  gi|1707034   722 ASKFANPEIGRRNLETVVAATLEASLLPQSnapAQLPAFEAAMQTLSDAA 771

                    tEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....Gie
                       YR++v+  P F +YF + tP +E   +niGsRPa Rk   ++++ ie
  gi|1707034   772 MASYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASRKLQDpknrKIE 821

                    sLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiKnlqkLkE
                     LRAiPW F+W q R  L  W G+G A    +d+ ++     K l  Lk
  gi|1707034   822 DLRAIPWGFSWGQCRLLLTGWYGFGSAVSAYLDgapdaaERTKRLTLLKK 871

                    mYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdk
                    m k+WPFF   l  ++mv AK D  +A+ y +L+    L+k   +++ ++
  gi|1707034   872 MNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVADRKLrKHVFERIVAE 921

                    YvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiR
                    ++ t + L +i GH   L   P L   ++ R +Y+  Ln +q   +KR R
  gi|1707034   922 WERTSQALAEITGHEGRLATNPLLARSIKNRFPYLDPLNHLQVELIKRHR 971

                    DPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKG
                                   A +           n   r   G+     Lt+ G
  gi|1707034   972 ----------------AGDT----------N--ARLRRGIH----LTING 989

                    iAAGmqntG<-*
                    iAAG+ ntG
  gi|1707034   990 IAAGLRNTG    998

gi|256776822|ref|ZP_05515285.1|: domain 1 of 1, from 3 to 906: score 313.5, E = 4.4e-91
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s D    +L                 L D   + L    G+dL + v
  gi|2567768     3    SADHTNAALRADIRR-----------LGDLLGETLVRQEGPDLLDLV 38

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         l      + D +   EL   L   d   a  + +a++    LAn+
  gi|2567768    39 ERVRALT-----RSDGEAAAEL---LGTTDLPTAAKLVRAFSTYFHLANV 80

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     E v   +R R    +         A     +  t+ +L        +
  gi|2567768    81 TEQV---HRSRELSAR--------RAAEGGILARTVDQLKDAD---ADHL 116

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     + +    v  v+tAHPt ++RR +L K  Ri   L  L A      + +
  gi|2567768   117 RQTVEHLGVRPVFTAHPTEAARRTVLNKLRRIAELLDTLAA----GGESR 162

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                      D  L   i   + tDE+R a+P P DE R  + Y+ E   + v   L
  gi|2567768   163 RSDLRLAENIDLLWQTDELRVARPEPADEARNAVYYLDELHAHAVGDVLE 212

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         L  +Gi   lP     + F  W+GGDRDG nP vtP vt +v +L
  gi|2567768   213 DLTAELERVGIE--LPATTRPLTFGTWIGGDRDG-NPNVTPQVTWEVLIL 259

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                              ++ ++DL   ls    n+   +  EEl    +rd
  gi|2567768   260 QHEHGISDALEIIDDLRAALSSSIRNS---AASEELLASLQRD--LELLP 304

                    EF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                    E ++++K +  +EPYR     +R KL ntRER    LA+    ++    y
  gi|2567768   305 EIsprYKRLNAEEPYRLKATCMRQKLVNTRER----LAKDAPHVPGRD-Y 349

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                        e L  L L   sL       iADG L   +R    FG+ L  +D+R
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  gi|2567768   350 LGTAEMLADLKLIQDSLRAHRGALIADGRLERAIRTLAAFGIQLATMDVR 399

                   qEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLlgsD
                     ++ +   l  +   L+  s+R  + + + R+  L  EL+ +RPL +s
  gi|2567768   400 EHADAHHHALGQLFDRLGEESWRyaDMPRDYRRKLLAKELRSRRPLAPSP 449

                   LPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAvELLq
                    P     +  l+ f+ + E+ ++   D   +Yiism+    Dv A  +L
  gi|2567768   450 APLDAAGAKTLGVFQTIREsferFGPDIVESYIISMCAGSDDVFAAAVLA 499

                   RECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK
                   RE g+   +++   + +vPL E   +L+ A   ++ + s   Y+  +  +
  gi|2567768   500 REAGLIDlhggwaKIGIVPLLETTDELKIADQLLDDMLSDPSYRRLVSLR 549

                   ...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                   ++ qevm+GYsDs K  G     W + +Aq  +  vA ++Gv+L lFHGR
  gi|2567768   550 gdvQEVMLGYSDSSKFGGITTSQWEIHRAQRLLRDVAHRHGVRLRLFHGR 599

                   GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                   GGtvGRGGGPtH AiL+qP  t++G ++vt qGEvi   +    L    L
  gi|2567768   600 GGTVGRGGGPTHDAILAQPWGTLEGEIKVTEQGEVISDKYLVPSLARENL 649

                   qRFtAAtLEHGm...nPPvsPk..PEWRkLmeemAvvAtEEYRsvvvKEP
                       AAtL     ++ P  s      W   me +   A   YR++v  +P
  gi|2567768   650 ELTVAATLQASAlhtAPRQSDEalARWDSTMETVSDAAHGAYRALV-DDP 698

                   RFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqtR
                       YF   tP      + +GsRP++R  sG G++ LRAiPW+F Wtq R
  gi|2567768   699 DLPAYFFASTPVDQLAELHLGSRPSRRPDSGaGLDGLRAIPWVFGWTQSR 748

                   FHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAK
                     +P W GvG   K A +     +  L Em + W FFR  l  +Em  AK
  gi|2567768   749 QIVPGWFGVGSGLKAAREAGLDGV--LDEMHQHWHFFRNFLSNVEMTLAK 796

                   GDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDP
                    D  iA  y + Lv +eLk   + + ++ + t   +L+i G  +lL+  P
  gi|2567768   797 TDLRIARHYVDTLVPDELKHVFDVIQAEHELTVREVLRITGEAELLDSNP 846

                   YLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnsk
                    LKq   +Rd+Y+  +  +q   L R R                A E
  gi|2567768   847 VLKQTFHVRDAYLDPISYLQVSLLDRQRT---------------ARER-- 879

                   kadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                             +e+  P L   L+Lt+ G+AAG+ ntG
  gi|2567768   880 ----------GEEPDPVLARALLLTVNGVAAGLRNTG    906

gi|254396574|ref|ZP_05011634.1|: domain 1 of 1, from 3 to 909: score 312.8, E = 6.9e-91
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      s D       P   +   +L      L D   + L    G++L + v
  gi|2543965     3    SADQ-----TPTASA---ELRADIRRLGDLLGETLVRQEGPELLDLV 41

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        l    +G   ++ L++     t L+ a  ++  +a++    LAn+
  gi|2543965    42 ERVRALTRT-DGEAAAELLGD-----TDLETAAKLV--RAFSTYFHLANV 83

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    E v+  +  R ++   G            +  t  +L       P+
  gi|2543965    84 TEQVHRGHEMRARRAAEGGL-----------LAITADRLKDAD---PQHL 119

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    e +Kn  v  v+tAHPt ++RRs+L K  Ri    a L    v   D++
  gi|2543965   120 RETVKNLNVRPVFTAHPTEAARRSVLNKLRRI----AELLESPVIAADRR 165

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     D  L   i   + tDE+R  +P P DE R  + Y+ E     v   L
  gi|2543965   166 RHDLRLAEHIDLIWQTDELRVVRPEPADEARNAIYYLDELHAGAVGDVLE 215

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                        L  +G+ E  P   PL  F  W+GGDRDG nP vtP vt +v +L
  gi|2543965   216 DLAAELERVGV-ELPPGTRPL-TFGTWIGGDRDG-NPNVTPAVTWEVLIL 262
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                    aRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkvvKyY
                             i+ ++ L   ls    n+   + A+EEl    + d
  gi|2543965   263 QHEHGITDAIEVIDYLRGLLS----NSIRYAGAtEELLASLQTD--LERL 306

                    iEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                     E ++++K +  +EPYR     +R KL ntRER    LA+G     +
  gi|2543965   307 PEIsprYKRLNAEEPYRLKATCIRQKLVNTRER----LAKGTPH-EDGRD 351

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y    e +  L L   sL e      ADG +  ++R  s FGL L  +D+
  gi|2543965   352 YLGTAELIADLTLIQTSLREHRGGLFADGRMDRVIRTLSAFGLQLATMDV 401

                    RqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLlgs
                    R  ++ +   l  +   L+  s+R  + + + Rq  L  EL+ +RPL +
  gi|2543965   402 REHADAHHHALGQLFDRLGEESWRyaDMPRDYRQKLLAKELRSRRPLAPT 451

                    DLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvEL
                      P     +  l+ f+ + E   + FG++  ++Yiism+    Dv A  +
  gi|2543965   452 PAPLDAAGQKTLGVFHTVKE-AFERFGPeviesYIISMCQGADDVFAAAV 500

                    LqRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                    L RE g+   + +   + +vPL E   +L+AA   +e + +   Y+  +
  gi|2543965   501 LAREAGLIDlhagwaKIGIVPLLETTDELKAADVILEGMLADPSYRRLVS 550

                    GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                     +++ qevm+GYsDs K  G     W + +Aq  +  vA ++Gv+L lFH
  gi|2543965   551 LRgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRHGVRLRLFH 600

                    GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                    GRGGtvGRGGGP H AiL+qP  t++G ++vt qGEvi   +    L
  gi|2543965   601 GRGGTVGRGGGPSHDAILAQPWGTLEGEIKVTEQGEVISDKYLIPSLARE 650

                    sLqRFtAAtLEHGm...nPPvsPkP..EWRkLmeemAvvAtEEYRsvvvK
                     L    AAtL     ++ P  s    + W   m+ +   A   YR +v
  gi|2543965   651 NLELTVAATLQASAlhtAPRQSDEAlsRWDAAMDTVSDAAHAAYRRLV-E 699

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtq
                    +P    YF  AtP      + +GsRP++R  sG G++ LRAiPW+F Wtq
  gi|2543965   700 DPDLPAYFFAATPVDQLAELHLGSRPSRRPDSGaGLDGLRAIPWVFGWTQ 749

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     R  +P W GvG   K   +     +  L Em  +W FFR  +  +Em
  gi|2543965   750 SRQIVPGWFGVGSGLKALREAGLDTV--LAEMHGNWHFFRNFIANVEMTL 797

                    AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                    AK D  iA  y + Lv E+Lk   + + ++   t   +Lk+ G  +lL
  gi|2543965   798 AKTDLRIARHYVDTLVPENLKHVFEVIEAEHALTVSEVLKVTGNDELLGS 847

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                     P L+q   +Rd+Y+  +  +q   LKR RD               A+E
  gi|2543965   848 NPVLQQTFAIRDAYLDPISYLQVALLKRQRD---------------AAER 882

                    skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                +e+  P L   L+Lt+ G+AAG+ ntG
  gi|2543965   883 ------------GEEADPLLARALLLTVNGVAAGLRNTG    909

gi|239941867|ref|ZP_04693804.1|: domain 1 of 1, from 2 to 909: score 312.7, E = 7.5e-91
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       s   q  +  P   +        D   l   L++ L    G++L +
  gi|2399418     2    SSADQTPAASPALRA--------DIRRLGDLLgETLVRQEGQELLDL 40

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     l    +G   ++ L+E     t L+ a  ++  +a++    LAn
  gi|2399418    41 VERVRALTRT-DGEAAAELLGE-----TELETAAQLV--RAFSTYFHLAN 82

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E v+ A+  R ++   G             +  t  +L       Pe
  gi|2399418    83 VTEQVHRAHEMRDRRSAEGGL-----------LARTADRLKDAD---PEH 118

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      e +Kn  v  v+tAHPt ++RRs+L K  Ri    a L    v   D+
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  gi|2399418   119 LRETVKNLNVRPVFTAHPTEAARRSVLNKLRRI----AELLETPVIEADR 164

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   + LD  L   i   + tDE+R  +P P DE R  + Y+ E   + v   L
  gi|2399418   165 RRLDLRLAENIDLIWQTDELRVVRPEPADEARNAIYYLDELHANAVGDVL 214

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                         L  +G+   lP     + F  W+GGDRDG nP vtP vt Dv +
  gi|2399418   215 EDLAAELDRVGVE--LPAGTRPLTFGTWIGGDRDG-NPNVTPAVTWDVLI 261

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkvvKy
                   L         ++ ++ L   ls    n+   + A+EEl    + d
  gi|2399418   262 LQHEHGITDALEMIDYLRGLLS----NSIRYAGAtEELLTSLQADLERLP 307

                   YiE.FWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                    i + +K +  +EPYR     +R KL ntRER    LA G    +    y
  gi|2399418   308 GISpRYKRLNAEEPYRLKATCIRQKLVNTRER----LAEGTPHRP-GCDY 352

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                       e +  LEL   sL        ADG +   +R    FGL L  +D+R
  gi|2399418   353 LGTAELIADLELIQTSLRAHRGGLFADGRMDRTIRTLAAFGLQLATMDVR 402

                   qEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLlgsD
                     ++ +   l  +   L+  s+R  + + + Rq  L  EL+ +RPL +
  gi|2399418   403 EHADAHHHALGQLFDRLGEESWRyaDMPRDYRQKLLAKELRSRRPLAPTP 452

                   LPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvELL
                    P     +  l+ f+ +     + FG++  ++Yiism+    Dv A  +L
  gi|2399418   453 APLDAAGEKTLGVFHTIKQ-AFERFGPeviesYIISMCQGADDVFAAAVL 501

                   qRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                    RE g+   + +   + +vPL E   +L+AA   ++ + +   Y+  +
  gi|2399418   502 AREAGLVDlhagwaKIGIVPLLETTDELKAADHILDEMLADPSYRRLVSL 551

                   K...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                   +++ qevm+GYsDs K  G     W + +Aq  +  vA +yGv+L lFHG
  gi|2399418   552 RgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRYGVRLRLFHG 601

                   RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                   RGGtvGRGGGP H AiL+qP  t++G ++vt qGEvi   +    L
  gi|2399418   602 RGGTVGRGGGPSHDAILAQPWGTLEGEIKVTEQGEVISDKYLIPALAREN 651

                   LqRFtAAtLEHGm...nPPvsPk..PEWRkLmeemAvvAtEEYRsvvvKE
                   L    AAtL     ++ P  s      W   m+ +   A   YR +v  +
  gi|2399418   652 LELTVAATLQASAlhtAPRQSDEalARWDAAMDTVSDAAHSAYRKLV-ED 700

                   PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWtq
                   P    YF   tP      + +GsRPa R+P+ G++ + LRAiPW+F Wtq
  gi|2399418   701 PDLSAYFLASTPVDQLADLHLGSRPA-RRPGSGVslDGLRAIPWVFGWTQ 749

                   tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                    R  +P W GvG   K   +     +  L Em + W FFR  +  +Em
  gi|2399418   750 SRQIVPGWFGVGSGLKALREAGLDTV--LDEMHEHWHFFRNFISNVEMTL 797

                   AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                   AK D  iA  y + Lv +eLk   + + ++   t + +L+i G   lL+
  gi|2399418   798 AKTDLRIARHYVDTLVPDELKHVFDGIEAEHALTVQEVLRITGGEKLLDT 847

                   DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                    P L+q   +Rd+Y+  +  +q   L R R                A+E
  gi|2399418   848 NPVLQQTFSIRDAYLDPISYLQVSLLARQRQ--------------AAER 882

                   skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                              +e+  P L   L+Lt+ G+AAG+ ntG
  gi|2399418   883 ------------GEEPDPLLSRALLLTVNGVAAGLRNTG    909

gi|116669180|ref|YP_830113.1|: domain 1 of 1, from 26 to 954: score 312.1, E = 1.1e-90
                   *->siDAqLRlLvPGKvse..dekLi.eYDALLlDkFLDiLqDLHGedLk
                       +   LR+ v  +vs    e L+++    LlD    +   L  ++ k
  gi|1166691    26    DLASELRADVR-RVSTllGESLVrQHGPELLDLVEQV--RLLTKESK 69
```

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                EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                Ea     +    +       ++ EL   L sL    a  + +a+     L
gi|1166691    70 EAARGGADATGPWSSHDVVAQVREL---LGSLPIDQATDLVRAFAFYFHL 116

                AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                An AE v   +R R  + +      E +      +EE        ++  P
gi|1166691   117 ANAAEQV---HRVRGLRTR-----QEKDGWLAKAVEE------ISGQAGP 152

                eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                +   e +    v  ++tAHPt + RRs+L K  R+   La +s  + t
gi|1166691   153 AVLQEVVNELDVRPIFTAHPTEASRRSVLDKIRRLSDVLA-VSTEEGTSA 201

                DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                 ++  D  L   i   + tDE+R  +PtP DE R  + Y+   + + +P
gi|1166691   202 RRRQ-DRQLAEVIDQMWQTDELRQVRPTPVDEARNAIYYLNSILTDAMPE 250

                FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                 L      L   G+   lP +   i+F sW+GGDRDG nP vt  vtR++
gi|1166691   251 MLSDLSELLGEHGVT--LPSQKAPIRFGSWIGGDRDG-NPNVTAGVTREI 297

                CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE.Elyrtaardkvv
                  +    A  + i  +++L+  ls    n+   + A++El      d
gi|1166691   298 LQIQNQHAVRISIAMIDELIAILS----NSTALAGADrELLDSIDTD--L 341

                KyYiEFWKqv...PPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                K      + v +   +EPYR  L  ++ KL nt  R    +A G s  +
gi|1166691   342 KNLPGLDRRVlelNAQEPYRLKLTCIKAKLLNTAKR----VAAGSSHEPG 387

                eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                   yt     L  L L   sL +      ADG+L  + R +  FGL L
gi|1166691   388 RD-YTSTAGVLAELGLLEESLRNHHAGLAADGALARVRRAIASFGLHLAT 436

                LDiRqEseRqtDvlDAittHLe..iGsYReWsEeKRqEWLlaELkGKRPL
                LDiR  ++ + D +  +   L+++   Y e s   R E L aEL  +RPL
gi|1166691   437 LDIREHADHHHDAVGQLMDRLGgpGVRYSELSRAERLEVLGAELGSRRPL 486

                lgsDLPktEEvkDvldafrvLAELPi.......DsFGaYiismataPsDv
                 g  + k + v+D  +++ v  E+    ++ ++D    Yiism+    Dv
gi|1166691   487 SGHPI-KLDGVAD--GTYDVFREIRRalktygpDVIETYIISMTRGADDV 533

                LAvELLqRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiD
                LA  +L RE g+ +  ++ +   +   PL E + +L+A    v++L s
gi|1166691   534 LAAAVLAREAGLvslfgdapYAKIGFAPLLETVEELRASAEIVDQLLSDP 583

                WYin..ridGK.qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyG
                 Y+   r+ G  qe+m+GYsDs K+ G +   W + k q  +  vA k+G
gi|1166691   584 SYRElvRLRGDvQEIMLGYSDSNKESGVMTSQWEIHKTQRKLRDVAAKHG 633

                vKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFG
                v++ lFHGRGG vGRGGGPt  Ai++qP   ++G ++ t qGEvi   +
gi|1166691   634 VRVRLFHGRGGSVGRGGGPTYDAIMAQPNGVLEGEIKFTEQGEVISDKYS 683

                EEnLCFrsLqRFtAAtLE.HGmn..PPvsP..kPEWRkLmeemAvvAtEE
                  +L    L    AA + +  ++++P  s +++  + ++me +   A
gi|1166691   684 LPELARENLELSLAAVMQgSALHrtPRTSEdqRERYGHVMETISDAAFAR 733

                YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiP
                YRs++  +P    YF   tP    G +niGsRP+KR  sG G+  LRAiP
gi|1166691   734 YRSLI-DDPDLPAYFMASTPVEQLGSLNIGSRPSKRPDSGaGLGGLRAIP 782

                WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                W+F Wtq R  +P W GvG   K A  ++  n  +L Em + W FFR  l
gi|1166691   783 WVFGWTQSRQIVPGWFGVGSGLKAA--REAGNTEQLTEMMDRWHFFRSVL 830

                DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                  +Em  AK D  iA+ y   Lv EeL+   + +R++Y  t   + k+ G
gi|1166691   831 SNVEMTLAKTDMDIAGYYVSTLVPEELHHLFRAIREEYDLTVAEIQKLTG 880

                HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                 + lL+  P LK  l +Rd Y+  +  +q   ++R+R
gi|1166691   881 EHVLLDAQPTLKRSLEIRDQYLDPISYLQVELMRRMR------------- 917
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                  KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      +E      e   +  + ++   L   +++t+ G+AAG+ ntG
  gi|1166691   918 ----AEG----SEGESIS-GAEIDERLQRAMLITVNGVAAGLRNTG    954

gi|240173274|ref|ZP_04751932.1|: domain 1 of 1, from 15 to 939: score 312.0, E = 1.2e-90
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      i    R           + ++ D  Ll   L+D + +  G+++ E
  gi|2401732    15    PIGDVHRTRLGREAT---EPMRADIRLLGSILgDTVREQNGDEIFEL 58

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v E   + A +  ++      E+     ++d   a+ v +a++H   LAn
  gi|2401732    59 V-ERARVEA-FRVRRSEIDRTEMARMFDGIDIHRALPVIRAFSHFALLAN 106

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  +AE+++   RR  +          ++   +s +  t+ kL
  gi|2401732   107 VAEDIHRERRRAGHIAA-------GEPPQDSSLAATYLKLEAAE-LDSVT 148

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK.DvtveD
                  v +ALK   v  v+tAHPt   RR +   + Ri   L  L A +    +D
  gi|2401732   149 VADALKGALVSPVITAHPTEIRRRTIFITQHRITE-LMRLHAEgHSETDD 197

                  KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                   + ++  L R +   + t  iR ++    DE+  G+  +    +k vP+
  gi|2401732   198 GRSIELELRRQVLTLWQTALIRLSRLQISDEIAVGLRLYRSAFFKVVPQV 247

                  LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                     v  AL+       l    P++k  sW+GGDRDG nP vt Ev R
  gi|2401732   248 NAEVRGALRDRWPDAEL-LSEPILKPGSWIGGDRDG-NPNVTAEVVRLAT 295

                  LLaRmmAanlYisqvEDLmFElsm....WRCndELRvRAEElyrtaardk
                    a   A   Y+  ++ L  Elsm+++      EL + A      a+ d
  gi|2401732   296 GSAAYTALSHYLAELDQLEQELSMssrlLTVTTELTALAGGCRDNARDD- 344

                  vvKyYiEFWKqvPPtEPYRviLGdvRDKLYnt.....RERaRHLLAtGis
                                EPYR  L  +R +L  t+ +       H L  G+
  gi|2401732   345 ---------------EPYRRALRVIRARLSATgaeilDQQPQHQLDLGLP 379

                  eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                         y    e    L++   sL   G   +AD  L  l   v  FG
  gi|2401732   380 P------YATPGELRADLDVIDASLRTHGSALLADDRLALLREAVHVFGF 423

                  sLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK
                   L  LD+Rq s+ + +v+  +    ++ + Y + +E+ R   L+ EL+ +
  gi|2401732   424 HLCGLDLRQNSDVHEEVVGELLAWAGVHpDYGSLPEDERVALLVGELSTR 473

                  RPLlgsDLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDv
                  RPL+g      ++ ++E+  v  a r +     ++   Y+ism+ + sD+
  gi|2401732   474 RPLIGGRAQISDqargELDIVAAAARAVRTYGAEAVPNYVISMCRSVSDM 523

                  LAvELLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsiD
                  L   +L +E g+   +++++  ++ + PLFE + DL+     ++    +
  gi|2401732   524 LEAAILLKEAGLLDasgpqpycPVGISPLFETIDDLRNGATILQATLDLP 573

                  WYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyG
                   Y+  +  +++ qevm+GYsDs KD G l+A W +Y+A   ++  A+k G
  gi|2401732   574 LYRGLVKARgdmQEVMLGYSDSNKDGGYLAANWAVYRAELALVETARKSG 623

                  vKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFG
                  ++L lFHGRGGtvGRGGGP   AiL+qPP  + GslR t qGEvi   +
  gi|2401732   624 IRLRLFHGRGGTVGRGGGPSYQAILAQPPGAVSGSLRLTEQGEVIAAKYA 673

                  EEnLCFrsLqRFtAAtLE......HGmnPPvsPkPEWRkLmeemAvvAtE
                  E ++  r L    AAtLE++  +  G+    +P      ++ee+A
  gi|2401732   674 EPQMARRNLESLLAATLEstlldvEGLGDTAAPA---YAVLEEVAALSQR 720

                  EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                   Y  +v   P FvEYF   tP  E G +niGsRP+ RkP   i  LRAiP
  gi|2401732   721 AYAELVHETPGFVEYFMASTPVSEIGSLNIGSRPTSRKPTSSIADLRAIP 770

                  WiFaWtqtRFHLPvWLGvGAAFKhAidK....DiKnlqkLkEmYkeWPFF
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                    W+ aW q R  LP W G G AF   i  +++++   l  L+++Y+ WPFF
  gi|2401732   771 WVLAWSQSRVMLPGWYGAGTAFERWIAAgpegEADKLDVLHDLYQRWPFF 820

                    RvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtkdlL
                    R  l  +  v AK D G+Aa y +L+  E L++   +++ d+   t  +
  gi|2401732   821 RSVLSNMAQVLAKSDLGLAAHYAELVADESLrRRVFDKIADEHHRTITMY 870

                    LkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtl
                     +i GH DlL   P L   +  R +Y+  Ln +q   L+R R
  gi|2401732   871 KRITGHDDLLVDNPALARSVFNRFPYLEPLNHLQVELLRRYR-------- 912

                    rPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqnt
                              E+    deLv+             ++Ltm G+A  + n
  gi|2401732   913 --------SGED----DELVQRG-----------ILLTMNGLASALRNS 938

                    G<-*
                    G
  gi|2401732   939 G    939

gi|48689|emb|CAA32450.1|: domain 1 of 1, from 1 to 919: score 312.0, E = 1.3e-90
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                    +    + ++ D   l + L++++ +  G+++ E
  gi|48689|e     1    -------------MT---DFLRDDIRFLGQILgEVIAEQEGQEVYEL 31

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      s +    k    ++ L  +  ++ Pa a  +A+a++H   LAn
  gi|48689|e    32 VEQARLTSFDIA--KGNAEMDSLVQVFDGITPAKATPIARAFSHFALLAN 79

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAE+    y    + +      D ++   +s ++ t  kL   +n   e
  gi|48689|e    80 LAEDL---YDEELREQA----LDAGDTPPDSTLDATWLKL-NEGNVGAEA 121

                    vFeALKnqsvDLvltAHPtqsvRRsLL..qK....naRiRnCLaqLsAKD
                    v + L+n  v  vltAHPt   RR + + qK  +++ R R  L
  gi|48689|e   122 VADVLRNAEVAPVLTAHPTETRRRTVFdaQKwittHMRERHALQSAEPTA 171

                    vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWk
                     t     E++  + R i   + t  iR a+P   DE+  G+ Y+   + +
  gi|48689|e   172 RTQSKLDEIEKNIRRRITILWQTALIRVARPRIEDEIEVGLRYYKLSLLE 221

                    GvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEv
                     +P+  R v   L+     E +P   P++k  sW+GGD DG nP vt E
  gi|48689|e   222 EIPRINRDVAVELRE-RFGEGVPLK-PVVKPGSWIGGDHDG-NPYVTAET 268

                    tRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaard
                           a       Y  q+  L  Els+    + +      l      d
  gi|48689|e   269 VEYSTHRAAETVLKYYARQLHSLEHELSLSDRMNKVTPQLLALADAGHND 318

                    kvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                                vP++  EPYR  +  vR ++  t        A  i e
  gi|48689|e   319 ------------VPsrVDEPYRRAVHGVRGRILATT-------AELIGED 349

                    sEeAvytkv.......EeFLEPLELCYksLCeCGDkviADGsLLDlLRqv
                    + e v+ kv ++  ++EeFL       +sL e  D  iAD  L  l+  +
  gi|48689|e   350 AVEGVWFKVftpyaspEEFLNDALTIDHSLRESKDVLIADDRLSVLISAI 399

                    stFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLla
                      FG  L  LD+Rq se   Dvl  + +  ++ ++YRe sE  + E Ll
  gi|48689|e   400 ESFGFNLYALDLRQNSESYEDVLTELFERAQVTAnYRELSEAEKLEVLLK 449

                    ELkGKRPLlgsDLPktEEvkDv.ldafrvLAELPiDsFGa.....Yiism
                    EL+  RPL++       Ev D +l+ fr   E  +  FG++  ++ iism
  gi|48689|e   450 ELRSPRPLIPHGSDEYSEVTDReLGIFRTASE-AVKKFGPrmvphCIISM 498

                    ataPsDvLAvELLqRECgv........kqtLrvvPLFEkLADLeAAPAav
                    a +  DvL   +L +E g+   ++++++ t+ v+PLFE + DL+A    +
  gi|48689|e   499 ASSVTDVLEPMVLLKEFGLiaangdnpRGTVDVIPLFETIEDLQAGAGIL 548

                    ekLFsiDWYinri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEii
                    + L+ iD Y+n + ++d  qevm+GYsDs KD G +sA W LY A   ++
  gi|48689|e   549 DELWKIDLYRNYLlqrDNVQEVMLGYSDSNKDGGYFSANWALYDAELQLV 598
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                    KvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGE
                       +  Gv + lFHGRGGtvGRGGGP   AiL+qP   ++Gs+R+t qGE
  gi|48689|e   599 ELCRSAGVNVRLFHGRGGTVGRGGGPSYDAILAQPRGAVQGSVRITEQGE 648

                    viEfsFGEEnLCFrsLqRFtAAtLEHGm..nPPvsPkPEWRkLmeemAvv
                    +i   +G  +   r L     AtLE  + +   +  +    ++m e+
  gi|48689|e   649 IISAKYGNPETARRNLEALVSATLEASLldVSELTDHQRAYDIMSEISEL 698

                    AtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLR
                        Y s+v  +  F++YF   tP  E G +niGsRP+ Rk    +e LR
  gi|48689|e   699 SLKKYASLVHEDQGFIDYFTQSTPLQEIGSLNIGSRPSSRKQTSSVEDLR 748

                    AiPWiFaWtqtRFHLPvWLGvGAAFKhAi...dKDiKnlqkLkEmYkeWP
                    AiPW+ +W q R  LP W GvG A    i+++++  + +  L+ + + WP
  gi|48689|e   749 AIPWVLSWSQSRVMLPGWFGVGTALEQWIgegEQATQRIAELQTLNESWP 798

                    FFRvtlDLlEmvFAKGDPGiAaLyDkLL....vaEeLkPFGksLRdkYvE
                    F    lD +  v  K +  +A Ly +L+++++vaE +      +R++Y
  gi|48689|e   799 FLPSVLDNMAQVMSKAELRLAKLYADLIpdteVAERVY---SVIREEYFL 845

                    tkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPs
                    tk++   i G  DlL+  P L   +  R +Y+  Lnv+q   ++R R
  gi|48689|e   846 TKKMFCVITGSDDLLDDNPLLARSVQRRYPYLLPLNVIQVEMMRRYR--- 892

                    ykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAA
                              K    E+       v  n            + Ltm G+
  gi|48689|e   893 ----------KGDQSEQ-------VSRN------------IQLTMNGLST 913

                    GmqntG<-*
                     + n G
  gi|48689|e   914 AVRNSG    919

gi|20196762|emb|CAC86385.1|: domain 1 of 1, from 1 to 398: score 312.0, E = 1.3e-90
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2019676     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2019676     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2019676     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                           s DLv+tAHPtqs+RRsLLqKnaRiRnCL+qL AKD+t +DK+
  gi|2019676     1 -------SADLVFTAHPTQSARRSLLQKNARIRNCLTQLKAKDITEDDKQ 43

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqAAFRtDEiRRaqPtPqDEmR+GmsYiHEtvWkGvPKFLR
  gi|2019676    44 ELDEALQREIQAAFRTDEIRRAQPTPQDEMRYGMSYIHETVWKGVPKFLR 93

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGi ERlPY vPLi+F+sWmGGDRDG nPRvtPEvtRDvCLL
  gi|2019676    94 RVDTALKNIGIKERLPYSVPLIRFCSWMGGDRDG-NPRVTPEVTRDVCLL 142

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    +RmmAanlYi+ +EDLmFElsmWRC dELR+RAEE+ +t+  +kv+KyYi
  gi|2019676   143 SRMMAANLYIDAIEDLMFELSMWRCDDELRARAEEVLSTPSAKKVTKYYI 192

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP+EPYRviL +vRDKLYntRERaRHLLAtG+sei+E+Av+t+v
  gi|2019676   193 EFWKQIPPNEPYRVILAAVRDKLYNTRERARHLLATGVSEIPEDAVFTNV 242

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    +eFLEPLELCYksLC+ GDk+iA+GsLLDlLRq++tFGL+LvKLDiRqEs
  gi|2019676   243 DEFLEPLELCYKSLCDSGDKAIAEGSLLDLLRQIFTFGLALVKLDIRQES 292

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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                    eR+tDv+DAittHL+iGsYR+W+EeKR +WLl+EL+GKRPLl++DLP+tE
  gi|2019676   293 ERHTDVVDAITTHLGIGSYRSWPEEKRFDWLLSELRGKRPLLPADLPMTE 342

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dv++a+rvLAELP DsFG+Yiism+taPsDvLAvELLqRECg++q+L
  gi|2019676   343 EIADVVGAMRVLAELPPDSFGPYIISMCTAPSDVLAVELLQRECGIRQPL 392

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLF
  gi|2019676   393 PVVPLF---------------------------------------------- 398

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|2019676     - ------------------------------------------------- -

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

  gi|2019676     - ------------------------------------------------- -

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|2019676     - ------------------------------------------------- -

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|2019676     - ------------------------------------------------- -

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|2019676     - ------------------------------------------------- -

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|2019676     - ------------------------------------------------- -

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|2019676     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|2019676     - -------------    -

gi|198283666|ref|YP_002219987.1|: domain 1 of 1, from 1 to 929: score 311.9, E = 1.4e-90
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                  K  +   L +   LL     ++L +  G  +  av
  gi|1982836     1    ---------MEKKALNGKALRNRVKLLGNLLGEVLREQAGHRVFNAV 38

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                                ++D +  e L   + +L   D +lv +a+     L n+
  gi|1982836    39 EQLRQGYIRLHKREDLRLRERLARFIDALPQDDLVLVIRAFNTYFSLVNI 88

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEE e  +  R ++++       +s       EEt++ L  ++   P
  gi|1982836    89 AEE-EFQHLHRRRLLQ------KGSMLWTGSFEETFRELQGQG-INPGQL 130

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L       v+tAHPt s RR +L    Ri      L    +  e+ +
  gi|1982836   131 QFLLDQIRYLPVFTAHPTESKRRTVLHALRRIFVTSKMLDDSALNDEEEQ 180

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    E+ + L   iq  + t+E+R  +P  qDE+  G+ Y+ + +++ vP   R
  gi|1982836   181 EVMDNLRAQIQILWETEEVRTNKPQVQDEVENGLFYFRDSLFEAVPLTYR 230

                    RvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDvCL
                        A + +  n  +  d+P  i+F sW+GGDRDG nP vt  +t
  gi|1982836   231 AARRAARRVFANADI--DIPaFIRFGSWIGGDRDG-NPNVTAAITGWALR 277

                    LaRmmAanlYisqvEDLmFElsm.WRCndELRvRAEElyrtaardkvvKy
                       +     Y + + DL   l  + R      v    l r a
  gi|1982836   278 TQSIEVLKEYQQRLSDLYQLLGHsSRFCAISPVLLASLERDADDF---PE 324
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                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                      E+  q  P EPYR  L  +  +L     R R L    + + s    y
  gi|1982836   325 LAEWVDQRFPSEPYRRKLRYMMTRL---DLRLRQLENGQVLNESAGPAYA 371

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                      E+FL+ L L   sL    D  iAD  + +++  v tFG  L  LDiRq
  gi|1982836   372 AAEDFLDDLLLVRDSLRGHNDGYIADNEVQEIIWLVQTFGFHLANLDIRQ 421

                    EseRqtDvlDAittHL.eiGsYReWsEeKRqEWLlaELkGKRPLl..gsD
                    Es  +   +  +   +++   Y e sEe R+  L   L+   PL+++ +D
  gi|1982836   422 ESSVHSRTIAELFAGIpGFANYVELSEEARMLALSDALRRPGPLVeqAPD 471

                    L.PktEEvkDvldafrvL.AELPiDsFGaYiismataPsDvLAvELLqRE
                    L+P+  E   +   +  L+ E+    FG Y+ism+   s ++ v +L +E
  gi|1982836   472 LsPMAAETCAMFRCIAQLrREVSTAGFGNYVISMTHEASHIMEVLVLAKE 521

                    Cgv....kqtL....rvvPLFEkLADLeAAPAavekLFsiDWYinri...
                     g+ + ++q L ++  v PLFE + DLe     +  L     Y   ++++
  gi|1982836   522 FGLagwsRQGLyseiAVTPLFETIHDLERMDTVMSTLLDNPVYAKILgsq 571

                    dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    d  qevm+GYsDs KD G ls  W LY+Aq  ++  A k  +++ +FHGR
  gi|1982836   572 DDIQEVMLGYSDSCKDGGILSSSWSLYQAQLRLAALADKRKIRIRVFHGR 621

                    GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                    GG vGRGGGPt  AiL+qPPDt+ G +++t qGEv+ f +   +     L
  gi|1982836   622 GGSVGRGGGPTYEAILAQPPDTVRGQIKITEQGEVLSFKYANLETAVYEL 671

                    qRFtAAtLEH..GmnPPvs.PkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                       tA  +  + G+    s+  P+  k+m e+       YR +    P F
  gi|1982836   672 TVGTAGLIKAsiGLVRSASgDNPDHLKIMAELTRTGEAVYRDLTEGTPGF 721

                    vEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqtRFH
                    ++YF  AtP  E  +mniGsRP+ R+ + + + s+RAiPWiFaW q R
  gi|1982836   722 MDYFYEATPLNEIAHMNIGSRPSHRQRGDrSMSSIRAIPWIFAWAQSRHV 771

                    LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                    LP W G+G A     +     lq L++mY+ WPFFR  +  + m  AK D
  gi|1982836   772 LPAWYGLGSALARWREDKPERLQALQDMYRHWPFFRALMGNIGMAMAKTD 821

                    PGiAaLyDkLLvaEe.LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                      iA+ y  L    +      +++ ++++  +  +L i G   lL   P
  gi|1982836   822 MAIAGEYAGLPNDRDaAIAIYRKIQAEFESSQAEMLAIVGADHLLADNPT 871

                    LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                    L   l  R+ Y+  Ln +q   L+R R                 dE
  gi|1982836   872 LAFSLQRRNVYMEPLNHIQLALLRRYRN----------------DET--- 902

                    adeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    + e  ++           D L+ t+  i AG  ntG
  gi|1982836   903 PPEFREIW---------LDPLLRTINAISAGQRNTG    929

gi|239988329|ref|ZP_04708993.1|: domain 1 of 1, from 2 to 909: score 311.6, E = 1.6e-90
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       s   q  +  P   +        D   l   L++ L    G++L +
  gi|2399883     2    SSADQTPAASPALRA--------DIRRLGDLLgETLVRQEGQELLDL 40

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     l    +G   ++ L+E     t L+ a  ++  +a++    LAn
  gi|2399883    41 VERVRALTRT-DGEAAAELLGE-----TELETAAQLV--RAFSTYFHLAN 82

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E v+ A+  R ++   G             +  t  +L       Pe
  gi|2399883    83 VTEQVHRAHEMRDRRSAEGGL-----------LARTADRLKDAD---PEH 118

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      e +Kn  v  v+tAHPt ++RRs+L K  Ri    a L    v   D+
  gi|2399883   119 LRETVKNLNVRPVFTAHPTEAARRSVLNKLRRI----AELLETPVIEADR 164

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
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                    + LD  L   i   + tDE+R  +P P DE R  + Y+ E   + v   L
  gi|2399883   165 RRLDLRLAENIDLIWQTDELRVVRPEPADEARNAIYYLDELHANAVGDVL 214

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                          L  +G+   lP     + F  W+GGDRDG nP vtP vt Dv +
  gi|2399883   215 EDLAAELDRVGVE--LPAGTRPLTFGTWIGGDRDG-NPNVTPAVTWDVLI 261

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkvvKy
                    L         ++ ++ L   ls    n+   + A+EEl    + d
  gi|2399883   262 LQHEHGITDALEMIDYLRGLLS----NSIRYAGAtEELLTSLQADLERLP 307

                    YiE.FWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                     i + +K +  +EPYR     +R KL ntRER    LA G    +    y
  gi|2399883   308 GISpRYKRLNAEEPYRLKATCIRQKLVNTRER----LAEGTPHRP-GCDY 352

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                        e +  LEL   sL        ADG +   +R    FGL L  +D+R
  gi|2399883   353 LGTAELIADLELIQTSLRAHRGGLFADGRMDRTIRTLAAFGLQLATMDVR 402

                    qEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLlgsD
                      ++ +   l  +   L+  s+R  + + + Rq  L  EL+ +RPL +
  gi|2399883   403 EHADAHHHALGQLFDRLGEESWRyaDMPRDYRQKLLAKELRSRRPLAPTP 452

                    LPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvELL
                     P     +  l+ f+ +     + FG++  ++Yiism+    Dv A  +L
  gi|2399883   453 APLDAAGEKTLGVFHTIKQ-AFERFGPeviesYIISMCQGADDVFAAAVL 501

                    qRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                     RE g+   + +   + +vPL E   +L+AA   ++ + +   Y+  +
  gi|2399883   502 AREAGLVDlhagwaKIGIVPLLETTDELKAADHILDEMLADPSYRRLVSL 551

                    K...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                    +++ qevm+GYsDs K  G     W + +Aq  +  vA +yGv+L lFHG
  gi|2399883   552 RgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRYGVRLRLFHG 601

                    RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                    RGGtvGRGGGP H AiL+qP  t++G ++vt qGEvi   +    L
  gi|2399883   602 RGGTVGRGGGPSHDAILAQPWGTLEGEIKVTEQGEVISDKYLIPALAREN 651

                    LqRFtAAtLEHGm...nPPvsPk..PEWRkLmeemAvvAtEEYRsvvvKE
                    L    AAtL     ++ P  s      W   m+ +   A   YR +v  +
  gi|2399883   652 LELTVAATLQASAlhtAPRQSDEalARWDAAMDTVSDAAHSAYRKLV-ED 700

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWtq
                    P    YF   tP      + +GsRPa R+P+ G++ + LRAiPW+F Wtq
  gi|2399883   701 PDLPAYFLASTPVDQLADLHLGSRPA-RRPGSGVslDGLRAIPWVFGWTQ 749

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     R  +P W GvG   K   +     +  L Em + W FFR  +  +Em
  gi|2399883   750 SRQIVPGWFGVGSGLKALREAGLDTV--LDEMHEHWHFFRNFISNVEMTL 797

                    AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                    AK D  iA  y + Lv +eLk   + + ++   t + +L+i G   lL+
  gi|2399883   798 AKTDLRIARHYVDTLVPDELKHVFDGIEAEHALTVQEVLRITGGEKLLDT 847

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                     P L+q   +Rd+Y+  +  +q   L R R                A+E
  gi|2399883   848 NPVLQQTFSIRDAYLDPISYLQVSLLARQRQ---------------AAER 882

                    skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                +e+  P L   L+Lt+ G+AAG+ ntG
  gi|2399883   883 ------------GEEPDPLLSRALLLTVNGVAAGLRNTG    909

gi|226229154|ref|YP_002763260.1|: domain 1 of 1, from 5 to 933: score 311.4, E = 1.9e-90
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                              l  P    e ++ ++ D  Ll + L+D + +  G d+
  gi|2262291     5    -------LDPPPARDEKDRPLRDDIRLLGRLLgDAVREQEGADVFQL 44

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v +    +  +     ++  e L   L  L P   + v +a++  L LAn
  gi|2262291    45 VEDTRRAAIRFAREGRAEDREALHVLLDPLPPDTMLSVVRAFSYFLQLAN 94
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                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                +AE+ +   RRR +    G    E+  t E  +E   + +   +  + e
gi|2262291    95 IAEDTHRGRRRRAHEVM-GSRPREG--TLEFALEMVRQAIGNDG-LAQER 140

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     +   v  vltAHPt   R s L     i   L q     +t e++
gi|2262291   141 LTAFFRSALVSPVLTAHPTEVQRQSTLTVMQQIATLLEQRDRMVLTGEER 190

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                 E D  L R +   + t  +R  +    DE++ G++Y+  t +  vP+
gi|2262291   191 TESDALLTRLVLTLWHTRIVRGERLRVVDEVKNGIAYFRSTFFTEVPRLH 240

                RRvDtALKni..GinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                   +  L    +G    l    P ++  sW+GGDRDG nP vt +v  +
gi|2262291   241 ANLEDLLSAQfpGSTWQL---TPFLQPGSWIGGDRDG-NPFVTADVLHET 286

                CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                  L       +Y++ +  L   ls+ R    L +    l   aar
gi|2262291   287 LRLQASATFDFYLQEIHALGQQLSLSRT---LHAVTPALEALAARS---- 329

                yYiEFWKqvPPtEPYRviLGdvRDKLYntRER......aRHLLAtGisei
                   +   q    EPYR  L  +  ++  t    + +++ R  L  G
gi|2262291   330 --PDTSAQ-RLDEPYRRALSGIYARVASTMSGlelpppVRAALGSGEPYA 376

                sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                s +A y       + L +   +L   G   +A G L  lL  v  FG  L
gi|2262291   377 SADALY-------DDLVIIRDALTTTGVGLLAAGRLRRLLMAVQGFGFHL 419

                vKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRP
                  LD+Rq ++ +  v+  +    ++ + Y    E +R   L  EL+G RP
gi|2262291   420 APLDLRQNADVHERVVTELFAQAGVCdNYAALDESQRVALLARELEGTRP 469

                LlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLA
                L  + L   EEv+  l  +   A L ++ +  +   Y+is +   sD L
gi|2262291   470 LHSPHLRYSEEVAGELAIVFTAARLRqrygASALPHYVISKCDGVSDLLE 519

                vELLqRECgvkq.......tLrvvPLFEkLADLeAAPAavekLFsiDWYi
                v L+ +E g+  ++++ +  L +vPLFE +ADL+ A  ++    ++  Y+
gi|2262291   520 VALMLKEAGLATggqqatlGLDIVPLFETIADLRRAGDTMRAALALPVYR 569

                nridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                  +  +++ qevm+GYsDs KD G l   W LY+Aq  +++   + Gv+L
gi|2262291   570 ALLRTRgdvQEVMLGYSDSNKDGGFLTSGWELYQAQTALMQAFGDAGVQL 619

                vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                  FHGRGG vGRGGGP   AiL+qP   + G +R t qGEvi   +   +
gi|2262291   620 RFFHGRGGSVGRGGGPSYDAILAQPAGAVTGQIRLTEQGEVIASKYATPD 669

                LCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEEYRsvv
                +  r L    AAtLE  +    s     + +R +me++   A   YR++v
gi|2262291   670 VGRRNLELLVAATLEATLTDHESGADQvtaFRPVMERLSAHAYAAYRALV 719

                vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWt
                +  P F  YFR  tP  E   +niGsRPa RkPs  ie LRAiPW+FaW
gi|2262291   720 YETPGFAQYFRESTPLAEIATLNIGSRPASRKPSDRIEDLRAIPWVFAWA 769

                qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                q R  LP W G+G A    +      l  L+ m + WPFFR  l  ++mv
gi|2262291   770 QCRCMLPGWYGFGSAVTAWLVEQPDGLPVLQRMAQHWPFFRTLLSNVDMV 819

                FAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtkdlLLkiAGHkDlL
                 AK D  +A+ y +L+  E L++     + +++  t+d L +i G   lL
gi|2262291   820 LAKSDLRVASRYSELVQDETLrRTIFAAIEAEWHRTRDALRQITGQDQLL 869

                EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                   P L   +  R +Y+  Ln +q   L+R R              E+ +
gi|2262291   870 ADNPLLVRSMANRFPYMDPLNHLQIALLQRHR--------------EHVA 905

                EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     +d+L++              + +t+ GiAAG+ n G
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  gi|2262291   906 SG-TAPDDLMRRG------------IHITINGIAAGLRNSG    933

gi|260457184|ref|ZP_05805553.1|: domain 1 of 1, from 3 to 909: score 311.1, E = 2.3e-90
                 *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                    s D       P       +L      L D   + L    G+dL + v
  gi|2604571     3    SADQ-----TPAANT---ELRADIRRLGDLLGETLVRQEGQDLLDLV 41

                 qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                      l  e +G   ++ L++     t L+ a  ++  +a++    LAn+
  gi|2604571    42 ERVRALTRE-DGEAAAELLGD-----TDLETAAQLV--RAFSTYFHLANV 83

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  E v+ A+  R ++   G             +  t  +L       P+
  gi|2604571    84 TEQVHRAHEMRDRRSAEGGL-----------LARTADRLKDAD---PDHL 119

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                  e +Kn  v  v+tAHPt ++RRs+L K  Ri    a L    v   D++
  gi|2604571   120 RETVKNLNVRPVFTAHPTEAARRSVLNKLRRI----AELLETPVIEADRR 165

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   D  L   i   + tDE+R  +P P DE R  + Y+ E   + v   L
  gi|2604571   166 RQDIRLAENIDLIWQTDELRVVRPEPADEARNAIYYLDELHANAVGDVLE 215

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                      L  +G+   lP     + F  W+GGDRDG nP vtP vt Dv +L
  gi|2604571   216 DLAAELERVGVE--LPAGTRPLTFGTWIGGDRDG-NPNVTPTVTWDVLIL 262

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkvvKyY
                           ++ v+ L   ls    n+     A++El    + d
  gi|2604571   263 QHEHGITDALELVDQLRGLLS----NSIRYTGAtDELLTSLQTD--LERL 306

                 iEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                  E ++++K +  +EPYR     vR KL ntRER    LA G    +
  gi|2604571   307 PEIsprYKRLNAEEPYRLKATCVRQKLVNTRER----LASGTPHRP-GCD 351

                 ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                 y    e +  L L   sL e      ADG +   +R    FGL L  +D+
  gi|2604571   352 YLGTAELIADLALIQTSLREHRGGLFADGRMDRTIRTLTAFGLQLATMDV 401

                 RqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLlgs
                 R  ++ +   l  +   L+  s+R ++ + + Rq  L  EL+ +RPL +
  gi|2604571   402 REHADAHHHTLGQLFDRLGEESWRytDMPRDYRQKLLAKELRSRRPLAPT 451

                 DLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvEL
                   P     +  l+ f+ +     + FG++  ++Yiism+    Dv A  +
  gi|2604571   452 PAPLDAAGEKTLGVFHTISQ-AFERFGPeviesYIISMCQGADDVFAAAV 500

                 LqRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                 L RE g+   +++   + +vPL E   +L+AA   ++ + +   Y+  +
  gi|2604571   501 LAREAGLLDlhggwaKIGIVPLLETTDELKAADVILDEMLADPSYRRLVS 550

                 GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                  +++ qevm+GYsDs K  G     W + +Aq  +  vA +yGv+L lFH
  gi|2604571   551 LRgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRYGVRLRLFH 600

                 GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                 GRGGtvGRGGGP H AiL+qP  t++G ++vt qGEvi   +    L
  gi|2604571   601 GRGGTVGRGGGPSHDAILAQPWGTLEGEIKVTEQGEVISDKYLIPALARE 650

                 sLqRFtAAtLEHGm...nPPvsPk..PEWRkLmeemAvvAtEEYRsvvvK
                  L    AAtL     ++ P  s      W   m+ +   A   YR +v
  gi|2604571   651 NLELTVAATLQASAlhtAPRQSDEalARWDAAMDTVSDAAHQAYRKLV-E 699

                 EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWt
                 +P    YF   tP      + +GsRP+ R+P+ G++ + LRAiPW+F Wt
  gi|2604571   700 DPDLPAYFLASTPVDQLADLHLGSRPS-RRPGSGVslDGLRAIPWVFGWT 748

                 qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                 q R  +P W GvG   K   +     +  L Em ++W FF   l  +Em
  gi|2604571   749 QSRQIVPGWFGVGSGLKALREAGLDTV--LDEMHEQWHFFQNFLSNVEMT 796
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                    FAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE
                     AK D  iA  y + Lv +eLk   + + ++ + t + +Lk+ G k+lL
  gi|2604571   797 LAKTDLRIARHYVDTLVPDELKHVFDVIQAEHELTVQEVLKVTGGKELLG 846

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                      P L+q   +Rd+Y+  +  +q   L R R               A+E
  gi|2604571   847 TNPVLQQTFAIRDAYLDPISYLQVSLLARQRQ---------------AAE 881

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                             +e+  P L   L+Lt+ G+AAG+ ntG
  gi|2604571   882 R------------GEEPDPLLARALLLTVNGVAAGLRNTG    909

gi|256767868|ref|ZP_05507042.1|: domain 1 of 1, from 3 to 928: score 311.0, E = 2.4e-90
                    *->siD..AqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                       s D+ Aq  +  P   s   +  +     l   +  L DL Ge L
  gi|2567678     3    SADqaAQAPVTQPADPSAPTRTAQTANAELRADIRRLGDLLGETL-- 47

                    avqECYElsAeYEGKkD.tkKLeELGakLts.LdPaDailvAkailHmLn
                    + qE  El    E  +  t+  +E  a L +++d   a  + +a++
  gi|2567678    48 VRQEGQELLDLVERVRAlTRTDGEAAAALLGdIDLETAAKLVRAFSTYFH 97

                    LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                    LAn+ E v+     R k ++       a    E  +      +
  gi|2567678    98 LANVTEQVH-----RGKELR-------AHRAAEGGLLARTADMLKDA--D 133

                    PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                    Pe   e +Kn  v  v+tAHPt ++RRs+L K  Ri   L
  gi|2567678   134 PEHLRETVKNLNVRPVFTAHPTEAARRSVLNKLRRIAALLEEPVS---GA 180

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                     D++  D  L   i   + tDE+R  +P P DE R  + Y+ E     v
  gi|2567678   181 GDRRRHDLRLAENIDLVWQTDELRVVRPEPADEARNAIYYLDELHAGAVG 230

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                      L      L+ +G+   lP     + F  W+GGDRDG nP vtP vtRD
  gi|2567678   231 DVLEDLAAELQRVGVE--LPAGTRPLTFGTWIGGDRDG-NPNVTPQVTRD 277

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkv
                    v +L         ++ v+ L   ls    n+   + A+EEl    + d
  gi|2567678   278 VLILQHEHGITDALELVDFLRSLLS----NSIRIAGAtEELLASLQAD-- 321

                    vKyYiEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseis
                         E ++++K +  +EPYR     +R KL ntRER    LA+G
  gi|2567678   322 LERLPEIsprYKRLNAEEPYRLKATCIRQKLLNTRER----LAKGTPH-E 366

                    EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                    E   y     e L  L L   sL e      ADG +   +R    FGL L
  gi|2567678   367 EGRDYLGTAELLADLTLIQTSLREHRGALFADGRMDRTIRTLAAFGLQLA 416

                    KLDiRqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRP
                     +D+R  ++ +   l  +   L+  s+R  + + + Rq  L  EL+ +RP
  gi|2567678   417 TMDVREHADAHHHALGQLFDRLGEESWRyaDMPRDYRQKLLAKELRSRRP 466

                    LlgsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvL
                    L +   P        l+ f  + +   + FG++  ++Yiism+    Dv
  gi|2567678   467 LAPTPAPLDAAGHKTLGVFSAIKD-AFEKFGPeviesYIISMCQGADDVF 515

                    AvELLqRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYi
                    A  +L RE g+   + +   + +vPL E   +L+AA   ++ + +   Y+
  gi|2567678   516 AAAVLAREAGLVDlhagwaKIGIVPLLETTDELRAADVILDEMLADPSYR 565

                    nridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                      +  +++ qevm+GYsDs K  G     W + +Aq  +  vA ++Gv+L
  gi|2567678   566 RLVSLRgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRHGVRL 615

                    vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                     lFHGRGGtvGRGGGP H AiL+qP  t++G ++vt qGEvi   +
  gi|2567678   616 RLFHGRGGTVGRGGGPSHDAILAQPWGTLEGEIKVTEQGEVISDKYLVPS 665

                    LCFrsLqRFtAAtLEHGm...nPPvs..PkPEWRkLmeemAvvAtEEYRs
                    L    L    AAtL     ++ P  s++    W   me +   A   YR
```

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  gi|2567678   666 LARENLELTVAATLQASAlhtAPRQSddALTRWDAAMEIVSDAAHGAYRE 715

                   vvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiF
                   +v  +P    YF  AtP      + +GsRP++R  sG G++ LRAiPW+F
  gi|2567678   716 LV-EDPDLPAYFFAATPVDQLADLHLGSRPSRRPDSGaGLDGLRAIPWVF 764

                   aWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLl
                    Wtq R  +P W GvG   K A+    +    L Em + W FFR  l  +
  gi|2567678   765 GWTQSRQIVPGWYGVGSGLK-ALREAGQD-TVLAEMGERWHFFRNFLSNV 812

                   EmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkD
                   Em  AK D  iA  y + Lv +eLk   +++ ++ + t   +L+i G
  gi|2567678   813 EMTLAKTDLRIARHYVDTLVPDELKHVFDRIQAEHELTVREVLRITGGEQ 862

                   lLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEy
                   lL+  P L+q   +Rd+Y+  +  +q   L R R
  gi|2567678   863 LLDSQPVLQQTFAVRDAYLDPISYLQVSLLARQRQ--------------- 897

                   AdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   A+              +e   P L   L+Lt+ G+AAG+ ntG
  gi|2567678   898 AAAR------------GEDPDPLLARALLLTVNGVAAGLRNTG    928

gi|254388786|ref|ZP_05004018.1|: domain 1 of 1, from 3 to 909: score 310.7, E = 3e-90
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      s D       P   +   +L      L D   + +    G++L E v
  gi|2543887     3    SADQ-----TPTASA---ELRADIRRLGDLLGETIVRQEGPELLELV 41

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        l    +G   ++ L++     t L+ a  ++  +a++    LAn+
  gi|2543887    42 EQVRALTRS-DGEAAAHLLGD-----TDLETAAKLV--RAFSTYFHLANV 83

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    E v+  +  R  +++         A   s +  t  +L       P+
  gi|2543887    84 TEQVHRGHELR--RLR---------AAEGSLLARTADRLKDAD---PAHL 119

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    e +Kn  v  v+tAHPt ++RRs+L K  Ri    a L      + D++
  gi|2543887   120 RETVKNLNVRPVFTAHPTEAARRSVLNKLRRI----AELLDTPAVPSDRR 165

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    +D  L   i   + tDE+R  +P P DE R  + Y+ E   + v   L
  gi|2543887   166 RIDLRLAENIDLIWQTDELRVVRPEPADEARNAIYYLDELHADAVGDVLE 215

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                        L  +G+   lP     + F  W+GGDRDG nP vtP vtR+v +L
  gi|2543887   216 DLAAELERVGLE--LPAGTRPLTFGTWIGGDRDG-NPNVTPAVTREVLIL 262

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                            +  ++ L   ls            +El    + d
  gi|2543887   263 QHEHGITDALALIDALRGQLSQ---SIRYTGATDELLASLQTD--LERLP 307

                   EF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                   E ++++K +  +EPYR     +  KL ntRER    LA+G    +    y
  gi|2543887   308 EIsprYKRLNAEEPYRLKATCIQQKLVNTRER----LAKGTPHQPGRD-Y 352

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                       e L  L L   sL e      ADG L   +R  s FGL L  +D+R
  gi|2543887   353 LGTSELLADLTLIQTSLREHRAGLFADGRLDRTIRTLSAFGLQLATMDVR 402

                   qEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLlgsD
                     ++ +   l  +   L+  s+R ++ + e Rq  L  EL+ +RPL +
  gi|2543887   403 EHADAHHHALGQLFDRLGEESWRysDMPREYRQKLLAKELRSRRPLAPTP 452

                   LPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvELL
                    P     +  l+ f+ + E   + FG++  ++Yiism+    Dv A  +L
  gi|2543887   453 APLDAAGAKTLGVFHTVKE-AFERFGPeviesYIISMCQGADDVFAAAVL 501

                   qRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                    RE g+   + +   + +vPL E   +L+AA   ++ + s   Y+  +
  gi|2543887   502 AREAGLIDlhagwaKIGIVPLLETTDELRAADVILDGMLSDPSYRRLVAL 551
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                    K...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                    +++ qevm+GYsDs K  G     W + +Aq  +  vA ++Gv+L lFHG
  gi|2543887   552 RgevQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRHGVRLRLFHG 601

                    RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf.....sFGEEn
                    RGGtvGRGGGPtH AiL+qP  t++G ++vt qGEvi  +   +s   En
  gi|2543887   602 RGGTVGRGGGPTHDAILAQPWGTLEGEIKVTEQGEVISDkylipSLAREN 651

                    LCFrsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKE
                    L         A  L       v     W   m+ +   A   YR++v  +
  gi|2543887   652 LELTVSATLQASALHTAPRQSVEALARWDAAMDTVSDAAHRVYRALV-ED 700

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqt
                    P    YF   tP      + +GsRP++R  sG G++ LRAiPW+F Wtq
  gi|2543887   701 PDLPAYFFASTPVDQLADLHLGSRPSRRPDSGaGLDGLRAIPWVFGWTQS 750

                    RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                    R  +P W GvG   K   +     +  L Em ++W FFR  +  +Em  A
  gi|2543887   751 RQIVPGWYGVGSGLKALREAGLDTV--LSEMHEQWHFFRNFIANVEMTLA 798

                    KGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                    K D  iA  y + Lv +eLk   + + ++   t   +Lk+ G   lL
  gi|2543887   799 KTDLRIARHYVDTLVPDELKHVFDTIEAEHRLTVSEVLKVTGGERLLGSN 848

                    PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                    P L+q   +Rd+Y+  +  +q   L R R               A+E
  gi|2543887   849 PVLQQTFAIRDAYLDPISYLQVSLLARQRG---------------AAER- 882

                    kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                               +e   P L   L+Lt+ G+AAG+ ntG
  gi|2543887   883 -----------GEPADPLLGRALLLTVNGVAAGLRNTG    909

gi|190891900|ref|YP_001978442.1|: domain 1 of 1, from 1 to 926: score 310.7, E = 3e-90
                    *->siDAqLR.lLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkE
                        +D qLR++   G+     +    D  Ll + L + +    G++ +E
  gi|1908919     1    -MDFQLRkAGMQGRRL-AARAQVKDVRLLGRLLcEAIEASDGKEARE 45

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    +v     ls     K  ++  + L      + P     v +a++    L
  gi|1908919    46 IVEQVRSLSVTGGRKTSPRLNDKLAPFCADIPPRTLKRVVRAFSQFSQLV 95

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE+   A+  R +++       E++      i   l  L   +    e
  gi|1908919    96 NIAED---AHHARAQRLS----IVEGEPAMPGTIARSLSVLAAAG-IEAE 137

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                     +   L    v  v+tAHPt   R+s++  +  +  CL+ L    +t ++
  gi|1908919   138 NIRKLLLEAVVSPVFTAHPTEVRRKSVIDIEQELARCLSRLDQAGLTAQE 187

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                         + L R     + t  +R  +    DE+  G+sY+  t+++ +P
  gi|1908919   188 VDRYQDDLERATTTLWQTNSLRGRKLQVVDEILNGLSYYDSTIFHAIPEV 237

                    LRRvDtALKniGinERlPYdv..PLikFssWmGGDRDGknPRvtPEvtRD
                        +  L+  G   +   d+ +P ++  sW+GGDRDG nP v  E  ++
  gi|1908919   238 YEDLENQLR--GSPWKFGQDAlpPFLRMGSWIGGDRDG-NPYVNGETLKE 284

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                       L       +Y+  +  L  Els+    d       +l+r a
  gi|1908919   285 ALRLQSERVFSFYLGELHSLGAELSL---DDRYVKVSRDLQRLATDS--- 328

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                                EPYR  +  +  +L  t   aR    t +   +  A
  gi|1908919   329 ----PDRSEQRRHEPYRLAISGIYARLAAT---ARKFGSTELVREPVAAA 371

                    ..ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                    ++y +  eF E L    ksL   G   iA G L  l R +  FG  Lv L
  gi|1908919   372 psYRNPAEFAEDLATISKSLIANGAEKIAAGKLRGLRRAIEVFGFHLVSL 421

                    DiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlg
                    D+Rq se +  v+  + + +  G +Y   +E  +   L  EL+    L+
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  gi|1908919   422 DLRQNSEVHQRVVHELFEKVRPGTgYEALAESDKIRLLTEELRSSQLLVT 471

                   sDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAvEL
                   +      E    l  +r  AE +++    s   Yiis a +PsD+L v +
  gi|1908919   472 PLKTYSAETMSELSVLREAAEahkrYGRASIPNYIISKAGSPSDILEVMV 521

                   LqRECgvkqt.......LrvvPLFEkLADLeAAPAavekLFsiDWYin..
                   L RE ++ ++++++  ++ ++PLFE + DL+     ++ + +i+ Y+
  gi|1908919   522 LFREVELFRPdepeaasVNIIPLFETISDLRRSHEVMQTVLAIEAYRAyl 571

                   .ridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                   + + GKqe+m+GYsDs KD G l   W LYkA    i+   + G++L lF
  gi|1908919   572 gALGGKQEIMLGYSDSNKDGGYLTSGWELYKAEMAFIQLFEREGIRLSLF 621

                   HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                   HGRGG vGRGGGP   Ai +qP   +  s+R t qGEvi   +    L
  gi|1908919   622 HGRGGSVGRGGGPSYEAITAQPAGAVADSIRLTEQGEVIAAKYSNPALGR 671

                   rsLqRFtAAtLEHGmnP..PvsPkPEWRkLmeemAvvAtEEYRsvvvKEP
                   r L    AAtLE  + P++   P P++   mee+   A   YRs+v+
  gi|1908919   672 RNLELLIAATLEASLLPsdAQEPDPDYLGAMEELSDLAFGVYRSLVYETE 721

                   RFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRF
                    F  +F   t   E  k+niGsRPa R  s  ie LRAiPW+F W q R
  gi|1908919   722 GFEKFFWETTIIGEIAKLNIGSRPASRSSSRRIEDLRAIPWVFGWSQSRI 771

                   HLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                    LP W G+G A +  +      l  L+ m ++WPFF   +  +Emv AK
  gi|1908919   772 MLPGWFGFGSAVRQWLAGQPDGLRTLQRMHRDWPFFQTLIANMEMVLAKT 821

                   DPGiAaLyDkLL..vaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                      iAa y +L ++ +   k F + ++d+++ t   L  i     lLE
  gi|1908919   822 NMAIAARYVDLApdTSTHEKIFAR-IKDEWEATTAALFGITDQASLLENN 870

                   PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                   P LKq +  R + +  Ln +q   L+R                 yA E
  gi|1908919   871 PALKQSIHHRFPCLDPLNHMQIDLLRR----------------HYAGERD 904

                   kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   ++ +e ++L                + GiAAG+ n G
  gi|1908919   905 QETEEALHLT----------------INGIAAGLRNSG    926

gi|227878424|ref|ZP_03996364.1|: domain 1 of 1, from 1 to 912: score 310.4, E = 3.8e-90
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           + +      s+ + + e   +L D   +  + + G+   + +
  gi|2278784     1    -----MTVKKLENNSDVNVVAEESKVLTDLLNESTKQVIGQAAFDKI 42

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   q    +sA       +k  +EL  ++ sL+  + i+vA+ +  +  L n+
  gi|2278784    43 QNLIKISA-------AKDYQELEKQIASLNNREMIVVARYFATLPLLINI 85

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    E+velA +  +    h D+    s t +         +v +  K  eE+
  gi|2278784    86 SEDVELASKVNVLNNTHQDYLGKLSDTID---------IVAQK-KNAEEI 125

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    e +    v  vltAHPtq  R+ +L     i   L           D+
  gi|2278784   126 LEHV---NVVPVLTAHPTQVQRKTILELTDQIHQLLRNYRDVKNGTIDRD 172

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   E  E +   i     tD iR  +     E+   ++Y+   +   + KF
  gi|2278784   173 EWTEQMRACIEILMQTDIIRGHKLKVANEITNVLAYYPKALIPAITKFTS 222

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   R     K  G+n      +  i    W+GGDRDG nP vt +       L
  gi|2278784   223 RYKELAKKHGLNAS---HATPITMGMWIGGDRDG-NPYVTADTLELSATL 268

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                      +    Yi q+  L   +sm             y  +  d  v +
  gi|2278784   269 QSQVIFEYYIKQINKLYRAISM----------STSYMEPSDD--VMHLS 305
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                    EFWKqvPP...tEPYRvi.......LGdvRDKLYntRERaRHLLAtGise
                    E      P +++EPYR      +++L     KL n   +   L    + +
  gi|2278784   306 ELSNDDSPfrtNEPYRRAfyyiqsrLVHTEQKLLNITNKNTFLKKRDLQN 355

                    isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                    +     y +  eF   LE+   sL e  D+++ D     +L  +  FG
  gi|2278784   356 LDKIPCYQNAQEFKADLEIIKNSLEEDHDHAVVDSYFTQILEAINIFGFH 405

                    LvKLDiRqEseRqtDvlDAitthLeiG.sYReWsEeKRqEWLlaELkGK.
                    L  +D+Rq+s  +   +  + +  +i + Y + sE+K+   Ll EL   +
  gi|2278784   406 LATIDMRQDSSVNEACVAELLKSAGICdNYSDLSEDKKIKLLLNELNNDp 455

                    RPLlgsDLPktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDv
                    R L     Pk E ++++  +  + r L ++L  D     iis + + sD+
  gi|2278784   456 RNLHANNKPKSELLQkelKIYKTARQLKDrLGEDVIKQHIISHTESVSDM 505

                    LAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYin
                    L   ++ +E  + +++k  ++vvPLFE + DL+ A   ++   s D  +
  gi|2278784   506 LEQAIMLKEYDLldnqKARIQVVPLFETVEDLNNAREIIKEFLSFDIVKK 555

                    ri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                     + +++  qevm+GYsDs KD G l+  W LYkAq ++ K+  + G+K++
  gi|2278784   556 WLvsqNNYQEVMLGYSDSNKDGGYLASCWNLYKAQKDLTKIGEEMGIKIT 605

                    lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                      HGRGGtvGRGGGP   Ai +qP   in  +R+t qGE+i   +G  +
  gi|2278784   606 FMHGRGGTVGRGGGPSYEAITAQPFKSINDRMRMTEQGEIIQNKYGNKDT 655

                    CFrsLqRFtAAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvv
                     +  L   + At++      +   ++  ++R  m+++     E YR +v+
  gi|2278784   656 AYYNLEMLASATIDRMASKQIVSEdhvADFRSSMDQIVAKSNEVYRKLVF 705

                    KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                      P F  YF  AtP  E   +n+GsRPa Rk       LRAiPW+F+W q
  gi|2278784   706 ENPNFLKYFFQATPIKEISGLNVGSRPASRKKLTDFSGLRAIPWVFSWSQ 755

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     R   P W GvG  FK  id D  nl+ L+ mY+ WPFF   l  ++mv
  gi|2278784   756 SRVMFPGWYGVGSGFKSFIDADPANLKELQNMYQGWPFFHSLLSNVDMVL 805

                    AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                     K    iA  y +L   E++k   + + ++++ tk+ +L+i GH +l+E
  gi|2278784   806 SKSNMRIAKQYADLCEDEQVKSVFDIINQEWELTKKVILQIEGHDELIED 855

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                     P LK+ l  R +Y   Ln +q   +KR R+ + +   +  +       +
  gi|2278784   856 APTLKKSLEYRMPYFNILNYIQLEMIKRDREDEIQGVYQSII-------P 898

                    skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                           + +n                  G+A G+ n G
  gi|2278784   899 -------ITIN-----------------GVASGLRNSG    912

gi|238028333|ref|YP_002912564.1|: domain 1 of 1, from 84 to 1031: score 310.3, E = 4.1e-90
                    *->siDAqLRlLvPGKvsed.ekLieYDALLlDkFL.DiLqDLHGedLkE
                             +  + G+  +d+++ +  D   l + L+D++ +  Ge + E
  gi|2380283    84    TAAERPKPKANGRTRDDkDQPLFEDIRYLGRLLgDVVREQEGEAVFE 130

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    +v      +  +    D +  + L    L  L P  ++ v +a++    LA
  gi|2380283   131 VVETIRQHAVKFRREDDREAAQALDKMLRKLTPEQTVSVVRAFSYFSHLA 180

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE+ +   RRRi+ +        +sA     +   l+ L   +  + +
  gi|2380283   181 NIAEDRHHNRRRRIHALA-------GSAPQAGTVAYALQALKAAG-DASA 222

                    EvFeALKnqsvDL.vltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    Ev       +  ++vltAHPt   R+s+L  +  i   La    +++t
  gi|2380283   223 EVIRRFFDEALIVpVLTAHPTEVQRKSILDAQHDIARLLAE-RDQELTAR 271

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++   D  L   +   + t  +R a+ t  DE+   +sY+  t  +  P
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  gi|2380283   272 ERAHNDALLRARVASLWQTRMLRDARLTVADEIDNALSYYRATFLHELPA 321

                   FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                       ++ AL   G+  R+P      +  sW+GGDRDG nP vt     +
  gi|2380283   322 LYADIEEALAEHGLAARVP---AFFQMGSWIGGDRDG-NPNVTAATLEEA 367

                   CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkvv
                         +    Y++qv  L  Els+    ++L v A++E+   aa
  gi|2380283   368 IHRQGAVILEHYLEQVHKLGAELSV----SDLLVGAsDEVRALAAAS--- 410

                   KyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGisei...
                           q P++  EPYR  L  +  ++      aR  L  G+  +++
  gi|2380283   411 ------PDQSPhrVDEPYRRALIGIYTRIAAS---ARVRLGEGVVAVrsa 451

                   .....sEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvs
                   +++ ++  A +y + E F   L +   sL       +A   L  l+R
  gi|2380283   452 grgapPVRATpYPDAEAFASDLRVLQDSLVAHHGALLATPRLAPLVRAAE 501

                   tFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaE
                   tFG  L  +D+Rq s+ +  v+  +    ++ ++Y   +E  +   Lla
  gi|2380283   502 TFGFHLASIDLRQSSDIHEAVIAELLARAGVEAdYAALPEADKLRVLLAA 551

                   LkGKRPLlgsDLPktEEvkDvldaf....rvLAELPiDsFGaYiismata
                   L   RPL  + +   E     l+ +++ ++v A     +   Yiis + +
  gi|2380283   552 LADPRPLRIPYVDYSELANSELGVLekarEVRARFGPRAVRNYIISHTET 601

                   PsDvLAvELLqRECgv.............kqtLrvvPLFEkLADLeAAPAa
                    sD + v LLq+E g+ +++ + +  + k++L v+PLFE +ADL+ AP
  gi|2380283   602 VSDLVEVLLLQKETGLldgtfgagaadaKHSLMVIPLFETIADLRNAPEI 651

                   vekLFsi...DWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEi
                   +   F++++    + r  G qevm+GYsDs KD G l   W LY+A   +
  gi|2380283   652 MGDYFALpgaAALVARQGGEQEVMLGYSDSNKDGGFLTSNWELYRAELAL 701

                   iKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqG
                   +   + +G++L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qG
  gi|2380283   702 VELFRAHGIRLRLFHGRGGTVGRGGGPTYEAILSQPPGTVNGQIRLTEQG 751

                   EviEfsFGEEnLCFrsLqRFtAAtLEHGmnP...PvsPkPEWRkLmeemA
                   Evi   F   ++  r L    AAtLE  + P+++  +  P +   ++ +
  gi|2380283   752 EVIASKFSNPEIGRRNLETVVAATLEASLLPrnnAPAQLPAFEAAVQTLS 801

                   vvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....
                    vA   YR++v+  P F +YF + tP  E   +niGsRPa Rk   ++++
  gi|2380283   802 DVAIATYRALVYETPGFTDYFFSSTPINEIAELNIGSRPASRKLQDpkhr 851

                   GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiKnlqk
                    ie LRAiPW F+W q R  L  W G+G AF   +d+ +++    + l
  gi|2380283   852 KIEDLRAIPWGFSWGQCRLLLTGWYGFGSAFAAYLDgagdeaERARRLAL 901

                   LkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk..PFGks
                   L+ m ++WPFF   l  ++mv  K D  +A+ y +L+    L+++ FG+
  gi|2380283   902 LQKMNRTWPFFSHLLSNMDMVLSKVDLAVASRYAELVADKKLRkhVFGR- 950

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   + ++++ t   L  i GH   L   P L   ++ R +Y+  Ln +q   +
  gi|2380283   951 IVAEWERTTAALAAITGHEARLATNPLLARSIKNRFPYLDPLNHLQVELI 1000

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KR R               A +           n   rv  G+     L
  gi|2380283  1001 KRHR---------------AGDT----------N--ARVRRGIH----L 1018

                   tmKGiAAGmqntG<-*
                   t+ GiAAG+ ntG
  gi|2380283  1019 TINGIAAGLRNTG    1031

gi|209516095|ref|ZP_03264955.1|: domain 1 of 1, from 67 to 1014: score 309.9, E = 5.3e-90
                   *->siDAqLRlLvPGKvsed.ekLieYDALLlDkFL.DiLqDLHGedLkE
                      +  A   +   G+  ed+++ +  D   l + L+D+L +  G+ + +
  gi|2095160    67    ASAAAPAVKSGGRTREDkDHPLFQDIRYLGRLLgDVLREQEGDAVFD 113
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                avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                +v      +  +    D    + L  kL  L P  ++ v +a++    LA
gi|2095160   114 VVETIRQTAVRFRREDDNAAAQTLDKKLRTLTPEQTVSVVRAFSYFSHLA 163

                nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                n+AE+ +   R Ri+ +        +s      i   l +Lv  +  +
gi|2095160   164 NIAEDRHRNRRHRIHALA-------GSTSQPGSIAYALERLVAAG-AAAT 205

                EvFeALKnqsvDL.vltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                 v +     +  ++vltAHPt   R+s+L  +  i   La    + +t
gi|2095160   206 PVLQRFFDDALIMpVLTAHPTEVQRKSILDAQHDIARLLAE-RDQPLTNR 254

                DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                ++   +  L   +   + t  +R ++ t  DE+   +sY+  t  +  P
gi|2095160   255 ERAHNEAMLRARVTSLWQTRMLRDSRLTVADEIENALSYYRSTFLEELPA 304

                FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    ++ ALK  G+  RlP   P  +  sW+GGDRDG nP vt E
gi|2095160   305 LYADIEEALKEHGLEARLP---PFFQMGSWIGGDRDG-NPNVTAETLENA 350

                CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      +    Y++qv  L  Elsm     +      El   +  +
gi|2095160   351 ITRQAAVIFEHYLEQVHKLGAELSMSNVLVDASDALNELAAVSPDH--SP 398

                yYiEFWKqvPPtEPYRviLGdvRDKLYn.tRER....aRHLLAtGiseis
                +  +        EPYR  L  +  +L  + R R ++++  L   G    +
gi|2095160   399 HRTD--------EPYRRALIGIYTRLAAsARVRlgegSVPLRSAGRGVPP 440

                EeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                  A++y +  +F+  L +   sL e     +A   L  l R    FG  L
gi|2095160   441 IRAIpYDDSADFVRDLHVLMDSLAEHHGAPLAAPRLAPLARAAEVFGFHL 490

                vKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRP
                  +D+Rq s+ +  v+  + +  ++ + Y   +E  +   LlaEL   R
gi|2095160   491 ASIDLRQSSDIHEAVIAELLKRAGVEdDYAALPEADKLNVLLAELAQPRA 540

                LlgsDLPktEEvkDvldafrvLAELPi..DsFGa.....YiismataPsD
                L    +P  E    v   + vL E  i+++ FGa+  ++Yiis + + sD
gi|2095160   541 L---RVPYAEYSDLVKSELAVLEEARItrEKFGAravrnYIISHTETVSD 587

                vLAvELLqRECgv............kqtLrvvPLFEkLADLeAAPAavek
                 + v LLq+E g+ +++ ++++++ +  L v+PLFE + DL+ AP  +
gi|2095160   588 LVEVMLLQKETGLlrgrlgdehdpaRAGLMVIPLFETIPDLRNAPHIMRD 637

                LFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKv
                L + ++i   i +    qevm+GYsDs KD G l   W LY+A   ++
gi|2095160   638 LIAlpgIGALIEHQGNEQEVMLGYSDSNKDGGFLTSNWELYRAELALVAL 687

                AKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEvi
                  + Gv L lFHGRGGtvGRGGGPt  AiLsqPP t++G +R t qGEvi
gi|2095160   688 FNERGVTLRLFHGRGGTVGRGGGPTYQAILSQPPGTVDGQIRLTEQGEVI 737

                EfsFGEEnLCFrsLqRFtAAtLEHGmnP...PvsPkPEWRkLmeemAvvA
                   F   ++  r L    AAtLE  + P+++ ++  P + + m+++   A
gi|2095160   738 ASKFANPEIGRRNLETVVAATLEASLLPhdhTLAELPVFEQTMQQLSDTA 787

                tEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....Gie
                   YR++v+  P F EYF   tP  E   +niGsRPa Rk   ++++ ie
gi|2095160   788 MATYRALVYETPGFKEYFFESTPIAEIAELNIGSRPASRKLQDpkqrKIE 837

                sLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiKnlqkLkE
                 LRAiPW F+W q R  L  W G+G A    +d+ +++    + l  Lk
gi|2095160   838 DLRAIPWGFSWGQCRLLLTGWYGFGSAVTEHLDsapsdaERARRLALLKK 887

                mYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdk
                m k WPFF   +  ++mv AK D  +A+ y  L+    L+k   +++ ++
gi|2095160   888 MHKSWPFFSNLMSNMDMVIAKTDLAVASRYAALVTDKKLrKHVFERIVAE 937

                YvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiR
                ++ t + L +i G  + L   P L   ++ R +Y+  Ln +q   LKR R
gi|2095160   938 WERTSKALSEITGKSERLAENPLLARSIKNRFPYLDPLNHLQVELLKRYR 987
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                  DPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKG
                                    A +           n   rv  G+     L + G
  gi|2095160   988 ----------------AGDT----------N--TRVRRGIH----LSING 1005

                  iAAGmqntG<-*
                  iAAG+ ntG
  gi|2095160  1006 IAAGLRNTG    1014

gi|292833131|gb|EFF91480.1|: domain 1 of 1, from 3 to 909: score 309.6, E = 6.6e-90
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                     s D q         s   +L      L D   + L    G++L + v
  gi|2928331     3    SADDQTTT------S--SELRADIRRLGDLLGETLVRQEGPELLDLV 41

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       l  e     D +   EL   L + +   a  + +a++    LAn+
  gi|2928331    42 EKVRRLTRE-----DGEAAAEL---LRGTELETAAKLVRAFSTYFHLANV 83

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   E v   +R +  + +         A     +  t  +L       Pe
  gi|2928331    84 TEQV---HRGKELRAR--------RAAEGGLLARTADRLKDAD---PEHL 119

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   + ++   v  v+tAHPt ++RRs+L K  Ri    a L    v   D++
  gi|2928331   120 RQTVQHLNVRPVFTAHPTEAARRSVLNKLRRI----AALLETPVLESDRR 165

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   LD  L   i   + tDE+R  +P P DE R  + Y+ E     v   L
  gi|2928331   166 RLDTRLAENIDLVWQTDELRVVRPEPTDEARNAIYYLDELHAGAVGDVLE 215

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                       L  +G+  +lP d   + F  W+GGDRDG nP vtP vt Dv +L
  gi|2928331   216 DLTAELERVGV--KLPDDTRPLTFGTWIGGDRDG-NPNVTPQVTWDVLIL 262

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkvvKyY
                            i+   D++ El  +  n+     A+EEl    + d
  gi|2928331   263 QHEHG----INDALDMVDELRGFLSNSIRYTGAtEELLASLQTD--LENL 306

                  iEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                   E ++++K +  +EPYR     +R KL nt+ R    LA   s   E+
  gi|2928331   307 PEIsprYKRLNAEEPYRLKATCIRQKLVNTKRR----LAR--STAHEDGR 350

                  .ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                  +y    e L  L L   sL +      ADG L   +R    FGL L  +D
  gi|2928331   351 dYLGTAELLADLRLLQDSLRQHRGGLFADGRLARTIRTLAAFGLQLATMD 400

                  iRqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLlg
                  +R  ++ +   l  +   L+  s+R  + + + R   L  EL+ +RPL +
  gi|2928331   401 VREHADAHHHALGQLFDRLGEESWRyaDMPRDYRAKLLAKELRSRRPLAP 450

                  sDLPktEEvkDvldaf....rvLAELPiDsFGaYiismataPsDvLAvEL
                     P     +  l+ f++ +r L     +   +Yiism+    Dv A  +
  gi|2928331   451 TPAPVDAAAAKTLGVFetvkRALSVFGPEVIESYIISMCQGADDVFAAAV 500

                  LqRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                  L RE g+   + +   + +vPL E   +L+AA   +e + s   Y+  +
  gi|2928331   501 LAREAGLIDlhagwaKIGIVPLLETTDELKAADTILEDMLSDPSYRRLVA 550

                  GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                   +++ qevm+GYsDs K  G     W + +Aq  +  vA +yGv+L lFH
  gi|2928331   551 LRgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRYGVRLRLFH 600

                  GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                  GRGGtvGRGGGP H AiL+qP  t++G ++vt qGEvi   +    L
  gi|2928331   601 GRGGTVGRGGGPSHDAILAQPWGTLEGEIKVTEQGEVISDKYLIPSLARE 650

                  sLqRFtAAtLEHGm...nPPvsPk..PEWRkLmeemAvvAtEEYRsvvvK
                   L    AAtL     ++ P  s      W   m+ +   A   YR +v
  gi|2928331   651 NLELTVAATLQASAlhtAPRQSDEalARWDAAMDVVSDAAHAAYRRLV-E 699

                  EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWt
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                    +P    YF   tP      + +GsRP+ R+P+ G++ + LRAiPW+F Wt
  gi|2928331   700 DPDLPTYFLASTPVDQLAELHLGSRPS-RRPGSGVslDGLRAIPWVFGWT 748

                    qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                    q R  +P W GvG   K   +     +  L Em ++W FFR  +  +Em
  gi|2928331   749 QSRQIVPGWFGVGSGLKALRETGLDTV--LGEMHEQWHFFRNFISNVEMT 796

                    FAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE
                     AK D  iA  y + Lv +eLk   + ++++ + t   +L++ G  +lL
  gi|2928331   797 LAKTDLRIAQHYVDTLVPDELKHVFDVIKAEHELTVAEVLRVTGESELLA 846

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                      P LKq   +Rd+Y+  +  +q   LKR RD               A+
  gi|2928331   847 AQPVLKQTFAIRDAYLDPISYLQVALLKRQRDTA-------------AAG 883

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +  ++d L+               L+Lt+ G+AAG+ ntG
  gi|2928331   884 Q--EPDPLLARA------------LLLTVNGVAAGLRNTG    909

gi|119897283|ref|YP_932496.1|: domain 1 of 1, from 1 to 917: score 309.5, E = 6.9e-90
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                              + P K +     ++ D  Ll + L+D + D  G    +
  gi|1198972     1    --------MTPDKDA----PLREDIRLLGRLLgDTVRDQQGAASFDL 35

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +      s  +   +D     EL   L +L    +i v +a++    LAn
  gi|1198972    36 IERIRQTSVRFRRDEDLAARRELEDTLDALSREQTIQVVRAFSYFSHLAN 85

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+ +   R R +++        +sA  E  +   + +        P +
  gi|1198972    86 IAEDQHHIRRSRAHLLA-------GSAPREGSLAHAVGHALDEQRLDPTD 128

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                             +  vltAHPt   R+s+L  ++ i   L       +t+++
  gi|1198972   129 LAAFFDTALISPVLTAHPTEVQRKSILNCQTVIARLLDERDRMQLTPDEA 178

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +   +AL R +   + t  +R a+    DE+  G+sY+  t  +  P+
  gi|1198972   179 EANLDALRRAVLTLWQTRMLRPAKLSVIDEVNNGLSYFETTFLRELPRLY 228

                    RRvDtALKniG...inERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                       +  L    +   n  lP     ++  sW+GGDRDG nP vt +v  +
  gi|1198972   229 AALEDRLAGAQpalANHELP---AFLQVGSWIGGDRDG-NPYVTADVLEE 274

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                       +   +A   Y++ +  L   ls+    + L    + l   a r
  gi|1198972   275 ALAMQARVALDYYLDELHTLGSQLSL---SQGLVGASDALLALADRS--- 318

                    KyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAt..Giseis
                            q P++  EPYR  +  +  +L  t    R LL +++    ++
  gi|1198972   319 ------PDQSPhrSDEPYRRAIAGIYARLSATY---RNLLGHppARHAVA 359

                    EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                    E   y +v    + L+   +sL   G  ++A G L  l R v  FG  L
  gi|1198972   360 EAEPYADVAALADDLDTLHRSLVANGTAALARGRLRHLRRAVRVFGFHLA 409

                    KLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPL
                     +D+Rq s+ +  v+  + +    G +Y    E  R   Ll EL   RPL
  gi|1198972   410 PIDLRQNSDVHERVVAELLEVARPGaAYLAQDEAGRCALLLDELATARPL 459

                    lgsDLPktEEvkDvldafrvL..AELPi..DsFGaYiismataPsDvLAv
                      + +   ++ +  l  fr  ++A L  ++ +    iis +   sD L
  gi|1198972   460 ASPHVRYSDDSEGELAIFRAArrAHLRYgrGAIHNCIISKTDDLSDLLEL 509

                    ELLqRECgvkqtLr......vvPLFEkLADLeAAPAavekLFsiDWYinr
                     +L +E g+ ++L +  + ++vPLFE + DLe A   +++LFsi  Y+
  gi|1198972   510 AVLLKEAGLLRPLEkaldvnIVPLFETIGDLENAAGVMDRLFSIPVYREL 559

                    idGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                    +  ++++qevm+GYsDs KD G l   W LYkA  E++ v  ++Gv+L l
  gi|1198972   560 LAARdqtQEVMLGYSDSNKDGGFLTSGWALYKAEGELVEVFGRHGVRLRL 609
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                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                    FHGRGG vGRGGGP   AiL+qP   ++G +R t qGEvi   +G  ++
  gi|1198972   610 FHGRGGSVGRGGGPSYQAILAQPDGAVQGQIRLTEQGEVIAAKYGNPEVG 659

                    FrsLqRFtAAtLEHGmnP...PvsPkPEWRkLmeemAvvAtEEYRsvvvK
                     r L    AAtLE  +  +++   P+  + + m+ +   A   YR +v+
  gi|1198972   660 RRNLEVLVAATLETSLRRdggDATPR-TFLDTMQALSDAAFTCYRGLVYE 708

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                     P F  YF   t   E   +niGsRPa Rk +  i+ LRAiPW+F+W q
  gi|1198972   709 TPGFEQYFWESTVISEIAGLNIGSRPASRKKGTRIDDLRAIPWVFSWSQC 758

                    RFHLPvWLGvGAAFKhAidKDiKn.lqkLkEmYkeWPFFRvtlDLlEmvF
                    R  LP W G+G A K  +    K +l  L+ mY+eW FF   l  ++mv
  gi|1198972   759 RLMLPGWFGFGSAVKQWLAAHPKDgLGLLQRMYREWSFFATLLSNMDMVL 808

                    AKGDPGiAaLyDkLLvaEeLk.PFGksLRdkYvEtkdlLLkiAGHkDlLE
                     K D  iA+ y +L+    L++   +++R ++++t d LL i    +lL+
  gi|1198972   809 SKTDLAIASRYAELVKDPVLRdSIFERIRSEWKDTVDALLAITEQVELLD 858

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                      P LK  +R R +Y+  Ln +q   L+R R+ +               E
  gi|1198972   859 ANPLLKRSIRNRFPYLDPLNHVQVELLRRHREGN--------------GE 894

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +  +  + +++                + GiAAG+ n G
  gi|1198972   895 D-ARIRNGIHIS----------------INGIAAGLRNSG    917

gi|254671222|emb|CBA08427.1|: domain 1 of 1, from 18 to 917: score 309.4, E = 7.3e-90
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2546712    18    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 55

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2546712    56 ETVKLLSTS----DDSAALIE--KVLPQLDEQQTHDLTLACGLFAQILNI 99

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+   RR i+          +    E  + Et+++L        + v
  gi|2546712   100 AEDVHHERRRQIHEEA-------GRGGAEGSLTETVRRLKAGK-ADGKSV 141

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                       L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|2546712   142 QRQLDNTSVTAVLTAHPTEVQRQTVLSFNRRIRALLPQrerCTNADALAR 191

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|2546712   192 LRREIDTILLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 237

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R+++   +       +P    ++k   W+GGDRDG nP v  E  R
  gi|2546712   238 LYRKMEHDFQTAYPDVCVP---NILKIGGWIGGDRDG-NPFVSAETLRFA 283

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                              +Y s ++ L  El +    +  Rv+      ta +dk
  gi|2546712   284 FRRHADAVFRFYRSELDKLYRELPL----SIRRVKVNG-DVTALSDKSPD 328

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEeAv
                      i        +EPYR  +  +   +     +aR L+L  G      e
  gi|2546712   329 EEI-----ARAEEPYRRAIAYI---MARAMGKARALgLGMGCKFGFLEP- 369

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y    eFL+ L    +sL + G + +A+G L Dl+R vs FG  ++ LD+
  gi|2546712   370 YASAQEFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPLDL 419

                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL+ +RPL+ + +
  gi|2546712   420 RQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAVLLRELSHQRPLYSPFI 469

                    PktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAvELLqR
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                      E  +  l  f++ +++  E   D+    iis +  PsD LA  LL +
  gi|2546712   470 TYSEHTRHELAIFNearkIKDEFGEDAVTQSIISNCEQPSDLLALALLLK 519

                   ECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                   E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   ++
  gi|2546712   520 ESGLlavengkpRSRINIVPLFETIEALENACPVMETMFRLDWYDALLES 569

                   K...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                   +++ qe+m+GYsDs KD G +   W LY+A   ++   Kky v++ lFHG
  gi|2546712   570 RgniQEIMLGYSDSNKDGGYVTSSWCLYQAELGLVELFKKYDVRMRLFHG 619

                   RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                   RGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +     r
  gi|2546712   620 RGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQRN 669

                   LqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvE
                   L    AAtLE G+ P    k    kLm+ +  v    YR ++   P F++
  gi|2546712   670 LETLVAATLEAGILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDFID 716

                   YFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPv
                   YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  LP
  gi|2546712   717 YFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLMLPA 766

                   WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                   W G+G A     +     l  L+E  +  PFF   l  +E v AK D  +
  gi|2546712   767 WYGFGSAVETLCEDKPETLAALREHAQSNPFFQAMLSNMEQVMAKTDITL 816

                   AaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                   A  y  L  ++E        ++++Y+  ++ LL +    +lL     L
  gi|2546712   817 AENYAGLSESpEKAAVIFGMIKEEYQRSRKALLDLLQTEELLRDNRSLAR 866

                   rlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkade
                    l LR +Y+  Ln +q   LKR+R                 E+   +
  gi|2546712   867 SLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNPHA 898

                   LvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   L+ +               Lt+ G+A G+ ntG
  gi|2546712   899 LLMVH--------------LTINGVAQGLRNTG    917

gi|254384995|ref|ZP_05000330.1|: domain 1 of 1, from 3 to 920: score 309.4, E = 7.4e-90
                   *->siDAq..LRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                      s D  ++  + + G  + + +L      L D   + L    G+dL +
  gi|2543849     3    SADQApsTSATASGAEAANAELRADIRRLGDLLGETLVRQEGQDLLD 49

                   avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    v     l    +G   ++ L++     t L+ a  ++  +a++    LA
  gi|2543849    50 LVERVRALTRT-DGIAAAELLGD-----TDLETAAKLV--RAFSTYFHLA 91

                   nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                   n+ E v+     R k ++       a    E  +      +       Pe
  gi|2543849    92 NVTEQVH-----RGKELR-------AHRAAEGGLLARTADMLKDA--DPE 127

                   EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                      + +Kn  v  v+tAHPt ++RRs+L K  Ri   L    A      +
  gi|2543849   128 HLRQTVKNLNVRPVFTAHPTEAARRSVLNKLRRIAALLEEPAA---GAGE 174

                   KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                   ++  D  L   i   + tDE+R  +P P DE R  + Y+ E     v
  gi|2543849   175 RRRHDLRLAENIDLVWQTDELRVVRPEPADEARNAIYYLDELHAGAVGDV 224

                   LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   L      L+ +G+ E  P   PL  F  W+GGDRDG nP vtP+vtRDv
  gi|2543849   225 LEDLAAELQRVGV-ELPPGTRPL-TFGTWIGGDRDG-NPNVTPDVTRDVL 271

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkvvK
                   +L         ++ v+ L   ls    n+     A+EEl    + d
  gi|2543849   272 ILQHEHGITDALELVDFLRGLLS----NSIRYTGAtEELLASLQAD--LE 315

                   yYiEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                      E ++++K +  +EPYR     vR KL ntRER    LA+G     E
  gi|2543849   316 RLPEIsprYKRLNAEEPYRLKATCVRQKLVNTRER----LAKGTPH-EEG 360
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                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y    e L  L L   sL e      ADG +   +R    FGL L  +
  gi|2543849   361 RDYLGTAELLTDLTLIQTSLREHRGALFADGRMDRTIRTLAAFGLQLATM 410

                    DiRqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLl
                    D+R  ++ +   l  +   L+  s+R  + + + R   L  EL+ +RPL
  gi|2543849   411 DVREHADAHHHALGQLFDRLGEESWRyaDMPRDYRGKLLAKELRSRRPLA 460

                    gsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAv
                    +   P     +  l+ f  + +   + FG++  ++Yiism+    Dv A
  gi|2543849   461 PTPAPLDAAGQKTLGVFFAIKD-AFEKFGPeviesYIISMCQGADDVFAA 509

                    ELLqRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                     +L RE g+   + +   + +vPL E   +L+AA   ++ + +   Y+
  gi|2543849   510 AVLAREAGLLDlhagwaKIGIVPLLETTDELRAADVILDEMLADPSYRRL 559

                    idGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                    +  +++ qevm+GYsDs K  G     W + +Aq  +  vA +yGv+L l
  gi|2543849   560 VSLRgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRYGVRLRL 609

                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                    FHGRGGtvGRGGGP H AiL+qP  t++G ++vt qGEvi   +    L
  gi|2543849   610 FHGRGGTVGRGGGPSHDAILAQPWGTLEGEIKVTEQGEVISDKYLVPSLA 659

                    FrsLqRFtAAtLEHGmnPPvsPk......PEWRkLmeemAvvAtEEYRsv
                       L    AAtL        +P++++   W   m+ +   A   YR++
  gi|2543849   660 RENLELTVAATLQASAL-HTAPRqsdddlARWDAAMDTVSDAAHGAYRAL 708

                    vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFa
                    v  +P    YF  AtP      + +GsRP++R  sG G++ LRAiPW+F
  gi|2543849   709 V-EDPDLPAYFFAATPVDQLADLHLGSRPSRRPDSGaGLDGLRAIPWVFG 757

                    WtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlE
                    Wtq R  +P W GvG   K    ++      L Em + W FFR  l  +E
  gi|2543849   758 WTQSRQIVPGWYGVGSGLKAL--REAGGEHALTEMGERWHFFRNFLSNVE 805

                    mvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDl
                    m  AK D  iA  y + Lv +eLk   +++ ++ + t   +L+i G + l
  gi|2543849   806 MTLAKTDLRIARHYVDTLVPDELKHVFDRIQAEHELTVREVLRITGGRQL 855

                    LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                    L+  P L+q   +Rd+Y+  +  +q   L R R                A
  gi|2543849   856 LDSNPVLQQTFAVRDAYLDPISYLQVSLLARQRA---------------A 890

                    dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +E             +e+  P L   L+Lt+ G+AAG+ ntG
  gi|2543849   891 AER------------GEEADPLLARALLLTVNGVAAGLRNTG    920

gi|221065752|ref|ZP_03541857.1|: domain 1 of 1, from 9 to 949: score 309.1, E = 9.3e-90
                    *->siDAqLRlLvPG.KvsedekLieYDALLlDkFL.DiLqDLHGedLkE
                       +  A      P +K  +d  Lie D  Ll + L+D++ +  G    E
  gi|2210657     9    AAHADKHGEKPArKTDKDLPLIE-DIRLLGRILgDVIREQEGGPAYE 54

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                     v     ls  +    D      L   L +L    ++ v +a+     LA
  gi|2210657    55 LVEQVRQLSVAFRRDADEAADKALKKLLKGLSSDQTVSVIRAFTYFSHLA 104

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    nLAE+ +   RRR    +       a  t E  iE  l +L   +  sP+
  gi|2210657   105 NLAED-RHHIRRRAVHER-------AGNTQEGSIEVALARLRWAG-ISPA 145

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL.........aqL
                     v + L    +  vltAHPt   R s+L  + Ri   L ++++   +aqL
  gi|2210657   146 TVVDTLARSFISPVLTAHPTEVQRQSILTAERRIAQLLaerddilmrAQL 195

                    s..AKD.vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsY
                    +++AKD +t+ +   ++  L   +   + t  +R ++ t  DE+   +sY
  gi|2210657   196 YnsAKDaLTPRELTRVEAQLRACVAQLWQTRLLRHSKLTVADEIENALSY 245

                    iHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGkn
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                    +  t  + +PK     +  L      E+lP +   ++   W+GGDRDG n
  gi|2210657   246 YEATFLQEIPKIYEQLEQEL-----GEKLP-EQSFLRMGQWIGGDRDG-N 288

                    PRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEl
                    P vt E           +A   Y+  v  L  Els+      L     E+
  gi|2210657   289 PFVTAESLELALSRQADVALRHYLREVHYLGGELSL---SANLVDITPEM 335

                    yrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAt
                    +  a       + +         EPYR  L  +  +L  t        A
  gi|2210657   336 QTLADAS--PDHNVH-----RSDEPYRRALTGIYARLAATLKQLTGGEAA 378

                    GiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvst
                      +  + +A y   + FL  L +   sL      ++A   L  l+R v
  gi|2210657   379 RHAVAPQNA-YASADAFLADLQIIDDSLSRYHGDALAPQRLRPLMRAVRV 427

                    FGLsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaEL
                    FG  L  +D+Rq s+++ +v+  +     +   Y    E+ +   L+  L
  gi|2210657   428 FGFYLSTVDLRQSSDKHEEVVRELLSVAKVElDYSLLEEDAKCALLVRLL 477

                    kGKRPL..lgsDL.PktEEvkDvldafrvLAE.LPiDsFGaYiismataP
                    +  RPL+ +g D +  t     + ++ + L E+L  ++    iis + +
  gi|2210657   478 EDARPLrvMGGDYgDHTRSELAIFETAKRLRErLGGEAIRHCIISHTETV 527

                    sDvLAvELLqRECgv.........kqtLrvvPLFEkLADLeAAPAavekL
                    sD L v LLq+E g+ +++ +++ +  L vvPLFE + DL+ A   + +
  gi|2210657   528 SDLLEVLLLQKEVGLlrgtlqdgaQCDLIVVPLFETIEDLRNAAPIMRRY 577

                    Fs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEii...
                    +  ++i   + +  G q++m+GYsDs KD G +   W LY+A   +++
  gi|2210657   578 YQlpgIAELVRKSGGEQDIMLGYSDSNKDGGIFTSNWELYRAEIALVdlf 627

                    .KvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqG
                    +  A +yG++L +FHGRGGtvGRGGGP   AiL+qPP t+ G +R t qG
  gi|2210657   628 dDLADHYGIRLRMFHGRGGTVGRGGGPSYQAILAQPPGTVRGQIRLTEQG 677

                    EviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvv.
                    Evi   +   ++  r L    AAtLE  +  P   kP  +  +e  A  +
  gi|2210657   678 EVIASKYANPEIGRRNLETLVAATLEATLLQPT--KPATKAFLEAAAFLs 725

                    ..AtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGies
                    ++    YR++v+  P F  YF + tP  E   +niGsRPa Rk    ie
  gi|2210657   726 etSMAAYRALVYETPGFTNYFFSSTPIREIAELNIGSRPASRKATQAIED 775

                    LRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid...KDiK.nlqkLkEmYk
                    LRAiPW F+W q R  LP W G+G A +  i++++KD K  l  L+ mY+
  gi|2210657   776 LRAIPWGFSWGQCRLTLPGWYGFGSAIQAFIHrpgKDAKaQLALLQKMYR 825

                    eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL..kPFGksLRdkYv
                    +WPFFR  l  ++mv AK D  +A+ y +L+    L+++ FG  + ++++
  gi|2210657   826 QWPFFRTLLSNMDMVLAKSDLNLASRYSELVTDTRLrrRIFG-AIEAEWQ 874

                    EtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDP
                     t + L +i G k  LE    L   +R R +Yi  Ln +q   ++R R
  gi|2210657   875 STVEALNQITGDKQRLEHNSALARSIRHRFPYIDPLNHLQVELVRRWR-- 922

                    sykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiA
                                  A     +  + ++L                + GiA
  gi|2210657   923 --------------AGQTDDRVKNGIHLS----------------INGIA 942

                    AGmqntG<-*
                    AG+ ntG
  gi|2210657   943 AGVRNTG    949

gi|167585804|ref|ZP_02378192.1|: domain 1 of 1, from 59 to 1007: score 309.1, E = 9.4e-90
                    *->siDAqLRlLvPGKvsedek...LieYDALLlDkFL.DiLqDLHGedL
                       +  A   +  PG    ++k+++L e D   l + L+D++ +  G+ +
  gi|1675858    59    ANGAAAVAAKPGVRTREDKdrpLFE-DIRFLGRLLgDVVREQEGDAV 104

                    kEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLn
                     ++v      +  +    D +  + L  kL  L P  ++ v +a++
  gi|1675858   105 FDVVETIRQTAVKFRREDDREAAQTLEKKLRKLTPEQTVSVVRAFSYFSH 154
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                LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                LAn+AE+ +   RRRi+ +        +sA     +   l +L   +  +
gi|1675858   155 LANIAEDRHHNRRRRIHALA-------GSAPQPGTVAFALDQLKQAG-GA 196

                PeEvFeALKnqsvDL.vltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt
                 ++v +     +  ++vltAHPt   R+s+L  +  i   La    +++t
gi|1675858   197 SKDVLQRFFDDALIVpVLTAHPTEVQRKSILDAQHDIARLLAE-RDQELT 245

                veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGv
                  +++  +  L   + A + t  +R a+ t  DE+   +sY+  t  +
gi|1675858   246 ARERQHNEAMLRARVTALWQTRMLRDARLTVGDEIENALSYYRATFLDEL 295

                PKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                P     ++ AL   G+  R+P      +  sW+GGDRDG nP vt
gi|1675858   296 PALYGDIEAALAEHGLPARVP---AFFQMGSWIGGDRDG-NPNVTAATLD 341

                DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                +       +    Y++qv  L  Els+    + L v A +  +  a
gi|1675858   342 EAIHRQSAVILEHYLEQVHKLGAELSV----SNLLVGASDAVKALAAA-- 385

                vKyYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER....aRHLLAtGi
                          q P++  EPYR  L  +  +L  + R R ++++  +   G
gi|1675858   386 ------SPDQSPhrVDEPYRRALIGIYTRLAAsARVRlgegTVPVRSAGR 429

                seisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstF
                   +  A +y + EeF+  L +   sL e     +A   L  l R    F
gi|1675858   430 GAAPVRATpYADSEEFVRDLKVLMESLDEHHGASLAAPRLAPLARAAEVF 479

                GLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELk
                G  L  +D+Rq s+ +  v+  +    ++ ++Y   +Ee +   Ll+ L
gi|1675858   480 GFHLASIDLRQSSDIHEAVVAELFARAGVEAdYAALAEEDKLRVLLTALA 529

                GKRPLlgsDLPktEEvkDvldafr....vLAELPiDsFGaYiismataPs
                  RPL  +        +  l+ f++ + v A     +   Yiis + + s
gi|1675858   530 DPRPLRSPYFEYSALAQSELGVFEkaraVRAQFGPRAVRNYIISHTETVS 579

                DvLAvELLqRECgv............kqtLrvvPLFEkLADLeAAPAave
                D + v LLq+E g+ ++  + ++++ k+ L v+PLFE + DL+ A   +
gi|1675858   580 DLVEVLLLQKETGLldgafgakhggaKNGLMVIPLFETIPDLRDASRIMR 629

                kLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiK
                  F+ +++D  + +  G qevm+GYsDs KD G l   W LY+A   ++
gi|1675858   630 EYFAlpgVDALVAHQGGEQEVMLGYSDSNKDGGFLTSNWELYRAELALVD 679

                vAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEv
                   + G+ L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGEv
gi|1675858   680 LFHERGITLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEV 729

                iEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv...sPkPEWRkLmeemAvv
                i   F   ++  r L    AAtLE  + P  + ++  P +   m+ +
gi|1675858   730 IASKFANPEIGRRNLETVVAATLEASLLPQSnapAQLPAFETAMQTLSDT 779

                AtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....Gi
                A   YR++v+  P F +YF + tP +E   +niGsRPa Rk   ++++ i
gi|1675858   780 AMAAYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASRKLQDpkhrRI 829

                esLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid..KD....iKnlqkLk
                e LRAiPW F+W q R  L  W G+G A    +d++KD  +++K l  Lk
gi|1675858   830 EDLRAIPWGFSWGQCRLLLTGWYGFGSAVAVYLDgsKDaaerSKRLALLK 879

                EmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRd
                 m k+WPFF   l  ++mv AK D  +A+ y +L+    L+k   +++ +
gi|1675858   880 KMNKTWPFFSNLLSNMDMVLAKTDLAVASRYAQLVADKKLrKHVFERIVA 929

                kYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRi
                +++ t + L +i G    L   P L   ++ R +Y+  Ln +q   +KR
gi|1675858   930 EWERTSQALTEITGQDTRLATNPLLARSIKNRFPYLDPLNHLQVELIKRH 979

                RDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmK
                R               A +           n   r   G+     Lt+
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  gi|1675858   980 R----------------AGDT----------N--ARLRRGIH----LTIN 997

                    GiAAGmqntG<-*
                    GiAAG+ ntG
  gi|1675858   998 GIAAGLRNTG    1007

gi|225858881|ref|YP_002740391.1|: domain 1 of 1, from 1 to 898: score 308.9, E = 1e-89
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           L  L     s +  +++ + L+l   L+Di + +  ++  E
  gi|2258588     1    ---MSLQKLE--NYS-NKSVVQEEVLILTELLeDITKNMLAPETFEK 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +    Els +    +D + L+ L   +tsL   + + + + ++ +  L n
  gi|2258588    42 IIQLKELSTQ----EDYQGLNRL---VTSLSNDEMVYISRYFSILPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+    s t          kLv       e
  gi|2258588    85 ISEDVDLAYEINHQNNIDQDYLGKLSTTI---------KLVAEK----EN 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      e L    v  vltAHPtq  R+s+L     i   L +     +    K
  gi|2258588   122 AVEILEHLNVVPVLTAHPTQVQRKSMLDLTNHIHSLLRKYRDVKLGLINK 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                          L R i     tD iR  +     E+   m Y+     k vP
  gi|2258588   172 DKWYNDLRRYIEIIMQTDMIREKKLKVTNEITNAMEYYNSSFLKAVPHLT 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                           +  G+n +   ++  i    W+GGDRDG nP vt E  +   L
  gi|2258588   222 TEYKRLAQAHGLNLK---QAKPITMGMWIGGDRDG-NPFVTAETLKQSAL 267

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                        +  n Y  ++  L  E+s+      +     E+ r ++ +     Y
  gi|2258588   268 TQCEVIMNYYDKKIYQLYREFSLSTSIVNVSKQVREMARQSKDN---SIY 314

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                     E        E YR  L d+  K+  t+          i +      y
  gi|2258588   315 RE-------KELYRRALFDIQSKIQATK-------TYLIEDEEVGTRYET 350

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      +F   L     sL e     +  G  ++lL  v  FG  L  +D+Rq+
  gi|2258588   351 ANDFYKDLIAIRDSLLENKGESLISGDFVELLQAVEIFGFYLASIDMRQD 400

                    seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK.RPLlgsDLP
                    s      +  + +  +i s+Y e sEe + + Ll EL+  +R L
  gi|2258588   401 SSVYEACVAELLKSAGIHSrYSELSEEEKCDLLLKELEEDpRILSATHAE 450

                    ktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLqRE
                    k E ++++  +  + rvL ++L  D     iis at+ sD+L   +L +E
  gi|2258588   451 KSELLAkelAIFKTARVLKDkLGDDVIRQTIISHATSLSDMLELAILLKE 500

                    Cgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                     g+ ++++  +++vPLFE + DL+    ++ k  s+   +  id +++ q
  gi|2258588   501 VGLvdteRARVQIVPLFETIEDLDHSEETMRKYLSLSLAKKWIDSRnnyQ 550

                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                    e+m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGRGGtv
  gi|2258588   551 EIMLGYSDSNKDGGYLSSCWTLYKAQQQLTAIGDEFGVKVTFFHGRGGTV 600

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                    GRGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
  gi|2258588   601 GRGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLV 650

                    AAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                     A +   +    s  +++  +  +m+++     + YR +v+    F +YF
  gi|2258588   651 SAAINRMITQKKSDTntpNRYEAIMDQVVDRSYDVYRDLVFGNEHFYDYF 700

                    RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                        P       niGsRPa Rk    i  LRAiPW+F+W q R   P W
  gi|2258588   701 FESSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWY 750
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                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    GvG  FK  i+K   n+  L++mY++WPFF   l  ++mv  K    iA
  gi|2258588   751 GVGSSFKEFINKNPENIAILRDMYQNWPFFQSLLSNVDMVLSKSNMNIAF 800

                    LyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                     y kL   E++k   + + ++++ tk+ +L i GH +lL   PYLK  l
  gi|2258588   801 EYAKLCEDEQVKAIYETILNEWQVTKNVILAIEGHDELLADNPYLKASLD 850

                    LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                     R +Y   Ln +q   +KR R        r +ls +  +E       L++
  gi|2258588   851 YRMPYFNILNYIQLELIKRQR--------RGELSSD--QER------LIH 884

                    LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +                + GiA G+ n G
  gi|2258588   885 IT----------------INGIATGLRNSG    898

gi|220911519|ref|YP_002486828.1|: domain 1 of 1, from 11 to 937: score 308.6, E = 1.3e-89
                    *->siDAqLRlLvPGKvse..dekLi.eYDALLlDkFLDiLqDLHGedLk
                        +   LR+ v  +vs    e L+++    LlD    +   L  ++ k
  gi|2209115    11    DLASELRADVR-RVSTllGESLVrQHGPELLDLVEQV--RLLTKESK 54

                    EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    Ea     +    +       ++ EL   L sL    a  + +a+     L
  gi|2209115    55 EAARGGADATGPWSAHDVVAQVREL---LGSLPIEQATDLVRAFAFYFHL 101

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                    An AE v   +R R  + +         A  +  +  t+  +  +    P
  gi|2209115   102 ANAAEQV---HRVRGLRTR---------AEKDGWLAKTVAEIAGQA--GP 137

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    e   e +    v  ++tAHPt + RRs+L K  ++   Laq      t
  gi|2209115   138 EVLQEVVNGLDVRPIFTAHPTEASRRSVLDKIRKLSDVLAQPTIEGTTAR 187

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++  D  L   i   + tDE+R  +PtP DE R  + Y+   + + +P
  gi|2209115   188 RRQ--DRQLAEIIDQMWQTDELRQVRPTPVDEARNAIYYLGGILTDAMPE 235

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     L      L   G+      d+P +kF sW+GGDRDG nP vt  vtR++
  gi|2209115   236 MLSELSELLSEHGVT-LAAQDAP-VKFGSWIGGDRDG-NPNVTAAVTREI 282

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      +    A  + i  +++L+  ls    n+   + A+ +   +      K
  gi|2209115   283 LQIQNQNAIRISIGMIDELISILS----NSTALAGADQVLLDSIDA-DLK 327

                    yYiEFWKqv...PPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                          K v +   +EPYR  L  ++ KL nt  R         s+
  gi|2209115   328 KLPGLDKRVlelNAQEPYRLKLTCIKAKLINTGKR-----VAANSNHEHG 372

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y   +e L  L+L   sL +      ADG+L  + R +  FGL L  L
  gi|2209115   373 RDYSSTDELLADLDLLELSLRNHSASLAADGALARVRRAIASFGLHLATL 422

                    DiRqEseRqtDvlDAittHLeiG..sYReWsEeKRqEWLlaELkGKRPLl
                    DiR  ++ + D +  +   ++  +  Y e s   R E L +EL  +RPL
  gi|2209115   423 DIREHADHHHDAVGQLMDRIGGPglHYAELSRKERFEVLGSELASRRPLS 472

                    gsDLPk...tEEvkDvldaf.rvLAELPiDsFGaYiismataPsDvLAvE
                    g  +  ++  +   Dv   ++r L     D    Yiism+    DvLA
  gi|2209115   473 GHPIKLdgaADGTYDVFREIrRALRMYGPDVIETYIISMTRGADDVLAAA 522

                    LLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsiDWYin
                    ++ RE g+ +  ++++   L   PL E + +L+A    +++L s   Y+
  gi|2209115   523 VIAREAGLVNlfgekpyaKLGFAPLLETVEELRASAEIIDQLLSDPSYRE 572

                    ..ridGK.qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                      r+ G  qevm+GYsDs K+ G +   W + k q  +  +A k+Gv++
  gi|2209115   573 lvRLRGDvQEVMLGYSDSNKESGVMTSQWEIHKTQRKLRDIAAKHGVRVR 622

                    lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                    lFHGRGG vGRGGGPt  AiL+qP   ++G ++ t qGEvi   +   +L
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  gi|2209115   623 LFHGRGGSVGRGGGPTYDAILAQPNGVLEGEIKFTEQGEVISDKYSLPEL 672

                   CFrsLqRFtAAtLEHGm...nPPvs..PkPEWRkLmeemAvvAtEEYRsv
                       L    AA L     +++P  s++ +  + ++me +   A E YRs+
  gi|2209115   673 ARENLELSLAAVLQGSAlhrDPRTSddQRERYAHVMETISDAAFERYRSL 722

                   vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFa
                   +   P    YF   tP    G +niGsRP+KR  sG G+  LRAiPW+F
  gi|2209115   723 I-DHPDLPAYFMASTPVEQLGSLNIGSRPSKRPDSGaGLGGLRAIPWVFG 771

                   WtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlE
                   Wtq R  +P W GvG   K A  ++  n  +L Em  +W FFR  l  +E
  gi|2209115   772 WTQSRQIVPGWFGVGSGLKAA--REAGNSEQLVEMIGQWHFFRSVLSNVE 819

                   mvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDl
                   m  AK D  iA+ y + Lv  eL+   + +R++Y+ t   +  + G + l
  gi|2209115   820 MTLAKTDLDIAGYYVDTLVPKELHHIFRAIREEYELTVTEVQNLTGEHVL 869

                   LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                   L+  P LK  l +Rd Y+  +  +q   L+R+R                A
  gi|2209115   870 LDAQPTLKRSLEVRDQYLDPISYLQVELLRRVRAE--------------A 905

                   dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    E    +++ +           L   +++t+ G+AAG+ ntG
  gi|2209115   906 GEG--MSNGEIDER--------LQRAMLITVNGVAAGLRNTG    937

gi|168494501|ref|ZP_02718644.1|: domain 1 of 1, from 1 to 898: score 308.6, E = 1.3e-89
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                          L  L     s +  +++ + L+l   L+Di + +  ++  E
  gi|1684945     1    ---MSLQKLE--NYS-NKSVVQEEVLILTELLeDITKNMLAPETFEK 41

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +    Els +    +D + L+ L   +tsL   + + + + ++ +  L n
  gi|1684945    42 IIQLKELSTQ----EDYQGLNRL---VTSLSNDEMVYISRYFSILPLLIN 84

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   + E+v+lAy    +     D+    s t          kLv       e
  gi|1684945    85 ISEDVDLAYEINHQNNIDQDYLGKLSTTI---------KLVAEK----EN 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     e L    v  vltAHPtq  R+s+L     i   L +     +    K
  gi|1684945   122 AVEILEHLNVVPVLTAHPTQVQRKSMLDLTNHIHSLLRKYRDVKLGLINK 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                         L R i     tD iR  +     E+   m Y+     k vP
  gi|1684945   172 DKWYNDLRRYIEIIMQTDMIREKKLKVTNEITNAMEYYNSSFLKAVPHLT 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                          +  G+n +   ++  i    W+GGDRDG nP vt E  +   L
  gi|1684945   222 TEYKRLAQAHGLNLK---QAKPITMGMWIGGDRDG-NPFVTAETLKQSAL 267

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                       +  n Y  ++  L  E+s+      +     E+ r ++ +     Y
  gi|1684945   268 TQCEVIMNYYDKKIYQLYREFSLSTSIVNVSKQVREMARQSKDN---SIY 314

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                    E        E YR  L d+  K+  t+          i +      y
  gi|1684945   315 RE-------KELYRRALFDIQSKIQATK-------TYLIEDEEVGTRYET 350

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     +F   L     sL e     +  G  ++lL  v  FG  L  +D+Rq+
  gi|1684945   351 ANDFYKDLIAIRDSLLENKGESLISGDFVELLQAVEIFGFYLASIDMRQD 400

                   seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK.RPLlgsDLP
                   s      +  + +  +i s+Y e sEe + + Ll EL+  +R L
  gi|1684945   401 SSVYEACVAELLKSAGIHSrYSELSEEEKCDLLLKELEEDpRILSATHAE 450

                   ktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLqRE
                   k E ++++  +  + rvL ++L  D     iis at+ sD+L   +L +E
  gi|1684945   451 KSELLAkelAIFKTARVLKDkLGDDVIRQTIISHATSLSDMLELAILLKE 500
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                    Cgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                     g+ ++++  +++vPLFE + DL+    ++ k  s+   +  id +++ q
  gi|1684945   501 VGLvdteRARVQIVPLFETIEDLDHSEETMRKYLSLSLAKKWIDSRnnyQ 550

                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                    e+m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGRGGtv
  gi|1684945   551 EIMLGYSDSNKDGGYLSSCWTLYKAQQQLTAIGDEFGVKVTFFHGRGGTV 600

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                    GRGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
  gi|1684945   601 GRGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLV 650

                    AAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                     A +   +    s  +++  +  +m+++     + YR +v+    F +YF
  gi|1684945   651 SAAINRMITQKKSDTntpNRYEAIMDQVVDRSYDIYRDLVFGNEHFYDYF 700

                    RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                        P       niGsRPa Rk    i  LRAiPW+F+W q R   P W
  gi|1684945   701 FESSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWY 750

                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    GvG  FK  i+K   n+  L++mY++WPFF   l  ++mv  K    iA
  gi|1684945   751 GVGSSFKEFINKNPENIAILRDMYQNWPFFQSLLSNVDMVLSKSNMNIAF 800

                    LyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                     y kL   E++k   + + ++++ tk+ +L i GH +lL   PYLK  l
  gi|1684945   801 EYAKLCEDEQVKAIYETILNEWQVTKNVILAIEGHDELLADNPYLKASLD 850

                    LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                     R +Y   Ln +q   +KR R        r +ls +  +E       L++
  gi|1684945   851 YRMPYFNILNYIQLELIKRQR--------RGELSSD--QER------LIH 884

                    LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +                + GiA G+ n G
  gi|1684945   885 IT----------------INGIATGLRNSG    898

gi|213965583|ref|ZP_03393777.1|: domain 1 of 1, from 14 to 942: score 308.5, E = 1.4e-89
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +   q    +  K     +L++ D   l + L+ ++ +  G+++
  gi|2139655    14    ASNGQSSSTATAKQQ---DLLREDIRHLGRILgQVIREQEGDEVFNL 57

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v       A +E  +    +e L      +dPa+a  v +a+ H   LAn
  gi|2139655    58 VENARR--AAFELHRGDGDIEKLTGLFRDIDPAEASPVIRAFTHFALLAN 105

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAE+ +       ++         ++   +s +E t +kL      s
  gi|2139655   106 LAEDLHEELGIEASLDA-------GDPPQDSTLEATWQKLRDAE-VSSSA 147

                    vFeALKnqsvDLvltAHPtqsvRRsL..LqKn....aRiRnCLaqLsAKD
                    + + +    v  vltAHPt   RR + ++qK+ +   R R  +
  gi|2139655   148 IADMMDHIEVVPVLTAHPTETRRRTVfdVQKHitaaMRRRHEIQAAPLNA 197

                    vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWk
                     t +   E+D  + R i   + t  iR  +P   DE+  G+ Y+   + +
  gi|2139655   198 RTADRLAEIDADIRRRILTLWQTALIRMNRPDIRDEVEVGLRYYQLSLLE 247

                    GvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEv
                     vP+  R v   L+ +G n +lP + P i+  sW+GGD DG nP vt +
  gi|2139655   248 AVPQINRDVVKHLRQLGGN-KLPAN-PTIRMGSWIGGDHDG-NPYVTEDT 294

                    tRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaard
                     R     a       Y+sq+  L  Els+    d L     +l   a r
  gi|2139655   295 LRYASDRAAGTILRHYFSQLHLLERELSL---SDRLTKVTVDLVALASRG 341

                    kvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGis..
                                vP++  EPYR  +  +R ++  t   a       i ++
  gi|2139655   342 ---------HNDVPnrEDEPYRRAVHGIRGRVAAT---AVNFFDESIIeg 379

                    eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                    + sE   y   Ee L+ L +   sL    D  iAD  L Dl+  v  FG
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  gi|2139655   380 DWSEFTPYDSAEELLDELSIIDDSLRSSHDDLIADHRLRDLMDSVEVFGF 429

                    sLvKLDiRqEseRqtDvlDAittHLe.iGsYReWsEeKRqEWLlaELkGK
                     L  +DiRq s+ + ++l  +    + +  Y    E  + E L  EL+
  gi|2139655   430 HLYSIDIRQNSDSHEEILTELFSAAGvVDNYAALKEADKVELLTKELQSS 479

                    RPLlgsDLPktEEvkDvldaf....rvLAELPiDsFGaYiismataPsDv
                    RPL+       E  +  l+ ++  +r +     D+    iism+t+ sD
  gi|2139655   480 RPLISTSTNLSEATARELGIMraasRAVRKYGRDAVPHCIISMCTSVSDL 529

                    LAvELLqRECgvkqt........LrvvPLFEkLADLeAAPAavekLFsiD
                    L   +L +E g+ ++++++++++ v+PLFE + DL+A    +   + i
  gi|2139655   530 LEPMILLKEVGLIRPngsqptgsVDVIPLFETIEDLQAGADVLRAAWDIP 579

                    WYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyG
                     Y+  +  +++ qevm+GYsDs KD G ++A W LY A   i+  AK+
  gi|2139655   580 VYRAYVSARgdlQEVMLGYSDSNKDGGYFAANWALYDAEVAIVAAAKDND 629

                    vKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFG
                    ++L lFHGRGGtvGRGGGP   AiL+qP   ++Gs+R+t qGE+i   +G
  gi|2139655   630 IRLRLFHGRGGTVGRGGGPSYEAILAQPSGAVQGSVRITEQGEIISAKYG 679

                    EEnLCFrsLqRFtAAtLEHGmnPPvsPkPEWR..kLmeemAvvAtEEYRs
                          r L     At+E  +      k   R +++m e+     E Y
  gi|2139655   680 HPAAARRNLAALVSATIESTLLDVDDLKNPSRahEIMSEISDLSREAYSK 729

                    vvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFa
                    ++  +P F+++F + tP  E G +niGsRP+ Rk    i  LRAiPW+ +
  gi|2139655   730 LMHEDPGFIDFFTSSTPVDEIGSLNIGSRPTSRKQTQTISDLRAIPWVLS 779

                    WtqtRFHLPvWLGvGAAFKhAi..dKDiKnlqkLkEmYkeWPFFRvtlDL
                    W q R  +P W GvG A +  i++d D   l  L+ + + WPFF   l
  gi|2139655   780 WSQQRSMVPGWFGVGSALQEWIgeDEDGSRLAELRQLNEIWPFFNSVLSN 829

                    lEmvFAKGDPGiAaLyDkLLvaE.eLkPFGksLRdkYvEtkdlLLkiAGH
                    +  v  K D  +A  y  L     +       +++++  t ++ Lk+ G
  gi|2139655   830 MAQVMSKADLNLARAYASLCQDKaDGERIYSIIKAEFDLTLEMFLKVTGY 879

                    kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                    k lLE  P L+  + +R +Y+  Ln++q   L+R R
  gi|2139655   880 KHLLEDNPLLRRSVDMRFPYLMPLNIIQLEMLRRYR---------------- 915

                    EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      A +n             ++v  G+     Ltm G+A  + n G
  gi|2139655   916 --AGDN------------RDKVRRGIQ----LTMNGLATALRNSG    942

gi|241889879|ref|ZP_04777177.1|: domain 1 of 1, from 3 to 896: score 308.5, E = 1.4e-89
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            L   v   +   ++ i+   +L +  L   q +  e+  E +
  gi|2418898     3    --NTRLESNVNENII--QEEIQ---ILTEMLLKATQKMISENTFEKI 42

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E   l+       D k  e L   +  L   +  +vA  ++ +  L n+
  gi|2418898    43 VELKALA-------DEKNYEKLNLIIKDLTQEEMEIVANFFSILPLLINI 85

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+lAy    k             t    + E +K +  k
  gi|2418898    86 AEDVDLAYEVNYKNNI--------GETYVGKLSESIKNIKDKN------- 120

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L n  v  vltAHPtq  R+ +L    ++   L +           +
  gi|2418898   121 --ILENINVVPVLTAHPTQVQRKTVLDLTEKLHTLLRKHRDVKNGLINER 168

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                        A+ + i      D iR  +     E+   + Y+     k v K +
  gi|2418898   169 KWKNAIQKHIEILTQSDIIREKKLKVANEITNVLEYYNLSFIKAVAKLMT 218

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         L    i   l  + P i    W+GGDRDG nP vt E      +
  gi|2418898   219 EYKLLLEENKIE--LKNETP-ITMGMWIGGDRDG-NPFVTAETLNLSAMK 264
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                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                       +    Yi+++  L   +sm    + +     El   a r   +  Y
  gi|2418898   265 QCELIIAYYIEKLNSLYRTFSM---SSHVAKGSKELEELANRSSDTSEYR 311

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    E        E YR  +  +++KL ntRE    LL     ei +   y  v
  gi|2418898   312 E-------KELYRRAISYIKEKLENTRE---YLLQD--KEIGDK--YLTV 347

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    +eF+  L +  ksL e    ++  G   +lL  v  FG  L  +D+Rq+s
  gi|2418898   348 DEFVADLIIIEKSLLENKGEILVTGEFEELLNVVKIFGFYLASIDMRQDS 397

                    eRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK.RPLlgsDLPk
                          +  +    +i + Y + sEe + E Ll  Lk  +RPL   D  k
  gi|2418898   398 SVYEASVAELLSSANIEkDYSSLSEEEKCELLLNQLKEDpRPLSINDENK 447

                    .tEEvkDvldafrvLAELPiDsFG.....aYiismataPsDvLAvELLqR
                    + EE++  l  fr    L  D  G++  +  iis +t+ sD L   ++ +
  gi|2418898   448 qSEELRKELAIFRTARKL-KDKLGdnvikQNIISHTTSVSDLLELAIMLK 496

                    ECgvk....qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...
                    E g+ +++   L+ vPLFE + DLe     ++k  s+D  +  +   ++
  gi|2418898   497 EVGLVgsdfARLQLVPLFETIEDLENSYEVMDKYLSLDIVKKWVSDNsry 546

                    qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                    qe+m+GYsDs KD G ls  W LYkAq E+     ky +K++ FHGRGGt
  gi|2418898   547 QEIMLGYSDSNKDGGYLSSGWSLYKAQQELSSLGEKYNIKVTFFHGRGGT 596

                    vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                    vGRGGGP   Ai+sqP   ++  +R t qGE+i   +G  +  +  L
  gi|2418898   597 VGRGGGPSYDAIISQPLGSVQDRIRLTEQGEIIAAKYGNSDAAYYNLEAL 646

                    tAAtLEHGmnP.....PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFv
                      A + H mn ++ ++ +   PE   +m+e+       YR +v+  P F
  gi|2418898   647 FSAVI-HRMNAdkvntDIRDIPEIQVIMDEIVEDSYNKYRELVFENPNFY 695

                    EYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLP
                     YF  AtP  E   +niGsRPa Rk    i  LRAiPW+F+W q R  LP
  gi|2418898   696 NYFFEATPIKEISSLNIGSRPASRKKITDIGGLRAIPWVFSWSQSRIMLP 745

                    vWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPG
                     W GvG AF   i+KD  n+ kL+ mYkeWPFF   l  ++mv AK D
  gi|2418898   746 GWYGVGTAFSNYINKDKGNIEKLRKMYKEWPFFTSLLSNVDMVMAKSDMD 795

                    iAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                    iA  y +L   Ee k   +++  ++  tk+ +L+i  Hk+ LE   YL q
  gi|2418898   796 IAREYANLCKEEETKKIYEEILREWNLTKQVVLEISEHKEFLEDNTYLTQ 845

                    rlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkade
                     l  R  Y  tLn +q   +KR R+                 E
  gi|2418898   846 SLENRLQYFNTLNLIQLELIKRSREGKLL-------------ES------ 876

                    LvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      ++n           t+ +t+ G+A G+ n G
  gi|2418898   877 --QIN-----------TIHITINGVATGLRNSG    896

gi|161524047|ref|YP_001579059.1|: domain 1 of 1, from 57 to 1004: score 307.2, E = 3.5e-89
                    *->siDAqLRlLvPGKvsed.ekLieYDALLlDkFL.DiLqDLHGedLkE
                       s          G+  ed+++ +  D   l + L+D++ +  G+ + +
  gi|1615240    57    SARTAATPKSGGRTREDkDRPLFEDIRFLGRLLgDVVREQEGDTVFD 103

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    +v      +  +    D +  + L  kL  L P  ++ v +a++    LA
  gi|1615240   104 VVETIRQTAVKFRREDDREAAQTLEKKLRKLTPEQTVSVVRAFSYFSHLA 153

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE+ +   RRRi+ +        +sA     +   l kL   +n s
  gi|1615240   154 NIAEDRHHNRRRRIHALA-------GSAPQPGTVAHALDKLKTTGNASKR 196

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                              +  vltAHPt   R+s+L  +  i   La    +++t  +
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  gi|1615240   197 VLQRFFDDALIVPVLTAHPTEVQRKSILDAQHDIARLLAE-RDQELTARE 245

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    ++  +  L   + A + t  +R a+ t  DE+   +sY+  t  +  P
  gi|1615240   246 RQHNEAMLRARVTALWQTRMLRDARLTVGDEIENALSYYRATFLEELPAL 295

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                       ++ AL   G+  R+P      +  sW+GGDRDG nP vt     +
  gi|1615240   296 YGDIEAALAEHGLAARVP---AFFQMGSWIGGDRDG-NPNVTAATLDEAI 341

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                         +    Y++qv  L  Els+    + L v A +  +  a
  gi|1615240   342 NRQAAVILEHYLEQVHKLGAELSV----SNLLVGANDAVKALAAA----- 382

                    YiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGisei.....
                          q P++  EPYR  L  +  +L      aR  L  G   +++ ++
  gi|1615240   383 ---SPDQSPhrVDEPYRRALIGIYTRLAAS---ARVRLGEGTVPVrsagr 426

                    ...sEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstF
                    + ++  A +y + +eF+  L +   sL e     +A   L  l+R    F
  gi|1615240   427 gapPVRATpYADSDEFVADLKVLTASLAEHHGASLAAPRLAPLMRAAEVF 476

                    GLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELk
                    G  L  +D+Rq s+ +  v+  +    ++ ++Y +  E  +   Lla L
  gi|1615240   477 GFHLASIDLRQSSDIHEAVVAELFARAGVVAdYASLEEADKLRVLLAALA 526

                    GKRPLlgsDLPktEEvkDvldaf....rvLAELPiDsFGaYiismataPs
                      RPL  + L      +  l+ f++ ++v A     +   Yiis + + s
  gi|1615240   527 DPRPLRSPYLEYSALAQSELGVFekarEVRAQFGARAVRNYIISHTETVS 576

                    DvLAvELLqREC............gvkqtLrvvPLFEkLADLeAAPAave
                    D + v LLq+E +  +++ + ++++ k++L v+PLFE + DL+ A   +
  gi|1615240   577 DLVEVLLLQKETgllegtlgapdgHAKNALMVIPLFETIPDLRDASRIMR 626

                    kLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiK
                      F+ +++D  i +    qevm+GYsDs KD G l   W LY+A   ++
  gi|1615240   627 EYFAlpgVDALIHHQGDEQEVMLGYSDSNKDGGFLTSNWELYRAELALVE 676

                    vAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEv
                      ++  + L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGEv
  gi|1615240   677 LFRERKITLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEV 726

                    iEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv...sPkPEWRkLmeemAvv
                    i   F   ++  r L    AAtLE  + P  + ++  P +   m+ +
  gi|1615240   727 IASKFANPEIGRRNLETVVAATLEASLLPQSnapAQLPAFEGAMQTLSDT 776

                    AtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....Gi
                    A   YR++v+  P F +YF   tP +E   +niGsRPa Rk   ++++ i
  gi|1615240   777 AMAAYRALVYETPGFTDYFFASTPITEIAELNIGSRPASRKLQDpknrRI 826

                    esLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi......KnlqkLk
                    e LRAiPW F+W q R  L  W G+G A    +d   +  +++K l  Lk
  gi|1615240   827 EDLRAIPWGFSWGQCRLLLTGWYGFGSAVAAYLDGAAdaaergKRLALLK 876

                    EmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk..PFGksLR
                     m k+WPFF   l  ++mv AK D  +A+ y +L+    L++  FG+ +
  gi|1615240   877 KMNKTWPFFANLLSNMDMVLAKTDLAVASRYAELVPDRKLRnaVFGR-IV 925

                    dkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKR
                    ++++ t   L +i GH + L   P L   ++ R +Y+  Ln +q   +KR
  gi|1615240   926 AEWERTSHALAEITGHEERLATNPLLARSIKNRFPYLDPLNHLQVELIKR 975

                    iRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtm
                     R               A +          n   r   G+     Lt+
  gi|1615240   976 HR----------------AGDT----------N--ARLRRGIH----LTI 993

                    KGiAAGmqntG<-*
                     GiAAG+ ntG
  gi|1615240   994 NGIAAGLRNTG    1004

gi|221211566|ref|ZP_03584545.1|: domain 1 of 1, from 57 to 1004: score 307.1, E = 3.8e-89
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                *->siDAqLRlLvPGKvsed.ekLieYDALLlDkFL.DiLqDLHGedLkE
                   s          G+  ed+++ +  D   l + L+D++ +  G+ + +
gi|2212115    57    SARTAATPKSGGRTREDkDRPLFEDIRFLGRLLgDVVREQEGDTVFD 103

                avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                +v      +  +    D +  + L  kL  L P  ++ v +a++    LA
gi|2212115   104 VVETIRQTAVKFRREDDREAAQTLEKKLRKLTPEQTVSVVRAFSYFSHLA 153

                nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                n+AE+ +   RRRi+ +        +sA     +   l kL   +n s
gi|2212115   154 NIAEDRHHNRRRRIHALA-------GSAPQPGTVAHALDKLKTTGNASKR 196

                EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                          +  vltAHPt   R+s+L  +  i   La    +++t  +
gi|2212115   197 VLQRFFDDALIVPVLTAHPTEVQRKSILDAQHDIARLLAE-RDQELTARE 245

                KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                ++  +  L   + A + t  +R a+ t  DE+   +sY+  t  +  P
gi|2212115   246 RQHNEAMLRARVTALWQTRMLRDARLTVGDEIENALSYYRATFLEELPAL 295

                LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   ++ AL   G+  R+P      +  sW+GGDRDG nP vt     +
gi|2212115   296 YGDIEAALAEHGLAARVP---AFFQMGSWIGGDRDG-NPNVTAATLDEAI 341

                LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     +    Y++qv  L  Els+    + L v A +  +  a
gi|2212115   342 NRQAAVILEHYLEQVHKLGAELSV----SNLLVGANDAVKALAAA----- 382

                YiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGisei.....
                      q P++  EPYR  L  +  +L      aR  L  G   +++ ++
gi|2212115   383 ---SPDQSPhrVDEPYRRALIGIYTRLAAS---ARVRLGEGTVPVrsagr 426

                ...sEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstF
                + ++  A +y + +eF+  L +   sL e     +A   L  l+R    F
gi|2212115   427 gapPVRATpYADSDEFVADLKVLTASLAEHHGASLAAPRLAPLMRAAEVF 476

                GLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELk
                G  L  +D+Rq s+ +  v+  +    ++ ++Y +  E  +   Lla L
gi|2212115   477 GFHLASIDLRQSSDIHEAVVAELFARAGVVAdYASLEEADKLRVLLAALA 526

                GKRPLlgsDLPktEEvkDvldaf....rvLAELPiDsFGaYiismataPs
                  RPL  + +      +  l+ f++ ++v A     +   Yiis + + s
gi|2212115   527 DPRPLRSPYIEYSALAQSELGVFekarEVRAQFGARAVRNYIISHTETVS 576

                DvLAvELLqREC............gvkqtLrvvPLFEkLADLeAAPAave
                D + v LLq+E +  +++ + ++++ k++L v+PLFE + DL+ A   +
gi|2212115   577 DLVEVLLLQKETgllegtlgapdgHAKNALMVIPLFETIPDLRDASRIMR 626

                kLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiK
                  F+ +++D  i +    qevm+GYsDs KD G l   W LY+A   ++
gi|2212115   627 EYFAlpgVDALIHHQGDEQEVMLGYSDSNKDGGFLTSNWELYRAELALVE 676

                vAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEv
                  ++  + L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGEv
gi|2212115   677 LFRERKITLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEV 726

                iEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv...sPkPEWRkLmeemAvv
                i   F   ++  r L    AAtLE  + P  + ++  P +   m+ +
gi|2212115   727 IASKFANPEIGRRNLETVVAATLEASLLPQSnapAQLPAFEGAMQTLSDT 776

                AtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....Gi
                A   YR++v+  P F +YF   tP +E   +niGsRPa Rk   ++++ i
gi|2212115   777 AMAAYRALVYETPGFTDYFFASTPITEIAELNIGSRPASRKLQDpknrRI 826

                esLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiKnlqkLk
                e LRAiPW F+W q R  L  W G+G A    +d+  +    +K l  Lk
gi|2212115   827 EDLRAIPWGFSWGQCRLLLTGWYGFGSAVAAYLDgaadaaERSKRLALLK 876

                EmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk..PFGksLR
                 m k+WPFF   l  ++mv AK D  +A+ y +L+    L++  FG+ +
gi|2212115   877 KMNKTWPFFANLLSNMDMVLAKTDLAVASRYAELVPDRKLRnaVFGR-IV 925
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                    dkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKR
                    ++++ t   L +i GH + L   P L   ++ R +Y+  Ln +q   +KR
  gi|2212115   926 AEWERTSHALAEITGHEERLATNPLLARSIKNRFPYLDPLNHLQVELIKR 975

                    iRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtm
                     R               A +          n   r   G+     Lt+
  gi|2212115   976 HR----------------AGDT----------N--ARLRRGIH----LTI 993

                    KGiAAGmqntG<-*
                     GiAAG+ ntG
  gi|2212115   994 NGIAAGLRNTG    1004

gi|254491458|ref|ZP_05104637.1|: domain 1 of 1, from 1 to 947: score 306.9, E = 4.2e-89
                    *->siDAqLRlLvPGKvs..edekLieYDALLlDkFLDiLqDLHGedLkE
                         D q  l    K s   d +L +    L     +++ +  G ++ E
  gi|2544914     1    MTDYQPVLSTVEKLSllSDKELRQHVRFLGHILGEVIDERAGREVFE 47

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                     v               +    EL + L  Ld +    v +a++    L
  gi|2544914    48 TVERLRQGFITLRKDDNAALRTELLSFLNTLDATTLKEVIRAFSLYFSLL 97

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n AEE    + R i+++        +         +tl +L   +  s +
  gi|2544914    98 NTAEEAFNYHNRMIQLRN-------GGELWNGSYLDTLTQLKQEG-VSLK 139

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                         L       v+tAHPt s RR L+    Ri     +L    +t+ D
  gi|2544914   140 QLQHLLDEMVYMPVFTAHPTESKRRTLMEILRRIFLLDEKLTNDPLTPFD 189

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                     +     + + +q  + tDE+R  +Pt  DE++ G+ Y+   +++ vP+
  gi|2544914   190 EERTRKEIKKQVQLLWSTDEVRAIKPTVRDEIKNGLYYFNVSLFDAVPRT 239

                    LRRvDtALKni...GinERlPYdvP.LikFssWmGGDRDGknPRvtPEvt
                     R ++ A++ + ++ i     + vP+L+kF sW+GGDRDG nP vt E t
  gi|2544914   240 YRNIENAIRRVysdEIAAGTEFTVPgLVKFGSWIGGDRDG-NPFVTAETT 288

                    RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk
                         L +      Y++ v  L + l        L    + l     +
  gi|2544914   289 EMAIQLQKRTVIRRYLDDVTKLSYVLTQ---SASLSTISDALADSLEQS- 334

                    vvKyYiEFWKqvPP...tEPYRviLGdvRDKLYntRERaRHLLAtGisei
                      + Y   ++  P +   EPYR  L  +R +L              ++
  gi|2544914   335 -EQQYAGAFRAKPDrflHEPYRRKLYMMRHRLEDNLRLIQQYFRPDLAPT 383

                    sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                    +    y + +e L  L L Y sL e GD  +A   L Dl+R v tFG  L
  gi|2544914   384 ALGVAYANEDELLQDLHLIYDSLVEHGDAELAGSELNDLIRLVETFGFYL 433

                    vKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRP
                      LDiRqEs R+ + l  + +  ++ + Y +  E  Rq  Ll+EL  +
  gi|2544914   434 YHLDIRQESTRHSEALADVLKVTGLCdDYHQLDETERQQ-LLTELLSRDA 482

                    LlgsDLPktE.EvkDvldafrvLAELPiD....sFGaYiismataPsDvL
                    L  +++P  ++  ++vl  f+ +  L  D + ++FG+Y+ism+   s +L
  gi|2544914   483 L--PEMPDIDgQNQEVLAVFKLMTRLHRDvsarAFGSYVISMTHQASHIL 530

                    AvELLqRECgvk.........qtLrvvPLFEkLADLeAAPAavekLFsiD
                     v +L R  g+ + ++++++   +rv PLFE + DL      +  L
  gi|2544914   531 EVLMLGRFAGLCgydehgqtfCHIRVSPLFETIEDLSHIEPVMSALLNNP 580

                    WYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyG
                     Y   +d  ++ qevm+GYsDs KD G l+  W LY+Aq  +   A+k+
  gi|2544914   581 QYCRLLDASgnlQEVMLGYSDSCKDGGILASGWNLYQAQKKVSGLAQKHN 630

                    vKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFG
                    vK  +FHGRGGt+GRGGGPtH AiLsqP  t++G ++ t qGEv+ f +G
  gi|2544914   631 VKCRMFHGRGGTIGRGGGPTHDAILSQPMGTVQGQIKFTEQGEVLSFKYG 680

                    EEnLCFrsLqRFtAAtLEHGmnPPvs....PkPEWRkLmeemAvvAtEEY
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                     +     L       L       +s++++  P++  +m+ +       Y
  gi|2544914   681 NIETAAYELG-MGVSGLMKASRSVISeteqVEPDFLTVMQAITQTGEASY 729

                    RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGie.sLRAiPW
                    R +      F +YF    P +E G mniGsRP+ Rk +   ++s+RAi W
  gi|2544914   730 RKLTEDTAGFLDYFYEVCPVTEIGMMNIGSRPSHRKAGDRSKsSVRAIGW 779

                    iFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlD
                    +F+W q R   LP W G+G A     + D   +  L+ m ++WPFFR  l
  gi|2544914   780 VFSWAQSRHTLPAWYGIGTALENWHQHDPEKIAFLRKMVQQWPFFRALLS 829

                    LlEmvFAKGDPGiAaLyDkLLv.aEeLkPFGksLRdkYvEtkdlLLkiAG
                       m   K D  iA+ y  L  +a + +   + + ++Y  t + +L +
  gi|2544914   830 NTQMSLSKADMSIASRYAALCEdAFQGQQVFELIAAEYDKTVEQVLFVVE 879

                    HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                       l+   P L+  lR R++Y+  +n +q   L+R RD
  gi|2544914   880 ADKLMAETPELRMSLRRREPYLDPINYIQIMLLQRYRDSA---------- 919

                    KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        dE+     e  +            D L+ t+  i AGm ntG
  gi|2544914   920 ---VDEQ-----EREQWS----------DPLLRTISAISAGMRNTG    947

gi|15903018|ref|NP_358568.1|: domain 1 of 1, from 1 to 898: score 306.8, E = 4.4e-89
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                            L  L     s +  +++ + L+l   L+Di + +  ++  E
  gi|1590301     1    ---MSLQKL---ENSSNKSVVQEEVLILTELLeDITKNMLAPETFEK 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +    Els +    +D + L+ L   +tsL   + + + + ++ +  L n
  gi|1590301    42 IIQLKELSTQ----EDYQGLNRL---VTSLSNDEMVYISRYFSILPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+    s t          kLv       e
  gi|1590301    85 ISEDVDLAYEINHQNNIDQDYLGKLSTTI---------KLVAEK----EN 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvteDK
                      e L    v  vltAHPtq  R+s+L     i   L +     +    K
  gi|1590301   122 AVEILEHLNVVPVLTAHPTQVQRKSMLDLTNHIHSLLRKYRDVKLGLINK 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                          L R i     tD iR  +     E+   m Y+     k vP
  gi|1590301   172 DKWYNDLRRYIEIIMQTDMIREKKLKVTNEITNAMEYYNSSFLKAVPHLT 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                           +  G+n +   ++  i    W+GGDRDG nP vt    +   L
  gi|1590301   222 TEYKRLAQAHGLNLK---QAKPITMGMWIGGDRDG-NPFVTAKTLKQSAL 267

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                        +  n Y  ++  L  E+s+      +     E+ r ++ +     Y
  gi|1590301   268 TQCEVIMNYYDKKIYQLYREFSLSTSIVNVSKQVREMARQSKDN---SIY 314

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                     E        E YR  L d+  K+  t+          i +      y
  gi|1590301   315 RE-------KELYRRALFDIQSKIQATK-------TYLIEDEEVGTRYET 350

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      +F   L     sL e     +  G  ++lL  v  FG  L  +D+Rq+
  gi|1590301   351 ANDFYKDLIAIRDSLLENKGESLISGDFVELLQAVEIFGFYLASIDMRQD 400

                    seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK.RPLlgsDLP
                    s      +  + +  +i s+Y e sEe + + Ll EL+  +R L
  gi|1590301   401 SSVYEACVAELLKSAGIHSrYSELSEEEKCDLLLKELEEDpRILSATHAE 450

                    ktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLqRE
                    k E ++++  +  + rvL ++L  D     iis at+ sD+L   +L +E
  gi|1590301   451 KSELLAkelAIFKTARVLKDkLGDDVIRQTIISHATSLSDMLELAILLKE 500

                    Cgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                     g+ ++++  +++vPLFE + DL+    ++ k  s+   +  id +++ q
  gi|1590301   501 VGLvdteRARVQIVPLFETIEDLDHSEETMRKYLSLSLAKKWIDSRnnyQ 550
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                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                    e+m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGRGGtv
  gi|1590301   551 EIMLGYSDSNKDGGYLSSCWTLYKAQQQLTAIGDEFGVKVTFFHGRGGTV 600

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                    GRGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
  gi|1590301   601 GRGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLV 650

                    AAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                     A +   +    s  +++  +  +m+++     + YR +v+    F +YF
  gi|1590301   651 SAAINRMITQKKSDTntpNRYEAIMDQVVDRSYDIYRDLVFGNEHFYDYF 700

                    RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                        P       niGsRPa Rk    i  LRAiPW+F+W q R   P W
  gi|1590301   701 FESSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWY 750

                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    GvG  FK  i+K   n+  L++mY++WPFF   l  ++mv  K    iA
  gi|1590301   751 GVGSSFKEFINKNPENIAILRDMYQNWPFFQSLLSNVDMVLSKSNMNIAF 800

                    LyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                     y kL   E++k   + + ++++ tk+ +L i GH +lL   PYLK  l
  gi|1590301   801 EYAKLCEDEQVKAIYETILNEWQVTKNVILAIEGHDELLADNPYLKASLD 850

                    LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                     R +Y   Ln +q   +KR R        r +ls +  +E       L++
  gi|1590301   851 YRMPYFNILNYIQLELIKRQR--------RGELSSD--QER------LIH 884

                    LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +                 + GiA G+ n G
  gi|1590301   885 IT----------------INGIATGLRNSG    898

gi|282865456|ref|ZP_06274507.1|: domain 1 of 1, from 3 to 909: score 306.6, E = 5.2e-89
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s D       P       +L      L D   + L    G++L + v
  gi|2828654     3    SADQ-----TPAANT---ELRADIRRLGDLLGETLVRQEGPELLDLV 41

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         l    +G   ++ L++     t L+ a  ++  +a++    LAn+
  gi|2828654    42 ERVRALTRT-DGEAAAQLLGD-----TDLETAAQLV--RAFSTYFHLANV 83

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     E v+ A+  R ++   G             +  t  +L       Pe
  gi|2828654    84 TEQVHRAHEMRDRRAAEGGL----------LARTADRLKDAD---PEHL 119

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     e +Kn  v  v+tAHPt ++RRs+L K  Ri    a L    v   D++
  gi|2828654   120 RETVKNLNVRPVFTAHPTEAARRSVLNKLRRI----AALLETPVIEADRR 165

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                      D  L   i   + tDE+R  +P P DE R  + Y+ E   + v   L
  gi|2828654   166 RQDLRLAENIDLIWQTDELRVVRPEPADEARNAIYYLDELHANAVGDVLE 215

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                         L  +G+   lP     + F  W+GGDRDG nP vtP vt Dv +L
  gi|2828654   216 DLAAELERVGVE--LPAGTRPLTFGTWIGGDRDG-NPNVTPKVTWDVLIL 262

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkvvKyY
                              ++ ++ L   ls    n+     A++El    + d
  gi|2828654   263 QHEHGITDALELIDHLRGLLS----NSIRYTGAtDELLTSLQTD--LELL 306

                    iEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                     E ++++K +  +EPYR     +R KL ntRER    LAtG    +
  gi|2828654   307 PEIsprYKRLNAEEPYRLKATCIRQKLVNTRER----LATGTPHRP-GCD 351

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y    e +  L L   sL e      ADG +   +R  s FGL L  +D+
  gi|2828654   352 YLGTSELIADLTLIQTSLREHRGGLFADGRMDRTIRTLSAFGLQLATMDV 401

                    RqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLlgs
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                    R  ++ +   l  +   L+  s+R  + + + Rq  L  EL+ +RPL +
  gi|2828654   402 REHADAHHHALGQLFDRLGEESWRyaDMPRDYRQKLLAKELRSRRPLAPT 451

                    DLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvEL
                      P     +  l+ f+ +     + FG++  ++Yiism+    Dv A  +
  gi|2828654   452 PAPLDAAGEKTLGVFHTITQ-AFERFGPeviesYIISMCQGADDVFAAAV 500

                    LqRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                    L RE g+   + +   + +vPL E   +L+AA   ++ + +   Y+  +
  gi|2828654   501 LAREAGLIDlhagwaKIGIVPLLETTDELKAADVILDDMLADPSYRRLVS 550

                    GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                     +++ qevm+GYsDs K  G     W + +Aq  +  vA +yGv+L lFH
  gi|2828654   551 LRgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRYGVRLRLFH 600

                    GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                    GRGGtvGRGGGP H AiL+qP  t++G ++vt qGEvi   +    L
  gi|2828654   601 GRGGTVGRGGGPSHDAILAQPWGTLEGEIKVTEQGEVISDKYLIPALARE 650

                    sLqRFtAAtLEHGm...nPPvsPk..PEWRkLmeemAvvAtEEYRsvvvK
                     L    AAtL     ++ P  s      W   m+ +   A   YR +v
  gi|2828654   651 NLELTVAATLQASAlhtAPRQSDEalARWDAAMDTVSDAAHTAYRKLV-E 699

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWt
                    +P    YF   tP      + +GsRP+ R+P+ G++ + LRAiPW+F Wt
  gi|2828654   700 DPDLPAYFLASTPVDQLADLHLGSRPS-RRPGSGVslDGLRAIPWVFGWT 748

                    qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                    q R  +P W GvG   K   +     +  L+Em  +W FF   l  +Em
  gi|2828654   749 QSRQIVPGWFGVGSGLKALREAGLDTV--LEEMHGQWHFFQNFLSNVEMT 796

                    FAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE
                     AK D  iA  y + Lv +eLk   + + ++ + t + +Lk+ G k+lL
  gi|2828654   797 LAKTDLRIARHYVDTLVPDELKHVFDVIEAEHELTVQEVLKVTGGKELLG 846

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                      P L+q   +Rd+Y+  +  +q   L R R                A+E
  gi|2828654   847 TSPVLQQTFAIRDAYLDPISYLQVSLLARQRQ---------------AAE 881

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                +e+  P L   L+Lt+ G+AAG+ ntG
  gi|2828654   882 R------------GEEPDPLLARALLLTVNGVAAGLRNTG    909

gi|76787926|ref|YP_329507.1|: domain 1 of 1, from 3 to 931: score 306.2, E = 6.9e-89
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                           +L        s + ++i  +  Ll + LD+  q L G +  +
  gi|7678792     3    --HPKLES------SSNKEIITEEVGLLKQLLDeATQKLIGSESFDK 41

                    vqECYElsA..eYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    +     ls +++Y G k+t          + +L   + ++v + ++ +  L
  gi|7678792    42 IEKIVSLSStdDYTGLKET---------ISALSNEEMVIVSRYFSILPLL 82

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                     n+ E+v+lAy    k     D+    s t +          v+ +
  gi|7678792    83 INISEDVDLAYEINYKNNLNQDYLGKLSTTID----------VVAG---H 119

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    e   + L    v  vltAHPtq  R+ +L   ++i   L +       +
  gi|7678792   120 ENAKDILEHVNVVPVLTAHPTQVQRKTVLELTSKIHDLLRKYRDVKAGIV 169

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++     L R i     tD iR  +   + E+   m Y+   + k v K
  gi|7678792   170 NQEKWYADLRRYIGIIMQTDTIREKKLKVKNEITNVMEYYNRSLIKAVTK 219

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                                Gi    P   PL     W+GGDRDG nP vt E  R
  gi|7678792   220 LTAEYKALAAKKGIHLENP--KPL-TMGMWIGGDRDG-NPFVTAETLRLS 265

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                     ++   +  n Yi+q+ +L   +s+      L     El   a + +
  gi|7678792   266 AMVQSEVIINHYIEQLNELYRNMSL---SINLTEVSPELVTLANQSQDNS 312
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                    yYiEFWKqvPPtEPYRviLGdvRDKLYnt.................RERa.
                     Y E       +EPYR     + DKL  t  + + +++++++  +R  ++
  gi|7678792   313 VYRE-------NEPYRKAFNFIQDKLVQTllnlkvgsspkekfvsRQESs 355

                    ....RHL...LAtGiseisEeAv..ytkvEeFLEPLELCYksLCeCGDkv
                    +  +R +++++A+  s+i  e  + y   EeF   L L  +sL + G
  gi|7678792   356 divgRYIkshIAQVASDIQTEELpaYATAEEFKQDLLLVKQSLVQYGQDS 405

                    iADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYR
                    + DG L  l+  v  FG  L  +D+Rq+s  +   +  + +  +i   Y
  gi|7678792   406 LVDGELACLIQAVDIFGFYLATIDMRQDSSINEACVAELLKSANIvDDYS 455

                    eWsEeKRqEWLlaELkGK.RPLlgsDLPktEEvkDvldafrvLAELP...
                    + sEe +   Ll EL   +R L     Pk E ++  l  f+   EL ++
  gi|7678792   456 SLSEEEKCQLLLKELTEDpRTLSSTHAPKSELLQKELAIFQTARELKdql 505

                    .iDsFGaYiismataPsDvLAvELLqRECgv....kqtLrvvPLFEkLAD
                    + D     iis + + sD+    ++ +E g+ + ++  +++vPLFE + D
  gi|7678792   506 gEDIINQHIISHTESVSDMFELAIMLKEVGLidanQARIQIVPLFETIED 555

                    LeAAPAavekLFsiDWYinri...dGKqevmvGYsDsGKDAGRlsAAWqL
                    L+     + +    +  +  i +++  qe+m+GYsDs KD G ls  W L
  gi|7678792   556 LDNSRDIMTQYLHYELVKKWIatnNNYQEIMLGYSDSNKDGGYLSSGWTL 605

                    YkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGs
                    YkAq E+ K+  + G+K++ FHGRGGtvGRGGGP   Ai sqP   i+
  gi|7678792   606 YKAQNELTKIGEENGIKITFFHGRGGTVGRGGGPSYEAITSQPFGSIKDR 655

                    lRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WR
                    +R t qGE+iE  +G  +  +  L     A ++  +   +    E +++R
  gi|7678792   656 IRLTEQGEIIENKYGNQDAAYYNLEMLISASIDRMVTRMITNPNEidnFR 705

                    kLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRk
                    + m+ +       YR +v+  P F +YF  A P  E   +niGsRPa Rk
  gi|7678792   706 ETMDGIVSESNAVYRNLVFDNPYFYDYFFEASPIKEVSSLNIGSRPAARK 755

                    PsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkE
                        i  LRAiPW+F+W q R   P W GvG AFKh i++D  nl kL+
  gi|7678792   756 TITEISGLRAIPWVFSWSQNRIMFPGWYGVGSAFKHFIEQDEANLAKLQT 805

                    mYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkY
                    mY++WPFF   l  ++mv  K    iA  y +L  + e++   + + +++
  gi|7678792   806 MYQKWPFFNSLLSNVDMVLSKSNMNIALQYAQLAGSKEVRDVFNIILNEW 855

                    vEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRD
                    + tkd++L i  H  lLE  P L   l  R +Y   Ln +q   +KR+R
  gi|7678792   856 QLTKDMILAIEQHDNLLEENPMLHASLDYRLPYFNVLNYVQIELIKRLRS 905

                    PsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGi
                     +             dE+    + L+++                + Gi
  gi|7678792   906 NQL-------------DED---YEKLIHIT----------------INGI 923

                    AAGmqntG<-*
                    A G+ n G
  gi|7678792   924 ATGLRNSG    931

gi|148989111|ref|ZP_01820501.1|: domain 1 of 1, from 1 to 898: score 306.1, E = 7.5e-89
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                            L  L     s +  +++ + L+l   L+Di + +  ++  E
  gi|1489891     1    ---MSLQKLE--NYS-NKSVVKEEVLILTELLeDITKNMLAPETFEK 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +    Els +    +D + L+ L   +tsL   + + + + ++ +  L n
  gi|1489891    42 IIQLKELSTQ----EDYQGLNRL---VTSLSNDEMVYISRYFSILPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+    s t          kLv       e
  gi|1489891    85 ISEDVDLAYEINHQNNIDQDYLGKLSTTI---------KLVAEK----EN 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
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                    e L    v  vltAHPtq  R+s+L     i   L +     +    K
  gi|1489891   122 AVEILEHLNVVPVLTAHPTQVQRKSMLDLTNHIHSLLRKYRDVKLGLINK 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                          L R i     tD iR  +     E+   m Y+     k vP
  gi|1489891   172 DKWYNDLRRYIEIIMQTDMIREKKLKVTNEITNAMEYYNSSFLKAVPHLT 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                           +  G+n +   ++  i    W+GGDRDG nP vt    +   L
  gi|1489891   222 TEYKRLAQAHGLNLK---QAKPITMGMWIGGDRDG-NPFVTAKTLKQSAL 267

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                        +  n Y  ++  L  E+s+      +     E+ r ++ +     Y
  gi|1489891   268 TQCEVIMNYYDKKIYQLYREFSLSTSIVNVSKQVREMARQSKDN---SIY 314

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                     E        E YR  L d+  K+  t+          i +      y
  gi|1489891   315 RE-------KELYRRALFDIQSKIQATK-------TYLIEDEEVGTRYET 350

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      +F   L     sL e   k +  G  ++lL  v  FG  L  +D+Rq+
  gi|1489891   351 ANDFYKDLIAIRDSLLENKGKSLISGDFVELLQAVEIFGFYLASIDMRQD 400

                    seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK.RPLlgsDLP
                    s      +  + +  +i s+Y e sEe + + Ll EL+  +R L
  gi|1489891   401 SSVYEACVAELLKSAGIHSrYSELSEEEKCDLLLKELEEDpRILSATHAE 450

                    ktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLqRE
                    k E ++++  +  + rvL ++L  D     iis at+ sD+L   +L +E
  gi|1489891   451 KSELLAkelAIFKTARVLKDkLGDDVIRQTIISHATSLSDMLELAILLKE 500

                    Cgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                     g+ ++++  +++vPLFE + DL+    ++ k  s+   +  id +++ q
  gi|1489891   501 VGLvdteRARVQIVPLFETIEDLDHSEETMRKYLSLSLAKKWIDSRnnyQ 550

                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                    e+m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGRGGtv
  gi|1489891   551 EIMLGYSDSNKDGGYLSSCWTLYKAQQQLTAIGDEFGVKVTFFHGRGGTV 600

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                    GRGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
  gi|1489891   601 GRGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLV 650

                    AAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                     A +   +    s  +++  +  +m+++     + YR +v+    F +YF
  gi|1489891   651 SAAINRMITQKKSDTntpNRYEAIMDQVVDRSYDIYRDLVFGNEHFYDYF 700

                    RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                        P       niGsRPa Rk    i  LRAiPW+F+W q R   P W
  gi|1489891   701 FESSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWY 750

                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    GvG  FK  i+K   n+  L++mY++WPFF   l  ++mv  K    iA
  gi|1489891   751 GVGSSFKEFINKNPENIAILRDMYQNWPFFQSLLSNVDMVLSKSNMNIAF 800

                    LyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                     y kL   E++k   + + ++++ tk+ +L i GH +lL   PYLK  l
  gi|1489891   801 EYAKLCEDEQVKAIYETILNEWQVTKNVILAIEGHDELLADNPYLKASLD 850

                    LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                     R +Y   Ln +q   +KR R        r +ls +  +E       L++
  gi|1489891   851 YRMPYFNILNYIQLELIKRQR--------RGELSSD--QER------LIH 884

                    LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +                + GiA G+ n G
  gi|1489891   885 IT---------------INGIATGLRNSG    898

gi|262046224|ref|ZP_06019187.1|: domain 1 of 1, from 1 to 912: score 305.9, E = 8.7e-89
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           + +      s+ + + e   +L D   +  + + G+   + +
  gi|2620462     1    -----MTVKKLENNSDVNVVAEESKVLTDLLNESTKQVIGQAAFDKI 42
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                q    +sA       +k  +EL  ++ sL+  + i+vA+ +  +  L n+
gi|2620462    43 QNLIKISA-------AKDYQELEKQIASLNNREMIVVARYFATLPLLINI 85

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                 E+velA +  +    h D+    s t +         +v +  K  eE+
gi|2620462    86 SEDVELASKVNVLNNTHQDYLGKLSDTID---------IVAQK-KNAEEI 125

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                 e +    v  vltAHPtq  R+ +L     i   L           D+
gi|2620462   126 LEHV---NVVPVLTAHPTQVQRKTILELTDQIHQLLRNYRDVKNGTIDRD 172

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                E  E +   i     tD iR  +     E+   ++Y+   +   + KF
gi|2620462   173 EWTEQMRACIEILMQTDIIRGHKLKVANEITNVLAYYPKALIPAITKFTS 222

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                R     K  G+n      +  i    W+GGDRDG nP vt +       L
gi|2620462   223 RYKELAKKHGLNAS---HATPITMGMWIGGDRDG-NPYVTADTLELSATL 268

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   +    Yi q+  L   + m              y  +  d  v +
gi|2620462   269 QSQVIFEYYIKQINKLYRAIFM-----------STSYMEPSDD--VMHLS 305

                EFWKqvPP...tEPYRvi.......LGdvRDKLYntRERaRHLLAtGise
                E      P +++EPYR      +++L     KL n   +   L    + +
gi|2620462   306 ELSNDDSPfrtNEPYRRAfyyiqsrLVHTEQKLLNITNKNTFLKKRDLQN 355

                isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                +     y +  eF   LE+   sL e  D++ D     +L  +  FG
gi|2620462   356 LDKIPCYQNAQEFKADLEIIKNSLEEDHDHAVVDSYFTQILEAINIFGFH 405

                LvKLDiRqEseRqtDvlDAitthLeiG.sYReWsEeKRqEWLlaELkGK.
                L  +D+Rq+s  +   +  + +  +i + Y + sE+K+   Ll EL   +
gi|2620462   406 LATIDMRQDSSVNEACVAELLKSAGICdNYSDLSEDKKIKLLLNELNNDp 455

                RPLlgsDLPktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDv
                R L     Pk E ++++  +  + r L ++L  D     iis + + sD+
gi|2620462   456 RNLHANNKPKSELLQkelKIYKTARQLKDrLGEDVIKQHIISHTESVSDM 505

                LAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYin
                L   ++ +E  + +++k  ++vvPLFE + DL+ A   ++   s D  +
gi|2620462   506 LEQAIMLKEYDLldnqKARIQVVPLFETVEDLNNAREIIKEFLSFDIVKK 555

                ri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                 + +++  qevm+GYsDs KD G l+  W LYkAq ++ K+  + G+K++
gi|2620462   556 WLvsqNNYQEVMLGYSDSNKDGGYLASCWNLYKAQKDLTKIGEEMGIKIT 605

                lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                  HGRGGtvGRGGGP   Ai +qP   in  +R+t qGE+i   +G  +
gi|2620462   606 FMHGRGGTVGRGGGPSYEAITAQPFKSINDRMRMTEQGEIIQNKYGNKDT 655

                CFrsLqRFtAAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvv
                 +  L   + At++      +   ++  ++R  m+++     E YR +v+
gi|2620462   656 AYYNLEMLASATIDRMASKQIVSEdhvADFRSSMDQIVAKSNEVYRKLVF 705

                KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                  P F  YF  AtP  E   +n+GsRPa Rk       LRAiPW+F+W q
gi|2620462   706 ENPNFLKYFFQATPIKEISGLNVGSRPASRKKLTDFSGLRAIPWVFSWSQ 755

                tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                 R   P W GvG  FK  id D  nl+ L+ mY+ WPFF   l  ++mv
gi|2620462   756 SRVMFPGWYGVGSGFKSFIDADPANLKELQNMYQGWPFFHSLLSNVDMVL 805

                AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                 K    iA  y +L   E++k   + + ++++ tk+ +L+i GH +l+E
gi|2620462   806 SKSNMRIAKQYADLCEDEQVKSVFDIINQEWELTKKVILQIEGHDELIED 855

                DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                 P LK+ l  R +Y   Ln +q   +KR R+ + +   +  +       +
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  gi|2620462   856 APTLKKSLEYRMPYFNILNYIQLEMIKRDREDEIQGVYQSII-------P 898

                   skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                          + +n                   G+A G+ n G
  gi|2620462   899 -------ITIN-----------------GVASGLRNSG    912

gi|225861034|ref|YP_002742543.1|: domain 1 of 1, from 1 to 898: score 305.6, E = 1.1e-88
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           L  L     s +  +++ + L+l   L+Di + +  ++  E
  gi|2258610     1    ---MSLQKLE--NYS-NKSVVQEEVLILTELLeDITKNMLAPETFEK 41

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +    Els +    +D + L+ L   +tsL   + + + + ++ +  L n
  gi|2258610    42 IIQLKELSTQ----EDYQGLNRL---VTSLSNDEMVYISRYFSILPLLIN 84

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   + E+v+lAy    +     D+    s t          kLv       e
  gi|2258610    85 ISEDVDLAYEINHQNNIDQDYLGKLSTTI---------KLVAEK----EN 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     e L    v  vltAHPtq  R+s+L     i   L +     +    K
  gi|2258610   122 AVEILEHLNVVPVLTAHPTQVQRKSMLDLTNHIHSLLRKYRDVKLGLINK 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                         L R i     tD iR  +     E+   m Y+     k vP
  gi|2258610   172 DKWYNDLRRYIEIIMQTDMIREKKLKVTNEITNAMEYYNSSFLKAVPHLT 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                          +  G+n +   ++  i    W+GGDRDG nP vt    +   L
  gi|2258610   222 TEYKRLAQAHGLNLK---QAKPITMGMWIGGDRDG-NPFVTAKTLKQSAL 267

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                       +  n Y  ++  L  E+s+      +     E+ r ++ +     Y
  gi|2258610   268 TQCEVIMNYYDKKIYQLYREFSLSTSIVNVSKQVREMARQSKDN---SIY 314

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                    E        E YR  L d+  K+  t+          i +      y
  gi|2258610   315 RE-------KELYRRALFDIQSKIQATK-------TYLIEDEEVGTRYET 350

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     +F   L     sL e     +  G  ++lL  v  FG  L  +D+Rq+
  gi|2258610   351 ANDFYKDLIAIRDSLLENKGESLISGDFVELLQAVEIFGFYLASIDMRQD 400

                   seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK.RPLlgsDLP
                   s      +  + +  +i s+Y e sEe + + Ll EL+  +R L
  gi|2258610   401 SSVYEACVAELLKSAGIHSrYSELSEEEKCDLLLKELEEDpRILSATHAE 450

                   ktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLqRE
                   k E ++++  +  + rvL ++L  D     iis at+ sD+L   +L +E
  gi|2258610   451 KSELLAkelAIFKTARVLKDkLGDDVIRQTIISHATSLSDMLELAILLKE 500

                   Cgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                    g+ ++++  +++vPLFE + DL+    ++ k  s+   +  id +++ q
  gi|2258610   501 VGLvdteRARVQIVPLFETIEDLDHSEETMRKYLSLSLAKKWIDSRnnyQ 550

                   evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                   e+m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGRGGtv
  gi|2258610   551 EIMLGYSDSNKDGGYLSSCWTLYKAQQQLTAIGDEFGVKVTFFHGRGGTV 600

                   GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                   GRGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
  gi|2258610   601 GRGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLV 650

                   AAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                    A +   +    s  +++  +  +m+++     + YR +v+    F +YF
  gi|2258610   651 SAAINRMITHKKSDTntpNRYEAIMDQVVDRSYDVYRDLVFGNEHFYDYF 700

                   RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                       P       niGsRPa Rk    i  LRAiPW+F+W q R   P W
  gi|2258610   701 FESSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWY 750
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                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    GvG  FK  i+K   n+  L++mY++WPFF   l  ++mv  K    iA
  gi|2258610   751 GVGSSFKEFINKNPENIAILRDMYQNWPFFQSLLSNVDMVLSKSNMNIAF 800

                    LyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                     y kL   E++k   + + ++++ tk+ +L i GH +lL   PYLK  l
  gi|2258610   801 EYAKLCEDEQVKAIYETILNEWQVTKNVILAIEGHDELLADNPYLKASLD 850

                    LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                     R +Y   Ln +q   +KR R        r +ls +  +E       L++
  gi|2258610   851 YRMPYFNILNYIQLELIKRQR--------RGELSSD--QER------LIH 884

                    LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +                + GiA G+ n G
  gi|2258610   885 IT----------------INGIATGLRNSG    898

gi|149006260|ref|ZP_01829972.1|: domain 1 of 1, from 1 to 898: score 305.5, E = 1.1e-88
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                            L  L     s +  +++ + L+l   L+Di + +  ++  E
  gi|1490062     1    ---MSLQKLE--NYS-NKSVVQEEVLILTELLeDITKNMLAPETFEK 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +    Els +    +D + L+ L   +tsL   + + + + ++ +  L n
  gi|1490062    42 IIQLKELSTQ----EDYQGLNRL---VTSLSNDEMVYISRYFSILPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+    s t          kLv       e
  gi|1490062    85 ISEDVDLAYEINHQNNIDQDYLGKLSTTI---------KLVAEK----EN 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      e L    v  vltAHPtq  R+s+L     i   L +     +    K
  gi|1490062   122 AVEILEHLNVVPVLTAHPTQVQRKSMLDLTNHIHSLLRKYRDVKLGLINK 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                          L R i     tD iR  +     E+   m Y+     k vP
  gi|1490062   172 DKWYNDLRRYIEIIMQTDMIREKKLKVTNEITNAMEYYNSSFLKAVPHLT 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                           +  G+n +   ++  i    W+GGDRDG nP vt    +   L
  gi|1490062   222 TEYKRLAQAHGLNLK---QAKPITMGMWIGGDRDG-NPFVTAKTLKQSAL 267

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                        +  n Y  ++  L  E+s+      +     E+ r ++ +     Y
  gi|1490062   268 TQCEVIMNYYDKKIYQLYREFSLSTSIVNVSKQVREMARQSKDN---SIY 314

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                     E        E YR  L d+  K+  t+          i +      y
  gi|1490062   315 RE-------KELYRRALFDIQSKIQATK-------TYLIEDEEVGTRYET 350

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      +F   L     sL e     +  G  ++lL  v  FG  L  +D+Rq+
  gi|1490062   351 ANDFYKDLIAIRDSLLENKGESLISGDFVELLQAVEIFGFYLASIDMRQD 400

                    seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK.RPLlgsDLP
                    s      +  + +  +i s+Y e sEe + + Ll EL+  +R L
  gi|1490062   401 SSVYEACVAELLKSAGIHSrYSELSEEEKCDLLLKELEEDpRILSATHAE 450

                    ktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLqRE
                    k E ++++  +  + rvL ++L  D     iis at+ sD+L    +L +E
  gi|1490062   451 KSELLAkelAIFKTARVLKDkLGDDVIRQTIISHATSLSDMLELAILLKE 500

                    Cgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                     g+ ++++  +++vPLFE + DL+    ++ k  s+   +  id +++ q
  gi|1490062   501 VGLvdteRARVQIVPLFETIEDLDHSEETMRKYLSLSLAKKWIDSRnnyQ 550

                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                    e+m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGRGGtv
  gi|1490062   551 EIMLGYSDSNKDGGYLSSCWTLYKAQQQLTAIGDEFGVKVTFFHGRGGTV 600

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                    GRGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
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  gi|1490062   601 GRGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLV 650

                   AAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                    A +   +    s  +++  +  +m+++     + YR +v+    F +YF
  gi|1490062   651 SAAINRMITQKKSDTntpNRYEAIMDQVVDRSYDVYRDLVFGNEHFYDYF 700

                   RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                       P       niGsRPa Rk    i  LRAiPW+F+W q R   P W
  gi|1490062   701 FESSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWY 750

                   GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                   GvG  FK  i+K   n+  L++mY++WPFF   l  ++mv  K    iA
  gi|1490062   751 GVGSSFKEFINKNPENIAILRDMYQNWPFFQSLLSNVDMVLSKSNMNIAF 800

                   LyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                    y kL   E++k   + + ++++ tk+ +L i GH +lL   PYLK  l
  gi|1490062   801 EYAKLCEDEQVKAIYETILNEWQVTKNVILAIEGHDELLADNPYLKASLD 850

                   LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                    R +Y   Ln +q   +KR R        r +ls +  +E       L++
  gi|1490062   851 YRMPYFNILNYIQLELIKRQR--------RGELSSD--QER------LIH 884

                   LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   +                 + GiA G+ n G
  gi|1490062   885 IT----------------INGIATGLRNSG    898

gi|269214612|ref|ZP_06158686.1|: domain 1 of 1, from 19 to 918: score 305.3, E = 1.3e-88
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2692146    19    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 56

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2692146    57 ETVKLLSTS----DDSAALIE--KVLPQLDERQTYDLTLACGLFAQILNI 100

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AE+v+   RR i+    G    E+s t      Et+++L        + v
  gi|2692146   101 AEDVHHERRRQIHEEA-GHGGAEGSLT------ETVRRLKAGK-ADGKSV 142

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                      L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|2692146   143 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 192

                   DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|2692146   193 LRREIDTVLLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 238

                   FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     R+++   +      R+P    ++k   W+GGDRDG nP v  E  R
  gi|2692146   239 LYRKMEHDFQTAYPDVRVP---DILKIGGWIGGDRDG-NPFVSAETLRFA 284

                   CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                             +Y   ++ L  El +    +  Rv+       a +dk
  gi|2692146   285 FRRHADAVFRFYRGELDKLYRELPL----SIRRVKVNG-DVMALSDKSPD 329

                   yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEeAv
                     i        +EPYR  +  +   +     +aR L+L  G       e
  gi|2692146   330 EEI-----ARTEEPYRRAIAYI---MARAMGKARALgLGMGCKFGFLEP- 370

                   ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                   y    eFL+ LE   +sL + G + +A+G L Dl+R vs FG  ++ LD+
  gi|2692146   371 YASAQEFLDDLEKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPLDL 420

                   RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                   Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL  +RPL+ + +
  gi|2692146   421 RQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELGHQRPLYSPFI 470

                   PktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqR
                      E++++E++   +a ++  E   D+    iis +  P D LA  LL +
  gi|2692146   471 TYSEhtrrELAIFNEARKIKDEFGEDAVTQSIISNCEQPGDLLALALLLK 520
```

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                    ECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                    E g+   +++++k  + +vPLFE +  Le A   +e +F +DWY   ++
  gi|2692146   521 ESGLlavengkpKSRINIVPLFETIEALENACPVMETMFRLDWYGALLES 570

                    K...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                    +++ qe+m+GYsDs KD G +   W LY+A   ++   KkyGv++ lFHG
  gi|2692146   571 RgniQEIMLGYSDSNKDGGYVTSSWCLYQAELGLVELFKKYGVRMRLFHG 620

                    RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                    RGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +     r
  gi|2692146   621 RGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQRN 670

                    LqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvE
                    L    AAtLE G+  P   k    kLm+ +  v    YR ++   P F++
  gi|2692146   671 LETLVAATLEAGI--PTDKKDPDAKLMQALSDVSFKYYRELITH-PDFID 717

                    YFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPv
                    YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  LP
  gi|2692146   718 YFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLMLPA 767

                    WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                    W G+G A     +     l  L+   ++ PFF   l  +E v AK D  +
  gi|2692146   768 WYGFGSAVETLCEGSPETLAALRGHARNNPFFQAMLSNMEQVMAKTDITL 817

                    AaLyDkLLvaEe.LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                    A  y  L  + ++ k     ++++Y   ++ LL +    +lL     L
  gi|2692146   818 AENYAGLSESPDkAKIIFGMIKEEYRRSRKALLDLLQTEELLRDNRSLAR 867

                    rlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkade
                     l LR +Y+  Ln +q   LKR+R                  E+   +
  gi|2692146   868 SLALRIPYLNALNGLQVAMLKRLR----------------KEP-DNPHA 899

                    LvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    L+ +               Lt+ G+A G+ ntG
  gi|2692146   900 LLMVH--------------LTINGVAQGLRNTG    918

gi|15900937|ref|NP_345541.1|: domain 1 of 1, from 1 to 898: score 305.3, E = 1.3e-88
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                            L  L     s +  +++ + L+l   L+Di + +  ++  E
  gi|1590093     1    ---MSLQKLE--NYS-NKSVVQEEVLILTELLeDITKNMLAPETFEK 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +    Els +    +D + L+ L   +tsL   + + + + ++ +  L n
  gi|1590093    42 IIQLKELSTQ----EDYQGLNRL---VTSLSNDEMVYISRYFSILPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+    s t          kLv       e
  gi|1590093    85 ISEDVDLAYEINHQNNIDQDYLGKLSTTI---------KLVAEK----EN 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      e L    v  vltAHPtq  R+s+L     i   L +     +    K
  gi|1590093   122 AVEILEHLNVVPVLTAHPTQVQRKSMLDLTNHIHSLLRKYRDVKLGLINK 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                          L R i     tD iR  +     E+   m Y+     k vP
  gi|1590093   172 DKWYNDLRRYIEIIMQTDMIREKKLKVTNEITNAMEYYNSSFLKAVPHLT 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                           +  G+n +    ++  i    W+GGDRDG nP vt     +   L
  gi|1590093   222 TEYKRLAQAHGLNLK---QAKPITMGMWIGGDRDG-NPFVTAKTLKQSAL 267

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                        +  n Y  ++  L  E+s+      +     E+ r ++ +     Y
  gi|1590093   268 TQCEVIMNYYDKKIYQLYREFSLSTSIVNVSKQVREMARQSKDN---SIY 314

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                     E        E YR  L d+  K+  t+          i +      y
  gi|1590093   315 RE-------KELYRRALFDIQSKIQATK-------TYLIEDEEVGTRYET 350

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      +F   L     sL e     +  G  ++lL  v  FG  L  +D+Rq+
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  gi|1590093   351 ANDFYKDLIAIRDSLLENKGESLISGDFVELLQAVEIFGFYLASIDMRQD 400

                   seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK.RPLlgsDLP
                   s      +  + +  +i s+Y e sEe + + Ll EL+  +R L
  gi|1590093   401 SSVYEACVAELLKSAGIHSrYSELSEEEKCDLLLKELEEDpRILSATHAE 450

                   ktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLqRE
                   k E ++++  +  + rvL ++L  D     iis at+ sD+L   +L +E
  gi|1590093   451 KSELLAkelAIFKTARVLKDkLGDDVIRQTIISHATSLSDMLELAILLKE 500

                   Cgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                    g+ ++++  +++vPLFE + DL+    ++ k  s+   +  id +++ q
  gi|1590093   501 VGLvdteRARVQIVPLFETIEDLDHSEETMRKYLSLSLAKKWIDSRnnyQ 550

                   evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                   e+m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGRGGtv
  gi|1590093   551 EIMLGYSDSNKDGGYLSSCWTLYKAQQQLTAIGDEFGVKVTFFHGRGGTV 600

                   GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                   GRGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
  gi|1590093   601 GRGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLV 650

                   AAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                    A +   +    s  +++  +  +m+++     + YR +v+    F +YF
  gi|1590093   651 SAAINRMITQKKSDTntpNRYETIMDQVVDRSYDIYRDLVFGNEHFYDYF 700

                   RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                       P       niGsRPa Rk    i  LRAiPW+F+W q R   P W
  gi|1590093   701 FESSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWY 750

                   GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                   GvG  FK  i+K   n+  L++mY++WPFF   l  ++mv  K    iA
  gi|1590093   751 GVGSSFKEFINKNPENIAILRDMYQNWPFFQSLLSNVDMVLSKSNMNIAF 800

                   LyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                    y kL   E++k   + + ++++ tk+ +L i GH +lL   PYLK  l
  gi|1590093   801 EYAKLCEDEQVKAIYETILNEWQVTKNVILAIEGHDELLADNPYLKASLD 850

                   LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                    R +Y   Ln +q   +KR R        r +ls +  +E       L++
  gi|1590093   851 YRMPYFNILNYIQLELIKRQR--------RGELSSD--QER------LIH 884

                   LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   +                 + GiA G+ n G
  gi|1590093   885 IT----------------INGIATGLRNSG    898

gi|149003977|ref|ZP_01828785.1|: domain 1 of 1, from 1 to 898: score 305.3, E = 1.3e-88
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           L  L     s +  +++ + L+l   L+Di + +  ++  E
  gi|1490039     1    ---MSLQKLE--NYS-NKSVVQEEVLILTELLeDITKNMLAPETFEK 41

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +    Els +    +D + L+ L   +tsL   + + + + ++ +  L n
  gi|1490039    42 IIQLKELSTQ----EDYQGLNRL---VTSLSNDEMVYISRYFSILPLLIN 84

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   + E+v+lAy    +     D+    s t          kLv       e
  gi|1490039    85 ISEDVDLAYEINHQNNIDQDYLGKLSTTI---------KLVAEK----EN 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     e L    v  vltAHPtq  R+s+L     i   L +     +    K
  gi|1490039   122 AVEILEHLNVVPVLTAHPTQVQRKSMLDLTNHIHSLLRKYRDVKLGLINK 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                         L R i     tD iR  +     E+   m Y+     k vP
  gi|1490039   172 DKWYNDLRRYIEIIMQTDMIREKKLKVTNEITNAMEYYNSSFLKAVPHLT 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                         +  G+n +   ++  i    W+GGDRDG nP vt    +   L
  gi|1490039   222 TEYKRLAQAHGLNLK---QAKPITMGMWIGGDRDG-NPFVTAKTLKQSAL 267
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                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                        +  n Y  ++  L  E+s+      +     E+ r ++ +     Y
  gi|1490039   268 TQCEVIMNYYDKKIYQLYREFSLSTSIVNVSKQVREMARQSKDN---SIY 314

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                     E        E YR  L d+  K+  t+          i +      y
  gi|1490039   315 RE-------KELYRRALFDIQSKIQATK-------TYLIEDEEVGTRYET 350

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      +F   L     sL e     +  G  ++lL  v  FG  L  +D+Rq+
  gi|1490039   351 ANDFYKDLIAIRDSLLENKGESLISGDFVELLQAVEIFGFYLASIDMRQD 400

                    seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK.RPLlgsDLP
                    s      +  + +  +i s+Y e sEe + + Ll EL+  +R L
  gi|1490039   401 SSVYEACVAELLKSAGIHSrYSELSEEEKCDLLLKELEEDpRILSATHAE 450

                    ktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLqRE
                    k E ++++  +  + rvL ++L  D     iis at+ sD+L   +L +E
  gi|1490039   451 KSELLAkelAIFKTARVLKDkLGDDVIRQTIISHATSLSDMLELAILLKE 500

                    Cgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                     g+ ++++  +++vPLFE + DL+    ++ k  s+   +  id +++ q
  gi|1490039   501 VGLvdteRARVQIVPLFETIEDLDHSEETMRKYLSLSLAKKWIDSRnnyQ 550

                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                    e+m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGRGGtv
  gi|1490039   551 EIMLGYSDSNKDGGYLSSCWTLYKAQQQLTTIGDEFGVKVTFFHGRGGTV 600

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                    GRGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
  gi|1490039   601 GRGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLV 650

                    AAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                     A +   +    s  +++  +  +m+++     + YR +v+    F +YF
  gi|1490039   651 SAAINRMITQKKSDTntpNRYEAIMDQVVDRSYDIYRDLVFGNEHFYDYF 700

                    RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                        P       niGsRPa Rk    i  LRAiPW+F+W q R   P W
  gi|1490039   701 FESSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWY 750

                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    GvG  FK  i+K   n+  L++mY++WPFF   l  ++mv  K    iA
  gi|1490039   751 GVGSSFKEFINKNPENIAILRDMYQNWPFFQSLLSNVDMVLSKSNMNIAF 800

                    LyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                     y kL   E++k   + + ++++ tk+ +L i GH +lL   PYLK  l
  gi|1490039   801 EYAKLCEDEQVKAIYETILNEWQVTKNVILAIEGHDELLADNPYLKASLD 850

                    LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                     R +Y   Ln +q   +KR R        r +ls +  +E       L++
  gi|1490039   851 YRMPYFNILNYIQLELIKRQR--------RGELSSD--QER------LIH 884

                    LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +                 + GiA G+ n G
  gi|1490039   885 IT----------------INGIATGLRNSG    898

gi|148994184|ref|ZP_01823499.1|: domain 1 of 1, from 1 to 898: score 305.2, E = 1.3e-88
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                            L  L     s +  +++ + L+l   L+Di + +  ++  E
  gi|1489941     1    ---MSLQKLE--NYS-NKSVVQEEVLILTELLeDITKNMLAPETFEK 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +    Els +    +D + L+ L   +tsL   + + + + ++ +  L n
  gi|1489941    42 IIQLKELSTQ----EDYQGLNRL---VTSLSNDEMVYISRYFSILPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+    s t          kLv       e
  gi|1489941    85 ISEDVDLAYEINHQNNIDQDYLGKLSTTI---------KLVAEK----EN 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      e L    v  vltAHPtq  R+s+L     i   L +     +    K
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  gi|1489941   122 AVEILEHLNVVPVLTAHPTQVQRKSMLDLTNHIHSLLRKYRDVKLGLINK 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                          L R i     tD iR  +     E+   m Y+     k vP
  gi|1489941   172 DKWYNDLRRYIEIIMQTDMIREKKLKVTNEITNAMEYYNSSFLKAVPHLT 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                           +  G+n +   ++  i    W+GGDRDG nP vt    +   L
  gi|1489941   222 TEYKRLAQAHGLNLK---QAKPITMGMWIGGDRDG-NPFVTAKTLKQSAL 267

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                        +  n Y  ++  L  E+s+      +     E+ r ++ +     Y
  gi|1489941   268 TQCEVIMNYYDKKIYQLYREFSLSTSIVNVSKQVREMARQSKDN---SIY 314

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                     E        E YR  L d+  K+  t+          i +      y
  gi|1489941   315 RE-------KELYRRALFDIQSKIQATK-------TYLIEDEEVGTRYET 350

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      +F   L     sL e     +  G  ++lL  v  FG  L  +D+Rq+
  gi|1489941   351 ANDFYKDLIAIRDSLLENKGESLISGDFVELLQAVEIFGFYLASIDMRQD 400

                    seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK.RPLlgsDLP
                    s      +  + +  +i s+Y e sEe + + Ll EL+  +R L
  gi|1489941   401 SSVYEACVAELLKSAGIHSrYSELSEEEKCDLLLKELEEDpRILSATHAE 450

                    ktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLqRE
                    k E ++++  +  + rvL ++L  D     iis at+ sD+L   +L +E
  gi|1489941   451 KSELLAkelAIFKTARVLKDkLGDDVIRQTIISHATSLSDMLELAILLKE 500

                    Cgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                     g+ ++++  +++vPLFE + DL+    ++ k  s+   +  id +++ q
  gi|1489941   501 VGLvdteRARVQIVPLFETIEDLDHSEETMRKYLSLSLAKKWIDSRnnyQ 550

                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                    e+m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGRGGtv
  gi|1489941   551 EIMLGYSDSNKDGGYLSSCWTLYKAQQQLTAIGDEFGVKVTFFHGRGGTV 600

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                    GRGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
  gi|1489941   601 GRGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLV 650

                    AAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                     A +   +    s  +++  +  +m+++     + YR +v+    F +YF
  gi|1489941   651 SAAINRMITQKKSDTntpNRYEAIMDQVVDRSYDIYRDLVFGNEHFYDYF 700

                    RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                        P       niGsRPa Rk    i  LRAiPW+F+W q R   P W
  gi|1489941   701 FESSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWY 750

                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    GvG  FK  i+K   n+  L++mY++WPFF   l  ++mv  K    iA
  gi|1489941   751 GVGSSFKEFINKNPENIAILRDMYQNWPFFQSLLSNVDMVLSKSNMNIAF 800

                    LyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                     y kL   E++k   + + ++++ tk+ +L i GH +lL   PYLK  l
  gi|1489941   801 EYAKLCEDEQVKAIYETILNEWQVTKNVILAIEGHDELLADNPYLKASLD 850

                    LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                     R +Y   Ln +q   +KR R        r +ls +  +E       L++
  gi|1489941   851 YRMPYFNILNYIQLELIKRQR--------RGELSSD--QER------LIH 884

                    LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +                + GiA G+ n G
  gi|1489941   885 IT----------------INGIATGLRNSG    898

gi|264679666|ref|YP_003279573.1|: domain 1 of 1, from 17 to 949: score 305.2, E = 1.4e-88
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                         D  +R     K  +d  Lie D  Ll + L+D++ +  G    E
  gi|2646796    17    --DKPVR-----KTDKDLPLIE-DIRLLGRILgDVIREQEGGPAYEL 55
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                vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                v     ls  +    D      L   L +L    ++ v +a+     LAn
gi|2646796    56 VEQVRQLSVAFRRDADEAADKALKKLLKGLSSDQTVSVIRAFTYFSHLAN 105

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                LAE+ +   RRR    +       a  t E  iE  l +L   +  s +
gi|2646796   106 LAED-RHHIRRRAVHER-------AGNTQEGSIEVALARLRWAG-ISTAT 146

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL.........aqLs
                v + L    +  vltAHPt   R s+L  + Ri   L ++++   +aqL+
gi|2646796   147 VVDTLAKSFISPVLTAHPTEVQRQSILTAERRIAQLLaerddilmrAQLY 196

                ..AKD.vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYi
                ++AKD +t+ +   ++  L   +   + t  +R ++ t  DE+   +sY+
gi|2646796   197 nsAKDaLTPRELTRVEAQLRACVAQLWQTRLLRHSKLTVADEIENALSYY 246

                HEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknP
                  t  + +PK     +  L      E+lP +   ++   W+GGDRDG nP
gi|2646796   247 EATFLQEIPKIYEQLEQEL-----GEKLP-EQSFLRMGQWIGGDRDG-NP 289

                RvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEly
                 vt E           +A   Y+  v  L  Els+      L     E++
gi|2646796   290 FVTAESLELALSRQADVALRHYLREVHYLGGELSL---SANLVDITPEMQ 336

                rtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtG
                  a       + +         EPYR  L  +  +L  t        A
gi|2646796   337 ALADAS--PDHNVH-----RSDEPYRRALTGIYARLAATLKQLTGGEAAR 379

                iseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstF
                 +  + +A y   + FL  L +   sL      ++A   L  l+R v  F
gi|2646796   380 HAVAPQNA-YASADAFLADLQIIDDSLSRYHGDALAPQRLRPLMRAVRVF 428

                GLsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELk
                G  L  +D+Rq s+++ +v+  +     +   Y    E+ +   L+  L+
gi|2646796   429 GFYLSTVDLRQSSDKHEEVVRELLSVAKVElDYSLLEEDAKCALLVRLLE 478

                GKRPL..lgsDL.PktEEvkDvldafrvLAE.LPiDsFGaYiismataPs
                  RPL+ +g D +  t     + ++ + L E+L +++    iis + + s
gi|2646796   479 DARPLrvMGGDYgDHTRSELAIFETAKRLRErLGSEAIRHCIISHTETVS 528

                DvLAvELLqRECgv.........kqtLrvvPLFEkLADLeAAPAavekLF
                D L v LLq+E g+ +++ +++ +  L vvPLFE + DL+ A   + + +
gi|2646796   529 DLLEVLLLQKEVGLlrgtlqdgaQCDLIVVPLFETIEDLRNAAPIMRRYY 578

                s...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEii....
                  ++i   + +  G q++m+GYsDs KD G +   W LY+A   +++  +
gi|2646796   579 QlpgIAELVRKSGGEQDIMLGYSDSNKDGGIFTSNWELYRAEIALVdlfd 628

                KvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGE
                  A +yG++L +FHGRGGtvGRGGGP   AiL+qPP t+ G +R t qGE
gi|2646796   629 DLADHYGIRLRMFHGRGGTVGRGGGPSYQAILAQPPGTVRGQIRLTEQGE 678

                viEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvv..
                vi   +   ++  r L    AAtLE  +  P   kP  +  +e  A  ++
gi|2646796   679 VIASKYANPEIGRRNLETLVAATLEATLLQPT--KPATKAFLEAAAFLse 726

                .AtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesL
                     YR++v+  P F  YF + tP  E   +niGsRPa Rk    ie L
gi|2646796   727 aSMAAYRALVYETPGFTNYFFSSTPIREIAELNIGSRPASRKATQAIEDL 776

                RAiPWiFaWtqtRFHLPvWLGvGAAFKhAid...KDiK.nlqkLkEmYke
                RAiPW F+W q R  LP W G+G A +  i++++KD K  l  L+ mY++
gi|2646796   777 RAIPWGFSWGQCRLTLPGWYGFGSAIQAFIHrpgKDAKaQLALLQKMYRQ 826

                WPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvE
                WPFFR  l  ++mv AK D  +A+ y +L+    L+++ FG  + ++++
gi|2646796   827 WPFFRTLLSNMDMVLAKSDLNLASRYSELVTDTRLrrRIFG-AIEAEWQS 875

                tkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPs
                t + L +i G k  LE    L   +R R +Yi  Ln +q   ++R R
gi|2646796   876 TVEALNQITGDKQRLEHNSALARSIRHRFPYIDPLNHLQVELVRRWR--- 922
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                  ykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAA
                               A     +  + ++L                 + GiAA
  gi|2646796   923 -------------AGQTDDRVKNGIHLS----------------INGIAA 943

                  GmqntG<-*
                  G+ ntG
  gi|2646796   944 GVRNTG    949

gi|284044871|ref|YP_003395211.1|: domain 1 of 1, from 5 to 881: score 305.2, E = 1.4e-88
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                     s     R+L P         ++ D LLl++ L+D+L +  G   +E
  gi|2840448     5    SSTTAARALDP---------LDRDTLLLERLLgDVLEEQNGRAFRER 42

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                       + +A      D++  e L + L +   a      +a +  L LAn
  gi|2840448    43 LFWLRDSAAALREGDDAQG-EQLLTFLRGQPAARLAPYVRACSMQLQLAN 91

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe.
                  +AEE e   RRR                t     E l   v    + P +
  gi|2840448    92 IAEELERLRRRREYDSD-----------TSVPQRESLAATVGAVSQVPRs 130

                  EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                   v eAL    v Lv+tAHPt + RRs+   +  +   + +L    v
  gi|2840448   131 RVAEALAQLDVRLVMTAHPTEATRRSVFDHQQTVWRIMEKLDDPRVGATR 180

                  KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                  ++ L++ L   +   + tDE+RR +P   DE+R  + ++   +++  P
  gi|2840448   181 RRALEDELREVLTTWWQTDEVRRMRPLVEDEVRRTLFFFEAVLFDALPPL 230

                  LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                        A          P   P+++F sW GGD DG nP v P
  gi|2840448   231 -----AAELSRCFDMPWPPATPVLRFGSWAGGDMDG-NPEVGPASIARTL 274

                  LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                   L R  A  l    ++ L  E+s     d+       l      d
  gi|2840448   275 HLHRGTALRLLHRRIDALAREFSQ---ADDHVFLSPALRASIEHDEAELP 321

                  YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                   +   +   P EP+R  LG +  ++  tR R     A G+s+ +E A
  gi|2840448   322 NVGSRRR-NPHEPFRRKLGLIAGRMQKTRRRE----AGGYSDPAELAA-- 364

                  kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                          LEL   sL       +A G++  lL qv tFG  L  LD+Rq
  gi|2840448   365 -------DLELVRNSLSSA---RVAGGAIARLLVQVRTFGFHLAALDVRQ 404

                  EseRqtDvlDAittHLeiGsYReWsEeKRqEWL...laELkGKRPLlgsD
                   +      l A    L +  Y e  E  Rq  L + +  L+G RP   +
  gi|2840448   405 SAGP----LQAAVAQL-VDGYAEADEAGRQALLaqaIPALEGTRP---PK 446

                  LPktEEvkDvldaf.rvLAELPiDsFGaYiismataPsDvLAvELLqREC
                   P  +Ev     a+ r + +    + G+ iisma  PsDvL    L R
  gi|2840448   447 APADDEVLAAFAAIaRGVRDHGARALGSVIISMAEQPSDVLCTLYLLRRA 496

                  gvkq....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridG...Kqe
                  gv +++ ++L++vPLFE + DL  A A++  L++   Y  +++G +++qe
  gi|2840448   497 GVGRdglpALPIVPLFETVDDLTGAQATMSTLYADPAYASHLNGcerRQE 546

                  vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                  +m+GYsDs KD G +sA W LY AqE ++  A ++ vKL  FHGRGG
  gi|2840448   547 IMLGYSDSAKDGGFISAQWELYAAQERLMAAADEHAVKLRFFHGRGGSTS 596

                  RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                  RGGGP H Ai++qPP  i G +R+t qGEvi + +   +L  r+L
  gi|2840448   597 RGGGPSHRAIVAQPPGSIRGRIRITEQGEVISQRYAHPELAQRALEQTLS 646

                  AtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAt
                    +   + PP  P   +R+  +++A      YR++++ + RF      A
  gi|2840448   647 GVVLATLAPPAEPPARYREEAQRLADDSRRAYRALIYDDERFDALLHQAS 696

                  PElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGA
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                  P  E   +niGsRPa R  +  +  LRAiPW+FaW q R  LP W G G
  gi|2840448   697 PLDELAELNIGSRPASR-GGRRLRELRAIPWVFAWMQNRLLLPAWYGAGS 745

                  AFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDk
                  A       D   l   +Em ++WPFFR+ +  lEm   K D G+A  y +
  gi|2840448   746 AL------DAGDLALQREMREQWPFFRMVISTLEMSLFKSDLGVAERYVE 789

                  LLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRds
                  L+  E  +     +Rd+ +   + +Lki G   lL G P L++rl  R++
  gi|2840448   790 LVTDEGARALWTPIRDEHERLVERVLKITGSDTLLGGTPALQKRLSHRNP 839

                  YittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpt
                  +i  L  +q   L+R R                Ad+
  gi|2840448   840 WIDPLSHVQVDLLRRAR----------------ADDA------------- 860

                  ervaPGLEDtLiLtmKGiAAGmqntG<-*
                  +   P     L+ t+ GiAAGm ntG
  gi|2840448   861 DAQTP-----LLHTVAGIAAGMRNTG    881

gi|293381352|ref|ZP_06627354.1|: domain 1 of 1, from 1 to 912: score 305.1, E = 1.5e-88
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         + +      s+ + + e   +L D   +  + + G+   + +
  gi|2933813     1    -----MTVKKLENNSDVNVVAEESKVLTDLLNESTKQVIGQAAFDKI 42

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                  q    +sA       +k  +EL  ++ sL+  + i+vA+ +  +  L n+
  gi|2933813    43 QNLIKISA-------AKDYQELEKQIASLNNREMIVVARYFATLPLLINI 85

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   E+velA +  +    h D+    s t +         +v +  K  eE+
  gi|2933813    86 SEDVELASKVNVLNNTHQDYLGKLSDTID---------IVAQK-KNAEEI 125

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   e +    v  vltAHPtq  R+ +L     i   L           D+
  gi|2933813   126 LEHV---NVVPVLTAHPTQVQRKTILELTDQIHQLLRNYRDVKNGTIDRD 172

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                  E  E +   i     tD iR  +     E+   ++Y+   +   + KF
  gi|2933813   173 EWTEQMRACIEILMQTDIIRGHKLKVANEITNVLAYYPKALIPAITKFTS 222

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                  R     K  G+n      +  i    W+GGDRDG nP vt +       L
  gi|2933813   223 RYKELAKKHGLNAS---HATPITMGMWIGGDRDG-NPYVTADTLELSATL 268

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                     +    Yi q+  L   +sm              y  +  d  v +
  gi|2933813   269 QSQVIFEYYIKQINKLYRAISM-----------STSYMGPSDD--VMHLS 305

                  EFWKqvPP...tEPYRvi.......LGdvRDKLYntRERaRHLLAtGise
                  E      P +++EPYR      +++L     KL n   +   L    + +
  gi|2933813   306 ELSNDDSPfrtNEPYRRAfyyiqsrLVHTEQKLLNITNKNTFLKKRDLQN 355

                  isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                  +     y +  eF   LE+   sL e  D+++ D     +L  +  FG
  gi|2933813   356 LDKIPCYQNAQEFKADLEIIKNSLEEDHDHAVVDSYFTQILEAINIFGFH 405

                  LvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK.
                  L  +D+Rq+s  +   +  + +  +i + Y + sE+K+   Ll EL   +
  gi|2933813   406 LATIDMRQDSSVNEACVAELLKSAGICdNYSDLSEDKKIKLLLNELNNDp 455

                  RPLlgsDLPktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDv
                  R L     Pk E ++++  +  + r L ++L  D     iis + + sD+
  gi|2933813   456 RNLHANNKPKSELLQkelKIYKTARQLKDrLGEDVIKQHIISHTESVSDM 505

                  LAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYin
                  L   ++ +E  + +++k  ++vvPLFE + DL+ A   ++   s D  +
  gi|2933813   506 LEQAIMLKEYDLldnqKARIQVVPLFETVEDLNNAREIIKEFLSFDIVKK 555

                  ri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                   + +++  qevm+GYsDs KD G l+  W LYkAq ++ K+  + G+K++
  gi|2933813   556 WLvsqNNYQEVMLGYSDSNKDGGYLASCWNLYKAQKDLTKIGEEMGIKIT 605
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                    lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                      HGRGGtvGRGG P    Ai +qP    in  +R+t qGE+i   +G  +
  gi|2933813   606 FMHGRGGTVGRGGSPSYEAITAQPFKSINDRMRMTEQGEIIQNKYGNKDT 655

                    CFrsLqRFtAAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvv
                     +  L   + At++      +   ++  ++R  m+++     E YR +v+
  gi|2933813   656 AYYNLEMLASATIDRMASKQIVSEdhvADFRSSMDQIVAKSNEVYRKLVF 705

                    KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                      P F  YF  AtP  E   +n+GsRPa Rk       LRAiPW+F+W q
  gi|2933813   706 ENPNFLKYFFQATPIKEISGLNVGSRPASRKKLTDFSGLRAIPWVFSWSQ 755

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     R   P W GvG  FK  id D  nl+ L+ mY+ WPFF   l  ++mv
  gi|2933813   756 SRVMFPGWYGVGSGFKSFIDADPANLKELQNMYQGWPFFHSLLSNVDMVL 805

                    AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                     K    iA  y +L   E++k   + + ++++ tk+ +L+i GH +l+E
  gi|2933813   806 SKSNMRIAKQYADLCEDEQVKSVFDIINQEWELTKKVILQIEGHDELIED 855

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                     P LK+ l  R +Y   Ln +q   +KR R+   +   +  +       +
  gi|2933813   856 APTLKKSLEYRMPYFNILNYIQLEMIKRDREDVIQGVYQSII-------P 898

                    skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                           + +n                  G+A G+ n G
  gi|2933813   899 -------ITIN------------------GVASGLRNSG    912

gi|168487465|ref|ZP_02711973.1|: domain 1 of 1, from 1 to 898: score 305.0, E = 1.6e-88
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           L  L     s +  +++ + L+l   L+Di + +  ++  E
  gi|1684874     1    ---MSLQKLE--NYS-NKSVVQEEVLILTELLeDITKNMLAPETFEK 41

                    vqECYElsA..eYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    +    Els +++Y G         L   +tsL   + + + + ++ +  L
  gi|1684874    42 IIQLKELSTqeDYQG---------LNCLVTSLSNDEMVYISRYFSILPLL 82

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                     n+ E+v+lAy    +     D+    s t          kLv
  gi|1684874    83 INISEDVDLAYEINHQNNIDQDYLGKLSTTI---------KLVAEK---- 119

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    e   e L    v  vltAHPtq  R+s+L     i   L +     +
  gi|1684874   120 ENAVEILEHLNVVPVLTAHPTQVQRKSMLDLTNHIHSLLRKYRDVKLGLI 169

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     K      L R i     tD iR  +     E+   m Y+     k vP
  gi|1684874   170 NKDKWYNDLRRYIEIIMQTDMIREKKLKVTNEITNAMEYYNSSFLKAVPH 219

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                             +  G+n +   ++  i    W+GGDRDG nP vt    +
  gi|1684874   220 LTTEYKRLAQAHGLNLK---QAKPITMGMWIGGDRDG-NPFVTAKTLKQS 265

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                     L    +  n Y  ++  L  E+s+      +     E+ r ++ +
  gi|1684874   266 ALTQCEVIMNYYDKKIYQLYREFSLSTSIVNVSKQVREMARQSKDN---S 312

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                     Y E        E YR  L d+  K+  t+          i +      y
  gi|1684874   313 IYRE-------KELYRRALFDIQSKIQATK-------TYLIEDEEVGTRY 348

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                        +F   L     sL e     +  G  ++lL  v  FG  L  +D+R
  gi|1684874   349 ETANDFYKDLIAIRDSLLENKGESLISGDFVELLQAVEIFGFYLASIDMR 398

                    qEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK.RPLlgsD
                    q+s      +  + +  +i s+Y e sEe + + Ll EL+  +R L
  gi|1684874   399 QDSSVYEACVAELLKSAGIHSrYSELSEEEKCDLLLKELEEDpRILSATH 448

                    LPktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLq
```

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                     k E ++++  +  + rvL ++L  D     iis at+ sD+L   +L
  gi|1684874   449 AEKSELLAkelAIFKTARVLKDkLGDDVIRQTIISHATSLSDMLELAILL 498

                    RECgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK..
                    +E g+ ++++  +++vPLFE + DL+    ++ k  s+   +  id +++
  gi|1684874   499 KEVGLvdteRARVQIVPLFETIEDLDHSEETMRKYLSLSLAKKWIDSRnn 548

                    .qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                     qe+m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGRGG
  gi|1684874   549 yQEIMLGYSDSNKDGGYLSSCWTLYKAQQQLTAIGDEFGVKVTFFHGRGG 598

                    tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                    tvGRGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
  gi|1684874   599 TVGRGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNLEM 648

                    FtAAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFvE
                       A +   +    s  +++  +  +m+++     + YR +v+    F +
  gi|1684874   649 LVSAAINRMITQKKSDTntpNRYEAIMDQVVDRSYDIYRDLVFGNEHFYD 698

                    YFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPv
                    YF    P       niGsRPa Rk    i  LRAiPW+F+W q R   P
  gi|1684874   699 YFFESSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPG 748

                    WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                    W GvG  FK  i+K   n+  L++mY++WPFF   l  ++mv  K    i
  gi|1684874   749 WYGVGSSFKEFINKNPENIAILRDMYQNWPFFQSLLSNVDMVLSKSNMNI 798

                    AaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                    A  y kL   E++k   + + ++++ tk+ +L i GH +lL   PYLK
  gi|1684874   799 AFEYAKLCEDEQVKAIYETILNEWQVTKNVILAIEGHDELLADNPYLKAS 848

                    lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                    l  R +Y   Ln +q   +KR R        r +ls +  +E       L
  gi|1684874   849 LDYRMPYFNILNYIQLELIKRQR--------RGELSSD--QER------L 882

                    vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +++                + GiA G+ n G
  gi|1684874   883 IHIT----------------INGIATGLRNSG    898

gi|221199352|ref|ZP_03572396.1|: domain 1 of 1, from 57 to 1004: score 304.9, E = 1.7e-88
                    *->siDAqLRlLvPGKvsed.ekLieYDALLlDkFL.DiLqDLHGedLkE
                       s          G+  ed+++ +  D   l + L+D++ +  G+ + +
  gi|2211993    57    SERTAATPKSGGRTREDkDRPLFEDIRFLGRLLgDVVREQEGDTVFD 103

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    +v      +  +    D +  + L  kL  L P  ++ v +a++    LA
  gi|2211993   104 VVETIRQTAVKFRREDDREAAQTLEKKLRKLTPEQTVSVVRAFSYFSHLA 153

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE+ +   RRRi+ +        +sA     +   l kL   +n s
  gi|2211993   154 NIAEDRHHNRRRRIHALA-------GSAPQPGTVAHALDKLKTTGNASKR 196

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                              +  vltAHPt   R+s+L  +  i   La    +++t  +
  gi|2211993   197 VLQRFFDDALIVPVLTAHPTEVQRKSILDAQHDIARLLAE-RDQELTARE 245

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    ++  +  L   + A + t  +R a+ t  DE+   +sY+  t  +  P
  gi|2211993   246 RQHNEAMLRARVTALWQTRMLRDARLTVGDEIENALSYYRATFLEELPAL 295

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                       ++ AL   G+  R+P      +  sW+GGDRDG nP vt     +
  gi|2211993   296 YGDIEAALAEHGLAARVP---AFFQMGSWIGGDRDG-NPNVTAATLDEAI 341

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                         +    Y++qv  L  Els+    + L v A +  +  a
  gi|2211993   342 NRQAAVILEHYLEQVHKLGAELSV----SNLLVGANDAVKALAAA----- 382

                    YiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGisei.....
                          q P++  EPYR  L  +  +L      aR  L  G   +++ ++
  gi|2211993   383 ---SPDQSPhrVDEPYRRALIGIYTRLAAS---ARVRLGEGTVPVrsagr 426
```

```
                    ...sEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstF
                    + ++  A +y + +eF+  L +   sL e     +A   L  l+R    F
  gi|2211993   427 gapPVRATpYADSDEFVADLKVLTASLAEHHGASLAAPRLTPLMRAAEVF 476

                    GLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELk
                    G  L  +D+Rq s+ +  v+  +    ++ ++Y +  E  +   Lla L
  gi|2211993   477 GFHLASIDLRQSSDIHEAVVAELFARAGVVAdYASLEEADKLRVLLAALA 526

                    GKRPLlgsDLPktEEvkDvldaf....rvLAELPiDsFGaYiismataPs
                      RPL  + +      +  l+ f++ ++v A     +   Yiis + + s
  gi|2211993   527 DPRPLRSPYIEYSALAQSELGVFekarEVRAQFGARAVRNYIISHTETVS 576

                    DvLAvELLqREC............gvkqtLrvvPLFEkLADLeAAPAave
                    D + v LLq+E +  ++  + ++++ k++L v+PLFE + DL+ A   +
  gi|2211993   577 DLVEVLLLQKETgllegalgapdgHAKNALMVIPLFETIPDLRDASRIMR 626

                    kLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiK
                      F+ +++D  i +    qevm+GYsDs KD G l   W LY+A   ++
  gi|2211993   627 EYFAlpgVDALIHHQGDEQEVMLGYSDSNKDGGFLTSNWELYRAELALVE 676

                    vAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEv
                      ++  + L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGEv
  gi|2211993   677 LFRERKITLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEV 726

                    iEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv...sPkPEWRkLmeemAvv
                    i   F   ++  r L    AAtLE  + P  + ++  P +   m+ +
  gi|2211993   727 IASKFANPEIGRRNLETVVAATLEASLLPQSnapAQLPAFEGAMQTLSDT 776

                    AtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....Gi
                    A   YR++v+  P F +YF   tP +E   +niGsRPa Rk   ++++ i
  gi|2211993   777 AMAAYRALVYETPGFTDYFFASTPITEIAELNIGSRPASRKLQDpknrRI 826

                    esLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiKnlqkLk
                    e LRAiPW F+W q R  L  W G+G A    +d+  ++   +K l  Lk
  gi|2211993   827 EDLRAIPWGFSWGQCRLLLTGWYGFGSAVATYLDgaadeaERSKRLALLK 876

                    EmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk..PFGksLR
                     m k+WPFF   l  ++mv AK D  +A+ y +L+    L++  FG+ +
  gi|2211993   877 KMNKTWPFFANLLSNMDMVLAKTDLAVASRYAELVPDRKLRnaVFGR-IV 925

                    dkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKR
                    ++++ t   L +i GH + L   P L   ++ R +Y+  Ln +q   +KR
  gi|2211993   926 AEWERTSRALAEITGHEERLATNPLLARSIKNRFPYLDPLNHLQVELIKR 975

                    iRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtm
                     R                A +           n   r   G+     Lt+
  gi|2211993   976 HR----------------AGDT----------N--ARLRRGIH----LTI 993

                    KGiAAGmqntG<-*
                     GiAAG+ ntG
  gi|2211993   994 NGIAAGLRNTG    1004

gi|256843881|ref|ZP_05549368.1|: domain 1 of 1, from 1 to 912: score 304.8, E = 1.8e-88
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            + +      s+ + + e   +L D   +  + + G+   + +
  gi|2568438     1    -----MTVKKLENNSDVNVVAEESKVLTDLLNESTKQVIGQAAFDKI 42

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    q    +sA       +k  +EL  ++ sL+  + i+vA+ +  +  L n+
  gi|2568438    43 QNLIKISA-------AKDYQELEKQIASLNNREMIVVARYFATLPLLINI 85

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     E+velA +  +    h D+    s t +         +v +  K  eE+
  gi|2568438    86 SEDVELASKVNVLNNTHQDYLGKLSDTID---------IVAQK-KNAEEI 125

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     e +    v  vltAHPtq  R+ +L     i   L           D+
  gi|2568438   126 LEHV---NVVPVLTAHPTQVQRKTILELTDQIHQLLRNYRDVKNGTIDRD 172

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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                    E  E +   i     tD iR  +     E+   ++Y+   +   + KF
  gi|2568438   173 EWTEQMRACIEILMQTDIIRGHKLKVANEITNVLAYYPKALIPAITKFTS 222

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R     K  G+n      +  i    W+GGDRDG nP vt +       L
  gi|2568438   223 RYKELAKKHGLNAS---HATPITMGMWIGGDRDG-NPYVTADTLELSATL 268

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                       +    Yi q+  L   +sm              y  +  d  v +
  gi|2568438   269 QSQVIFEYYIKQINKLYRAISM-----------STSYMEPSDD--VMHLS 305

                    EFWKqvPP...tEPYRvi.......LGdvRDKLYntRERaRHLLAtGise
                    E      P +++EPYR      +++L     KL n   +   L    + +
  gi|2568438   306 ELSNDDSPfrtNEPYRRAfyyiqsrLVHTEQKLLNITNKNTFLKKRDLQN 355

                    isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                    +     y +  eF   LE+   sL e  D+++ D     +L  +  FG
  gi|2568438   356 LDKIPCYQNAQEFKADLEIIKNSLEEDHDHAVVDSYFTQILEAINIFGFH 405

                    LvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK.
                    L  +D+Rq+s  +   +  + +  +i + Y + sE+K+   Ll EL   +
  gi|2568438   406 LATIDMRQDSSVNEACVAELLKSAGICdNYSDLSEDKKIKLLLNELNNDp 455

                    RPLlgsDLPktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDv
                    R L     Pk E ++++  +  + r L ++L  D     iis + + sD+
  gi|2568438   456 RNLHANNKPKSELLQkelKIYKTARQLKDrLGEDVIKQHIISHTESVSDM 505

                    LAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYin
                    L   ++ +E  + +++k  ++vvPLFE + DL+ A   ++   s D  +
  gi|2568438   506 LEQAIMLKEYDLldnqKARIQVVPLFETVEDLNNAREIIKEFLSFDIVKK 555

                    ri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                     + +++  qevm+GYsDs KD G l+  W LYkAq ++ K+  + G+K++
  gi|2568438   556 WLvsqNNYQEVMLGYSDSNKDGGYLASCWNLYKAQKDLTKIGEEMGIKIT 605

                    lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                      HGRGGtvGRGG P   Ai +qP   in  +R+t qGE+i   +G  +
  gi|2568438   606 FMHGRGGTVGRGGSPSYEAITAQPFKSINDRMRMTEQGEIIQNKYGNKDT 655

                    CFrsLqRFtAAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvv
                     +  L   + At++      +   ++  ++R  m+++     E YR +v+
  gi|2568438   656 AYYNLEMLASATIDRMASKQIVSEdhvADFRSSMDQIVAKSNEVYRKLVF 705

                    KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                      P F  YF  AtP  E   +n+GsRPa Rk       LRAiPW+F+W q
  gi|2568438   706 ENPNFLKYFFQATPIKEISGLNVGSRPASRKKLTDFSGLRAIPWVFSWSQ 755

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     R   P W GvG  FK  id D  nl+ L+ mY+ WPFF   l  ++mv
  gi|2568438   756 SRVMFPGWYGVGSGFKSFIDADPANLKELQNMYQGWPFFHSLLSNVDMVL 805

                    AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                     K    iA  y +L   E++k   + + ++++ tk+ +L+i GH +l+E
  gi|2568438   806 SKSNMRIAKQYADLCEDEQVKSVFDIINQEWELTKKVILQIEGHDELIED 855

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                     P LK+ l  R +Y   Ln +q   +KR R+   +   +  +       +
  gi|2568438   856 APTLKKSLEYRMPYFNILNYIQLEMIKRDREDVIQGVYQSII-------P 898

                    skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                           + +n                  G+A G+ n G
  gi|2568438   899 -------ITIN-----------------GVASGLRNSG    912

gi|22536923|ref|NP_687774.1|: domain 1 of 1, from 3 to 931: score 304.8, E = 1.8e-88
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                           +L        s + ++i  +  Ll + LD+  q L G +  +
  gi|2253692     3    --HPKLES------SSNKEIITEEVGLLKQLLDeATQKLIGSESFDK 41

                    vqECYElsA..eYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    +     ls +++Y G k+t         + +L   + ++v + ++ +  L
  gi|2253692    42 IEKIVSLSLtdDYTGLKET---------ISALSNEEMVIVSRYFSILPLL 82
```

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                AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                 n+ E+v+lAy    k     D+    s t +          v+ +
gi|2253692     83 INISEDVDLAYEINYKNNLNQDYLGKLSTTID----------VVAG---H 119

                eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                e   + L    v  vltAHPtq  R+ +L   ++i   L +       +
gi|2253692    120 ENAKDILEHVNVVPVLTAHPTQVQRKTVLELTSKIHDLLRKYRDVKAGIV 169

                DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                 ++     L R i     tD iR  +   + E+   m Y+   + k v K
gi|2253692    170 NQEKWYADLRRYIGIIMQTDTIREKKLKVKNEITNVMEYYNRSLIKAVTK 219

                FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                           Gi    P   PL     W+GGDRDG nP vt E  R
gi|2253692    220 LTAEYKALAAKKGIHLENP--KPL-TMGMWIGGDRDG-NPFVTAETLRLS 265

                CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                 ++   +  n Yi+q+ +L   +s+      L     El   a + +
gi|2253692    266 AMVQSEVIINHYIEQLNELYRNMSL---SINLTEVSPELVTLANQSQDNS 312

                yYiEFWKqvPPtEPYRviLGdvRDKLYnt.............RERa.
                 Y E       +EPYR     + DKL  t  + + +++++++  +R  ++
gi|2253692    313 VYRE-------NEPYRKAFNFIQDKLVQTllnlkvgsspkekfvsRQESs 355

                ....RHL...LAtGiseisEeAv..ytkvEeFLEPLELCYksLCeCGDkv
                +  +R +++++A+  s+i  e  + y   EeF   L L  +sL + G
gi|2253692    356 divgRYIkshIAQVASDIQTEELpaYATAEEFKQDLLLVKQSLVQYGQDS 405

                iADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYR
                + DG L  l+  v  FG  L  +D+Rq+s  +   +  + +  +i   Y
gi|2253692    406 LVDGELACLIQAVDIFGFYLATIDMRQDSSINEACVAELLKSANIvDDYS 455

                eWsEeKRqEWLlaELkGK.RPLlgsDLPktEEvkDvldafrvLAELP...
                + sEe +   Ll EL   +R L     Pk E ++  l  f+   EL ++
gi|2253692    456 SLSEEEKCQLLLKELTEDpRTLSSTHAPKSELLQKELAIFQTARELKdql 505

                .iDsFGaYiismataPsDvLAvELLqRECgv....kqtLrvvPLFEkLAD
                + D     iis + + sD+    ++ +E g+ + ++  +++vPLFE + D
gi|2253692    506 gEDIINQHIISHTESVSDMFELAIMLKEVGLidanQARIQIVPLFETIED 555

                LeAAPAavekLFsiDWYinri...dGKqevmvGYsDsGKDAGRlsAAWqL
                L+     + +    +  +  i +++  qe+m+GYsDs KD G ls  W L
gi|2253692    556 LDNSRDIMTQYLHYELVKKWIatnNNYQEIMLGYSDSNKDGGYLSSGWTL 605

                YkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGs
                YkAq E+ K+  + G+K++ FHGRGGtvGRGGGP   Ai sqP   i+
gi|2253692    606 YKAQNELTKIGEENGIKITFFHGRGGTVGRGGGPSYEAITSQPFGSIKDR 655

                lRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WR
                +R t qGE+iE  +G  +  +  L     A ++  +   +    E +++R
gi|2253692    656 IRLTEQGEIIENKYGNQDAAYYNLEMLISASIDRMVTRMITNPNEidnFR 705

                kLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRk
                + m+ +       YR +v+  P F +YF  A P  E   +niGsRPa Rk
gi|2253692    706 ETMDGIVSESNAVYRNLVFDNPYFYDYFFEASPIKEVSSLNIGSRPAARK 755

                PsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkE
                    i  LRAiPW+F+W q R   P W GvG AFKh i++D  nl kL+
gi|2253692    756 TITEISGLRAIPWVFSWSQNRIMFPGWYGVGSAFKHFIEQDEANLAKLQT 805

                mYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkY
                mY++WPFF   l  ++mv  K    iA  y +L  + e++   + + +++
gi|2253692    806 MYQKWPFFNSLLSNVDMVLSKSNMNIALQYAQLAGSKEVRDVFNIILNEW 855

                vEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRD
                + tkd++L i  H  lLE  P L   l  R +Y   Ln +q   +KR+R
gi|2253692    856 QLTKDMILAIEQHDNLLEENPMLHASLDYRLPYFNVLNYVQIELIKRLRS 905

                PsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGi
                 +              dE+    + L+++                + Gi
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  gi|2253692   906 NQL-------------DED---YEKLIHIT---------------INGI 923

                   AAGmqntG<-*
                   A G+ n G
  gi|2253692   924 ATGLRNSG    931

gi|148985039|ref|ZP_01818282.1|: domain 1 of 1, from 1 to 898: score 304.8, E = 1.9e-88
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           L  L     s +  +++ + L+l   L+Di + +  ++  E
  gi|1489850     1    ---MSLQKLE--NYS-NKSVVKEEVLILTELLeDITKNMLAPETFEK 41

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +    Els +    +D + L+ L   +tsL   + + + + ++ +  L n
  gi|1489850    42 IIQLKELSTQ----EDYQGLNRL---VTSLSNDEMVYISRYFSILPLLIN 84

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   + E+v+lAy    +     D+    s t          kLv       e
  gi|1489850    85 ISEDVDLAYEINHQNNIDQDYLGKLSTTI---------KLVAEK----EN 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     e L    v  vltAHPtq  R+s+L     i   L +     +    K
  gi|1489850   122 AVEILEHLNVVPVLTAHPTQVQRKSMLDLTNHIHSLLRKYRDVKLGLINK 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                         L R i     tD iR  +     E+   m Y+     k vP
  gi|1489850   172 DKWHNDLRRYIEIIMQTDMIREKKLKVTNEITNAMEYYNSSFLKAVPHLT 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                          +  G+n +   ++  i    W+GGDRDG nP vt    +   L
  gi|1489850   222 TEYKRLAQAHGLNLK---QAKPITMGMWIGGDRDG-NPFVTAKTLKQSAL 267

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                       +  n Y  ++  L  E+s+      +     E+ r ++ +     Y
  gi|1489850   268 TQCEVIMNYYDKKIYQLYREFSLSTSIVNVSKQVREMARQSKDN---SIY 314

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                    E        E YR  L d+  K+  t+          i +      y
  gi|1489850   315 RE-------KELYRRALFDIQSKIQATK-------TYLIEDEEVGTRYET 350

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     +F   L     sL e     +  G  ++lL  v  FG  L  +D+Rq+
  gi|1489850   351 ANDFYKDLIAIRDSLLENKGESLISGDFVELLQAVEIFGFYLASIDMRQD 400

                   seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK.RPLlgsDLP
                   s      +  + +  +i s+Y e sEe + + Ll EL+  +R L
  gi|1489850   401 SSVYEACVAELLKSAGIHSrYSELSEEEKCDLLLKELEEDpRILSATHAE 450

                   ktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLqRE
                   k E ++++  +  + rvL ++L  D     iis at+ sD+L   +L +E
  gi|1489850   451 KSELLAkelAIFKTARVLKDkLGDDVIRQTIISHATSLSDMLELAILLKE 500

                   Cgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                    g+ ++++  +++vPLFE + DL+    ++ k  s+   +  id +++ q
  gi|1489850   501 VGLvdteRARVQIVPLFETIEDLDHSEETMRKYLSLSLAKKWIDSRnnyQ 550

                   evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                   e+m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGRGGtv
  gi|1489850   551 EIMLGYSDSNKDGGYLSSCWTLYKAQQQLTAIGDEFGVKVTFFHGRGGTV 600

                   GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                   GRGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
  gi|1489850   601 GRGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLV 650

                   AAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                    A +   +    s  +++  +  +m+++     + YR +v+    F +YF
  gi|1489850   651 SAAINRMITQKKSDTntpNRYEAIMDQVVDRSYDIYRDLVFGNEHFYDYF 700

                   RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                       P       niGsRPa Rk    i  LRAiPW+F+W q R   P W
  gi|1489850   701 FESSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWY 750
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                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    GvG  FK  i+K   n+  L++mY++WPFF   l  ++mv  K    iA
  gi|1489850   751 GVGSSFKEFINKNPENIAILRDMYQNWPFFQSLLSNVDMVLSKSNMNIAF 800

                    LyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                     y kL   E++k   + + ++++ tk+ +L i GH +lL   PYLK  l
  gi|1489850   801 EYAKLCEDEQVKAIYETILNEWQVTKNVILAIEGHDELLADNPYLKASLD 850

                    LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                     R +Y   Ln +q   +KR R        r +ls +  +E       L++
  gi|1489850   851 YRMPYFNILNYIQLELIKRQR--------RGELSSD--QER------LIH 884

                    LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +                + GiA G+ n G
  gi|1489850   885 IT----------------INGIATGLRNSG    898

gi|168576207|ref|ZP_02722101.1|: domain 1 of 1, from 1 to 898: score 304.4, E = 2.4e-88
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                            L  L     s +  +++ + L+l   L+Di + +  ++  E
  gi|1685762     1    ---MSLQKLE--NYS-NKSVVKEEVLILTELLeDITKNMLAPETFEK 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +    Els +    +D + L+ L   +tsL   + + + + ++ +  L n
  gi|1685762    42 IIQLKELSTQ----EDYQGLNRL---VTSLSNDEMVYISRYFSILPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+    s t          kLv       e
  gi|1685762    85 ISEDVDLAYEINHQNNIDQDYLGKLSTTI---------KLVAEK----EN 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      e L    v  vltAHPtq  R+s+L     i   L +     +    K
  gi|1685762   122 AVEILEHLNVVPVLTAHPTQVQRKSMLDLTNHIHSLLRKYRDVKLGLINK 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                          L R i     tD iR  +     E+   m Y+     k vP
  gi|1685762   172 DKWHNDLRRYIEIIMQTDMIREKKLKVTNEITNAMEYYNSSFLKAVPHLT 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                           +  G+n +   ++  i    W+GGDRDG nP vt    +   L
  gi|1685762   222 TEYKRLAQAHGLNLK---QAKPITMGMWIGGDRDG-NPFVTAKTLKQSAL 267

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                        +  n Y  ++  L  E+s+      +     E+ r ++ +     Y
  gi|1685762   268 TQCEVIMNYYDKKIYQLYREFSLSTSIVNVSKQVREMARQSKDN---SIY 314

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                     E        E YR  L d+  K+  t+          i +      y
  gi|1685762   315 RE-------KELYRRALFDIQSKIQATK-------TYLIEDEEVGTRYET 350

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      +F   L     sL e     +  G  ++lL  v  FG  L  +D+Rq+
  gi|1685762   351 ANDFYKDLIAIRDSLLENKGESLISGDFVELLQAVEIFGFYLASIDMRQD 400

                    seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK.RPLlgsDLP
                    s      +  + +  +i s+Y e sEe + + Ll EL+  +R L
  gi|1685762   401 SSVYEACVAELLKSAGIHSrYSELSEEEKCDLLLKELEEDpRILSATHAE 450

                    ktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLqRE
                    k E ++++  +  + rvL ++L  D     iis at+ sD+L    +L +E
  gi|1685762   451 KSELLAkelAIFKTARVLKDkLGDDVIRQTIISHATSLSDMLELAILLKE 500

                    Cgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                     g+ ++++  +++vPLFE + DL+    ++ k  s+   +  id +++ q
  gi|1685762   501 VGLvdteRARVQIVPLFETIEDLDHSEETMRKYLSLSLAKKWIDSRnnyQ 550

                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                    e+m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGRGGtv
  gi|1685762   551 EIMLGYSDSNKDGGYLSSCWTLYKAQQQLTAIGDEFGVKVTFFHGRGGTV 600

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                    GRGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
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  gi|1685762   601 GRGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLV 650

                   AAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                    A +   +    s  +++  +  +m+++     + YR +v+    F +YF
  gi|1685762   651 SAAINRMITQKKSDTntpNRYEAIMDQVVDRSYDIYRDLVFGNEHFYDYF 700

                   RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                       P       niGsRPa Rk    i  LRAiPW+F+W q R   P W
  gi|1685762   701 FDSSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWY 750

                   GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                   GvG  FK  i+K   n+  L++mY++WPFF   l  ++mv  K    iA
  gi|1685762   751 GVGSSFKEFINKNPENIAILRDMYQNWPFFQSLLSNVDMVLSKSNMNIAF 800

                   LyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                    y kL   E++k   + + ++++ tk+ +L i GH +lL   PYLK  l
  gi|1685762   801 EYAKLCEDEQVKAIYETILNEWQVTKNVILAIEGHDELLADNPYLKASLD 850

                   LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                    R +Y   Ln +q   +KR R        r +ls +  +E       L++
  gi|1685762   851 YRMPYFNILNYIQLELIKRQR--------RGELSSD--QER------LIH 884

                   LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   +                 + GiA G+ n G
  gi|1685762   885 IT----------------INGIATGLRNSG    898

gi|169833797|ref|YP_001694494.1|: domain 1 of 1, from 1 to 898: score 303.9, E = 3.4e-88
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                          L  L     s +  +++ + L+l   L+Di + +  ++  E
  gi|1698337     1    ---MSLQKLE--NYS-NKSVVKEEVLILTELLeDITKNMLAPETFEK 41

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +    Els +    +D + L+ L   +tsL   + + + + ++ +  L n
  gi|1698337    42 IIQLKELSTQ----EDYQGLNRL---VTSLSNDEMVYISRYFSILPLLIN 84

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   + E+v+lAy    +     D+    s t          kLv       e
  gi|1698337    85 ISEDVDLAYEINHQNNIDQDYLGKLSTTI---------KLVAEK----EN 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     e L    v  vltAHPtq  R+s+L     i   L +     +    K
  gi|1698337   122 AVEILEHLNVVPVLTAHPTQVQRKSMLDLTNHIHSLLRKYRDVKLGLINK 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                         L R i     tD iR  +     E+   m Y+     k vP
  gi|1698337   172 DKWYNDLRRYIEIIMQTDMIREKKLKVTNEITNAMEYYNSSFLKAVPHLT 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                          +  G+n +   ++  i    W+GGDRDG nP vt    +   L
  gi|1698337   222 TEYKRLAQAHGLNLK---QAKPITMGMWIGGDRDG-NPFVTAKTLKQSAL 267

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                       +  n Y  ++  L  E+s+      +     E+ r ++ +     Y
  gi|1698337   268 TQCEVIMNYYDKKIYQLYREFSLSTSIVNVSKQVREMARQSKDN---SIY 314

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                    E        E YR  L d+  K+  t+          i +      y
  gi|1698337   315 RE-------KELYRRALFDIQSKIQATK-------TYLIEDEEVGTRYET 350

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     +F   L     sL e     +  G  ++lL  v  FG  L  +D+Rq+
  gi|1698337   351 ANDFYKDLIAIRDSLLENKGESLISGDFVELLQAVEIFGFYLASIDMRQD 400

                   seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK.RPLlgsDLP
                   s      +  + +  +i s+Y e sEe + + Ll EL+  +R L
  gi|1698337   401 SSVYEACVAELLKSAGIHSrYSELSEEEKCDLLLKELEEDpRILSATHAE 450

                   ktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLqRE
                   k E ++++  +  + rvL ++L  D     iis at+ sD+L   +L +E
  gi|1698337   451 KSELLAkelAIFKTARVLKDkLGEDVIRQTIISHATSLSDMLELAILLKE 500
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                    Cgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                     g+ ++++  +++vPLFE + DL+    ++ k  s+   +  id +++ q
  gi|1698337   501 VGLvdteRARVQIVPLFETIEDLDHSEETMRKYLSLSLAKKWIDSRnnyQ 550

                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                    e+m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGRGGtv
  gi|1698337   551 EIMLGYSDSNKDGGYLSSCWTLYKAQQQLTAIGDEFGVKVTFFHGRGGTV 600

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                    GRGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
  gi|1698337   601 GRGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLV 650

                    AAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                     A +   +    s  +++  +  +m+++     + YR +v+    F +YF
  gi|1698337   651 SAAINRMITQKKSDTntpNRYEAIMDQVVDRSYDIYRDLVFGNEHFYDYF 700

                    RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                        P       niGsRPa Rk    i  LRAiPW+F+W q R   P W
  gi|1698337   701 FESSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWY 750

                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    GvG  FK  i+K   n+  L++mY++WPFF   l  ++mv  K    iA
  gi|1698337   751 GVGSSFKEFINKNPENIAILRDMYQNWPFFQSLLSNVDMVLSKSNMNIAF 800

                    LyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                     y kL   E++k   + + ++++ tk+ +L i GH +lL   PYLK  l
  gi|1698337   801 EYAKLCEDEQVKAIYETILNEWQVTKNVILAIEGHDELLADNPYLKASLD 850

                    LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                     R +Y   Ln +q   +KR R        r +ls +  +E       L++
  gi|1698337   851 YRMPYFNILNYIQLELIKRQR--------RGELSSD--QER------LIH 884

                    LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +                + GiA G+ n G
  gi|1698337   885 IT----------------INGIATGLRNSG    898

gi|206560970|ref|YP_002231735.1|: domain 1 of 1, from 38 to 989: score 303.7, E = 3.9e-88
                    *->siDAqLR.lLvP..GKvsedek...LieYDALLlDkFL.DiLqDLHG
                       +  A  R++++P+ G    d+k+++L e D   l + L+D++ +  G
  gi|2065609    38    AAGAPARkAVAPkaGTRTRDDKdgpLFE-DIRFLGRLLgDVVREQEG 83

                    edLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailH
                    + + ++v      +  +    D++  + L  kL  L P  ++ v +a++
  gi|2065609    84 DTVFDVVETIRQTAVKFRREDDSEAAQTLEKKLRKLTPEQTVSVVRAFSY 133

                    mLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkl
                       LAn+AE+ +   RRRi+ +        +sA     +   l +L   +
  gi|2065609   134 FSHLANIAEDRHHNRRRRIHALA-------GSAPQPGTVAYALDQLKTTG 176

                    nKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKD
                    n s            +  vltAHPt   R+s+L  +  i   La    ++
  gi|2065609   177 NASKRLLQRFFDDALIVPVLTAHPTEVQRKSILDAQHDIARLLAE-RDQE 225

                    vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWk
                    +t  +++  +  L   + A + t  +R ++ t  DE+   +sY+  t  +
  gi|2065609   226 LTARERQYNEAMLRARVTALWQTRMLRDSRLTVGDEIENALSYYRATFLD 275

                    GvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEv
                      P     ++ AL   G+  R+P       +  sW+GGDRDG nP vt
  gi|2065609   276 ELPALYGDIEAALAEHGLSARVP---AFFQMGSWIGGDRDG-NPNVTAAT 321

                    tRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaard
                      +       +    Y++qv  L  Els+    + L v A +  +  a
  gi|2065609   322 LDEAINRQAAVILEHYLEQVHKLGAELSV----SNLLVGANDAVKALAAA 367

                    kvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                               q P++  EPYR  L  +  +L      aR  L  G   +
  gi|2065609   368 --------SPDQSPhrVDEPYRRALIGIYTRLAAS---ARVRLGEGTVPV 406

                    ........sEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLR
                    ++ +++ ++  A++y + E F+  L +   sL e     +A   L  l+R
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  gi|2065609   407 rsagrgapPVRAIpYEDSEAFVADLKVLTASLDEHHGASLAAPRLAPLVR 456

                   qvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWL
                       FG  L  +D+Rq s+ +  v+  +    ++ ++Y   +Ee +   L
  gi|2065609   457 AAEVFGFHLASIDLRQSSDIHEAVVAELFARAGVEAdYAALAEEDKLRVL 506

                   laELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGa.....Yiis
                   la L   RPL  + L      +  l+ f+   E+    FGa+  ++Yiis
  gi|2065609   507 LAALADPRPLRSPYLEYSALAQSELGVFEKAREVRTQ-FGAravrnYIIS 555

                   mataPsDvLAvELLqRECgv............kqtLrvvPLFEkLADLeA
                    + + sD + v LLq+E g+ +++ + ++++ k++L v+PLFE + DL+
  gi|2065609   556 HTETVSDLVEVLLLQKETGLlegtlgvpgrdaKNSLMVIPLFETIPDLRD 605

                   APAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkA
                   A   +   F+ ++iD  i +    qevm+GYsDs KD G l   W LY+A
  gi|2065609   606 ASRIMRDYFAlpgIDALIAHQGAEQEVMLGYSDSNKDGGFLTSNWELYRA 655

                   qEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRv
                      ++   ++  + L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R
  gi|2065609   656 ELALVDLFRERKITLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRL 705

                   tvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv...sPkPEWRkLm
                   t qGEvi   F    +  r L    AAtLE  + P  + ++  P +   m
  gi|2065609   706 TEQGEVIASKFSNPSIGRRNLETVVAATLEASLLPQSnapAQLPAFEAAM 755

                   eemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG
                   + +   A   YR++v+  P F +YF + tP +E   +niGsRPa Rk
  gi|2065609   756 QTLSDSAMAAYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASRKLQD 805

                   ....GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiK
                   ++++ ie LRAiPW F+W q R  L  W G+G A    +d+ ++     K
  gi|2065609   806 pkqrKIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVSAYLDgapdaaERTK 855

                   nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPF
                    +  Lk m k+WPFF   l  ++mv AK D  +A+ y +L+    L+k
  gi|2065609   856 RVTLLKKMNKTWPFFSNLLSNMDMVLAKTDLAVASRYAQLVSDRKLrKHV 905

                   GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                    +++ ++++ t + L +i GH   L   P L   ++ R +Y+  Ln +q
  gi|2065609   906 FERIVAEWERTSQALAEITGHEGRLATNPLLARSIKNRFPYLDPLNHLQV 955

                   YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                     +KR R               A +           n   r   G+
  gi|2065609   956 ELIKRHR----------------AGDT----------N--ARLRRGIH-- 975

                   LiLtmKGiAAGmqntG<-*
                     Lt+ GiAAG+ ntG
  gi|2065609   976 --LTINGIAAGLRNTG    989

gi|149925330|ref|ZP_01913594.1|: domain 1 of 1, from 1 to 919: score 303.4, E = 4.7e-88
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +  qL         e +  ++ D  Ll   L++i+ +  G  +  a
  gi|1499253     1    -MNKQLND------EEKDSQLRDDIRLLGALLgEIIAEQQGLPVFAA 40

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   + E   ls +Y    D      L a+L +L   ++i + ++++    L n
  gi|1499253    41 IEEVRQLSVQYRRFDDNAARTKLEARLEALTQDETISLIRSFSIFSMLSN 90

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE+ +l  R R + +        +    E+ ++ t+  L   +    +
  gi|1499253    91 IAEDCHLIRRNRQHELA-------GMPAREASLDYTIAELSRVG-VNRDA 132

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   v   LK      vltAHPt   R+s+L  +  i   +       +t e+
  gi|1499253   133 VLARLKKTESVPVLTAHPTEVQRKSVLDAQQSIIALIRHRDEIQLTLEEA 182

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                       + L   +q  F t  +RR +    DE+   ++Y+  t +  vP+
  gi|1499253   183 NAWRDELKAAVQRLFQTRLLRRNKLSVIDEVNNALAYFDSTFFAQVPQVY 232
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                    RRvDtALKniGinERlPYdv.PL...ikFssWmGGDRDGknPRvtPEvtR
                    R+    L        lP + +PL++ +   sW+GGDRDG nP vt  v
  gi|1499253   233 RKLQSLLSLPSTDNFLPVNEdPLgkvLTVGSWIGGDRDG-NPFVTAQVLD 281

                    DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                        +        Y+  v  L+ E+s+            +l  t+  d
  gi|1499253   282 TTLKIQSSKVLEHYLAEVNCLIREFSVTDYFLKPNPPLTDLANTSGED-- 329

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                      + ++        E  R    ++R +L  t       L + +
  gi|1499253   330 SAHRMD--------ETLRRACVAIRNRLQAT-------LQQAVQGECTAQ 364

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                     y      L  L   + +L e G + iA+G L  l R+v  FG sL+ LD
  gi|1499253   365 AYSSPAGLLSDLNTLFSALSENGMQRIAEGRLALLARKVKVFGFSLMALD 414

                    iRqEseRqtDvlDAittH..LeiGsYReWsEeKRqEWLlaELkGKRPLlg
                    +Rq s+    v+  + + ++L+   Y   sE  R   L aEL+  R L+
  gi|1499253   415 LRQNSDVFEAVVADLLKQstLGKTDYLASSEAERVALLCAELRTPRLLFS 464

                    sDLPktEEvkDvldafr..vLAE..LPiDsFGaYiismataPsDvLAvEL
                      L   E     +  fr+  LA + L + +    iis + + sD L   +
  gi|1499253   465 DSLQYSERTHSEMAIFRkaKLAHqvLGVSAIQNCIISKTASVSDLLELAV 514

                    LqRECgv......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                    L +E ++ +  ++  ++ +vPLFE + DL+AAPA ++ LF i  Y+  +
  gi|1499253   515 LLKEAHLlnvatgELAVNIVPLFETIEDLQAAPAIMATLFDIAEYRALVA 564

                    GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                     +++ qevm+GYsDs KD G +   W LY+A   ++ v  k+G+K+ lFH
  gi|1499253   565 SRghvQEVMLGYSDSNKDGGFVTSGWSLYQAEIGLVDVFAKHGIKIRLFH 614

                    GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                    GRGG vGRGGG    AiL qPP  ++G +R t qGEvi   +G E L  r
  gi|1499253   615 GRGGSVGRGGGSSYHAILGQPPGAVDGRIRLTEQGEVIAAKYGIESLGRR 664

                    sLqRFtAAtLEHGmnPPvsPkP..EWRkLmeemAvvAtEEYRsvvvKEPR
                     L     A L    +  +    ++ + +Lm ++   A   YR +v+
  gi|1499253   665 NLEVLVSANLMVSEHTELTREVpsKYLELMAKLSNHAFNAYRDLVYNTDG 714

                    FvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFH
                    F EYF+  t   E   +niGsRPa Rk    ie LRAiPW+F+W q R
  gi|1499253   715 FLEYFKQSTVISEIASLNIGSRPASRKANWTIEDLRAIPWVFSWAQSRVM 764

                    LPvWLGvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                    LP W G+G A  +          l  L+ m k+WPFF   l  l mv AK
  gi|1499253   765 LPGWYGFGIAVAtLRSSLTEAELLDLQAMAKQWPFFNTMLSTLNMVLAKA 814

                    DPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                    D  iA+ y  ++   eL++k FG+ + ++     + LL + G  +lL
  gi|1499253   815 DMAIASRYAAMVEDAELreKVFGR-IAAEHARAVEGLLWLTGQEELLSDN 863

                    PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                    P LK  +  R +Y+  Ln +q   L+R R  +              dE
  gi|1499253   864 PLLKRSIEARFPYVDPLNHVQVELLRRHRQGEL-------------DER- 899

                    kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       +  v+L                 + GiA G+ n G
  gi|1499253   900 --VARGVHLS----------------INGIATGLRNSG    919

gi|258654566|ref|YP_003203722.1|: domain 1 of 1, from 25 to 945: score 303.4, E = 4.8e-88
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         DA LR+ v    s           L+ +    L DL  e+++
  gi|2586545    25    DRDAALRADVRRVGS------LLGQTLVRQQGPELLDLV-EQVRGLT 64

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    +   E +A  E +  t K+ E+   L +L  a a  + +a+     LAn
  gi|2586545    65 KQSREAAAATERQSATLKVREM---LAALPIAVATELVRAFATYFQLANG 111

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE v   +  R  + +  +  D+  A    +i  tl      +  +  E
```

```
gi|2586545   112 AEQV---HQVRELRAR--ETGDDHLAAVVQEIVTTL------GTDALREA 150

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   eAL  q    v+tAHPt + RRs+L K   +   L            ++
gi|2586545   151 VEALEVQP---VFTAHPTEASRRSVLLKLQALADILVVPTPAGSAARTRQ 197

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    D  L   i   + tDEiR  +PtP DE R  + Y+   v + +P
gi|2586545   198 --DRKLAEVIDLLWQTDEIRQFRPTPVDEARNALFYLEAIVGDTIPALTD 245

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                      A+   G+ E  P   PL+   sW+GGDRDG nP vt  vtR+v  L
gi|2586545   246 DLAAAMAQHGV-ELSPEATPLL-LGSWIGGDRDG-NPNVTAAVTREVLAL 292

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                      A  + i ++++L+  ls       +    +El    + d    +
gi|2586545   293 QHQSAIAIAIGKIDELLLALS---SSTVIAGASDELVASIRTD--LDHLP 337

                  EF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                    +++ K +   EP R  L  v+ KL ntR R     A+   e   +  y
gi|2586545   338 LLdprVKELNKDEPIRLKLTCVKAKLINTRARVNAGRAH---EPGRD--Y 382

                  tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                      e L  L +  +sL + G    A G L    R     GL +  +DiR
gi|2586545   383 ASKGELLADLAIVHRSLEQHGGALAAAGILATAQRALAVSGLNVAYMDIR 432

                  qEseRqtDvlDAittHLeiGs..YReWsEeKRqEWLlaELkGKRPLlgsD
                    se +  v+  +   L+   ++Y + s  +R+ WL  EL   RPL
gi|2586545   433 EHSEAHHQVIAQLVDRLGELDrpYDSMSRPQRMRWLSKELTSHRPL--TT 480

                  LPktEEvkDvldafrvLAEL..PiDsFGa.....YiismataPsDvLAvE
                  LP   + +    +f v  E+++   ++G++   +Yi sm+    D+LA
gi|2586545   481 LPAPLDAAGT-KTFSVFSEIkdAQATYGPevivtYITSMTMGADDILAAA 529

                  LLqRECgv...........kqtLrvv...PLFEkLADLeAAPAavekLFs
                  +L RE g+ +  ++++++++ +   ++  PL E + +L+     v+ L s
gi|2586545   530 VLAREAGLidvygtpgdptRGPFAAIgfaPLLETVEELRKSAEVVDELLS 579

                  iDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKk
                     Y+  +  +++ qe+m+GYsDs K  G     W + k    +   A +
gi|2586545   580 DPTYREIVRLRgdvQEIMLGYSDSNKQSGITTSQWEIHKTERLLRDLAAR 629

                  yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                  +Gv L+lFHGRGGtvGRGGGPt   iL+qP   i G+++ t qGEvi
gi|2586545   630 HGVSLTLFHGRGGTVGRGGGPTYDSILAQPYGVITGAIKFTEQGEVISGK 679

                  FGEEnLCFrsLqRFtAAtLEHGmnPPvsPkP.....EWRkLmeemAvvAt
                  +G  +L    L    AAtL        s +  ++ ++W + me++   A
gi|2586545   680 YGMPDLAKENLALTVAATLRATTLHTESRQTaqelrDWDQWMEQVSDAAF 729

                  EEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKR.kPsGGiesLRA
                    Y  ++  +P    YF   tP    G++niGsRPa+R+  +GGi  LRA
gi|2586545   730 AAYVGLI-DDPDLPAYFLASTPTEQLGQLNIGSRPARRpDSGGGIGGLRA 778

                  iPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRv
                  iPW+F Wtq R  +P W GvG   + A  ++    q+L+ m ++W FFR
gi|2586545   779 IPWVFGWTQSRQIVPGWFGVGSGLRAA--REAGGEQMLRTMHRKWHFFRT 826

                  tlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLki
                   +  +Em  AK D GiAa+y + Lv   L+   + ++++   t   +L++
gi|2586545   827 FISNVEMTLAKTDMGIAAMYVESLVPAPLRRLFEVIKAEHDLTVAEVLRV 876

                  AGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPh
                   G  +lL+  P LK  l +R++Y+  +  +q   L RiR
gi|2586545   877 TGEAELLDDQPALKRTLGVREPYLAPISYLQVDLLNRIRSQ--------- 917

                  lsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-
                       AdE+               v P L   ++Lt+ G+AAGm ntG
gi|2586545   918 -----ADEQ---------------VDPQLRRAMLLTINGVAAGMRNTG   945

                  *
```

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  gi|2586545     -   -

gi|78067222|ref|YP_369991.1|: domain 1 of 1, from 58 to 1008: score 302.4, E = 9.8e-88
                   *->siDAqLRlLvP...GKvsedekLieYDAL.LlDkFL.DiLqDLHGed
                      +  A   + +P+++ +  ed +   +D ++ l + L+D++ +  G+
  gi|7806722    58    ARTAARTAAAPksgTRTREDKDGPLFDDIrFLGRLLgDVVREQEGDT 104

                   LkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmL
                   + ++v      +  +    D++  + L  kL  L P  ++ v +a++
  gi|7806722   105 VFDVVETIRQTAVKFRREDDSEAAQTLEKKLRKLTPEQTVSVVRAFSYFS 154

                   nLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnK
                    LAn+AE+ +   RRRi+ +        +sA     +   l +L   +n
  gi|7806722   155 HLANIAEDRHHNRRRRIHALA-------GSASQPGTVAYALEQLKTTGNA 197

                   sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt
                   s            +  vltAHPt   R+s+L  +  i   La    +++t
  gi|7806722   198 SKRLLQRFFDDALIVPVLTAHPTEVQRKSILDAQHDIARLLAE-RDQELT 246

                   veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGv
                     +++  +  L   + A + t  +R a+ t  DE+   +sY+  t  +
  gi|7806722   247 GRERQYNESMLRARVTALWQTRMLRDARLTVGDEIENALSYYRATFLDEL 296

                   PKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                   P     ++ AL   G+  R+P      +  sW+GGDRDG nP vt
  gi|7806722   297 PALYGDIEAALAEHGLSARVP---AFFQMGSWIGGDRDG-NPNVTAPTLE 342

                   DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                   +       +    Y++qv  L  Els+    + L v A +  +  a
  gi|7806722   343 EAINRQAAVILEHYLEQVHKLGAELSV----SNLLVGANDAVKALAAA-- 386

                   vKyYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER....aRHLLAtGi
                            q P++  EPYR  L  +  +L  + R R ++++  +   G
  gi|7806722   387 ------SPDQSPhrVDEPYRRALIGIYTRLAAsARVRlgegTVPVRSAGR 430

                   seisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstF
                      +  A +y + E F+  L +   sL e     +A   L  l+R    F
  gi|7806722   431 GAAPVRATpYADSEAFVADLKVLTASLDEHHGTSLAAPRLAPLVRAAEVF 480

                   GLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELk
                   G  L  +D+Rq s+ +  v+  +    ++ ++Y   +Ee +   Lla L
  gi|7806722   481 GFHLASIDLRQSSDIHEAVVAELFARAGVEAdYAALAEEDKLRVLLAALA 530

                   GKRPLlgsDLPktEEvkDvldaf....rvLAELPiDsFGaYiismataPs
                     RPL  +        +  l+ f++ ++v A     +   Yiis + + s
  gi|7806722   531 DPRPLRSPYFEYSALAQSELGVFekarEVRAQFGARAVRNYIISHTETVS 580

                   DvLAvELLqRECgv.............kqtLrvvPLFEkLADLeAAPAave
                   D + v LLq+E g+ ++  + ++++ k++L v+PLFE + DL+ A   +
  gi|7806722   581 DLVEVLLLQKETGLldgalgvpggdaKNSLMVIPLFETIPDLRDAARIMR 630

                   kLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiK
                     F+ ++iD  i +    qevm+GYsDs KD G l   W LY+A   ++
  gi|7806722   631 EYFAlpgIDALIAHQGAEQEVMLGYSDSNKDGGFLTSNWELYRAELALVD 680

                   vAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEv
                     ++  + L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGEv
  gi|7806722   681 LFRDRKITLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEV 730

                   iEfsFGEEnLCFrsLqRFtAAtLEHGmnP...PvsPkPEWRkLmeemAvv
                   i   F   ++  r L    AAtLE  + P+++  +  P +   m+ +
  gi|7806722   731 IASKFANPEIGRRNLETVVAATLEATLLPqnnAPAQLPAFEAAMQTLSDS 780

                   AtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....Gi
                   A   YR++v+  P F +YF + tP +E   +niGsRPa Rk   ++++ i
  gi|7806722   781 AMAAYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASRKLQDpkqrKI 830

                   esLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiKnlqkLk
                   e LRAiPW F+W q R  L  W G+G A    +d+ +++    K +  Lk
  gi|7806722   831 EDLRAIPWGFSWGQCRLLLTGWYGFGSAVSAYLDgaqddaERTKRVALLK 880
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                    EmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRd
                     m k+WPFF   l  ++mv AK D  +A+ y +L+    L+k   +++ +
  gi|7806722   881 KMNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVSDRKLrKHVFERIVA 930

                    kYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRi
                    +++ t + L +i GH   L   P L   ++ R +Y+  Ln +q   +KR
  gi|7806722   931 EWERTSQALAEITGHEGRLATNPLLARSIKNRFPYLDPLNHLQVELIKRH 980

                    RDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmK
                    R               A +           n   r   G+     Lt+
  gi|7806722   981 R----------------AGDT----------N--ARLRRGIH----LTIN 998

                    GiAAGmqntG<-*
                    GiAAG+ ntG
  gi|7806722   999 GIAAGLRNTG    1008

gi|116690446|ref|YP_836069.1|: domain 1 of 1, from 59 to 1009: score 302.2, E = 1.1e-87
                    *->siDAqLRlLvP..GKvsedek...LieYDALLlDkFL.DiLqDLHGe
                          A   +++P+ G    d+k+++L e D   l + L+D++ +  G+
  gi|1166904    59    TSPAARNAVAPkaGTRTRDDKdgpLFE-DIRFLGRLLgDVVREQEGD 104

                    dLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHm
                     + ++v      +  +    D++  + L  kL  L P  ++ v +a++
  gi|1166904   105 TVFDVVETIRQTAVKFRREDDSEAAQTLEKKLRKLTPEQTVSVVRAFSYF 154

                    LnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkln
                      LAn+AE+ +   RRRi+ +        +sA     +   l +L   +n
  gi|1166904   155 SHLANIAEDRHHNRRRRIHALA-------GSAPQPGTVAYALDQLKTTGN 197

                    KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                     s            +  vltAHPt   R+s+L  +  i   La    +++
  gi|1166904   198 ASKRLLQRFFDDALIVPVLTAHPTEVQRKSILDAQHDIARLLAE-RDQEL 246

                    tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                    t  +++  +  L   + A + t  +R a+ t  DE+   +sY+  t  +
  gi|1166904   247 TARERQYNETMLRARVTALWQTRMLRDARLTVGDEIENALSYYRATFLDE 296

                    vPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                     P     ++ AL   G+  R+P      +  sW+GGDRDG nP vt
  gi|1166904   297 LPALYGDIEAALAEHGLSARVP---AFFQMGSWIGGDRDG-NPNVTAATL 342

                    RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk
                     +       +    Y++qv  L  Els+    + L v A +  +  a
  gi|1166904   343 DEAINRQAAVILEHYLEQVHKLGAELSV----SNLLVGANDAVKALAAA- 387

                    vvKyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGisei.
                               q P++  EPYR  L  +  +L      aR  L  G   ++
  gi|1166904   388 -------SPDQSPhrVDEPYRRALIGIYTRLAAS---ARVRLGEGTVPVr 427

                    .......sEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                    + +++ ++  A++y + E F+  L +   sL e     +A   L  l+R
  gi|1166904   428 sagrgapPVRAIpYEDSEAFVADLKMLTASLDEHHGASLAAPRLAPLVRA 477

                    vstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLl
                       FG  L  +D+Rq s+ +  v+  +    ++ ++Y   +Ee +   Ll
  gi|1166904   478 AEVFGFHLASIDLRQSSDIHEAVVAELFARAGVEAdYAALAEEDKLRVLL 527

                    aELkGKRPLlgsDLPktEEvkDvldaf....rvLAELPiDsFGaYiisma
                    a L   RPL  + L      +  l+ f++ ++v A     +   Yiis +
  gi|1166904   528 AALADPRPLRSPYLEYSALAQSELGVFekarEVRAQFGARAVRNYIISHT 577

                    taPsDvLAvELLqREC............gvkqtLrvvPLFEkLADLeAAP
                     + sD + v LLq+E +  +++ + ++++ k++L v+PLFE + DL+ A
  gi|1166904   578 ETVSDLVEVLLLQKETgllegtlgvpgsHAKNSLMVIPLFETIPDLRDAS 627

                    AavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqE
                      +   F+ ++iD  i +    qevm+GYsDs KD G l   W LY+A
  gi|1166904   628 RIMRDYFAlpgIDALIAHQGAEQEVMLGYSDSNKDGGFLTSNWELYRAEL 677

                    EiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtv
```

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                     ++   ++  + L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t
  gi|1166904   678 ALVDLFRERKITLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTE 727

                    qGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv...sPkPEWRkLmee
                    qGEvi   F    +  r L    AAtLE  + P  + ++  P +   m+
  gi|1166904   728 QGEVIASKFSNPSIGRRNLETVVAATLEASLLPQSnapAQLPAFEAAMQT 777

                    mAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG..
                    +   A   YR++v+  P F +YF + tP +E   +niGsRPa Rk   ++
  gi|1166904   778 LSDSAMAAYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASRKLQDpk 827

                    ..GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiKnl
                    ++ ie LRAiPW F+W q R  L  W G+G A    +d+ +++    K +
  gi|1166904   828 qrKIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVSAYLDgaqddaERAKRV 877

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGk
                      Lk m k+WPFF   l  ++mv AK D  +A+ y +L+    L+k   +
  gi|1166904   878 TLLKKMNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVSDRKLrKHVFE 927

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    ++ ++++ t   L +i G    L   P L   ++ R +Y+  Ln +q
  gi|1166904   928 RIVAEWERTSRALAEITGQEGRLATNPLLARSIKNRFPYLDPLNHLQVEL 977

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    +KR R               A +           n   r   G+
  gi|1166904   978 IKRHR----------------AGDT----------N--ARLRRGIH---- 995

                    LtmKGiAAGmqntG<-*
                    Lt+ GiAAG+ ntG
  gi|1166904   996 LTINGIAAGLRNTG    1009

gi|107023363|ref|YP_621690.1|: domain 1 of 1, from 44 to 994: score 302.2, E = 1.1e-87
                    *->siDAqLRlLvP..GKvsedek...LieYDALLlDkFL.DiLqDLHGe
                          A   +++P+ G    d+k+++L e D   l + L+D++ +  G+
  gi|1070233    44    TSPAARNAVAPkaGTRTRDDKdgpLFE-DIRFLGRLLgDVVREQEGD 89

                    dLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHm
                     + ++v      +  +    D++  + L  kL  L P  ++ v +a++
  gi|1070233    90 TVFDVVETIRQTAVKFRREDDSEAAQTLEKKLRKLTPEQTVSVVRAFSYF 139

                    LnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkln
                      LAn+AE+ +   RRRi+ +        +sA     +   l +L   +n
  gi|1070233   140 SHLANIAEDRHHNRRRRIHALA-------GSAPQPGTVAYALDQLKTTGN 182

                    KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                     s            +  vltAHPt   R+s+L  +  i   La    +++
  gi|1070233   183 ASKRLLQRFFDDALIVPVLTAHPTEVQRKSILDAQHDIARLLAE-RDQEL 231

                    tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                    t  +++  +  L   + A + t  +R a+ t  DE+   +sY+  t  +
  gi|1070233   232 TARERQYNETMLRARVTALWQTRMLRDARLTVGDEIENALSYYRATFLDE 281

                    vPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                     P     ++ AL   G+  R+P      +  sW+GGDRDG nP vt
  gi|1070233   282 LPALYGDIEAALAEHGLSARVP---AFFQMGSWIGGDRDG-NPNVTAATL 327

                    RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk
                     +       +    Y++qv  L  Els+    + L v A +  +  a
  gi|1070233   328 DEAINRQAAVILEHYLEQVHKLGAELSV----SNLLVGANDAVKALAAA- 372

                    vvKyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGisei.
                              q P++  EPYR  L  +  +L      aR  L  G   ++
  gi|1070233   373 -------SPDQSPhrVDEPYRRALIGIYTRLAAS---ARVRLGEGTVPVr 412

                    .......sEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                    + +++ ++  A++y + E F+  L +   sL e     +A   L  l+R
  gi|1070233   413 sagrgapPVRAIpYEDSEAFVADLKMLTASLDEHHGASLAAPRLAPLVRA 462

                    vstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLl
                       FG  L  +D+Rq s+ +  v+  +    ++ ++Y   +Ee +   Ll
  gi|1070233   463 AEVFGFHLASIDLRQSSDIHEAVVAELFARAGVEAdYAALAEEDKLRVLL 512
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                    aELkGKRPLlgsDLPktEEvkDvldaf....rvLAELPiDsFGaYiisma
                    a L   RPL  + L      +  l+ f++ ++v A     +   Yiis +
  gi|1070233   513 AALADPRPLRSPYLEYSALAQSELGVFekarEVRAQFGARAVRNYIISHT 562

                    taPsDvLAvELLqREC.............gvkqtLrvvPLFEkLADLeAAP
                     + sD + v LLq+E +  +++ + ++++ k++L v+PLFE + DL+ A
  gi|1070233   563 ETVSDLVEVLLLQKETgllegtlgvpgsHAKNSLMVIPLFETIPDLRDAS 612

                    AavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqE
                      +   F+ ++iD  i +    qevm+GYsDs KD G l   W LY+A
  gi|1070233   613 RIMRDYFAlpgIDALIAHQGAEQEVMLGYSDSNKDGGFLTSNWELYRAEL 662

                    EiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtv
                     ++   ++  + L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t
  gi|1070233   663 ALVDLFRERKITLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTE 712

                    qGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv...sPkPEWRkLmee
                    qGEvi   F    +  r L    AAtLE  + P  + ++  P +   m+
  gi|1070233   713 QGEVIASKFSNPSIGRRNLETVVAATLEASLLPQSnapAQLPAFEAAMQT 762

                    mAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG..
                    +   A   YR++v+  P F +YF + tP +E   +niGsRPa Rk   ++
  gi|1070233   763 LSDSAMAAYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASRKLQDpk 812

                    ..GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiKnl
                    ++ ie LRAiPW F+W q R  L  W G+G A    +d+ +++    K +
  gi|1070233   813 qrKIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVSAYLDgaqddaERAKRV 862

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGk
                      Lk m k+WPFF   l  ++mv AK D  +A+ y +L+    L+k   +
  gi|1070233   863 TLLKKMNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVSDRKLrKHVFE 912

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    ++ ++++ t   L +i G    L   P L   ++ R +Y+  Ln +q
  gi|1070233   913 RIVAEWERTSRALAEITGQEGRLATNPLLARSIKNRFPYLDPLNHLQVEL 962

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    +KR R               A +           n   r   G+
  gi|1070233   963 IKRHR----------------AGDT----------N--ARLRRGIH---- 980

                    LtmKGiAAGmqntG<-*
                    Lt+ GiAAG+ ntG
  gi|1070233   981 LTINGIAAGLRNTG    994

gi|237745485|ref|ZP_04575965.1|: domain 1 of 1, from 9 to 957: score 302.0, E = 1.3e-87
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                L   +vs + +    D  +l + L+D++ +  Ge +
  gi|2377454     9    ---SSNHPLSSRQVSPEKE----DIRMLGRMLgDVIREKEGEAIFNL 48

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      +  +    D    + L   L  L    ai v +a++    LAn
  gi|2377454    49 VEKVRRTAVSFRRNPDLYSADTLNNLLRNLSRNQAISVVRAFSYFSHLAN 98

                    LA..EEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                    +A +   +lAyR      k         A     +   l  L   +  +
  gi|2377454    99 IAvdKHANLAYRAARIAGK---------APEKGSLSYALNMLDQSG-VAG 138

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    +E+   L    +  vltAHPt   R+s L  +  i   La     D+t+
  gi|2377454   139 AEIKKLLHETFISPVLTAHPTEVQRKSTLDSEREIARLLAE-HGTDLTPK 187

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++k   E L   i   + t  +R ++    DE+   +sY+  t  +  P
  gi|2377454   188 ERKHNTEMLSARIAGLWQTRLLRYTRLSVADEINNALSYYRITFLRELPE 237

                    FLRRvDtALKniGinERlPYdvP.....LikFssWmGGDRDGknPRvtPE
                        +   +       R    +P+++++ ++  sW+GGDRDG nP v  +
  gi|2377454   238 LYHSIQEEIAERYPESRDGVPAPgseskYLQMGSWIGGDRDG-NPNVNAD 286

                    vtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaar
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                           +   +Y++ +  L  Els+    + +     El  t+
  gi|2377454   287 TMLHALERQSHLIMEFYLEEIHNLGAELSISSLLNHVSPELQELANTSSD 336

                    dkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseis
                         + ++        EPYR  L ++  ++  t  R   +     sei
  gi|2377454   337 T--SLHRVD--------EPYRRALIAIYSRMAAT-ARDYGMTSLSRSEIG 375

                    EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                        y   +eF   L +   sL +     +    L  l   v  FG  L
  gi|2377454   376 VGEAYLSPDEFGKDLQIMIDSLNQNAGGLLVRARLGSLKAAVDIFGFHLA 425

                    KLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPL
                     LD+Rq s+ +  vl  i    ++ + Y + +EeK+ E L+ EL+  R L
  gi|2377454   426 TLDMRQSSDVHERVLTEIFAAAQVEpDYASLPEEKKIELLIGELSKPRLL 475

                    lgsDLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAv
                    + +     EE +  l  +r+ + +       +   Yiis + + sD L v
  gi|2377454   476 YSPFAQYSEETASELKIMRtaryIREQYGKRAITNYIISHTETVSDLLEV 525

                    ELLqRECgvkqt..................LrvvPLFEkLADLeAAPAav
                     LLq+E g+ +++++++   +++ ++ + +L  +PLFE + DL+ A   +
  gi|2377454   526 YLLQKESGLLHPrrnsglaasqqwedaeldLMAIPLFETIPDLRLAATIM 575

                    ekLFsiDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEii
                    +   si + +  i  +++ qevm+GYsDs KD G     W LYkA   ++
  gi|2377454   576 KEAMSIPFIRELIRKQgdlQEVMLGYSDSNKDGGYTTSNWELYKAEKQLV 625

                    KvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGE
                        + GvKL lFHGRGGtvGRGGGPt  AiL+qP  t+nG +R t qGE
  gi|2377454   626 ALFNEMGVKLRLFHGRGGTVGRGGGPTYEAILAQPHGTVNGQIRLTEQGE 675

                    viEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPEWRkL......mee
                    +i   F   ++  r L    AAtLE  + P    k    k+++ ++ +ee
  gi|2377454   676 MIASKFAHAEIGSRNLELLVAATLEASLMPEDQNKKYADKMhdfetaLEE 725

                    mAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi
                    +   A   YR +v+  P F +YF   tP  E   +niGsRPa Rk s  i
  gi|2377454   726 ISALAYQAYRHLVYETPGFTDYFFQSTPIAEIAELNIGSRPASRKSSRRI 775

                    esLRAiPWiFaWtqtRFHLPvWLGvGAAF.KhAidKD..iKn..lqkLkE
                    e LRAiPW F+W q R  LP W G+G A +++  +KD+++Kn+++  L+
  gi|2377454   776 EDLRAIPWSFSWGQCRVLLPGWYGFGSAItQWLDEKDpgVKNrkIALLQS 825

                    mYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk.PFGksLRdk
                    mYkeWPFF   l  ++mv  K D  iA  y +L+    L++    ++ ++
  gi|2377454   826 MYKEWPFFESMLSNMDMVLSKADLAIAYRYSELVTDQKLRdSIFSEICAE 875

                    YvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiR
                     + t +    i   k+ L   P L + l+ R +Yi  Ln +q   +KR R
  gi|2377454   876 HQRTLESFEIITSQKERLVNNPALAKALKDRLAYIDPLNHLQVELIKRHR 925

                    DPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKG
                     P               En         L    r   G+     Lt+ G
  gi|2377454   926 NPGSN------------PEN---------LD--ARATRGIH----LTING 948

                    iAAGmqntG<-*
                    i AGm ntG
  gi|2377454   949 ISAGMRNTG    957

gi|144899948|emb|CAM76812.1|: domain 1 of 1, from 6 to 933: score 302.0, E = 1.3e-87
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         D  LR+    +v           L       +L +   +++ E v
  gi|1448999     6    --DKNLRA----RVK----------LFGNILGTVLAEQERPQVLETV 36

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                             +    +D+ K   L   + +LdP     v +a+     LAn+
  gi|1448999    37 EALRKGFIDLRQHEDPAKRRALMRLIGALDPHTLSHVVRAFATYFLLANI 86

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEE + A   R +  +       ++       ++tl++L   +  s
  gi|1448999    87 AEE-DFANQQRRRHVQ------SGERLWYGSFDDTLRQLKAEG-VSAGQL 128
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                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   + L       v+tAHPt + RR++L  + R+      L    +    ++
  gi|1448999   129 QQMLDALRFQPVFTAHPTEAKRRAVLEAQRRLYVLARRLNDPNLAEHQRR 178

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   LD  +   +q  ++tDE+R  +P   DE++ G+ Y+ Et+++ vP+  R
  gi|1448999   179 SLDQQILNQVQVLWKTDEVRIQKPVVEDEIKNGLFYFRETLFDTVPRVYR 228

                  RvDtALKniGinE..RlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDv
                    + AL n+   E++   + vP  ++F sW+GGDRDG nP vt +vt+
  gi|1448999   229 NLERALDNVYADEggAKAFRVPaFLRFGSWIGGDRDG-NPFVTHDVTKMA 277

                  CLLaRmmAanlYisqvEDLmFElsmWRCndELR.vRAEElyrtaardkvv
                    L        Y   +E+L   l      + +R+    E   ta  d +v
  gi|1448999   278 VRLQSREVLKHYRRRIEELQVQLT--HSASLVRpSPVFEARMTADED-IV 324

                  KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                               EPYR  L  +  +L     R   LL  G ++    A
  gi|1448999   325 AEAFGAKPGRYAFEPYRRKLHLMHYRLGRQIARIETLLDGG-ADPGRGAG 373

                  ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                  y   ++ L  L     sL   GD  +A   L D++  v tFG  L  LDi
  gi|1448999   374 YGSEDDLLADLLAISDSLISHGDSNVAAAELQDMIALVRTFGFFLAELDI 423

                  RqEseRqtD.vlDAittHLeiGsYReWsEeKRqEWLlaELk..GKRPLlg
                  RqEs R+t  v +   +  ++  Y e  E  R   L   L++ G   L+
  gi|1448999   424 RQESSRHTQaVAELFAKAPNLPDYNELNESARVGVLADLLShaGTPLLYA 473

                  sDLPk.tEEvkDvldafrvL.AELPiDsFGaYiismataPsDvLAvELLq
                   DL  +t E+  v+ ++  L+ E+   +FGaY+ism+   s vL v  L
  gi|1448999   474 QDLSDgTREILRVMRTMADLrREISPRAFGAYVISMTHQASHVLEVLFLA 523

                  RECgv..kqt.......LrvvPLFEkLADLeAAPAavekLFsiDWYinri
                     g+ +++ +++ + ++rv PLFE + DL     ++e+L  +  Y+  +
  gi|1448999   524 SFAGLcgRHQdgswhcdIRVAPLFETIDDLAKIEPTLEQLLDVGTYRALL 573

                  d...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                   +++  qevm+GYsDs KD G l+  W LYkAq  i +     G    +F
  gi|1448999   574 KqsgNIQEVMLGYSDSCKDGGILASSWSLYKAQRLISRSTETRGLACRVF 623

                  HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                  HGRGG vGRGGGPtH AiL+qPP t+nG ++ t qGEv+   +   +
  gi|1448999   624 HGRGGSVGRGGGPTHDAILAQPPGTVNGDIKFTEQGEVLSAKYSNADTAT 673

                  rsLqRFtAAtLE..HGmnPPvsP.kPEWRkLmeemAvvAtEEYRsvvvKE
                    L       +  +  m     P++ ++ ++m+++A      YR +  +
  gi|1448999   674 YELTMGVSGLIKasRCMSVACTPdRADFIEIMDDLAQRGETSYRDLTDRT 723

                  PRFvEYFRlAtPElEYGkmniGsRPaKR.kPsGGiesLRAiPWiFaWtqt
                  P F++YF   tP  E G +niGsRP+ R+k      s+RAiPW+FaW q
  gi|1448999   724 PGFIDYFYEGTPVAEIGLLNIGSRPSHRsKGDRSKYSVRAIPWVFAWAQS 773

                  RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                  R  +P W G+G A K     D   lq L+ m +eWPFFR  l    m
  gi|1448999   774 RQTIPAWYGIGSALKGWRGDDAERLQTLRAMVREWPFFRALLSNSAMSLS 823

                  KGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                  K +  iA  y +L        F +++  ++ E    +L++    +lL
  gi|1448999   824 KSEMSIAREYADLCGEAGGSVF-DRIQGEFNESNTQMLEVFEADELLGDN 872

                  PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                    L   l  R++Y+  +n +q   L+  RD               A E
  gi|1448999   873 RQLAMSLARRNPYLDPINHIQIIALRHYRD---------------APES- 906

                  kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     +e ++              L+  +  +AAGm ntG
  gi|1448999   907 -DQAERLRWQ----------LPLLRSINALAAGMRNTG    933

gi|225856712|ref|YP_002738223.1|: domain 1 of 1, from 1 to 898: score 301.7, E = 1.6e-87
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
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                     L  L     s +  +++ + L+l   L+Di + +  ++  E
gi|2258567     1    ---MSLQKLE--NYS-NKSVVQEEVLILTELLeDITKNMLAPETFEK 41

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +    Els +    +D + L+ L   +tsL   + + + + ++ +  L n
gi|2258567    42 IIQLKELSTQ----EDYQGLNRL---VTSLSNDEMVYISRYFSILPLLIN 84

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   + E+v+lAy    +     D+    s t          kLv       e
gi|2258567    85 ISEDVDLAYEINHQNNIDQDYLGKLSTTI---------KLVAEK----EN 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     e L    v  vltAHPtq  R+s+L     i   L +     +    K
gi|2258567   122 AVEILEHLNVVPVLTAHPTQVQRKSMLDLTNHIHSLLRKYRDVKLGLINK 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                         L R i     tD iR  +     E+   m Y+     k vP
gi|2258567   172 DKWYNDLRRYIEIIMQTDMIREKKLKVTNEITNAMEYYNSSFLKAVPHLT 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                          +  G+n +   ++  i    W+GGDRDG nP vt    +   L
gi|2258567   222 TEYKRLAQAHGLNLK---QAKPITMGMWIGGDRDG-NPFVTAKTLKQSAL 267

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                       +  n Y  ++  L  E+s+      +     E+ r ++ +     Y
gi|2258567   268 TQCEVIMNYYDKKIYQLYREFSLSTSIVNVSKQVREMARQSKDN---SIY 314

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                    E        E YR  L d+  K+  t+          i +      y
gi|2258567   315 RE-------KELYRRALFDIQSKIQATK-------TYLIEDEEVGTRYET 350

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     +F   L     sL e     +  G  ++lL  v  FG  L  +D+Rq+
gi|2258567   351 ANDFYKDLIAIRDSLLENKGESLISGDFVELLQAVEIFGFYLASIDMRQD 400

                   seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK.RPLlgsDLP
                   s      +  + +  +i s+Y e sEe + + Ll EL+  +R L
gi|2258567   401 SSVYEACVAELLKSAGIHSrYSELSEEEKCDLLLKELEEDpRILSATHAE 450

                   ktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLqRE
                   k E ++++  +  + rvL ++L  D     iis at  sD+L   +L +E
gi|2258567   451 KSELLAkelAIFKTARVLKDkLGDDVIRQTIISHATNLSDMLELAILLKE 500

                   Cgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                    g+ ++++  +++vPLFE + DL+    ++ k  s+   +  id +++ q
gi|2258567   501 VGLvdteRARVQIVPLFETIEDLDHSEETMRKYLSLSLAKKWIDSRnnyQ 550

                   evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                   e+m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGRGGtv
gi|2258567   551 EIMLGYSDSNKDGGYLSSCWTLYKAQQQLTAIGDEFGVKVTFFHGRGGTV 600

                   GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                   GRGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
gi|2258567   601 GRGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLV 650

                   AAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                    A +   +    s  +++  +  +m+++     + YR +v+    F +YF
gi|2258567   651 SAAINRMITQKKSDTntpNRYEAIMDQVVDRSYDIYRDLVFGNEHFYDYF 700

                   RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                       P       niGsRPa Rk    i  LRAiPW+F+W q R   P W
gi|2258567   701 FESSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWY 750

                   GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                   GvG  FK  i+K   n+  L++mY++WPFF   l  ++mv  K    iA
gi|2258567   751 GVGSSFKEFINKNPENIAILRDMYQNWPFFQSLLSNVDMVLSKSNMNIAF 800

                   LyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                    y kL   E++k   + + ++++ tk+ +L i GH +lL   PYLK  l
gi|2258567   801 EYAKLCEDEQVKAIYEIILNEWQVTKNVILAIEGHDELLADNPYLKASLD 850
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                   LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                    R +Y   Ln +q   +KR R        r +ls +  +E       L++
  gi|2258567   851 YRMPYFNILNYIQLELIKRQR--------RGELSSD--QER------LIH 884

                   LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   +                 + GiA G+ n G
  gi|2258567   885 IT----------------INGIATGLRNSG    898

gi|222152768|ref|YP_002561945.1|: domain 1 of 1, from 1 to 902: score 301.6, E = 1.7e-87
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                             ++     s ++ +i  +  +l   L++i  D+ G++
  gi|2221527     1    ------MAVKKLESSSNQAIIAEEVAILKTILEtITRDMVGDETFLK 41

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +     ls +     D  +Le +   + sL   + +++ + ++ +  L n
  gi|2221527    42 IEQIVKLSEQ----DDYIQLEKM---IESLTDDEMVIMSRYFSILPLLIN 84

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   + E+v+lAy    +  k   +    s t    iEE     v       e
  gi|2221527    85 ISEDVDLAYEINFQNNKGINYLGKLSHT----IEE-----VASK----EN 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLs.AKDvtveD
                     + L n +v  vltAHPtq  R+ +L    +i   L q  + K   +++
  gi|2221527   122 AKDILENVTVVPVLTAHPTQVQRKTVLELTNKIHGLLRQYRdVKSGVINE 171

                   KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    k L+E L R +     tD iR  +   + E+   m+Y+H  +   v
  gi|2221527   172 EKWLEE-LRRYVEIIMQTDIIREKKLKVKNEITNVMAYYHSSIIPAV--- 217

                   LRRvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRDv
                     R   A K +     l  + P +i    W+GGDRDG nP vt E
  gi|2221527   218 -TRLTLAYKELAKEKGLELENPKpITMGMWIGGDRDG-NPFVTAETLQLS 265

                   CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                     +   +    Y++++  L   ls+    +        l   aa    +
  gi|2221527   266 ASIQSQVIIEYYLEKLSKLYRSLSL---SSRFSKTSKALDDLAALSSDTS 312

                   yYiEFWKqvPPtEPYRviLGdvRDKLYnt....RERaRHLLAtGiseisE
                    Y E        EPYR     +  K+ nt ++ +E a H   +  s+i E
  gi|2221527   313 IYRE-------HEPYRKAFHYIQSKMSNTltsiKENASH--DKQPSDIYE 353

                   eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                    A     E+F   L +   sL + G+  +  G   DlL  v  FG  L
  gi|2221527   354 TA-----EDFKKDLLIIKDSLVQNGEGTLISGDFSDLLQAVDVFGFFLAS 398

                   LDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaELkGK.RPL
                   +D+Rq+s  q   +  + +  +i   Y    E  +   Ll EL+  +R L
  gi|2221527   399 IDMRQDSSVQEACVAELLKSANIvDDYSALNETEKCQILLKELEEDpRIL 448

                   lgsDLPktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDvLAv
                       + k E ++++  +  a r L ++L  D     iis + + sD+
  gi|2221527   449 SATAVEKSELLEkelAIYKAARYLKDkLGEDVIKQHIISHTESVSDMFEL 498

                   ELLqRECgv..kqtLrv..vPLFEkLADLeAAPAavekLFsiDWYinrid
                    ++ +E g+ +k+  rv+ vPLFE + DL+   A +    s D  +n i
  gi|2221527   499 AIMLKEVGLldKHMARVqiVPLFETIEDLDNSNAIMTEYLSYDIVKNWIA 548

                   GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                     ++ qe+m+GYsDs KD G l+  W LYkAq E+  +  k G+K++ FH
  gi|2221527   549 SNhnyQEIMLGYSDSNKDGGYLASGWTLYKAQNELTEIGSKNGIKITFFH 598

                   GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                   GRGGtvGRGGGP   Ai sqP   i+  +R t qGE+iE  FG  +  +
  gi|2221527   599 GRGGTVGRGGGPSYDAITSQPFGSIKDKIRLTEQGEIIENKFGNKDAAYY 648

                   sLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEEYRsvvvKEP
                    L     A +   +   +    E +++R+ me +       YR +v+  P
  gi|2221527   649 NLEMLISASINRMVSRMLTNPNEidgFRETMEGIVSYSNKVYRDLVFDNP 698

                   RFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRF
                    F +YF  A P  E   +niGsRPa Rk    i+ LRAiPW+F+W q R
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  gi|2221527   699 NFYDYFFEASPIKEVSSLNIGSRPAARKTITEITGLRAIPWVFSWSQNRI 748

                   HLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                     P W GvG AFK  idK+  nl kL+ mYk+WPFF   l  ++mv  K
  gi|2221527   749 MFPGWYGVGSAFKDFIDKEEGNLAKLQHMYKTWPFFHSLLSNVDMVLSKS 798

                   DPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                      iA  y +L  + e+k     L d+++ tk+++L i  H +lLE  P
  gi|2221527   799 NMNIAYQYAQLANTQEVKDIYYILLDEWQLTKNIILAIENHDELLEDHPS 848

                   LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                   LK  l  R +Y   Ln +q   +KR+R
  gi|2221527   849 LKHSLEFRLPYFNILNYIQIELIKRLRQ---------------------- 876

                   adeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                          n   +   G E  +  t+ GiA G+ n G
  gi|2221527   877 -------N---QLGEGYEKLIHTTINGIATGLRNSG    902

gi|25028259|ref|NP_738313.1|: domain 1 of 1, from 2 to 919: score 301.5, E = 1.8e-87
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                      ++L++ D   l + L++++ +  G  + E
  gi|2502825     2    -----------------NELLRDDIRYLGRILgEVISEQEGHHVFEL 31

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v      s +    k    ++ L  +  ++dP Da  vA+a+ H   LAn
  gi|2502825    32 VERARRTSFDIA--KGRAEMDSLVEVFAGIDPEDATPVARAFTHFALLAN 79

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   LAE+ + A  R   +         ++   +s +E t  kL   +     E
  gi|2502825    80 LAEDLHDAAQREQALNS-------GEPAPDSTLEATWVKLDDAG-VGSGE 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRi......RnCLaqLsAKD
                   v   ++n  v  vltAHPt   RR +   +  i+   ++R  L  L
  gi|2502825   122 VAAVIRNALVAPVLTAHPTETRRRTVFDAQKHItalmeeRHLLLALPTHA 171

                   vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWk
                    t     +++  + R i   + t  iR a+P   DE+  G+ Y+   +
  gi|2502825   172 RTQSKLDDIERNIRRRITILWQTALIRVARPRIEDEVEVGLRYYKLSLLA 221

                   GvPKFLRRvDtALKniGinERlPYdvP...LikFssWmGGDRDGknPRvt
                    +P+    v   L       R   d+P++ +++  sW+GGD DG nP vt
  gi|2502825   222 EIPRINHDVTVEL-----ARRFGGDIPttaMVRPGSWIGGDHDG-NPFVT 265

                   PEvtRDvCLLaRmmAanlYisqvEDLmFEls....mWRCndELRvRAEEl
                    E        a       Y+ q+  L  Els +++m    dELRv A+
  gi|2502825   266 AETVTYATHRAAETVLKYYVKQLHALEHELSlsdrMNVISDELRVLADAG 315

                   yrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAt
                   +    +                 EPYR  +  +R +          +LAt
  gi|2502825   316 QNDMPSR--------------VDEPYRRAIHGMRGR----------MLAT 341

                   GiseisEeAv..........ytkvEeFLEPLELCYksLCeCGDkviADGs
                     + i EeAv+++  ++ ++yt+  eF   L++   sL    D +iAD
  gi|2502825   342 TAALIGEEAVegtwfktftpYTDTHEFKRDLDIVDGSLRMSRDDIIADDR 391

                   LLDlLRqvstFGLsLvKLDiRqEseRqtDvl.DAittHLeiGsYReWsEe
                   L  l      FG  L  LD+Rq s+   Dvl++   t      YR   E
  gi|2502825   392 LAMLRSALDSFGFNLYSLDLRQNSDGFEDVLtELFATAQTEKNYRGLTEA 441

                   KRqEWLlaELkGKRPLlgsDLPktEEvkDv.ldafrvLAELPiDsFGaY.
                    + + L+ EL+  RPL++   P   E    +l+ f   AE  +  FG+
  gi|2502825   442 EKLDLLIRELSTPRPLIPHGDPDYSEATNReLGIFSKAAE-AVRKFGPLm 490

                   ....iismataPsDvLAvELLqRECgvkqt........LrvvPLFEkLAD
                    ++ iisma +  D+L   +L +E g+ ++++++++++ v+PLFE + D
  gi|2502825   491 vphcIISMASSVTDILEPMVLLKEFGLIRAngknptgsVDVIPLFETIDD 540

                   LeAAPAavekLFsiDWYinridGK...qevmvGYsDsGKDAGRlsAAWqL
                   L+     +e L+ iD Y+n ++ +++ qevm+GYsDs KD G ++A W L
  gi|2502825   541 LQRGAGILEELWDIDLYRNYLEQRdnvQEVMLGYSDSNKDGGYFAANWAL 590
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                    YkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGs
                    Y A   ++   +   vKL lFHGRGGtvGRGGGP   AiL+qP   + G+
  gi|2502825   591 YDAELRLVELCRGRNVKLRLFHGRGGTVGRGGGPSYDAILAQPKGAVRGA 640

                    lRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs.PkPE.WRk
                    +Rvt qGE+i   +G  +   r L     AtLE  +   v  P  E+  +
  gi|2502825   641 VRVTEQGEIISAKYGNPDTARRNLEALVSATLEASLLDDVElPNRErAHQ 690

                    LmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkP
                    +m e+       Y s+v  +P F+ YF   tP  E G +niGsRP+ Rk
  gi|2502825   691 IMGEISELSFRRYSSLVHEDPGFIQYFTQSTPLQEIGSLNIGSRPSSRKQ 740

                    sGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAi...dKDiKnlqkL
                       +e LRAiPW+ +W q R  LP W GvG A +  i++++     +  L
  gi|2502825   741 TNTVEDLRAIPWVLSWSQSRVMLPGWFGVGTALREWIgegEGAAERIAEL 790

                    kEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLR
                    +E+ + WPFF   lD +  v  K +  +A Ly +L+   e+  +  + +
  gi|2502825   791 QELNRCWPFFTSVLDNMAQVMSKAELRLARLYADLIPDREVADrIYETIF 840

                    dkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKR
                     +Y  tk++   i G +DlL+  P L   +R R +Y+  Lnv+q   ++R
  gi|2502825   841 GEYFLTKEMFCTITGSQDLLDDNPALARSVRSRFPYLLPLNVIQVEMMRR 890

                    iRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtm
                     R                dE        v  n            + Ltm
  gi|2502825   891 YRS---------------GDEG-----TAVPRN------------IRLTM 908

                    KGiAAGmqntG<-*
                     G+   + n G
  gi|2502825   909 NGLSTALRNSG    919

gi|195977846|ref|YP_002123090.1|: domain 1 of 1, from 1 to 927: score 301.2, E = 2.2e-87
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            ++ L        e + e  A+L +    i   + G++    +
  gi|1959778     1    ---MSVKKLESYNNQ--EIIAEEVAILKEILESITRRMIGDEAFARI 42

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E  +ls     K+D   Le L ak+      D  l+ + ++ +  L n+
  gi|1959778    43 EEIIDLSE----KQDYVLLEQLIAKISN---KDMELISRYFSILPLLINI 85

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiE.EtlKkLvlklnKsPeE
                     E+v+lAy    +     D+      t  s  E+E  K L  k
  gi|1959778    86 SEDVDLAYEINRQNNTNQDYLGKLALTIASAAEkENAKELLEKV------ 129

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                            +v  vltAHPtq  R+ +L   + i n L         v  +
  gi|1959778   130 --------TVVPVLTAHPTQVQRKTVLELTSSIHNLLRRYRDVKAGVMNQ 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                          L R i     tD iR  +   + E+   m Y+   + + +
  gi|1959778   172 NKWYSELYRYIDILMQTDIIREKKLKLVKNEITNVMQYYNSSLIQAITALT 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                     +  t  K  Gi   l  +   i    W+GGDRDG nP vt E  R
  gi|1959778   222 SKYKTLAKDKGI---LLDNPKPINMGMWIGGDRDG-NPFVTAETLRLSAT 267

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    +   +   +Yi+++  L   +s+    + L     E+ r a        Y
  gi|1959778   268 VQSEVILRFYIDKLSALYQTFSL---SSALIKTSPEVERLASLSSDQSIY 314

                    iEFWKqvPPtEPYRviLGdvRDKLYntRER......aRHL.........
                     E       +EPYR     +  +L  t     +++ +  L ++ + + ++
  gi|1959778   315 RE-------NEPYRRAFHYIQARLSQTLQElvgqpaSDQLasrmpatvgs 357

                    LAtGiseisEeA......vytkvEeFLEPLELCYksLCeCGDkviADGsL
                    L  G+  i  + ++++ + y     F   L +  +sL   GD  + +G L
  gi|1959778   358 LQSGVTSIVTNSsdqqapAYKTAAAFKADLVMIEQSLIAAGDSSLVEGDL 407

                    LDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeK
                     ++L  v  FG  L  +D+Rq+s  q   +  + +  +i   Y   sEe+
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  gi|1959778   408 QEVLQAVDIFGFFLASIDLRQDSSVQEACVAELLKNAGIvENYSALSEEQ 457

                    RqEWLlaELkGK.RPLlgsDLPktEEvkDvldafrvLAELP....iDsFG
                    + E Ll EL   +R L  + + k E ++  l  +    EL ++ + +
  gi|1959778   458 KCEVLLKELTEDpRTLSSAAVEKSELLEKELAIYTAARELKdklgEEVIK 507

                    aYiismataPsDvLAvELLqRECgv....kqtLrvvPLFEkLADLeAAPA
                      iis + + sD+    ++ +E g+ ++++  +++vPLFE + DL+ A A
  gi|1959778   508 QHIISHTESVSDMFELAIMLKEVGLidqrQARVQIVPLFETIEDLDNARA 557

                    avekLFsiDWYinri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEE
                     + +  s D  +  i ++ G qe+m+GYsDs KD G l+  W LYkAq E
  gi|1959778   558 IMTQYLSYDIVKSWIatnAGYQEIMLGYSDSNKDGGYLASGWTLYKAQNE 607

                    iiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvq
                    + K+  + G+ ++ FHGRGGtvGRGGGP   Ai sqP   i+  +R t q
  gi|1959778   608 LTKIGEDNGISITFFHGRGGTVGRGGGPSYEAITSQPFGSIKDRIRLTEQ 657

                    GEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeem
                    GE+iE  +G  ++ +  L     A +   +   +    E +++Rk+m+e+
  gi|1959778   658 GEIIENKYGNQDVAYYNLEMLISASINRMVTRMLTNPDEidgFRKIMDEI 707

                    AvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGie
                           YR +v+  P F +YF  A P  E   +niGsRPa Rk    i
  gi|1959778   708 VEDSNRIYRELVFDNPHFYDYFFEASPIKEVSSLNIGSRPAARKTITDIS 757

                    sLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWP
                     LRAiPW+F+W q R  LP W  vG AFK  idK+  nl kL+ mY++WP
  gi|1959778   758 GLRAIPWVFSWSQNRIMLPGWYAVGSAFKRFIDKEEGNLAKLQHMYDKWP 807

                    FFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdl
                    FF   l  ++mv  K    iA  y +L  + e+    + + d+++ tk+
  gi|1959778   808 FFHSLLSNVDMVLSKSNMNIAFQYAQLAESKEVCEVFHTILDEWQLTKNV 857

                    LLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvt
                    +L iA H +lLE  P LKq l  R +Y   Ln +q   +KR+R
  gi|1959778   858 ILAIAQHDELLEETPSLKQSLDFRLPYFNVLNYIQIELIKRLR------- 900

                    lrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqn
                           E  dE+    + L++                  + GiA G+ n
  gi|1959778   901 ------HEQLDED---YEKLIHTT----------------INGIATGLRN 925

                    tG<-*
                     G
  gi|1959778   926 SG    927

gi|189219750|ref|YP_001940391.1|: domain 1 of 1, from 2 to 931: score 301.1, E = 2.3e-87
                    *->siDAqLRlLvPGKvsedekLieYDALLl.DkFLDiLqDLHGedLkEa
                       s+  qL  L       d  L+      l+D    ++  L Ge +  +
  gi|1892197     2    SVRKQLSSLQRISPEHDFSLLSRTIHFLgDTLGKVITQLEGEKILSI 48

                    vqECYElsAe.YEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                          l+ e+  GK+++ +   L   + +Ld   a  +A a+     L
  gi|1892197    49 EETIRKLAKEsRKGKEEATR--KLSDIVRGLDIDMAYRMAMAFTCYFELV 96

                    nLAEE...velAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnK
                    nLAEE+ +v++  +RRi ++          A     iE  + +L
  gi|1892197    97 NLAEEnyrVRILMKRRINQLN-----HPQKAIPKESIESAISQLKKAK-V 140

                    sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt
                      eE+ e L    + Lv+tAHPt   R  +L K   i   L + s
  gi|1892197   141 KKEEIQEILEKMEIVLVFTAHPTEIKRQTILNKLCEISSYLKKES---FN 187

                    veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGv
                          +   + R i   + t+  R  +P   DE+R G+ Y+  t+W+ +
  gi|1892197   188 SKPSPAIHSTVERLIASLWLTERSRSKNPQVLDEVRTGLWYFEHTLWDVI 237

                    PKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                    P         L        +      i F sW+GGDRDG n  vt   t
  gi|1892197   238 PELHNELQRVLDI--YYPGVTLKPKWISFGSWIGGDRDG-NFQVTTKTTA 284
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                    DvCLLaRmmAanlYisqvEDL..mFElsmWRC...ndELRvRAEElyrta
                       +L R +A     + +E L+++F +s  R +++   +R   E l++ +
  gi|1892197   285 TTFILQRNLALRKVSQSLERLseIFSISSQRIpptKKVIRLLNEKLKSFP 334

                    ardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRER.aRHLLAtGis
                      +     Y        P+EPYR +L + +  + n   + +   L   +
  gi|1892197   335 SLKEEYERY--------PNEPYRLVLLALKKEVENSINKiSENDLLDFFH 376

                    eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                    +   +     + e LE L   + +      ++  +G    l   +  FG+
  gi|1892197   377 DCKPDTTLKAITEVLEALKENFDA---PQTRIFLEGEFQKLAQCIEVFGI 423

                    sLvKLDiRqEseRqtDvlDAitt...HLeiGsYReWsEeKRqEWLlaELk
                     +  LDiRq s  + + ++ i + ++H ei sY    E  +   L   L+
  gi|1892197   424 HIFSLDIRQHSAIHEEAIEEILRlngHPEI-SYALLDEKEKVGLLNKLLE 472

                    GKRPLlgsDLPkt.EEvkDvldafrv....LAELPiDsFGaYiismataP
                    G  P l s   + ++ +k+vl+ + v ++++A L  +  G Y+ism+
  gi|1892197   473 GPLPSLHSLYNRAsDKLKEVLGPILVfsrsIAILGKEVCGCYLISMTSGL 522

                    sDvLAvELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                    sD+L v  L + C  + ++ + PLFE L DL+  P +++ L s   Y+
  gi|1892197   523 SDILEVLYLCKIC--RCSIDIAPLFETLSDLKSSPQTLQDLLSHPLYRKY 570

                    idG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                    ++ +++Kq vm+GYsDs KD G +   W L++ qE +  v + +Gv Lvl
  gi|1892197   571 LQErsdKQIVMLGYSDSNKDCGYMTSNWWLFQIQEKLHEVCRVHGVSLVL 620

                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                    FHGRGGt+ RGGGP   AiL+qP   ++G +R+t qGEv+   + + ++
  gi|1892197   621 FHGRGGTIARGGGPAAKAILAQPKGLLEGKIRITEQGEVLSTRYHDFDIA 670

                    FrsLqRFtAAtL...EHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvK
                    Fr L   t   L       +  + Pk  W k +e +A      Y  +  +
  gi|1892197   671 FRILEQTTYGVLlaiHKSRKKTILPK-SWEKTIECIAEESYRAYTHLLHQ 719

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                    EP F  ++   tP  E G + i sRP  R      e LRAiPW+F+W qt
  gi|1892197   720 EPDFLRFWQEVTPINEIGSLKIASRPIFRFRLNNFEDLRAIPWVFSWMQT 769

                    RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                    RF +P W G+G   K  i+   K l  L+ mY++W FF   +D   +  A
  gi|1892197   770 RFVIPGWYGIGSSLKKVIETSPKALSILQKMYEKWTFFQTVIDNAQLSLA 819

                    KGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                    K D  iA Ly +L    +L +     + ++Y+ t + +Lki     +L+
  gi|1892197   820 KTDIDIARLYCDLASDKNLaQRIFSIIEAEYKKTVETILKITLQNNILDH 869

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                    +P L+  + LR++Y+  Ln +q   +KR R        +P+ + E
  gi|1892197   870 EPILQRSIQLRNPYVDPLNYIQVEMIKRNR------AGQPPTALEIDKIK 913

                    skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                          +++L                + Gi AG+ ntG
  gi|1892197   914 -----SVIELT----------------INGISAGLRNTG    931

gi|293365250|ref|ZP_06611967.1|: domain 1 of 1, from 1 to 898: score 301.1, E = 2.3e-87
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                            L  L     s +  +++ + L+l   L+Di + +  ++  E
  gi|2933652     1    ---MSLQKLE--NYS-NKAVVQEEVLILTELLeDITKNMLAPETFEK 41

                    vqECYElsA..eYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    +    Els +++Y G  D          +tsL   + i + + ++ +  L
  gi|2933652    42 IIQLKELSTseNYQGLND---------LVTSLSNEEMIYISRYFSILPLL 82

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                     n+ E+v+lAy    +     D+    s t          k+v
  gi|2933652    83 INISEDVDLAYEINHQNNVDQDYLGKLSTTI---------KMVAEK-ENA 122

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    +E+ e L    v  vltAHPtq  R+s+L     i   L +     +
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  gi|2933652   123 AEILEKL---NVVPVLTAHPTQVQRKSMLDLTNHIHTLLRKYRDVKLGLI 169

                   DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    K+     L R i     tD iR  +     E+   m Y+     + vP+
  gi|2933652   170 NKEKWHTDLRRYIEIIMQTDMIREKKLKVTNEITNVMEYYQSSFLNAVPR 219

                   FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                            K  Gi    P     i    W+GGDRDG nP vt E
  gi|2933652   220 LTAEYKKLAKEQGIELEHPKP---ITMGMWIGGDRDG-NPFVTAETLNKS 265

                   CLLaRmmAanlYisqvEDLm..FElsmWRCndELRvRAEElyrtaardkv
                    L    +  n Y +++  L ++F ls    n   +vR   l++   +
  gi|2933652   266 ALTQCEVIMNYYDEKIYNLYreFSLSTSIVNVSDKVREMALKSQDNSI-- 313

                   vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                      Y E        E YR  L d+  K+  t+       A  i +   +
  gi|2933652   314 ---YRE-------KELYRRALFDIQAKMQATK-------AYLIEDKDLQP 346

                   vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                    y   +eF   L     sL e     +  G  ++l+  v  FG  L  +D
  gi|2933652   347 RYATADEFYQDLLAIRDSLLENKGEYLISGEFVELMQAVEIFGFYLASID 396

                   iRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaELkGKRPLlgs
                   +Rq+s  +   +  +    +i+  Y + sE+ +   Ll EL+    +l +
  gi|2933652   397 MRQDSSVHEACVAELLASAGInDHYSDLSEDEKCALLLKELEEDPRILSA 446

                   DLPktEEvkD....vldafrvLAE.LPiDsFGaYiismataPsDvLAvEL
                         E+ +++ ++  a r L ++L        iis at+ sD+L   +
  gi|2933652   447 THAEKSELLEkelsIFKAARKLKDkLGENVIRQTIISHATSVSDMLELAI 496

                   LqRECgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK
                   + +E g+ + +k  +++vPLFE + DL+    ++ + Fs+   +  i  K
  gi|2933652   497 MLKEVGLvdaqKARVQIVPLFETIEDLDHSEETMRRYFSLPLAKKWIASK 546

                   ...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                   ++ qe+m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGR
  gi|2933652   547 dnyQEIMLGYSDSNKDGGYLSSCWTLYKAQQQLTAIGDEFGVKVTFFHGR 596

                   GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                   GGtvGRGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
  gi|2933652   597 GGTVGRGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNL 646

                   qRFtAAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRF
                        A +   +    s  +++  +  +m+++     + YR +v+    F
  gi|2933652   647 EMLVSAAINRMITKKKSDTntsNRYEAIMDQVVDRSYDIYRDLVFGNEHF 696

                   vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                    +YF    P       niGsRPa Rk    i  LRAiPW+F+W q R
  gi|2933652   697 YDYFFESSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMF 746

                   PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                   P W GvG  FK  id+D Kn+  L++mY++WPFF   l  ++mv  K
  gi|2933652   747 PGWYGVGSSFKEFIDQDPKNIEFLRDMYQNWPFFQSLLSNVDMVLSKSNM 796

                   GiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLK
                    iA  y kL   Ee++     + d+++ tkd +L i G  +lL    YLK
  gi|2933652   797 NIAFEYAKLCEDEEVQAIYYTILDEWQLTKDVILAIEGYDELLAENSYLK 846

                   qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                     l  R +Y   Ln +q   +KR R        r +ls   AdE+
  gi|2933652   847 DSLNYRMPYFNILNYIQLELIKRQR--------RGELS---ADEE----- 880

                   eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    L++                 + GiA G+ n G
  gi|2933652   881 KLIHTT----------------INGIATGLRNSG    898

gi|77409086|ref|ZP_00785802.1|: domain 1 of 1, from 3 to 931: score 300.9, E = 2.7e-87
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                          +L        s + ++i  +  Ll + LD+  q L G +  +
  gi|7740908     3    --HPKLES------SSNKEIITEEVGLLKQLLDeATQKLIGSESFDK 41
```

```
                vqECYElsA..eYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                +     ls +++Y G k+t         + +L   + ++v + ++ +  L
gi|7740908    42 IEKIVSLSStdDYTGLKET---------ISALSNEEMVIVSRYFSILPLL 82

                AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                 n+ E+v+lAy    k     D+    s t +          v+ +
gi|7740908    83 INISEDVDLAYEINYKNNLNQDYLGKLSTTID----------VVAG---H 119

                eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                e   + L    v  vltAHPtq  R+ +L   ++i   L +       +
gi|7740908   120 ENAKDILEHVNVVPVLTAHPTQVQRKTVLELTSKIHDLLRKYRDVKAGIV 169

                DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                 ++     L R i     tD iR  +   + E+   m Y+   + k v K
gi|7740908   170 NQEKWYADLRRYIGIIMQTDTIREKKLKVKNEITNVMEYYNRSLIKAVTK 219

                FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                            Gi    P   PL     W+GGDRDG nP vt E  R
gi|7740908   220 LTAEYKALAAKKGIHLENP--KPL-TMGMWIGGDRDG-NPFVTAETLRLS 265

                CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                 ++   +  n Yi+q+ +L   +s+     E+     El   a + +
gi|7740908   266 AMVQSEVIINHYIEQLNELYRNMSLSISLTEV---SPELVTLANQSQDNS 312

                yYiEFWKqvPPtEPYRviLGdvRDKLYnt.................RERa.
                 Y E       +EPYR     + DKL  t  + + ++ ++++  +R  ++
gi|7740908   313 VYRE-------NEPYRKAFNFIQDKLVQTllnlkvgsypkekfvsRQESs 355

                ....RHL...LAtGiseisEeAv..ytkvEeFLEPLELCYksLCeCGDkv
                +  +R +++++A+  s+i  e  + y   EeF   L L  +sL + G
gi|7740908   356 givgRYIkshIAQVASDIQTEELpaYATAEEFKQDLLLVKQSLVQHGQDS 405

                iADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYR
                + DG L  l+  v  FG  L  +D+Rq+s  +   +  + +  +i   Y
gi|7740908   406 LVDGELACLIQAVDIFGFYLATIDMRQDSSINEACVAELLKSANIvDDYS 455

                eWsEeKRqEWLlaELkGK.RPLlgsDLPktEEvkDvldafrvLAELP...
                + sEe +   Ll EL   +R L     Pk E ++  l  f+   EL ++
gi|7740908   456 SLSEEEKCQLLLKELTEDpRTLSSTHTPKSELLQKELAIFQTARELKdql 505

                .iDsFGaYiismataPsDvLAvELLqRECgv....kqtLrvvPLFEkLAD
                + D     iis + + sD+    ++ +E g+ + ++  +++vPLFE + D
gi|7740908   506 gEDIIKQHIISHTESVSDMFELAIMLKEVGLidanQARIQIVPLFETIED 555

                LeAAPAavekLFsiDWYinri...dGKqevmvGYsDsGKDAGRlsAAWqL
                L+     + +       +  i++++  qe+m+GYsDs KD G ls  W L
gi|7740908   556 LDNSRDIMTQYLHYGLVKKWIttnNNYQEIMLGYSDSNKDGGYLSSGWTL 605

                YkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGs
                YkAq E+ K+  + G+K++ FHGRGGtvGRGGGP   Ai sqP   i+
gi|7740908   606 YKAQNELTKIGEENGIKITFFHGRGGTVGRGGGPSYEAITSQPFGSIKDR 655

                lRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WR
                +R t qGE+iE  +G  +  +  L     A ++  +   +    E +++R
gi|7740908   656 IRLTEQGEIIENKYGNQDAAYYNLEMLISASIDRMVTRMITNLNEidnFR 705

                kLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRk
                + m+ +       YR +v+  P F +YF  A P  E   +niGsRPa Rk
gi|7740908   706 ETMDGIVAESNAVYRNLVFDNPYFYDYFFEASPIKEVSSLNIGSRPAARK 755

                PsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkE
                    i  LRAiPW+F+W q R   P W GvG AFK  i++D  nl kL+
gi|7740908   756 TITEISGLRAIPWVFSWSQNRIMFPGWYGVGSAFKQFIEQDEANLAKLQT 805

                mYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkY
                mY++WPFF   l  ++mv  K    iA  y +L  + e++   + + +++
gi|7740908   806 MYQKWPFFNSLLSNVDMVLSKSNMNIALQYAQLAGSKEVRDVFNIILNEW 855

                vEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRD
                + tkd++L i  H  lLE  P L   l  R +Y   Ln +q   +KR+R
gi|7740908   856 QLTKDMILAIEQHDNLLEENPMLHASLDYRLPYFNVLNYVQIELIKRLRS 905
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                  PsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGi
                   +              dE+    + L+++                 + Gi
  gi|7740908   906 NQL-------------DED---YEKLIHIT---------------INGI 923

                  AAGmqntG<-*
                  A G+ n G
  gi|7740908   924 ATGLRNSG    931

gi|194397283|ref|YP_002037699.1|: domain 1 of 1, from 1 to 898: score 300.4, E = 3.8e-87
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                          L  L     s +  +++ + L+l   L+Di + +  ++  E
  gi|1943972     1    ---MSLQKLE--NYS-NKSVVKEEVLILTELLeDITKNMLAPETFEK 41

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  +    Els +    +D + L+ L   +tsL   + + + + ++ +  L n
  gi|1943972    42 IIQLKELSTQ----EDYQGLNRL---VTSLSNDEMVYISRYFSILPLLIN 84

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  + E+v+lAy    +     D+    s t          kLv       e
  gi|1943972    85 ISEDVDLAYEINHQNNIDQDYLGKLSTTI---------KLVAEK----EN 121

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    e L    v  vltAHPtq  R+s+L     i   L +     +    K
  gi|1943972   122 AVEILXHLNVVPVLTAHPTQVQRKSMLDLTNHIHSLLRKYRDVKLGLINK 171

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                        L R i     tD iR  +     E+   m Y+     k vP
  gi|1943972   172 DKWHNDLRRYIEIIMQTDMIREKKLKVTNEITNAMEYYNSSFLKAVPHLT 221

                  RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                         +  G+n +   ++  i    W+GGDRDG nP vt    +   L
  gi|1943972   222 TEYKRLAQAHGLNLK---QAKPITMGMWIGGDRDG-NPFVTAKTLKQSAL 267

                  LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                      +  n Y  ++  L  E+s+      +     E+ r ++ +     Y
  gi|1943972   268 TQCEVIMNYYDKKIYQLYREFSLSTSIVNVSKQVREMARQSKDN---SIY 314

                  iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                   E        E YR  L d+  K+  t+          i +      y
  gi|1943972   315 RE-------KELYRRALFDIQSKIQATK-------TYLIEDEEVGTRYET 350

                  vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    +F   L     sL e     +  G  ++lL  v  FG  L  +D+Rq+
  gi|1943972   351 ANDFYKDLIAIRDSLLENKGESLISGDFVELLQAVEIFGFYLASIDMRQD 400

                  seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK.RPLlgsDLP
                  s      +  + +  +i s+Y e sEe + + Ll EL+  +R L
  gi|1943972   401 SSVYEACVAELLKSAGIHSrYSELSEEEKCDLLLKELEEDpRILSATHAE 450

                  ktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLqRE
                  k E ++++  +  + rvL ++L  D     iis at+ sD+L   +L +E
  gi|1943972   451 KSELLAkelAIFKTARVLKDkLGDDVIRQTIISHATSLSDMLELAILLKE 500

                  Cgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                   g+ ++++  +++vPLFE + DL+    ++ k  s+   +  id +++ q
  gi|1943972   501 VGLvdteRARVQIVPLFETIEDLDHSEETMRKYLSLSLAKKWIDSRnnyQ 550

                  evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                  e+m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGRGGtv
  gi|1943972   551 EIMLGYSDSNKDGGYLSSCWTLYKAQQQLTAIGDEFGVKVTFFHGRGGTV 600

                  GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                  GRGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
  gi|1943972   601 GRGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLV 650

                  AAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                   A +   +    s  +++  +  +m+++     + YR + +    F +YF
  gi|1943972   651 SAAINRMITQKKSDTntpNRYEAIMDQVVDRSYDIYRDLXFGNEHFYDYF 700

                  RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
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                      P       niGsRPa Rk    i  LRAiPW+F+W q R   P W
  gi|1943972   701 FESSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWY 750

                  GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                  GvG  FK  i+K   n+  L++mY++WPFF   l  ++mv  K    iA
  gi|1943972   751 GVGSSFKEFINKNPENIAILRDMYQNWPFFQSLLSNVDMVLSKSNMNIAF 800

                  LyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                   y kL   E++k   + + ++++ tk+ +L i GH +lL   PYLK  l
  gi|1943972   801 EYAKLCEDEQVKAIYETILNEWQVTKNVILAIEGHDELLADNPYLKASLD 850

                  LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                   R +Y   Ln +q   +KR R        r +ls +  +E       L++
  gi|1943972   851 YRMPYFNILNYIQLELIKRQR--------RGELSSD--QER------LIH 884

                  LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                  +                 + GiA G+ n G
  gi|1943972   885 IT----------------INGIATGLRNSG    898

gi|224826000|ref|ZP_03699103.1|: domain 1 of 1, from 1 to 901: score 300.2, E = 4.5e-87
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      +  q + L P + s            l++ L+++L +  Ge++ E
  gi|2248260     1    -MTDQDKDL-PLRAS---------IARLERLLgEVLLEQEGEQVYEE 36

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v     + A+     + ++     ++L  L P+ +  + +a      L n
  gi|2248260    37 VR---AIPADALTGGERSR-----SVLERLSPGATTALVRACGLYSQLFN 78

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  +AE+ +   RRR ++         +sA     +   l +L   +
  gi|2248260    79 IAEDLHHTRRRRAHQIA-------GSAPQQGSLAGALARLKQDG-VDFGQ 120

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      L   sv  vltAHPt   R s+L  +  +R  L+qL   ++t+e+
  gi|2248260   121 LAATLADASVVAVLTAHPTEVQRQSVLDGHRAVRKFLSQLNSPELTPEEE 170

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   EL+  L R +   + t EiR  +    DE+  G++Y   t +  +PK
  gi|2248260   171 SELEAKLKRVMLTLWQTSEIRPFKLSIRDEIENGVAYHPLTFFSAMPKLY 220

                  RRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDvC
                   R     + i        + P+ ++  sW+GGDRDG nP v   v R
  gi|2248260   221 ERLG---RLIADHWEQQVELPsFLRVGSWIGGDRDG-NPNVDAGVMRHAI 266

                  LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                        A   Y+  +  L  Els+      + v A      aa+  +
  gi|2248260   267 TRQAEEAFRHYFYELAGLYRELSL--SERHVSVSAAVQALSAASPDLAES 314

                  YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                    E        EPYR  L  +  +L     R   +   G   + E   y
  gi|2248260   315 RRE--------EPYRRALATIEGRLSASAARL-GVESRGRWTLGEP--YA 353

                  kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                  +    +  L     sL e G   +A+G L  lLR    FG  L+ LD+Rq
  gi|2248260   354 DCAALVADLQALVDSLREHGSGLLAEGRLGRLLRSLDVFGFFLMPLDMRQ 403

                  EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   +  +  v+  +    ++  Y    E  R   Ll EL   R L+ + L
  gi|2248260   404 HAAIHEAVVGELFARAGLEEYVALDEAARVRVLLRELATPRLLYSPYLTY 453

                  tEEvkDvldafrvLA....ELPiDsFGaYiismataPsDvLAvELLqREC
                    E +  l  fr  A+ ++E  +D+    iis + + sD+LA  LL +E
  gi|2248260   454 SAEAEKELAIFREAAriqrEFGVDAIAQSIISNCATVSDILALALLLKEA 503

                  gv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK.
                  g+ + +++ ++ ++  vPLFE +ADL+ A   ++ LF++ WY   +  ++
  gi|2248260   504 GLirldngipQASINLVPLFETIADLQNATLVMDALFALPWYQQLLKSRg 553

                  ..qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRG
                    qevm+GYsDs KD G l   W LY A   +++     GvKL lFHGRG
  gi|2248260   554 miQEVMLGYSDSNKDGGYLTSQWELYLAEQRLVQSFAAAGVKLKLFHGRG 603
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                    GtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLq
                    G vGRGGGP   Ai++qP   + G +R+t qGEvi   + + ++  r L
  gi|2248260   604 GSVGRGGGPSYEAIMAQPAGSVAGRIRITEQGEVIASKYSDPDIGARNLE 653

                    RFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                       AAtLE  + P      +  ++ +e+   A   YR +v   P F+ YF
  gi|2248260   654 ALVAATLEASLSPHACHAVD-EEVFNELSGHAFTAYRELV-ETPGFMQYF 701

                    RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                      AtP     k+niGsRPa Rk    i  LRAiPW+F+W q R  LP W
  gi|2248260   702 LEATPISAIAKLNIGSRPASRKSLNSIRDLRAIPWVFSWAQSRVMLPGWY 751

                    GvGAAFKhAidKDiKn.lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiA
                    G+G A    + +    +l +L+  Y   PFF v l  +E v AKGD  iA
  gi|2248260   752 GFGSAVSAYLGRHGDEgLARLQQAYASSPFFQVVLSNMEQVMAKGDLNIA 801

                    aLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                      + +L+    L  + FG+ + +++  t++    i G + lLE  P L
  gi|2248260   802 KGFADLVSDRRLADnlFGR-ISEEWHKTQQAFFAISGQQKLLEKNPTLGR 850

                    rlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkade
                     l +R +Y+  Ln +q   L+R+R+       +P        E+   a+
  gi|2248260   851 SLDIRLPYLDALNLLQTELLRRLRE-------QP--------ED---AEA 882

                    LvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    L  +               Lt+ Gi AG+ n G
  gi|2248260   883 LYAIH--------------LTINGISAGLRNSG    901

gi|76810271|ref|YP_332639.1|: domain 1 of 1, from 128 to 1085: score 300.1, E = 4.8e-87
                    *->siD.AqLRlLvP.........GKvsed.ekLieYDALLlDkFL.DiL
                        +D+A  R L+P++  + +++G+  ed+++ +  D   l + L+D++
  gi|7681027   128    KLDgAAARPLAPtnaasakpqGRTREDkDRPLFEDIRYLGRLLgDVV 174

                    qDLHGedLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvA
                     +  G+ + ++v      +  +    D    + L   L  L P  ++ v
  gi|7681027   175 REQEGDAVFDVVETIRQTAVKFRREDDKAAAQTLEKMLRKLTPEQTVSVV 224

                    kailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKk
                    +a++    LAn+AE+ +   RRRi+ +        +sA     +   l k
  gi|7681027   225 RAFSYFSHLANIAEDRHHNRRRRIHALA-------GSAAQAGTVAYALDK 267

                    LvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq
                    L   ++ s + + +      +  vltAHPt   R+s+L  +  i    a
  gi|7681027   268 LKQAGDASSKTIKQFFEGALIVPVLTAHPTEVQRKSILDAQHDI----AR 313

                    LsAKDvtveDKkEL..DEALHRE.iqAAFRtDEiRRaqPtPqDEmRaGms
                    L A    +   +EL + EAL R ++   + t  +R a+ t  DE+   +s
  gi|7681027   314 LLAERDQPLTARELahNEALLRArVTTLWQTRMLRDARLTVADEIENALS 363

                    YiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGk
                    Y+  t  +  P     ++ AL   G+  R+P      +  sW+GGDRDG
  gi|7681027   364 YYRATFLDELPALYADIEEALAEHGLRARVP---AFFQMGSWIGGDRDG- 409

                    nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEE
                    nP vt     +       +    Y++qv  L  Els+    + L v A +
  gi|7681027   410 NPNVTAATLDEAISRQAAVIFEHYLEQVHKLGAELSV----SNLLVGASD 455

                    lyrtaardkvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER...
                      +  a            q P++  EPYR  L  v  +L  + R R ++
  gi|7681027   456 ALKALAAA--------SPDQSPhrVDEPYRRALIGVYTRLAAsARVRlge 497

                    .aRHLLAtGiseisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsL
                    ++  +   G    +  A +y + EeF   L +   sL       +A   L
  gi|7681027   498 gTVPVRSAGRGAAPVRATpYADAEEFAADLRVLTDSLALHHGESLATPRL 547

                    LDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeK
                      l+R    FG  L  +D+Rq s+ +  v+  +    ++ ++Y   +E
  gi|7681027   548 APLMRAAEVFGFHLASIDLRQSSDIHEAVVAELLARGGVEAdYAALPEAD 597

                    RqEWLlaELkGKRPLlgsDLPktEEvkDvldafr....vLAELPiDsFGa
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                    +   Lla L   RPL  + L   +  k  l+ +++ + + A     +
  gi|7681027   598 KLRVLLAALADPRPLRSPYLDYSDLAKSELGVLErahaIRAQFGARAVRN 647

                    YiismataPsDvLAvELLqRECgv.............kqtLrvvPLFEkLA
                    Yiis + + sD + v LLq+E g+ +++ ++++ + ++ L v+PLFE +A
  gi|7681027   648 YIISHTETVSDLVEVLLLQKETGLfegtlgtphanaRNGLMVIPLFETIA 697

                    DLeAAPAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWq
                    DL+ A   +   F+ +++     +    qevm+GYsDs KD G l   W
  gi|7681027   698 DLRNASDIMRAFFAlpgVGELLAHQGHEQEVMLGYSDSNKDGGFLTSNWE 747

                    LYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinG
                    LY+A   ++    + G+KL lFHGRGGtvGRGGGPt  AiLsqPP t+nG
  gi|7681027   748 LYRAELALVDLFDERGIKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNG 797

                    slRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEW
                     +R t qGEvi   F   ++  r L    AAtLE  + P  ++Pk+ P +
  gi|7681027   798 QIRLTEQGEVIASKFANPEIGRRNLETVVAATLEATLAPHSnAPKqlPAF 847

                    RkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKR
                       m+ +   A   YR++v+  P F +YF + tP +E   +niGsRPa R
  gi|7681027   848 EATMQTLSDAAMASYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASR 897

                    kPsG....GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......
                    k   ++++ ie LRAiPW F+W q R  L  W G+G A    +d+ ++
  gi|7681027   898 KLQDpknrKIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVAAYLDgapdaa 947

                    KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL
                       K +  Lk m k+WPFF   l  ++mv AK D  +A+ y +L+    L
  gi|7681027   948 ERGKRVALLKKMNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVADKKL 997

                    .kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLn
                    +k   +++ +++  t d L +i G +  L   P L   ++ R +Y+  Ln
  gi|7681027   998 rKHVFERIVAEWHRTADALAEITGAHARLAANPLLARSIKNRFPYLDPLN 1047

                    vfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPG
                     +q   +KR R               A +           n   r   G
  gi|7681027  1048 HLQVELIKRHR----------------AGDT----------N--ARLRRG 1069

                    LEDtLiLtmKGiAAGmqntG<-*
                    +     Lt+ GiAAG+ ntG
  gi|7681027  1070 IH----LTINGIAAGLRNTG    1085

gi|254261244|ref|ZP_04952298.1|: domain 1 of 1, from 37 to 994: score 300.1, E = 4.8e-87
                    *->siD.AqLRlLvP.........GKvsed.ekLieYDALLlDkFL.DiL
                        +D+A  R L+P++  + +++G+  ed+++ +  D   l + L+D++
  gi|2542612    37    KLDgAAARPLAPtnaasakpqGRTREDkDRPLFEDIRYLGRLLgDVV 83

                    qDLHGedLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvA
                     +  G+ + ++v      +  +    D    + L   L  L P  ++ v
  gi|2542612    84 REQEGDAVFDVVETIRQTAVKFRREDDKAAAQTLEKMLRKLTPEQTVSVV 133

                    kailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKk
                    +a++    LAn+AE+ +   RRRi+ +        +sA     +   l k
  gi|2542612   134 RAFSYFSHLANIAEDRHHNRRRRIHALA-------GSAAQAGTVAYALDK 176

                    LvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq
                    L   ++ s + + +      +  vltAHPt   R+s+L  +  i    a
  gi|2542612   177 LKQAGDASSKTIKQFFEGALIVPVLTAHPTEVQRKSILDAQHDI----AR 222

                    LsAKDvtveDKkEL..DEALHRE.iqAAFRtDEiRRaqPtPqDEmRaGms
                    L A    +   +EL + EAL R ++   + t  +R a+ t  DE+   +s
  gi|2542612   223 LLAERDQPLTARELahNEALLRArVTTLWQTRMLRDARLTVADEIENALS 272

                    YiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGk
                    Y+  t  +  P     ++ AL   G+  R+P      +  sW+GGDRDG
  gi|2542612   273 YYRATFLDELPALYADIEEALAEHGLRARVP---AFFQMGSWIGGDRDG- 318

                    nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEE
                    nP vt     +       +    Y++qv  L  Els+    + L v A +
  gi|2542612   319 NPNVTAATLDEAISRQAAVIFEHYLEQVHKLGAELSV----SNLLVGASD 364
```

```
                    lyrtaardkvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER...
                      +  a             q P++  EPYR  L  v  +L  + R R ++
  gi|2542612   365 ALKALAAA--------SPDQSPhrVDEPYRRALIGVYTRLAAsARVRlge 406

                    .aRHLLAtGiseisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsL
                    ++  +   G    +  A +y + EeF   L +   sL       +A   L
  gi|2542612   407 gTVPVRSAGRGAAPVRATpYADAEEFAADLRVLTDSLALHHGESLATPRL 456

                    LDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeK
                      l+R    FG  L  +D+Rq s+ +  v+  +    ++ ++Y   +E
  gi|2542612   457 APLMRAAEVFGFHLASIDLRQSSDIHEAVVAELLARGGVEAdYAALPEAD 506

                    RqEWLlaELkGKRPLlgsDLPktEEvkDvldafr....vLAELPiDsFGa
                    +   Lla L   RPL  + L   +  k  l+ +++ + + A     +
  gi|2542612   507 KLRVLLAALADPRPLRSPYLDYSDLAKSELGVLErahaIRAQFGARAVRN 556

                    YiismataPsDvLAvELLqRECgv.............kqtLrvvPLFEkLA
                    Yiis + + sD + v LLq+E g+ +++ ++++ + ++ L v+PLFE +A
  gi|2542612   557 YIISHTETVSDLVEVLLLQKETGLfegtlgtphanaRNGLMVIPLFETIA 606

                    DLeAAPAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWq
                    DL+ A   +   F+ +++     +    qevm+GYsDs KD G l   W
  gi|2542612   607 DLRNASDIMRAFFAlpgVGELLAHQGHEQEVMLGYSDSNKDGGFLTSNWE 656

                    LYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinG
                    LY+A   ++    + G+KL lFHGRGGtvGRGGGPt  AiLsqPP t+nG
  gi|2542612   657 LYRAELALVDLFDERGIKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNG 706

                    slRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEW
                     +R t qGEvi   F   ++  r L    AAtLE  + P  ++Pk+ P +
  gi|2542612   707 QIRLTEQGEVIASKFANPEIGRRNLETVVAATLEATLAPHSnAPKqlPAF 756

                    RkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKR
                       m+ +   A   YR++v+  P F +YF + tP +E   +niGsRPa R
  gi|2542612   757 EATMQTLSDAAMASYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASR 806

                    kPsG....GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......
                    k   ++++ ie LRAiPW F+W q R  L  W G+G A    +d+ ++
  gi|2542612   807 KLQDpknrKIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVAAYLDgapdaa 856

                    KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL
                       K +  Lk m k+WPFF   l  ++mv AK D  +A+ y +L+    L
  gi|2542612   857 ERGKRVALLKKMNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVADKKL 906

                    .kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLn
                    +k   +++ +++  t d L +i G +  L   P L   ++ R +Y+  Ln
  gi|2542612   907 rKHVFERIVAEWHRTADALAEITGAHARLAANPLLARSIKNRFPYLDPLN 956

                    vfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPG
                     +q   +KR R               A +           n   r   G
  gi|2542612   957 HLQVELIKRHR----------------AGDT----------N--ARLRRG 978

                    LEDtLiLtmKGiAAGmqntG<-*
                    +     Lt+ GiAAG+ ntG
  gi|2542612   979 IH----LTINGIAAGLRNTG    994

gi|53718655|ref|YP_107641.1|: domain 1 of 1, from 37 to 994: score 300.0, E = 5.2e-87
                    *->siD.AqLRlLvP.........GKvsed.ekLieYDALLlDkFL.DiL
                        +D+A  R L+P++  + +++G+  ed+++ +  D   l + L+D++
  gi|5371865    37    KLDgAAARPLAPtnaasakpqGRTREDkDRPLFEDIRYLGRLLgDVV 83

                    qDLHGedLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvA
                     +  G+ + ++v      +  +    D    + L   L  L P  ++ v
  gi|5371865    84 REQEGDAVFDVVETIRQTAVKFRREDDKAAAQTLEKMLRKLTPEQTVSVV 133

                    kailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKk
                    +a++    LAn+AE+ +   RRRi+ +        +sA     +   l k
  gi|5371865   134 RAFSYFSHLANIAEDRHHNRRRRIHALA-------GSAAQAGTVAYALDK 176

                    LvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq
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                L   ++ s + + +      +  vltAHPt   R+s+L  +  i    a
gi|5371865   177 LKQAGDASSKTIKQFFEGALIVPVLTAHPTEVQRKSILDAQHDI----AR 222

                LsAKDvtveDKkEL..DEALHRE.iqAAFRtDEiRRaqPtPqDEmRaGms
                L A    +   +EL + EAL R ++   + t  +R a+ t  DE+   +s
gi|5371865   223 LLAERDQPLTARELahNEALLRArVTTLWQTRMLRDARLTVADEIENALS 272

                YiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGk
                Y+  t  +  P     ++ AL   G+  R+P      +  sW+GGDRDG
gi|5371865   273 YYRATFLDELPALYADIEEALAEHGLRARVP---AFFQMGSWIGGDRDG- 318

                nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEE
                nP vt     +       +    Y++qv  L  Els+    + L v A +
gi|5371865   319 NPNVTAATLDEAISRQAAVIFEHYLEQVHKLGAELSV----SNLLVGASD 364

                lyrtaardkvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER...
                  +  a             q P++  EPYR  L  v  +L  + R R ++
gi|5371865   365 ALKALAAA--------SPDQSPhrVDEPYRRALIGVYTRLAAsARVRlge 406

                .aRHLLAtGiseisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsL
                ++  +   G    +  A +y + EeF   L +   sL       +A   L
gi|5371865   407 gTVPVRSAGRGAAPVRATpYADAEEFAADLRVLTDSLALHHGESLATPRL 456

                LDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeK
                  l+R    FG  L  +D+Rq s+ +  v+  +    ++ ++Y   +E
gi|5371865   457 APLMRAAEVFGFHLASIDLRQSSDIHEAVVAELLARGGVEAdYAALPEAD 506

                RqEWLlaELkGKRPLlgsDLPktEEvkDvldafr....vLAELPiDsFGa
                +   Lla L   RPL  + L   +  k  l+ +++ + + A     +
gi|5371865   507 KLRVLLAALADPRPLRSPYLDYSDLAKSELGVLErahaIRAQFGARAVRN 556

                YiismataPsDvLAvELLqRECgv.............kqtLrvvPLFEkLA
                Yiis + + sD + v LLq+E g+ +++ ++++ + ++ L v+PLFE +A
gi|5371865   557 YIISHTETVSDLVEVLLLQKETGLfegtlgtphanaRNGLMVIPLFETIA 606

                DLeAAPAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWq
                DL+ A   +   F+ +++     +    qevm+GYsDs KD G l   W
gi|5371865   607 DLRNASDIMRAFFAlpgVGELLAHQGHEQEVMLGYSDSNKDGGFLTSNWE 656

                LYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinG
                LY+A   ++    + G+KL lFHGRGGtvGRGGGPt  AiLsqPP t+nG
gi|5371865   657 LYRAELALVDLFDERGIKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNG 706

                slRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEW
                 +R t qGEvi   F   ++  r L    AAtLE  + P  ++Pk+ P +
gi|5371865   707 QIRLTEQGEVIASKFANPEIGRRNLETVVAATLEATLAPHSnAPKqlPAF 756

                RkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKR
                   m+ +   A   YR++v+  P F +YF + tP +E   +niGsRPa R
gi|5371865   757 EAAMQTLSDAAMASYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASR 806

                kPsG....GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......
                k   ++++ ie LRAiPW F+W q R  L  W G+G A    +d+ ++
gi|5371865   807 KLQDpknrKIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVAAYLDgapdaa 856

                KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL
                   K +  Lk m k+WPFF   l  ++mv AK D  +A+ y +L+    L
gi|5371865   857 ERGKRVALLKKMNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVADKKL 906

                .kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLn
                +k   +++ +++  t d L +i G +  L   P L   ++ R +Y+  Ln
gi|5371865   907 rKHVFERIVAEWHRTADALAEITGAHARLAANPLLARSIKNRFPYLDPLN 956

                vfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPG
                 +q   +KR R                A +           n   r   G
gi|5371865   957 HLQVELIKRHR----------------AGDT----------N--ARLRRG 978

                LEDtLiLtmKGiAAGmqntG<-*
                +     Lt+ GiAAG+ ntG
gi|5371865   979 IH----LTINGIAAGLRNTG    994
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gi|126440608|ref|YP_001058119.1|: domain 1 of 1, from 37 to 994: score 300.0, E = 5.2e-87
                  *->siD.AqLRlLvP.........GKvsed.ekLieYDALLlDkFL.DiL
                      +D+A  R L+P++  + +++G+  ed+++ +  D   l + L+D++
  gi|1264406    37    KLDgAAARPLAPtnaasakpqGRTREDkDRPLFEDIRYLGRLLgDVV 83

                  qDLHGedLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvA
                   +  G+ + ++v      +  +    D    + L   L  L P  ++ v
  gi|1264406    84 REQEGDAVFDVVETIRQTAVKFRREDDKAAAQTLEKMLRKLTPEQTVSVV 133

                  kailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKk
                  +a++    LAn+AE+ +   RRRi+ +        +sA     +   l k
  gi|1264406   134 RAFSYFSHLANIAEDRHHNRRRRIHALA-------GSAAQAGTVAYALDK 176

                  LvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq
                  L   ++ s + + +      +  vltAHPt   R+s+L  +  i    a
  gi|1264406   177 LKQAGDASSKTIKQFFEGALIVPVLTAHPTEVQRKSILDAQHDI----AR 222

                  LsAKDvtveDKkEL..DEALHRE.iqAAFRtDEiRRaqPtPqDEmRaGms
                  L A    +   +EL + EAL R ++   + t  +R a+ t  DE+   +s
  gi|1264406   223 LLAERDQPLTARELahNEALLRArVTTLWQTRMLRDARLTVADEIENALS 272

                  YiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGk
                  Y+  t  +  P     ++ AL   G+  R+P      +  sW+GGDRDG
  gi|1264406   273 YYRATFLDELPALYADIEEALAEHGLRARVP---AFFQMGSWIGGDRDG- 318

                  nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEE
                  nP vt     +       +    Y++qv  L  Els+    + L v A +
  gi|1264406   319 NPNVTAATLDEAISRQAAVIFEHYLEQVHKLGAELSV----SNLLVGASD 364

                  lyrtaardkvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER...
                    +  a             q P++  EPYR  L  v  +L  + R R ++
  gi|1264406   365 ALKALAAA--------SPDQSPhrVDEPYRRALIGVYTRLAAsARVRlge 406

                  .aRHLLAtGiseisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsL
                  ++  +   G    +  A +y + EeF   L +   sL       +A   L
  gi|1264406   407 gTVPVRSAGRGAAPVRATpYADAEEFAADLRVLTDSLALHHGESLATPRL 456

                  LDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeK
                    l+R    FG  L  +D+Rq s+ +  v+  +    ++ ++Y   +E
  gi|1264406   457 APLMRAAEVFGFHLASIDLRQSSDIHEAVVAELLARGGVEAdYAALPEAD 506

                  RqEWLlaELkGKRPLlgsDLPktEEvkDvldafr....vLAELPiDsFGa
                  +   Lla L   RPL  + L   +  k  l+ +++ + + A     +
  gi|1264406   507 KLRVLLAALADPRPLRSPYLDYSDLAKSELGVLErahaIRAQFGARAVRN 556

                  YiismataPsDvLAvELLqRECgv.............kqtLrvvPLFEkLA
                  Yiis + + sD + v LLq+E g+ +++ ++++ + ++ L v+PLFE +A
  gi|1264406   557 YIISHTETVSDLVEVLLLQKETGLfegtlgtphanaRNGLMVIPLFETIA 606

                  DLeAAPAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWq
                  DL+ A   +   F+ +++     +    qevm+GYsDs KD G l   W
  gi|1264406   607 DLRNASDIMRAFFAlpgVGELLAHQGHEQEVMLGYSDSNKDGGFLTSNWE 656

                  LYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinG
                  LY+A   ++    + G+KL lFHGRGGtvGRGGGPt  AiLsqPP t+nG
  gi|1264406   657 LYRAELALVDLFDERGIKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNG 706

                  slRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEW
                   +R t qGEvi   F   ++  r L    AAtLE  + P  ++Pk+ P +
  gi|1264406   707 QIRLTEQGEVIASKFANPEIGRRNLETVVAATLEATLAPHSnAPKqlPAF 756

                  RkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKR
                     m+ +   A   YR++v+  P F +YF + tP +E   +niGsRPa R
  gi|1264406   757 EAAMQTLSDAAMASYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASR 806

                  kPsG....GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......
                  k   ++++ ie LRAiPW F+W q R  L  W G+G A    +d+ ++
  gi|1264406   807 KLQDpknrKIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVAAYLDgapdaa 856

                  KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL
                     K +  Lk m k+WPFF   l  ++mv AK D  +A+ y +L+    L
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  gi|1264406   857 ERGKRVALLKKMNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVADKKL 906

                   .kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLn
                   +k   +++ +++  t d L +i G +  L   P L   ++ R +Y+  Ln
  gi|1264406   907 rKHVFERIVAEWHRTADALAEITGAHARLAANPLLARSIKNRFPYLDPLN 956

                   vfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPG
                    +q   +KR R               A +           n   r   G
  gi|1264406   957 HLQVELIKRHR----------------AGDT----------N--ARLRRG 978

                   LEDtLiLtmKGiAAGmqntG<-*
                   +     Lt+ GiAAG+ ntG
  gi|1264406   979 IH----LTINGIAAGLRNTG    994

gi|126451534|ref|YP_001065355.1|: domain 1 of 1, from 67 to 1024: score 300.0, E = 5.2e-87
                   *->siD.AqLRlLvP.........GKvsed.ekLieYDALLlDkFL.DiL
                       +D+A  R L+P++  + +++G+  ed+++ +  D   l + L+D++
  gi|1264515    67    KLDgAAARPLAPtnaasakpqGRTREDkDRPLFEDIRYLGRLLgDVV 113

                   qDLHGedLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvA
                    +  G+ + ++v      +  +    D    + L   L  L P  ++ v
  gi|1264515   114 REQEGDAVFDVVETIRQTAVKFRREDDKAAAQTLEKMLRKLTPEQTVSVV 163

                   kailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKk
                   +a++    LAn+AE+ +   RRRi+ +        +sA     +   l k
  gi|1264515   164 RAFSYFSHLANIAEDRHHNRRRRIHALA-------GSAAQAGTVAYALDK 206

                   LvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq
                   L   ++ s + + +      +  vltAHPt   R+s+L  +  i    a
  gi|1264515   207 LKQAGDASSKTIKQFFEGALIVPVLTAHPTEVQRKSILDAQHDI----AR 252

                   LsAKDvtveDKkEL..DEALHRE.iqAAFRtDEiRRaqPtPqDEmRaGms
                   L A    +   +EL + EAL R ++   + t  +R a+ t  DE+   +s
  gi|1264515   253 LLAERDQPLTARELahNEALLRArVTTLWQTRMLRDARLTVADEIENALS 302

                   YiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGk
                   Y+  t  +  P     ++ AL   G+  R+P      +  sW+GGDRDG
  gi|1264515   303 YYRATFLDELPALYADIEEALAEHGLRARVP---AFFQMGSWIGGDRDG- 348

                   nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEE
                   nP vt     +       +    Y++qv  L  Els+    + L v A +
  gi|1264515   349 NPNVTAATLDEAISRQAAVIFEHYLEQVHKLGAELSV----SNLLVGASD 394

                   lyrtaardkvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER...
                     +  a             q P++  EPYR  L  v  +L  + R R ++
  gi|1264515   395 ALKALAAA--------SPDQSPhrVDEPYRRALIGVYTRLAAsARVRlge 436

                   .aRHLLAtGiseisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsL
                   ++  +   G    +  A +y + EeF   L +   sL       +A   L
  gi|1264515   437 gTVPVRSAGRGAAPVRATpYADAEEFAADLRVLTDSLALHHGESLATPRL 486

                   LDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeK
                     l+R    FG  L  +D+Rq s+ +  v+  +    ++ ++Y   +E
  gi|1264515   487 APLMRAAEVFGFHLASIDLRQSSDIHEAVVAELLARGGVEAdYAALPEAD 536

                   RqEWLlaELkGKRPLlgsDLPktEEvkDvldafr....vLAELPiDsFGa
                   +   Lla L   RPL  + L   +  k  l+ +++ + + A     +
  gi|1264515   537 KLRVLLAALADPRPLRSPYLDYSDLAKSELGVLErahaIRAQFGARAVRN 586

                   YiismataPsDvLAvELLqRECgv............kqtLrvvPLFEkLA
                   Yiis + + sD + v LLq+E g+ +++ ++++ + ++ L v+PLFE +A
  gi|1264515   587 YIISHTETVSDLVEVLLLQKETGLfegtlgtphanaRNGLMVIPLFETIA 636

                   DLeAAPAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWq
                   DL+ A   +   F+ +++     +    qevm+GYsDs KD G l   W
  gi|1264515   637 DLRNASDIMRAFFAlpgVGELLAHQGHEQEVMLGYSDSNKDGGFLTSNWE 686

                   LYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinG
                   LY+A   ++    + G+KL lFHGRGGtvGRGGGPt  AiLsqPP t+nG
  gi|1264515   687 LYRAELALVDLFDERGIKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNG 736
```

```
                    slRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEW
                     +R t qGEvi   F   ++  r L    AAtLE  + P  ++Pk+ P +
  gi|1264515   737 QIRLTEQGEVIASKFANPEIGRRNLETVVAATLEATLAPHSnAPKqlPAF 786

                    RkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKR
                       m+ +   A   YR++v+  P F +YF + tP +E   +niGsRPa R
  gi|1264515   787 EAAMQTLSDAAMASYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASR 836

                    kPsG....GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......
                    k   ++++ ie LRAiPW F+W q R  L  W G+G A    +d+ ++
  gi|1264515   837 KLQDpknrKIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVAAYLDgapdaa 886

                    KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL
                       K +  Lk m k+WPFF   l  ++mv AK D  +A+ y +L+    L
  gi|1264515   887 ERGKRVALLKKMNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVADKKL 936

                    .kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLn
                    +k   +++ +++  t d L +i G +  L   P L   ++ R +Y+  Ln
  gi|1264515   937 rKHVFERIVAEWHRTADALAEITGAHARLAANPLLARSIKNRFPYLDPLN 986

                    vfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPG
                     +q   +KR R               A +           n   r   G
  gi|1264515   987 HLQVELIKRHR----------------AGDT----------N--ARLRRG 1008

                    LEDtLiLtmKGiAAGmqntG<-*
                    +     Lt+ GiAAG+ ntG
  gi|1264515  1009 IH----LTINGIAAGLRNTG    1024

gi|167003501|ref|ZP_02269287.1|: domain 1 of 1, from 37 to 994: score 299.9, E = 5.6e-87
                    *->siD.AqLRlLvP.........GKvsed.ekLieYDALLlDkFL.DiL
                        +D+A  R L+P++  + +++G+  ed+++ +  D   l + L+D++
  gi|1670035    37    KLDgAAARPLAPtnaasakpqGRTREDkDRPLFEDIRYLGRLLgDVV 83

                    qDLHGedLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvA
                     +  G+ + ++v      +  +    D    + L   L  L P  ++ v
  gi|1670035    84 REQEGDAVFDVVETIRQTAVKFRREDDKAAAQTLEKMLRKLTPEQTVSVV 133

                    kailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKk
                    +a++    LAn+AE+ +   RRRi+ +        +sA     +   l k
  gi|1670035   134 RAFSYFSHLANIAEDRHHNRRRRIHALA-------GSAAQAGTVAYALDK 176

                    LvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq
                    L   ++ s + + +      +  vltAHPt   R+s+L  +  i    a
  gi|1670035   177 LKQAGDASSKTIKQFFEGALIVPVLTAHPTEVQRKSILDAQHDI----AR 222

                    LsAKDvtveDKkEL..DEALHRE.iqAAFRtDEiRRaqPtPqDEmRaGms
                    L A    +   +EL + EAL R ++   + t  +R a+ t  DE+   +s
  gi|1670035   223 LLAERDQPLTARELahNEALLRArVTTLWQTRMLRDARLTVADEIENALS 272

                    YiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGk
                    Y+  t  +  P     ++ AL   G+  R+P      +  sW+GGDRDG
  gi|1670035   273 YYRATFLDELPALYADIEEALAEHGLRARVP---AFFQMGSWIGGDRDG- 318

                    nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEE
                    nP vt     +       +    Y++qv  L  Els+    + L v A +
  gi|1670035   319 NPNVTAATLDEAISRQAAVIFEHYLEQVHKLGAELSV----SNLLVGASD 364

                    lyrtaardkvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER...
                      +  a             q P++  EPYR  L  v  +L  + R R ++
  gi|1670035   365 ALKALAAA--------SPDQSPhrVDEPYRRALIGVYTRLAAsARVRlge 406

                    .aRHLLAtGiseisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsL
                    ++  +   G    +  A +y + EeF   L +   sL       +A   L
  gi|1670035   407 gTVPVRSAGRGAAPVRATpYADAEEFAADLRVLTDSLALHHGESLATPRL 456

                    LDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeK
                      l+R    FG  L  +D+Rq s+ +  v+  +    ++ ++Y   +E
  gi|1670035   457 APLMRAAEVFGFHLASIDLRQSSDIHEAVVAELLARGGVEAdYAALPEAD 506

                    RqEWLlaELkGKRPLlgsDLPktEEvkDvldafr....vLAELPiDsFGa
                    +   Lla L   RPL  + L   +  k  l+ +++ + + A     +
```

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  gi|1670035   507 KLRVLLAALADPRPLRSPYLDYSDLAKSELGVLErahaIRAQFGARAVRN 556

                   YiismataPsDvLAvELLqRECgv.............kqtLrvvPLFEkLA
                   Yiis + + sD + v LLq+E g+ +++ ++++ + ++ L v+PLFE +A
  gi|1670035   557 YIISHTETVSDLVEVLLLQKETGLfegtlgtphanaRNGLMVIPLFETIA 606

                   DLeAAPAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWq
                   DL+ A   +   F+ +++     +    qevm+GYsDs KD G l   W
  gi|1670035   607 DLRNASDIMRAFFAlpgVGELLAHQGHEQEVMLGYSDSNKDGGFLTSNWE 656

                   LYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinG
                   LY+A   ++    + G+KL lFHGRGGtvGRGGGPt  AiLsqPP t+nG
  gi|1670035   657 LYRAELALVDLFDERGIKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNG 706

                   slRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEW
                    +R t qGEvi   F   ++  r L    AAtLE  + P  ++Pk+ P +
  gi|1670035   707 QIRLTEQGEVIASKFANPEIGRRNLETVVAATLEATLAPHSnAPKqlPAF 756

                   RkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKR
                      m+ +   A   YR++v+  P F +YF + tP +E   +niGsRPa R
  gi|1670035   757 EAAMQTLSDAAMASYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASR 806

                   kPsG....GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......
                   k   ++++ ie LRAiPW F+W q R  L  W G+G A    +d+ ++
  gi|1670035   807 KLQDpknrKIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVAAYLDgapdaa 856

                   KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL
                      K +  Lk m k+WPFF   l  ++mv AK D  +A+ y +L+    L
  gi|1670035   857 ERGKRVALLKKMNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVADKKL 906

                   .kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLn
                   +k   +++ +++  t d L +i G +  L   P L   ++ R +Y+  Ln
  gi|1670035   907 rKHVFERIVAEWHRTADALAEITGAHARLAANPLLAHSIKNRFPYLDPLN 956

                   vfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPG
                    +q   +KR R               A +           n   r   G
  gi|1670035   957 HLQVELIKRHR----------------AGDT----------N--ARLRRG 978

                   LEDtLiLtmKGiAAGmqntG<-*
                   +     Lt+ GiAAG+ ntG
  gi|1670035   979 IH----LTINGIAAGLRNTG    994

gi|260101538|ref|ZP_05751775.1|: domain 1 of 1, from 1 to 898: score 299.9, E = 5.6e-87
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                    v           +L     +    L G++L   +
  gi|2601015     1    ---------MTEEVK----------ILTNLLNESTEQLIGKELFTKI 28

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   q    +sA+       k  +EL  ++ sLd  + i+vA+ +  +  L n+
  gi|2601015    29 QNLIKISAD-------KNYQELEDQIASLDNREMIVVARYFATLPLLINI 71

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    E+velA +  +      D+    + t +         +v +  K  +E+
  gi|2601015    72 SEDVELASKVYVLNNTNQDYLGKLNDTID---------IVAQK-KNAKEI 111

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    e +    v  vltAHPtq  R+ +L    +i   L         +  ++
  gi|2601015   112 LEKV---NVVPVLTAHPTQVQRKTVLELTDKIHKLLRNYREVKNGIINRE 158

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   E  E L   i     tD iR  +     E+   + Y+H  +   + KF
  gi|2601015   159 EWTEELRACIEILMQTDIIRGHKLKVSNEITNVLTYYHKSLISAITKFTA 208

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   R     K  G+   +P   P i    W+GGDRDG nP vt +  +    L
  gi|2601015   209 RYKELAKKHGLD--IPDATP-ITMGMWIGGDRDG-NPYVTADTLKLSATL 254

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                      +    Yi q+  L   +s+             y  +  +  v +
  gi|2601015   255 QSQVIFEYYIKQINQLYRSISL-----------STSYMKPSTE--VMHLS 291
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                    EFWKqvPP...tEPYRvi.......LGdvRDKLYntRERaRHLLAtGise
                    E      P +++EPYR      +++L     KL n       L    +
  gi|2601015   292 ELSNDDSPfrtNEPYRRAfyyiesrLVRSEQKLLNITNQHSFLKERDVEH 341

                    isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                    +     y +  eF   LE+  +sL e  D++       ++L  +  FG
  gi|2601015   342 LDQIPAYENAQEFKADLEIIKRSLEENHDQAVVKSYFTEILEAIDVFGFH 391

                    LvKLDiRqEseRqtDvlDAitthLeiG.sYReWsEeKRqEWLlaELkGK.
                    L  +D+Rq+s  +   +  + +  ei + Y + sE  +   Ll EL   +
  gi|2601015   392 LATIDMRQDSSVNEACVAELLKSAEICdHYSDLSEKEKVSLLLNELNNDp 441

                    RPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDv
                    R L     Pk E ++  l  ++   +L ++ + D     iis + + sD+
  gi|2601015   442 RNLHANNKPKSELLQKELKIYKTARDLKdrlgEDVIKQHIISHTESVSDM 491

                    LAvELLqRECgvkqt....LrvvPLFEkLADLeAAPAavekLFsiD....
                    L   ++ +E  +   ++ +++vvPLFE + DL+ A   ++    +D  ++
  gi|2601015   492 LEQAIMLKEYDLLDNqsarVQVVPLFETVEDLNNARDIIKEYLNLDivkk 541

                    WYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                    W + + +  qevm+GYsDs KD G l+  W LYkAq ++  +  + G+K+
  gi|2601015   542 WLVSQHN-YQEVMLGYSDSNKDGGYLASCWNLYKAQKDLTAIGEELGIKI 590

                    vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                    +  HGRGGtvGRGGGP   Ai +qP  tin  +R+t qGE+i   +G  +
  gi|2601015   591 TYMHGRGGTVGRGGGPSYEAITAQPFKTINDRIRMTEQGEIIQNKYGNKD 640

                    LCFrsLqRFtAAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvv
                      +  L     At++      +   +   ++R  m+e+     E Y+ +v
  gi|2601015   641 AAYYNLEMLVSATVDRIASKQIVSEeyiADFRSSMDEIVTESNEIYKKLV 690

                    vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWt
                    +  P F +YF  AtP  E   +niGsRPa Rk      sLRAiPW+F+W
  gi|2601015   691 FENPNFLDYFLQATPIKEISNLNIGSRPASRKKLSDFSSLRAIPWVFSWS 740

                    qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                    q R   P W GvG AFKh id D  nlq L+ mY+ WPFF   l  ++mv
  gi|2601015   741 QSRVMFPGWYGVGSAFKHFIDADKNNLQELRHMYQGWPFFHALLSNVDMV 790

                    FAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE
                      K    iA  y +L   E  k   + + ++++ tk+++L+i GH DlL
  gi|2601015   791 LSKSNMEIAKQYAELCQDEKTKSVFDIIYQEWKLTKQIILQIEGHDDLLS 840

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                      P LK  l  R +Y   Ln +q   +KR R  + +   r  +
  gi|2601015   841 DAPNLKNSLAARMPYFNILNYIQLEMIKRDRKDEIQGVFRSII------- 883

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +       + +n                  G+A G+ n G
  gi|2601015   884 P-------ITIN-----------------GVASGLRNSG    898

gi|160897676|ref|YP_001563258.1|: domain 1 of 1, from 10 to 949: score 299.8, E = 5.7e-87
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       + D         K  +d  Lie D  Ll + L+D++ +  G    E
  gi|1608976    10    ARDDRRDDKPVRKTDKDLPLIE-DIRLLGRILgDVIREQEGVAAFEL 55

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls  +    D      L   L +L    ++ v +a+     LAn
  gi|1608976    56 IEQVRQLSVTFRRDADETADRALKRLLKGLTTDQTVSVIRAFTYFSHLAN 105

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAE+ +   RRR    +       a  t E  iE   l +L   +  s
  gi|1608976   106 LAED-RHHIRRRAVHER-------AGNTQEGSIEVALARLRWAG-ISAGT 146

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL.........aqLs
                    v + L    v  vltAHPt   R s+L  +  i   L  +++   +aqL+
  gi|1608976   147 VAQTLAKSYVAPVLTAHPTEVQRQSILVAERDISQLLaaredivarAQLY 196

                    ..AKDvtveDKkELDEA.LHREiqAAFRtDEiRRaqPtPqDEmRaGmsYi
                    ++AKD       E  EA+L   +   + t  +R ++ t  DE+   +sY+
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  gi|1608976   197 nsAKDALTPRELERNEAqLRARVSQLWQTRLLRYSKLTVADEIENALSYY 246

                    HEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknP
                      t  + +PK     +  L n      lP    L +   W+GGDRDG nP
  gi|1608976   247 EATFLREIPKLYAQLEQELGNT-----LPVHSFL-RMGHWIGGDRDG-NP 289

                    RvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsm.WRCnd...ELRvRA
                     vt             +A   Y+  v  L  Els++ R  d ++E+ + A
  gi|1608976   290 NVTAQSLELALSRQADVALRHYLREVHYLGGELSLsQRLADvtpEMQALA 339

                    EElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntR......
                    E    t                   EPYR  L  +  +L  t +  +++
  gi|1608976   340 ERSPDTNEHR--------------SDEPYRRALTGIYARLAATLkvltgg 375

                    ERaRHLLAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsL
                    E aRH +A      + +A y   EeFL  L +   sL      v+A   L
  gi|1608976   376 EAARHAVA------PQNA-YASPEEFLADLRVIDDSLSRNHGEVLAPQRL 418

                    LDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeK
                      l+R v  FG  L  +D+Rq s+++ +v+  +     + + Y    E+
  gi|1608976   419 RPLMRAVQVFGFHLATVDLRQSSDKHEEVVAELLAAARLEpDYSGLQEDA 468

                    RqEWLlaELkGKRPL..lgsDLPktE..EvkDvldafrvLAELPiDsFGa
                    +   L+  L+  RPL+ +g+D     ++E++    a r  A L  ++
  gi|1608976   469 KCALLVRLLEEARPLrvVGADYSEHArgELAIFETARRLRAALGAEAIRH 518

                    YiismataPsDvLAvELLqRECg.vkqtL........rvvPLFEkLADLe
                     iis + + sD L v LLq+E g ++ tL+++   +  vvPLFE + DL+
  gi|1608976   519 CIISHTESVSDLLEVLLLQKEAGlLRGTLddgaicdvIVVPLFETIGDLR 568

                    AAPAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYk
                     A   + + F  +++   + r  G q++m+GYsDs KD G +   W LY+
  gi|1608976   569 SASPIMRRYFQlpgVAAMVQRSGGEQDIMLGYSDSNKDGGIFTSNWELYR 618

                    AqEEii....KvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtin
                    A   +++  +  A  +G+ L +FHGRGGtvGRGGGP   AiL+qPP t+
  gi|1608976   619 AEISLVelfdELADSHGISLRMFHGRGGTVGRGGGPSYQAILAQPPGTVR 668

                    GslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPEWRk
                    G +R t qGEvi   +   ++  r L    AAtLE  +  P   kP  R
  gi|1608976   669 GQIRLTEQGEVIASKYANPEIGRRNLETLVAATLEATLLQPT--KPATRA 716

                    LmeemAvv...AtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaK
                     ++  A  ++     YR++v+  P F  YF + tP  E   +niGsRPa
  gi|1608976   717 FLDAAAFLsdaSMGAYRALVYETPGFTSYFFSSTPIREIAELNIGSRPAS 766

                    RkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid...KDiK.n
                    RkPs  ie LRAiPW F+W q R  LP W G+GAA K  id+++KD K
  gi|1608976   767 RKPSQKIEDLRAIPWGFSWGQCRLTLPGWYGFGAAVKAFIDqpgKDGKaQ 816

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFG
                    l  L+ mY++WPFFR  l  ++mv AK D  +A+ y +L+    L++
  gi|1608976   817 LALLQKMYRQWPFFRTLLSNMDMVLAKSDLNLASRYADLVPDARLrRRIF 866

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                      + +++  t d L +i G k  L     L   +R R +Yi
  gi|1608976   867 SAIEAEWHSTVDALARITGDKQRLAHNEALARSIRHRFPYI--------- 907

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                          DP ++  l+ +l + + + +    de +k             +
  gi|1608976   908 ------DPLHH--LQVELVRRWRAGQ---TDERIKTG-----------I 934

                    iLtmKGiAAGmqntG<-*
                     L + GiAAG+ ntG
  gi|1608976   935 HLSINGIAAGVRNTG    949

gi|89143166|emb|CAJ44471.1|: domain 1 of 1, from 1 to 940: score 299.8, E = 5.9e-87
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                              +      s+++++i  +  +l   L+D    + Ge+
  gi|8914316     1    ------MAFNKLESSNNQEIISEEVGILKELLdDATRGMAGEQGLTT 41
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                vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                +q   El        D    e L   +  +   D ++  + ++ +  L n
gi|8914316    42 IQHLVEL-------YDEGDYEALTQAISEMTNDDMVVASRYFSLLPLLIN 84

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                + E+v+lAy    k        DE+     s   Et+  +v       +
gi|8914316    85 ISEDVDLAYEVNRKNNI-----DESYLGKLS---ETFD-VVAES----DN 121

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLs.AKD.vtve
                  + L n  v  vltAHPtq  R+ +L     i   L +  + KD++
gi|8914316   122 ARDILENVNVVPVLTAHPTQVQRKTMLELTNHIHELLRKHRdVKDgLINK 171

                DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                DK   D  L R +    +tD iR  +   + E+   m Y+   + k + K
gi|8914316   172 DKWYAD--LRRYVEIMMKTDIIREKKLKVKNEITNVMEYYNSSLIKAISK 219

                FLRRvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRD
                         K + +   +  d P +i    W+GGDRDG nP vt E  +
gi|8914316   220 ----LSHEFKRLAVEKGIELDNPTpITMGMWIGGDRDG-NPFVTAETLKL 264

                vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                   L   +  n Yi++v  L   +s+    + L    E +   a+    +
gi|8914316   265 CATLQSEVILNYYIEKVVNLYRSFSL---SSRLTEVSETVAEMAKLSPDT 311

                KyYiEFWKqvPPtEPYRviLGdvRDKLYnt..........RERaRHLLAt
                  Y E       +EPYR     +  KL  t    + ++ ++ER    L
gi|8914316   312 SVYRE-------NEPYRRAFSYIQSKLIQTllffkagnfsKERVAKRLSE 354

                Gi.......seisEeAv.................ytkvEeFLEPLELCY
                 ++ ++ ++ e+  + v+++ +++ +  ++++++ y   E F + L
gi|8914316   355 NVrlgsvstGEVVADFVhdrlsqslqavsqqttefYETAEAFHDDLLAIK 404

                ksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAit
                 sL e  D v+  G   +lL  v  FG  L  +D+Rq+s  +   +  +
gi|8914316   405 NSLLENDDSVLISGDFEELLQAVEVFGFYLATIDMRQDSSVHEACVAELL 454

                tHLei.GsYReWsEeKRqEWLlaELkGK.RPLlgsDLPktEEvkDvldaf
                +  +i   Y e  E  +   Ll EL+  +R L    + k E ++  l  f
gi|8914316   455 KSANIvDNYSELTEVEKVAVLLKELQEDpRTLSSTNVSKSETLEKELAIF 504

                rvLAELPiDsFG.....aYiismataPsDvLAvELLqRECgv....kqtL
                r  A L  D  G++  +  iis + + sD+    +L +E g+ ++++  +
gi|8914316   505 RT-ARLLKDYLGeevikQHIISHTESVSDMFELAILLKEVGLvdteRARV 553

                rvvPLFEkLADLeAAPAavekLFsiDWYinri...dGKqevmvGYsDsGK
                ++vPLFE + DLe     +++    D  +  i++++  qe+m+GYsDs K
gi|8914316   554 QIVPLFETIEDLENSNEIMKQYLGYDIVKRWIknsNNYQEIMLGYSDSNK 603

                DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                D G ls  W LYkAq E+ K+  + G+K++ FHGRGGtvGRGGGP   Ai
gi|8914316   604 DGGYLSSGWTLYKAQNELTKIGEERGIKITFFHGRGGTVGRGGGPSYDAI 653

                LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                 sqP  ti+  +R t qGEvi   +G  +  +  L     AtL+  +
gi|8914316   654 TSQPFGTIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLVSATLDRMVTRQ 703

                vsPkPE...WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGk
                +    E  ++R++m+ +       YR +v+    F EYF  A P  E
gi|8914316   704 ITDPDElvdFREIMDSIVQDSNGVYRDLVFGNEHFYEYFFEASPIKEVSS 753

                mniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid
                +niGsRPa Rk    i  LRAiPW+F+W q R  LP W GvG AF h i+
gi|8914316   754 LNIGSRPAARKTITDISGLRAIPWVFSWSQNRIMLPGWYGVGSAFNHYIE 803

                KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL
                 +  nl kL+ m+++WPFFR  l  ++mv  K D  iA  y +L  +Ee+
gi|8914316   804 AEEGNLEKLQHMFETWPFFRSLLSNVDMVLSKSDMNIAFHYAQLAESEEV 853

                kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnv
                +   + + d+++ tk+ +L i  H D LE  P+LK  l  R +Y   Ln
gi|8914316   854 RSVFNIILDEWQLTKNVILAIEKHDDFLEESPFLKASLDFRLPYFNVLNY 903
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                  fqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGL
                  +q   +KR+R  +              dE       L+++
  gi|8914316   904 IQIELIKRLRNNNLT-----------DDEI-----SLIHIT--------- 928

                  EDtLiLtmKGiAAGmqntG<-*
                         + GiA G+ n G
  gi|8914316   929 -------INGIATGLRNSG    940

gi|218767367|ref|YP_002341879.1|: domain 1 of 1, from 1 to 900: score 299.7, E = 6.4e-87
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2187673     1    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 38

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2187673    39 ETVKLLSTS----DDSAALIE--KVLPQLDEQQTHDLTLACGLFAQILNI 82

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AE+v+   RR i+          +    E  + Et+++L        + v
  gi|2187673    83 AEDVHHERRRQIHEEA-------GRGGAEGSLTETVRRLKAGK-ADGKSV 124

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                     L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|2187673   125 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 174

                  DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                   ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|2187673   175 LRREIDTILLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 220

                  FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    R+++   +      R+P    ++k   W+GGDRDG nP v  E  R
  gi|2187673   221 LYRKMEHDFQTAYPDVRVP---DILKIGGWIGGDRDG-NPFVSAETLRFA 266

                  CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                            +Y   ++ L  E +ls+ R      v A   ++
  gi|2187673   267 FRRHADAVFRFYRGELDKLYRElpLSIRRVKVNGDVMALSDKSPDEET-- 314

                  vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                               +EPYR  +  +   +     +aR L+L  G      e
  gi|2187673   315 ----------ARAEEPYRRAIAYI---MARAMGKARALgLGMGCKFGFLE 351

                  AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                    y    eFL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
  gi|2187673   352 P-YASAQEFLDDLKKLQHSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 400

                  DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                  D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL+ +RPL+ +
  gi|2187673   401 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELSHQRPLYSP 450

                  DLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAvELL
                   +   +  +  l  f++ +++  E   D+    iis +  PsD LA  LL
  gi|2187673   451 FITYSDHTRHELAIFNearkIKDEFGEDAVTQSIISNCEQPSDLLALALL 500

                  qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                   +E g+   +++++k  + +vPLFE +  Le A   +e +F +DWY   +
  gi|2187673   501 LKETGLlavengkpKSRINIVPLFETIEALENACPVMETMFRLDWYGALL 550

                  dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                  + +++ qe+m+GYsDs KD G +   W LY+A   ++   Kky v++ lF
  gi|2187673   551 ESRgniQEIMLGYSDSNKDGGYVTSSWCLYQAELGLVELFKKYDVRMRLF 600

                  HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                  HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|2187673   601 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 650

                  rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                  r L    AAtLE  + P    k    kLm+++  v    YR ++   P F
  gi|2187673   651 RNLETLVAATLEASILP--DKKDPDAKLMQDLSDVSFKYYRELITH-PDF 697

                  vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
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                    ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
  gi|2187673   698 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 747

                    PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                    P W G+G A     +     l  L+E  +  PFF   l  +E v AK D
  gi|2187673   748 PAWYGFGSAVETLCEGNPDTLAALREHAQSNPFFQAMLSNMEQVMAKTDI 797

                    GiAaLyDkLLvaEe.LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     +A  y  L  + ++ k     ++++Y   ++ LL +    +lL     L
  gi|2187673   798 TLAENYAGLSESPDkAKVIFGMIKEEYRRSRKALLDLLQTEELLRDNRSL 847

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                       l LR +Y+  Ln +q   LKR+R                  E+   +
  gi|2187673   848 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 879

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      L+ +               Lt+ G+A G+ ntG
  gi|2187673   880 HALLMVH--------------LTINGVAQGLRNTG    900

gi|11267798|pir||D81953: domain 1 of 1, from 18 to 917: score 299.7, E = 6.4e-87
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|1126779    18    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 55

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|1126779    56 ETVKLLSTS----DDSAALIE--KVLPQLDEQQTHDLTLACGLFAQILNI 99

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+   RR i+          +    E  + Et+++L        + v
  gi|1126779   100 AEDVHHERRRQIHEEA-------GRGGAEGSLTETVRRLKAGK-ADGKSV 141

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                       L n sv  vltAHPt    R  +L  n RiR  L q+++    D
  gi|1126779   142 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 191

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|1126779   192 LRREIDTILLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 237

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R+++   +      R+P    ++k   W+GGDRDG nP v  E  R
  gi|1126779   238 LYRKMEHDFQTAYPDVRVP---DILKIGGWIGGDRDG-NPFVSAETLRFA 283

                    CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                              +Y   ++ L  E +ls+ R      v A   ++
  gi|1126779   284 FRRHADAVFRFYRGELDKLYRElpLSIRRVKVNGDVMALSDKSPDEET-- 331

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                                 +EPYR  +  +   +     +aR L+L  G      e
  gi|1126779   332 ----------ARAEEPYRRAIAYI---MARAMGKARALgLGMGCKFGFLE 368

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y    eFL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
  gi|1126779   369 P-YASAQEFLDDLKKLQHSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 417

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL+ +RPL+ +
  gi|1126779   418 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELSHQRPLYSP 467

                    DLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAvELL
                     +   +  +  l  f++ +++  E   D+    iis +  PsD LA  LL
  gi|1126779   468 FITYSDHTRHELAIFNearkIKDEFGEDAVTQSIISNCEQPSDLLALALL 517

                    qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                     +E g+   +++++k  + +vPLFE +  Le A   +e +F +DWY   +
  gi|1126779   518 LKETGLlavengkpKSRINIVPLFETIEALENACPVMETMFRLDWYGALL 567

                    dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                    + +++ qe+m+GYsDs KD G +   W LY+A   ++   Kky v++ lF
  gi|1126779   568 ESRgniQEIMLGYSDSNKDGGYVTSSWCLYQAELGLVELFKKYDVRMRLF 617
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                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|1126779   618 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 667

                    rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                    r L    AAtLE  + P    k    kLm+++  v    YR ++   P F
  gi|1126779   668 RNLETLVAATLEASILP--DKKDPDAKLMQDLSDVSFKYYRELITH-PDF 714

                    vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                    ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
  gi|1126779   715 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 764

                    PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                    P W G+G A     +     l  L+E  +  PFF   l  +E v AK D
  gi|1126779   765 PAWYGFGSAVETLCEGNPDTLAALREHAQSNPFFQAMLSNMEQVMAKTDI 814

                    GiAaLyDkLLvaEe.LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     +A  y  L  + ++ k     ++++Y   ++ LL +    +lL     L
  gi|1126779   815 TLAENYAGLSESPDkAKVIFGMIKEEYRRSRKALLDLLQTEELLRDNRSL 864

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                       l LR +Y+  Ln +q   LKR+R                  E+   +
  gi|1126779   865 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 896

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      L+ +               Lt+ G+A G+ ntG
  gi|1126779   897 HALLMVH--------------LTINGVAQGLRNTG    917

gi|222111549|ref|YP_002553813.1|: domain 1 of 1, from 7 to 949: score 299.6, E = 6.6e-87
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                         DA        K  +d  Li+ D  Ll + L+D++ +  G    +
  gi|2221115     7    KTDAAAASAPARKTDKDLPLIQ-DIRLLGRILgDVIREQEGVAAYDL 52

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls  +    D +    L   L +L    ++ v +a+     LAn
  gi|2221115    53 VEQVRKLSVAFRRDADHEADKALKKLLKGLTGDQTVSVIRAFTYFSHLAN 102

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAE+ +   RRR    +       a    E  iE  l +L   +  +P
  gi|2221115   103 LAED-RHHIRRRAVHER-------AGSAQEGSIEVALARLRWAG-IAPRT 143

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL.........aqLs
                    v + L    v  vltAHPt   R+s+L  +  i   L+++++ + +aqL+
  gi|2221115   144 VAQTLATSYVAPVLTAHPTEVQRKSILDAEREIALLLtqrddiqarAQLY 193

                    ..AKD.vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYi
                    ++AKD++t+ +    +  L   +   + t  +R ++ t  DE+   +sY+
  gi|2221115   194 nsAKDtLTPRELAANEAQLRARVAQLWQTRLLRYSKLTVADEIENALSYY 243

                    HEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknP
                      t  + +PK     +   + +G    +   +  ++   W+GGDRDG nP
  gi|2221115   244 EYTFLHEIPKIYAELE---RELGGSHPV---ASFLRMGQWIGGDRDG-NP 286

                    RvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEly
                     v  +           +A   Y+  v  L  Els+    + + v AE l+
  gi|2221115   287 NVSADTLALALRRQAEVALRHYLTEVHHLGRELSL--SSNLVQVSAEMLQ 334

                    rtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntR......ERaR
                      a++     +           EPYR  L  v  +L  t ++ +++E aR
  gi|2221115   335 LAARSPDTSEH--------RRDEPYRRALTGVYARLAATLrdltggEAAR 376

                    HLLAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlL
                    H +A      + +A y    +FL  L +   sL      ++    L  l+
  gi|2221115   377 HAVA------PQNA-YASAGDFLADLRVIEASLRSHRGAALVGERLRPLM 419

                    RqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEW
                    R v  FG  L  +D+Rq s+ +  v+  +     + s+Y   +E  R+
  gi|2221115   420 RAVEVFGFHLATVDLRQSSDQHERVVAELLATARVESdYEALPEPARRAL 469

                    LlaELkGKRPLlgsDLPktE....EvkDvldafrvLAE.LPiDsFGaYii
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                    Ll  L   RPL     P  E++++Ev+ + ++ r + E+   D+   Yii
  gi|2221115   470 LLRLLCDARPLRVVGAPYSEhttgEVA-IFETARQMRErYGDDAIRHYII 518

                    smataPsDvLAvELLqRECgv.........kqtLrvvPLFEkLADLeAAP
                    s + + sD L v LLq+E g+ +++ +++ +  L vvPLFE + DL+ A
  gi|2221115   519 SHTETVSDLLEVLLLQKEVGLlqgtldtgaRADLIVVPLFETIEDLRNAA 568

                    AavekLFsiDWYinrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqE
                      +   ++i      +  ++  q++m+GYsDs KD G +   W LY+A
  gi|2221115   569 PIMREFYAIPGIAQLVRasgAEQDIMLGYSDSNKDGGIFTSNWELYRAEI 618

                    EiiKv.....AKkyG..vKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtin
                     ++   ++ +A + G++++L +FHGRGGtvGRGGGP   AiL+qPP t+
  gi|2221115   619 ALVALfdemnAAQAGtpIQLRMFHGRGGTVGRGGGPSYQAILAQPPGTVR 668

                    GslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHG.mnPPvsPkPEWR
                    G +R t qGEvi   +   ++  r L    AAtLE   ++P  s    +
  gi|2221115   669 GQIRLTEQGEVIASKYANPEIGRRNLETLVAATLEATlLQPTKSATKAFL 718

                    kLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRk
                    +  e++     E YR++v+  P F +YF   tP  E   +niGsRPa Rk
  gi|2221115   719 EAAEQLSQASMEAYRALVYETPGFTDYFFNSTPIREIAELNIGSRPASRK 768

                    PsGGiesLRAiPWiFaWtqtRFHLPvWLGvGA...AFKhAidKDiK.nlq
                     s  ie LRAiPW F+W q R  LP W G+GA  +AF hA  KD K  l
  gi|2221115   769 ASQQIEDLRAIPWGFSWGQCRLTLPGWFGFGAavdAFTHAPGKDPKaQLA 818

                    kLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL..kPFGk
                     L+ mY++WPFFR  l  ++mv AK D  +A+ y +L+    L++k FG
  gi|2221115   819 LLQKMYRQWPFFRTLLSNMDMVLAKSDLALASRYSELVADARLrkKVFG- 867

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                     + ++++ t d L +i G k  L     L   +R R +Yi  L  +q
  gi|2221115   868 VIEAEWQRTADALTRITGEKQRLAANTALARSIRHRFPYIDPLHHLQVEL 917

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    ++R R  +              dE     +  +++
  gi|2221115   918 VRRWRAGQ-------------GDER---VQTGIHIS-------------- 937

                    LtmKGiAAGmqntG<-*
                      + GiAAG+ ntG
  gi|2221115   938 --INGIAAGLRNTG    949

gi|170733766|ref|YP_001765713.1|: domain 1 of 1, from 59 to 1009: score 299.5, E = 7.2e-87
                    *->siDAqLRlLvP..GKvsedek...LieYDALLlDkFL.DiLqDLHGe
                       +  A   +++P+ G    d+k+++L e D   l + L+D++ +  G+
  gi|1707337    59    ASPAARNAVAPkaGTRTRDNKdgpLFE-DIRFLGRLLgDVVREQEGD 104

                    dLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHm
                     + ++v      +  +    D++  + L  kL  L P  ++ v +a++
  gi|1707337   105 TVFDVVETIRQTAVKFRREGDSEAAQTLEKKLRKLTPEQTVSVVRAFSYF 154

                    LnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkln
                      LAn+AE+ +   RRRi+ +        +sA     +   l +L   +n
  gi|1707337   155 SHLANIAEDRHHNRRRRIHALA-------GSAPQPGTVAYALDQLKTTGN 197

                    KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                     s            +  vltAHPt   R+s+L  +  i   La    +++
  gi|1707337   198 ASKRLLQRFFDDALIVPVLTAHPTEVQRKSILDAQHDIARLLAE-RDQEL 246

                    tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                    t  +++  +  L   + A + t  +R a+ t  DE+   +sY+  t  +
  gi|1707337   247 TARERQYNETMLRARVTALWQTRMLRDARLTVGDEIENALSYYRATFLDE 296

                    vPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                     P     ++ AL   G+  R+P      +  sW+GGDRDG nP vt
  gi|1707337   297 LPALYGDIEAALAEHGLSARVP---AFFQMGSWIGGDRDG-NPNVTAATL 342

                    RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk
                     +       +    Y++qv  L  Els+    + L v A +  +  a
  gi|1707337   343 DEAINRQAAVILEHYLEQVHKLGAELSV----SNLLVGANDAVKALAAA- 387
```

```
                    vvKyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGisei.
                              q P++  EPYR  L  +  +L      aR  L  G   ++
  gi|1707337   388 -------SPDQSPhrVDEPYRRALIGIYTRLAAS---ARVRLGEGTVPVr 427

                    .......sEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                    + +++ ++  A++y + E F+  L +   sL e     +A   L  l+R
  gi|1707337   428 sagrgapPVRAIpYEDSEAFVADLKVLTASLDEHHGASLAAPRLAPLVRA 477

                    vstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLl
                       FG  L  +D+Rq s+ +  v+  +    ++ ++Y   +Ee +   Ll
  gi|1707337   478 AEVFGFHLASIDLRQSSDIHEAVVAELFARAGVEAdYAALAEEDKLRVLL 527

                    aELkGKRPLlgsDLPktEEvkDvldaf....rvLAELPiDsFGaYiisma
                    a L   RPL  + L      +  l+ f++ ++v A     +   Yiis +
  gi|1707337   528 AALADPRPLRSPYLEYSALAQSELGVFekarEVRAQFGARAVRNYIISHT 577

                    taPsDvLAvELLqREC............gvkqtLrvvPLFEkLADLeAAP
                     + sD + v LLq+E +  +++ + ++++ k++L v+PLFE + DL+ A
  gi|1707337   578 ETVSDLVEVLLLQKETgllegtlgvpgsHAKNSLMVIPLFETIPDLRDAS 627

                    AavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqE
                      +   F+ ++iD  i +    qevm+GYsDs KD G l   W LY+A
  gi|1707337   628 RIMRDYFAlpgIDALIAHQGAEQEVMLGYSDSNKDGGFLTSNWELYRAEL 677

                    EiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtv
                     ++   ++  + L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t
  gi|1707337   678 ALVDLFRERKITLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTE 727

                    qGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv...sPkPEWRkLmee
                    qGEvi   F    +  r L    AAtLE  + P  + ++  P +   m+
  gi|1707337   728 QGEVIASKFSNPSIGRRNLETVVAATLEASLLPQSnapAQLPAFEAAMQT 777

                    mAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG..
                    +   A   YR++v+  P F +YF + tP +E   +niGsRPa Rk   ++
  gi|1707337   778 LSDSAMAAYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASRKLQDpk 827

                    ..GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiKnl
                    ++ ie LRAiPW F+W q R  L  W G+G A    +d+ +++    K +
  gi|1707337   828 qrKIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVSAYLDgaqddaERAKRV 877

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGk
                      Lk m k+WPFF   l  ++mv AK D  +A+ y +L+    L+k   +
  gi|1707337   878 TLLKKMNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVSDRKLrKHVFE 927

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    ++ ++++ t   L +i G    L   P L   ++ R +Y+  Ln +q
  gi|1707337   928 RIVAEWERTSRALAEITGQEGRLATNPLLARSIKNRFPYLDPLNHLQVEL 977

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    +KR R               A +           n   r   G+
  gi|1707337   978 IKRHR----------------AGDT----------N--ARLRRGIH---- 995

                    LtmKGiAAGmqntG<-*
                    Lt+ GiAAG+ ntG
  gi|1707337   996 LTINGIAAGLRNTG    1009

gi|77413069|ref|ZP_00789270.1|: domain 1 of 1, from 3 to 931: score 299.4, E = 7.8e-87
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                           +L        s + ++i  +  Ll + LD+  q L G +  +
  gi|7741306     3    --HPKLES------SSNKEIITEEVGLLKQLLDeATQKLIGSESFDK 41

                    vqECYElsA..eYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    +     ls +++Y G k+t         + +L   + ++v + ++ +  L
  gi|7741306    42 IEKIVSLSStdDYTGLKET---------ISALSNEEMVIVSRYFSILPLL 82

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                     n+ E+v+lAy    k     D+    s t +          v+ +
  gi|7741306    83 INISEDVDLAYEINYKNNLNQDYLGKLSTTID----------VVAG---H 119

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
```

```
                e   + L    v  vltAHPtq  R+ +L   ++i   L +       +
gi|7741306   120 ENAKDILEHVNVVPVLTAHPTQVQRKTVLELTSKIHDLLRKYRDVKAGIV 169

                DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                 ++     L R i     tD iR  +   + E+   m Y+   + k v K
gi|7741306   170 NQEKWYADLRRYIGIIMQTDTIREKKLKVKNEITNVMEYYNRSLIKAVTK 219

                FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                            Gi    P   PL     W+GGDRDG nP vt E  R
gi|7741306   220 LTAEYKALAAKKGIHLENP--KPL-TMGMWIGGDRDG-NPFVTAETLRLS 265

                CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                 ++   +  n Yi+q+ +L   +s+     E+     El   a + +
gi|7741306   266 AMVQSEVIINHYIEQLNELYRNMSLSISLTEV---SPELVTLANQSQDNS 312

                yYiEFWKqvPPtEPYRviLGdvRDKLYnt.............RERa.
                 Y E       +EPYR     +  KL  t  + + ++ ++++  +R  ++
gi|7741306   313 VYRE-------NEPYRKAFNFIQGKLVQTllnlkvgsypkekfvsRQESs 355

                ....RHL...LAtGiseisEeAv..ytkvEeFLEPLELCYksLCeCGDkv
                +  +R +++++A+  s+i  e  + y   EeF   L L  +sL + G
gi|7741306   356 divgRYIkshVAQVASDIQTEELpaYATAEEFKQDLLLVKQSLVQYGQDS 405

                iADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYR
                + DG L  l+  v  FG  L  +D+Rq+s  +   +  + + +  +i   Y
gi|7741306   406 LVDGELACLIQAVDIFGFYLATIDMRQDSSINEACVAELLKSANIvDDYS 455

                eWsEeKRqEWLlaELkGK.RPLlgsDLPktEEvkDvldafrvLAELP...
                + sEe +   Ll EL   +R L     Pk E ++  l  f+   EL ++
gi|7741306   456 SLSEEEKCQLLLKELTEDpRTLSSTHTPKSELLQKELAIFQTARELKdql 505

                .iDsFGaYiismataPsDvLAvELLqRECgv....kqtLrvvPLFEkLAD
                + D     iis + + sD+    ++ +E g+ + ++  +++vPLFE + D
gi|7741306   506 gEDIIKQHIISHTESVSDMFELAIMLKEVGLidanQARIQIVPLFETIED 555

                LeAAPAavekLFsiDWYinri...dGKqevmvGYsDsGKDAGRlsAAWqL
                L+     + +       +  i +++  qe+m+GYsDs KD G ls  W L
gi|7741306   556 LDNSRDIMTQYLHYGLVKKWIatnNNYQEIMLGYSDSNKDGGYLSSGWTL 605

                YkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGs
                YkAq E+ K+  + G+K++ FHGRGGtvGRGGGP   Ai sqP   i+
gi|7741306   606 YKAQNELTKIGEENGIKITFFHGRGGTVGRGGGPSYEAITSQPFGSIKDR 655

                lRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WR
                +R t qGE+iE  +G  +  +  L     A ++  +   +    E +++R
gi|7741306   656 IRLTEQGEIIENKYGNQDAAYYNLEMLISASIDRMVTRMITNPNEidnFR 705

                kLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRk
                + m+ +       YR +v+  P F +YF  A P  E   +niGsRPa Rk
gi|7741306   706 ETMDGIVAESNAVYRNLVFDNPYFYDYFFEASPIKEVSSLNIGSRPAARK 755

                PsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkE
                    i  LRAiPW+F+W q R   P W GvG AFKh i++D  nl kL+
gi|7741306   756 TITEISGLRAIPWVFSWSQNRIMFPGWYGVGSAFKHFIEQDEANLAKLQT 805

                mYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkY
                mY++WPFF   l  ++mv  K    iA  y +L  + e++   + + +++
gi|7741306   806 MYQKWPFFNSLLSNVDMVLSKSNMNIALQYAQLAGSKEVRDVFNIILNEW 855

                vEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRD
                + tkd++L i  H  lLE  P L   l  R +Y   Ln +q   +KR+R
gi|7741306   856 QLTKDMILAIEQHDNLLEENPMLHASLDYRLPYFNVLNYVQIELIKRLRS 905

                PsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGi
                 +              dE+    + L+++                + Gi
gi|7741306   906 NQL------------DED---YEKLIHIT---------------INGI 923

                AAGmqntG<-*
                A G+ n G
gi|7741306   924 ATGLRNSG    931
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gi|254247510|ref|ZP_04940831.1|: domain 1 of 1, from 59 to 1009: score 299.3, E = 8e-87
                  *->siDAqLRlLvP..GKvsedek...LieYDALLlDkFL.DiLqDLHGe
                        A   +++P+ G    d+k+++L e D   l + L+D++ +  G+
  gi|2542475    59    TSPAARNAVAPkaGTRTRDDKdgpLFE-DIRFLGRLLgDVVREQEGD 104

                  dLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHm
                   + ++v      +  +    D++  + L  kL  L P  ++ v +a++
  gi|2542475   105 TVFDVVETIRQTAVKFRREDDSEAAQTLEKKLRKLTPEQTVSVVRAFSYF 154

                  LnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkln
                    LAn+AE+ +   RRRi+ +        +sA     +   l +L   +n
  gi|2542475   155 SHLANIAEDRHHNRRRRIHALA-------GSAPQPGTVAYALDQLKTTGN 197

                  KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                   s           +  vltAHPt   R+s+L  +  i   La    +++
  gi|2542475   198 ASKRLLQRFFDDALIVPVLTAHPTEVQRKSILDAQHDIARLLAE-RDQEL 246

                  tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                  t  +++  +  L   + A + t  +R a+ t  DE+   +sY+  t  +
  gi|2542475   247 TARERQYNETMLRARVTALWQTRMLRDARLTVGDEIENALSYYRATFLDE 296

                  vPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                   P     ++ AL   G+  R+P      +  sW+GGDRDG nP vt
  gi|2542475   297 LPALYGDIEAALAEHGLSARVP---AFFQKGSWIGGDRDG-NPNVTAATL 342

                  RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk
                   +       +    Y++qv  L  Els+    + L v A +  +  a
  gi|2542475   343 DEAINRQAAVILEHYLEQVHKLGAELSV----SNLLVGANDAVKALAAA- 387

                  vvKyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGisei.
                            q P++  EPYR  L  +  +L      aR  L  G   ++
  gi|2542475   388 -------SPDQSPhrVDEPYRRALIGIYTRLAAS---ARVRLGEGTVPVr 427

                  .......sEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                  + +++ ++  A++y + E F+  L +   sL e     +A   L  l+R
  gi|2542475   428 sagrgapPVRAIpYEDSEAFVADLKVLTASLDEHHGASLAAPRLAPLVRA 477

                  vstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLl
                     FG  L  +D+Rq s+ +  v+  +    ++ ++Y   +Ee +   Ll
  gi|2542475   478 AEVFGFHLASIDLRQSSDIHEAVVAELFARAGVEAdYAALAEEDKLRVLL 527

                  aELkGKRPLlgsDLPktEEvkDvldaf....rvLAELPiDsFGaYiisma
                  a L   RPL  + L      +  l+ f++ ++v A     +   Yiis +
  gi|2542475   528 AALADPRPLRSPYLEYSALAQSELGVFekarEVRAQFGARAVRNYIISHT 577

                  taPsDvLAvELLqREC............gvkqtLrvvPLFEkLADLeAAP
                   + sD + v LLq+E +  +++ + ++++ k++L v+PLFE + DL+ A
  gi|2542475   578 ETVSDLVEVLLLQKETgllegtlgvpgsHAKNSLMVIPLFETIPDLRDAS 627

                  AavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqE
                    +   F+ ++iD  i +    qevm+GYsDs KD G l   W LY+A
  gi|2542475   628 RIMRDYFAlpgIDALIAHQGAEQEVMLGYSDSNKDGGFLTSNWELYRAEL 677

                  EiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtv
                   ++   ++  + L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t
  gi|2542475   678 ALVDLFRERKITLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTE 727

                  qGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv...sPkPEWRkLmee
                  qGEvi   F    +  r L    AAtLE  + P  + ++  P +   m+
  gi|2542475   728 QGEVIASKFSNPSIGRRNLETVVAATLEASLLPQSnapAQLPAFEAAMQT 777

                  mAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG..
                  +   A   YR++v+  P F +YF + tP +E   +niGsRPa Rk   ++
  gi|2542475   778 LSDSAMAAYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASRKLQDpk 827

                  ..GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiKnl
                  ++ ie LRAiPW F+W q R  L  W G+G A    +d+ +++    K +
  gi|2542475   828 qrRIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVSAYLDgaqddaERAKRV 877

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGk
                    Lk m k+WPFF   l  ++mv AK D  +A+ y +L+    L+k   +
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```
  gi|2542475   878 TLLKKMNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVSDRKLrKHVFE 927

                   sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                   ++ ++++ t   L +i G    L   P L   ++ R +Y+  Ln +q
  gi|2542475   928 RIVAEWERTSRALAEITGQEGRLATNPLLARSIKNRFPYLDPLNHLQVEL 977

                   LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                   +KR R               A +           n   r   G+
  gi|2542475   978 IKRHR----------------AGDT----------N--ARLRRGIH---- 995

                   LtmKGiAAGmqntG<-*
                   Lt+ GiAAG+ ntG
  gi|2542475   996 LTINGIAAGLRNTG    1009

gi|282873614|ref|ZP_06282580.1|: domain 1 of 1, from 2 to 909: score 299.1, E = 9.7e-87
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDi..LqDLHGedLkE
                      s   q  +  P   +                 Di++L DL Ge L
  gi|2828736     2    SSADQTPAASPALRA----------------DIrrLGDLLGETL-- 29

                   avqECYElsAeYEGKkD.tkKLeELGakLts.LdPaDailvAkailHmLn
                   + qE  El    E  +  t+  +E  a L ++ d   a  + +a++
  gi|2828736    30 VRQEGQELLDLVERVRAlTRTDGEAAAELLGdTDLETAARLVRAFSTYFH 79

                   LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                   LAn+ E v+ A+  R ++   G             +  t  +L
  gi|2828736    80 LANVTEQVHRAHEMRDRRAAEGGL-----------LARTADRLKDAD--- 115

                   PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                   Pe   e +Kn  v  v+tAHPt ++RRs+L K  Ri    a L
  gi|2828736   116 PEHLRETVKNLNVRPVFTAHPTEAARRSVLNKLRRI----AALLETPAIE 161

                   eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                    D++ LD  L   i   + tDE+R  +P P DE R  + Y+ E     v
  gi|2828736   162 ADRRRLDLRLAENIDLIWQTDELRVVRPEPADEARNAIYYLDELHTGAVG 211

                   KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                     L      L  +G+   lP     + F  W+GGDRDG nP vtP vt D
  gi|2828736   212 DVLEDLAAELERVGVE--LPAGTRPLTFGTWIGGDRDG-NPNVTPAVTWD 258

                   vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                   v +L         ++ ++ L   ls    n+   + A E   t+ +  +
  gi|2828736   259 VLILQHEHGITDALEMIDHLRGLLS----NSIRYAGATEELLTSLQTDLE 304

                   Ky..YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                   + ++    +K +  +EPYR     +R KL ntRER    LA G    +
  gi|2828736   305 RLpgISPRYKRLNAEEPYRLKATCIRQKLVNTRER----LAEGTPHRP-G 349

                   AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                     y    e +  LEL   sL        ADG +   +R    FGL L  +
  gi|2828736   350 CDYLGTAELIADLELIQTSLRAHKGGLFADGRMDRTIRTLGAFGLQLATM 399

                   DiRqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLl
                   D+R  ++ +   l  +   L+  s+R  + + + Rq  L  EL+ +RPL
  gi|2828736   400 DVREHADAHHHALGQLFDRLGEESWRyaDMPRDYRQKLLAKELRSRRPLA 449

                   gsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAv
                   +   P     +  l+ f+ +     + FG++  ++Yiism+    Dv A
  gi|2828736   450 PTPAPLDAAGEKTLGVFHTIKQ-AFERFGPeviesYIISMCQGADDVFAA 498

                   ELLqRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                    +L RE g+   + +   + +vPL E   +L+AA   ++ + +   Y+
  gi|2828736   499 AVLAREAGLVDlhagwaKIGIVPLLETTDELKAADVILDEMLADPSYRRL 548

                   idGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                   +  +++ qevm+GYsDs K  G     W + +Aq  +  vA +yGv+L l
  gi|2828736   549 VSLRgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRYGVRLRL 598

                   FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                   FHGRGGtvGRGGGP H AiL+qP  t++G ++vt qGEvi   +    L
  gi|2828736   599 FHGRGGTVGRGGGPSHDAILAQPWGTLEGEIKVTEQGEVISDKYLIPALA 648
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                    FrsLqRFtAAtLEHGm...nPPvsPk..PEWRkLmeemAvvAtEEYRsvv
                       L    AAtL     ++ P  s      W   m+ +   A   YR +v
  gi|2828736   649 RENLELTVAATLQASAlhtAPRQSDEalARWDAAMDTVSDAAHSAYRKLV 698

                    vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFa
                      +P    YF   tP      + +GsRP+ R+P+ G++ + LRAiPW+F
  gi|2828736   699 -EDPDLPAYFLASTPVDQLADLHLGSRPS-RRPGSGVslDGLRAIPWVFG 746

                    WtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlE
                    Wtq R  +P W GvG   K   +     +  L Em + W FFR  l  +E
  gi|2828736   747 WTQSRQIVPGWYGVGSGLKALREAGLDTV--LDEMHEHWHFFRNFLSNVE 794

                    mvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDl
                    m  AK D  iA  y + Lv +eLk   + + ++   t   +Lk+ G  +l
  gi|2828736   795 MTLAKTDLRIARHYVDTLVPDELKHVFDAIEAEHALTVREVLKVTGSTEL 844

                    LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                    L   P L+q   +Rd+Y+  +  +q   L R R                A
  gi|2828736   845 LGTSPVLQQTFGIRDAYLDPISYLQVSLLARQRQ---------------A 879

                    dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +E             +e+  P L   L+Lt+ G+AAG+ ntG
  gi|2828736   880 AER------------GEEPDPLLARALLLTVNGVAAGLRNTG    909

gi|182438172|ref|YP_001825891.1|: domain 1 of 1, from 2 to 909: score 299.0, E = 1e-86
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDi..LqDLHGedLkE
                       s   q  +  P   +                 Di++L DL Ge L
  gi|1824381     2    SSADQTPAASPALRA-----------------DIrrLGDLLGETL-- 29

                    avqECYElsAeYEGKkD.tkKLeELGakLts.LdPaDailvAkailHmLn
                    + qE  El    E  +  t+  +E  a L ++ d   a  + +a++
  gi|1824381    30 VRQEGQELLDLVERVRAlTRTDGEAAAELLGdTDLETAARLVRAFSTYFH 79

                    LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                    LAn+ E v+ A+  R ++   G            +  t  +L
  gi|1824381    80 LANVTEQVHRAHEMRDRRAAEGGL-----------LARTADRLKDAD--- 115

                    PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                    Pe   e +Kn  v  v+tAHPt ++RRs+L K  Ri    a L
  gi|1824381   116 PEHLRETVKNLNVRPVFTAHPTEAARRSVLNKLRRI----AALLETPAIE 161

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                     D++ LD  L   i   + tDE+R  +P P DE R  + Y+ E     v
  gi|1824381   162 ADRRRLDLRLAENIDLIWQTDELRVVRPEPADEARNAIYYLDELHTGAVG 211

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                      L      L  +G+   lP     + F  W+GGDRDG nP vtP vt D
  gi|1824381   212 DVLEDLAAELERVGVE--LPAGTRPLTFGTWIGGDRDG-NPNVTPAVTWD 258

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRA.EElyrtaardkv
                    v +L         ++ ++ L   ls    n+   + A+EEl    + d
  gi|1824381   259 VLILQHEHGITDALEMIDHLRGLLS----NSIRYAGAtEELLTSLQADLE 304

                    vKyYiE.FWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                        i + +K +  +EPYR     +R KL ntRER    LA G    +
  gi|1824381   305 RLPGISpRYKRLNAEEPYRLKATCIRQKLVNTRER----LAEGTPHRP-G 349

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y    e +  LEL   sL        ADG +   +R    FGL L  +
  gi|1824381   350 CDYLGTAELIADLELIQTSLRAHKGGLFADGRMDRTIRTLGAFGLQLATM 399

                    DiRqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLl
                    D+R  ++ +   l  +   L+  s+R  + + + Rq  L  EL+ +RPL
  gi|1824381   400 DVREHADAHHHALGQLFDRLGEESWRyaDMPRDYRQKLLAKELRSRRPLA 449

                    gsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAv
                    +   P     +  l+ f+ +     + FG++  ++Yiism+    Dv A
  gi|1824381   450 PTPAPLDAAGEKTLGVFHTIKQ-AFERFGPeviesYIISMCQGADDVFAA 498

                    ELLqRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                     +L RE g+   + +   + +vPL E   +L+AA   ++ + +   Y+
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  gi|1824381   499 AVLAREAGLVDlhagwaKIGIVPLLETTDELKAADVILDEMLADPSYRRL 548

                   idGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                   +  +++ qevm+GYsDs K  G     W + +Aq  +  vA +yGv+L l
  gi|1824381   549 VSLRgdvQEVMLGYSDSSKFGGITTSQWEIHRAQRRLRDVAHRYGVRLRL 598

                   FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                   FHGRGGtvGRGGGP H AiL+qP  t++G ++vt qGEvi   +    L
  gi|1824381   599 FHGRGGTVGRGGGPSHDAILAQPWGTLEGEIKVTEQGEVISDKYLIPALA 648

                   FrsLqRFtAAtLEHGm...nPPvsPk..PEWRkLmeemAvvAtEEYRsvv
                      L    AAtL     ++ P  s      W   m+ +   A   YR +v
  gi|1824381   649 RENLELTVAATLQASAlhtAPRQSDEalARWDAAMDTVSDAAHSAYRKLV 698

                   vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFa
                     +P    YF   tP      + +GsRP+ R+P+ G++ + LRAiPW+F
  gi|1824381   699 -EDPDLPAYFLASTPVDQLADLHLGSRPS-RRPGSGVslDGLRAIPWVFG 746

                   WtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlE
                   Wtq R  +P W GvG   K   +     +  L Em + W FFR  l  +E
  gi|1824381   747 WTQSRQIVPGWYGVGSGLKALREAGLDTV--LDEMHEHWHFFRNFLSNVE 794

                   mvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDl
                   m  AK D  iA  y + Lv +eLk   + + ++   t   +Lk+ G  +l
  gi|1824381   795 MTLAKTDLRIARHYVDTLVPDELKHVFDAIEAEHALTVREVLKVTGSTEL 844

                   LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                   L   P L+q   +Rd+Y+  +  +q   L R R                A
  gi|1824381   845 LGTSPVLQQTFGIRDAYLDPISYLQVSLLARQRQ---------------A 879

                   dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   +E             +e+  P L   L+Lt+ G+AAG+ ntG
  gi|1824381   880 AER------------GEEPDPLLARALLLTVNGVAAGLRNTG    909

gi|258594352|ref|ZP_05709164.1|: domain 1 of 1, from 4 to 971: score 298.8, E = 1.2e-86
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDi.LqDLHGedLkEa
                                G   ed   +     Ll + L  ++++L G  + E
  gi|2585943     4    ---GVFTSTLTGWQPEDSATLAGQVGLLGRLLGRsIKELRGAAVLEQ 47

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v +   l  +      ++    +  ++  Ld  + + + +a+     L n
  gi|2585943    48 VEDLRQLCKQAMVENRPELRRQVAQRIADLDCREIVHLLHAYTAFFHLVN 97

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     E +e+    R         +   +      i+  ++ L  ++  s +
  gi|2585943    98 KVEQMEITRVYREPDPSPPPATPGENSRRRETIDAAVRGLKEQG-CSLQQ 146

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                       L    +   ltAHPt + RRs+L K+  +   L  L    +t +++
  gi|2585943   147 TLAVLSRLDIQPTLTAHPTEARRRSILYKQKQVASLLGRLRREALTTDER 196

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    EL   +   i     tD+iR ++Pt  DE+  G+ ++   +W  vP+
  gi|2585943   197 DELLGEISNQIGLLLTTDDIRQTRPTVDDEVESGLYFVRNAIWATVPRIY 246

                   RRvDtAL.KniGin.ERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                   R    AL +  G  +E lP    L++F sW+G DRDG nP vt  v R
  gi|2585943   247 RDLRAALwRHYGESpEILPV---LLRFRSWIGSDRDG-NPNVTAAVSRRT 292

                   CLLaRmmAanlYisqvEDLmFElsmWRCn....dELRvRAEElyrtaard
                       R +   lY++ + +L  Els+     ++++ LR   EE  rt a d
  gi|2585943   293 YHYQRRVVLQLYLDELCELRRELSLSSRQappsEALRNSLEEDGRTLAID 342

                   kvvKyYiEFWKqvPPtEPYRv....iLGdvRDKLYntRERaRHLLAtGis
                          E  +    +EPYR + + i+   R  L+    R R L A  +
  gi|2585943   343 -------EQRRRHYRNEPYRLkityIMARLRSLLWQMENRPRELAAGDY- 384

                   eisEeAvytkvEeFLEPLELCYksLCeCG.DkviADGsLLDlLRqvstFG
                            +   FL  L L   sL e G  + +  G L  lL  v tFG
  gi|2585943   385 ---------HCPAFLADLQLLAASLRESGfSRLVSQGRLGRLLVRVRTFG 425
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                    LsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkG
                      Lv LD Rq s+ + + +  + +  ++  +Y + +Ee+R   L  EL
  gi|2585943   426 FHLVALDFRQHSQVHEETVALLLRLAGVEEdYLSLPEERRLALLQEELGN 475

                    KRPLlgsDLPktEEvkDvldafrvLAELPi...DsFGaYiismataPsDv
                     RPLl+       E +D l+++  + EL   ++ s G+Yiism+   sD
  gi|2585943   476 PRPLLPRGCELPPEARDLLETLALIGELQRldpASVGSYIISMTHQVSDL 525

                    LAvELLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsiD
                    L v LL +E g+ + ++++ ++ L+ vPLFE + DLe     vek+ +
  gi|2585943   526 LEVLLLAKEAGIWRlrdggvesRLQLVPLFETIEDLELSGRLVEKMLANP 575

                    WYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyG
                     Y+ ++  +++ qevm+GYsDs KD G   A W L +AqE + +v ++yG
  gi|2585943   576 VYRQHLAAQndfQEVMLGYSDSNKDGGYWMANWALHRAQERLGQVCRQYG 625

                    vKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFG
                    v L lFHGRGGtvGRGGG    Ai++ P    nG +R t qGEvi f +
  gi|2585943   626 VDLRLFHGRGGTVGRGGGRSSQAIVAMPEVVHNGRIRFTEQGEVISFRYA 675

                    EEnLCFrsL.qRF.............................tAAtLE...
                      +L  r L+q F    ++ ++  +  +++ +++  ++  ++AA  E+++
  gi|2585943   676 FADLAHRHLeQIFyamirtagrvarlaeqqaepgaageaveAAADAEpgr 725

                    .HGmnPPvsPk..PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtP
                      G++  v+P +  E+  Lm+e+A      YR +v ++P F  ++   tP
  gi|2585943   726 lEGIEAGVAPErlQEFSALMDEVAQRSMQAYRELV-RDPEFWAWYTRVTP 774

                    ElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWtqtRFHLPvWLGvG
                         ++ i sRP  Rk +G ++ + LRAiPW+FaW qtR+ +P W GvG
  gi|2585943   775 IEQISRLPIASRPVSRKAAGDVdlDGLRAIPWVFAWIQTRYIVPGWYGVG 824

                    AAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyD
                    AA    +    +  q Lk mY++WPFFR+ +D       +    iAa y
  gi|2585943   825 AALGE-LSGTERGRQTLKQMYEQWPFFRMLIDNARREMGRTRLEIAADYA 873

                    kLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRd
                     L     +k F  ++  ++ E ++ LL++ G  +lL G P ++  + LR+
  gi|2585943   874 ALANDLAVKDFHAQISRDFAEGRQALLELSGEEELLGGSPEVQRSIALRN 923

                    sYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnp
                    +Y   Ln +q   L+R                 y d
  gi|2585943   924 PYTDVLNLLQVELLRR-----------------YHDSG------------ 944

                    tervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +++    L D L L + GiAA mq tG
  gi|2585943   945 GDEEREALWDALFLSVNGIAAAMQSTG    971

gi|167561969|ref|ZP_02354885.1|: domain 1 of 1, from 4 to 952: score 298.7, E = 1.3e-86
                    *->siDAqLRlLvP.GKvsed.ekLieYDALLlDkFL.DiLqDLHGedLk
                       +  A      P+G+  ed+++ +  D   l + L+D++ +  G+d+
  gi|1675619     4    ARPASAAPAKPhGRTREDkDRPLFEDIRYLGRLLgDVVREQEGDDVF 50

                    EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                     +v      +  +    D+   + L   L  L P  ++ v +a++    L
  gi|1675619    51 HVVETIRQTAVKFRREDDSAAAQTLEKMLRKLTPEQTVSVVRAFSYFSHL 100

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                    An+AE+ +   RRRi+ +        +sA     +   l kL   ++ sP
  gi|1675619   101 ANIAEDRHHNRRRRIHALA-------GSAPQAGTVAYALDKLKEAGDASP 143

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    + +        +  vltAHPt   R+s+L  +  i   La    + +t
  gi|1675619   144 KVIKRFFEGALIVPVLTAHPTEVQRKSILDAQHDIAHLLAE-RDQPLTAR 192

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    +    +  L   +   + t  +R a+ t  DE+   +sY+  t  +  P
  gi|1675619   193 EFAHNEALLRARVTTLWQTRMLRDARLTVADEIENALSYYRATFLDELPA 242

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                        ++ AL   G+  R+P      +  sW+GGDRDG nP vt     +
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  gi|1675619   243 LYADIEEALAEHGLPARVP---AFFQMGSWIGGDRDG-NPNVTAATLDEA 288

                   CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                         +    Y++qv  L  Els+    + L v A +  +  a
  gi|1675619   289 INRQAAVIFEHYLEQVHKLGAELSV----SNLLVGANDALKALAAA---- 330

                   yYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER....aRHLLAtGise
                          q P++  EPYR  L  v  +L  + R R +++a  +   G
  gi|1675619   331 ----SPDQSPhrVDEPYRRALIGVYTRLAAsARVRlgegAVPVRSAGRGA 376

                   isEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                    +  A +y + EeF   L +   sL       +A   L  l+R    FG
  gi|1675619   377 APVRATpYADAEEFAADLRVLTDSLALHHGESLATPRLAPLMRAAEVFGF 426

                   sLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK
                    L  +D+Rq s+ +  v+  +    ++ + Y   +E  +   Lla L
  gi|1675619   427 HLASIDLRQSSDIHEAVIAELLARGGVEpDYAALAEADKLRVLLAALADP 476

                   RPLlgsDLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDv
                   RPL  + L   +  k  l+ +++ + + A     +   Yiis + + sD
  gi|1675619   477 RPLRSPYLDYSDLAKSELGVLErahaIRAQFGPRAVRNYIISHTETVSDL 526

                   LAvELLqRECgv............kqtLrvvPLFEkLADLeAAPAavekL
                   + v LLq+E g+ +++ ++++ + ++ L  +PLFE +ADL+ AP  +
  gi|1675619   527 VEVLLLQKETGLfegtlgtphanaRNGLMAIPLFETIADLRNAPDIMREF 576

                   Fs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvA
                   F+ +++   + +    qevm+GYsDs KD G l   W LY+A   ++
  gi|1675619   577 FAlpgVGELVAHQGHEQEVMLGYSDSNKDGGFLTSNWELYRAELALVDLF 626

                   KkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviE
                    + G+KL lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGEvi
  gi|1675619   627 SERGIKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEVIA 676

                   fsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEWRkLmeemAvvAt
                     F   ++  r L    AAtLE  + P  ++Pk+ P +   m+ +   A
  gi|1675619   677 SKFANPEIGRRNLETVVAATLEATLLPHRnAPKqlPAFEAAMQALSDAAM 726

                   EEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....Gies
                     YR++v+  P F +YF + tP +E   +niGsRPa Rk   ++++ ie
  gi|1675619   727 ASYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASRKLQDpknrKIED 776

                   LRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid..KDi....KnlqkLkEm
                   LRAiPW F+W q R  L  W G+G A    +d++KD+ ++ K +  Lk m
  gi|1675619   777 LRAIPWGFSWGQCRLLLTGWYGFGSAVAAFLDgtKDVaeraKRVALLKKM 826

                   YkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkY
                    k+WPFF   l  ++mv AK D  +A+ y +L+    L+k   +++  ++
  gi|1675619   827 NKTWPFFAHLLSNMDMVLAKTDLAVASRYAQLVADKKLrKHVFERIVSEW 876

                   vEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRD
                     t d L +i G    L   P L   ++ R +Y+  Ln +q   +KR R
  gi|1675619   877 HRTSDALAEITGSDARLAANPLLARSIKNRFPYLDPLNHLQVELIKRHRS 926

                   PsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGi
                                  d n        +L             + Lt+ Gi
  gi|1675619   927 ---------------GDTN-------ARLR----------RGIHLTINGI 944

                   AAGmqntG<-*
                   AAG+ ntG
  gi|1675619   945 AAGLRNTG    952

gi|167618301|ref|ZP_02386932.1|: domain 1 of 1, from 40 to 994: score 298.6, E = 1.3e-86
                   *->siDAqLRlLvP.........GKvsed.ekLieYDALLlDkFL.DiLq
                         A  R ++P++  + +++G+  ed+++ +  D   l + L+D++
  gi|1676183    40    --GAAARTIAPtnaasakphGRTREDkDRPLFEDIRYLGRLLgDVVR 84

                   DLHGedLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAk
                   +  G+ + ++v      +  +    D    + L   L  L P  ++ v +
  gi|1676183    85 EQEGDAVFDVVETIRQTAVKFRREDDKTAAQTLEKMLRKLTPEQTVSVVR 134
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                ailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkL
                a++    LAn+AE+ +   RRRi+ +        +sA     +   l kL
gi|1676183   135 AFSYFSHLANIAEDRHHNRRRRIHALA-------GSAPQAGTVAYALDKL 177

                vlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL
                   ++ s + + +      +  vltAHPt   R+s+L  +  i   La
gi|1676183   178 RQAGDASSKTIKQFFEGALIVPVLTAHPTEVQRKSILDAQHDIARLLAE- 226

                sAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHE
                  + +t  ++   +  L   +   + t  +R a+ t  DE+   +sY+
gi|1676183   227 RDQPLTARERAHNEALLRARVTTLWQTRMLRDARLTVADEIENALSYYRA 276

                tvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRv
                t  +  P     ++ AL   G+  R+P      +  sW+GGDRDG nP v
gi|1676183   277 TFLDELPALYTDIEEALAEHGLPARVP---AFFQMGSWIGGDRDG-NPNV 322

                tPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrt
                t     +       +    Y++qv  L  Els+    + L v A +  +
gi|1676183   323 TAATLDEAINRQAAVIFEHYLEQVHKLGAELSV----SNLLVGASDALKA 368

                aardkvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER....aRH
                 a            q P++  EPYR  L  v  +L  + R R +++a
gi|1676183   369 LAAA--------SPDQSPhrVDEPYRRALIGVYTRLAAsARVRlgegAVP 410

                LLAtGiseisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlL
                +   G    +  A +y + EeF+  L +   sL       +A   L  l+
gi|1676183   411 VRSAGRGAAPVRATpYADAEEFVADLRVLTDSLAVHHGESLATPRLAPLM 460

                RqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEW
                R    FG  L  +D+Rq s+ +  v+  +    ++ + Y   +E  +
gi|1676183   461 RAAEVFGFHLASIDLRQSSDIHEAVIAELLARGGVEpDYAALPEADKLRV 510

                LlaELkGKRPLlgsDLPktEEvkDvldafr....vLAELPiDsFGaYiis
                Lla L   RPL  + L   +  k  l+ +++ + + A     +   Yiis
gi|1676183   511 LLAALADPRPLRSPYLDYSDLAKSELGVLErahaIRAQFGARAVRNYIIS 560

                mataPsDvLAvELLqRECgv............kqtLrvvPLFEkLADLeA
                 + + sD + v LLq+E g+ +++ + ++ + ++ L v+PLFE +ADL+
gi|1676183   561 HTETVSDLVEVLLLQKETGLfegtlgaphanaRNGLMVIPLFETIADLRN 610

                APAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkA
                A   +   F+ +++     +    qevm+GYsDs KD G l   W LY+A
gi|1676183   611 ASDIMREFFAlpgVGELLAHQGHEQEVMLGYSDSNKDGGFLTSNWELYRA 660

                qEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRv
                   ++    + G+KL lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R
gi|1676183   661 ELALVDLFHERGIKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRL 710

                tvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEWRkLm
                t qGEvi   F   ++  r L    AAtLE  + P  ++Pk+ P +   m
gi|1676183   711 TEQGEVIASKFANPEIGRRNLETVVAATLEATLAPHSnAPKqlPAFEAAM 760

                eemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG
                + +   A   YR++v+  P F +YF + tP +E   +niGsRPa Rk
gi|1676183   761 QTLSDAAMASYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASRKLQD 810

                ....GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiK
                ++++ ie LRAiPW F+W q R  L  W G+G A    +d+ ++     K
gi|1676183   811 pkhrKIEDLRAIPWGFSWGQCRLLLTGWYGFGGAVAAYLDgapdaaERGK 860

                nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPF
                 +  L+ m k+WPFF    l  ++mv AK D  +A+ y +L+    L+k
gi|1676183   861 RVALLRKMNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVADKKLrKHV 910

                GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                 +++ +++  t   L +i G +  L   P L   ++ R +Y+  Ln +q
gi|1676183   911 FERIVAEWHRTASALAEITGAQARLAANPLLARSIKNRFPYLDPLNHLQV 960

                YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                  +KR R               A +           n   r   G+
gi|1676183   961 ELIKRHR----------------AGDT----------N--ARLRRGIH-- 980
```

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                  LiLtmKGiAAGmqntG<-*
                    Lt+ GiAAG+ ntG
  gi|1676183   981 --LTINGIAAGLRNTG    994

gi|167580195|ref|ZP_02373069.1|: domain 1 of 1, from 40 to 994: score 298.5, E = 1.4e-86
                  *->siDAqLRlLvP.........GKvsed.ekLieYDALLlDkFL.DiLq
                        A  R ++P++  + +++G+  ed+++ +  D   l + L+D++
  gi|1675801    40    --GAAARTIAPtnaasakphGRTREDkDRPLFEDIRYLGRLLgDVVR 84

                  DLHGedLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAk
                  +  G+ + ++v      +  +    D    + L   L  L P  ++ v +
  gi|1675801    85 EQEGDAVFDVVETIRQTAVKFRREDDKAAAQTLEKMLRKLTPEQTVSVVR 134

                  ailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkL
                  a++    LAn+AE+ +   RRRi+ +        +sA     +   l kL
  gi|1675801   135 AFSYFSHLANIAEDRHHNRRRRIHALA-------GSAPQAGTVAYALDKL 177

                  vlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL
                     ++ s + + +      +  vltAHPt   R+s+L  +  i   La
  gi|1675801   178 RQAGDASSKTIKQFFEGALIVPVLTAHPTEVQRKSILDAQHDIARLLAE- 226

                  sAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHE
                    + +t  ++   +  L   +   + t  +R a+ t  DE+   +sY+
  gi|1675801   227 RDQPLTARERAHNEALLRARVTTLWQTRMLRDARLTVADEIENALSYYRA 276

                  tvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRv
                  t  +  P     ++ AL   G+  R+P      +  sW+GGDRDG nP v
  gi|1675801   277 TFLDELPALYTDIEEALAEHGLPARVP---AFFQMGSWIGGDRDG-NPNV 322

                  tPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrt
                  t     +       +    Y++qv  L  Els+    + L v A +  +
  gi|1675801   323 TAATLDEAINRQAAVIFEHYLEQVHKLGAELSV----SNLLVGASDALKA 368

                  aardkvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER....aRH
                   a             q P++  EPYR  L   v  +L  + R R +++a
  gi|1675801   369 LAAA--------SPDQSPhrVDEPYRRALIGVYTRLAAsARVRlgegAVP 410

                  LLAtGiseisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlL
                  +   G    +  A +y + EeF+  L +   sL       +A   L  l+
  gi|1675801   411 VRSAGRGAAPVRATpYADAEEFVADLRVLTDSLAVHHGESLATPRLAPLM 460

                  RqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEW
                  R    FG  L  +D+Rq s+ +  v+  +    ++ + Y   +E  +
  gi|1675801   461 RAAEVFGFHLASIDLRQSSDIHEAVIAELLARGGVEpDYAALPEADKLRV 510

                  LlaELkGKRPLlgsDLPktEEvkDvldafr....vLAELPiDsFGaYiis
                  Lla L   RPL  + L   +  k  l+ +++ + + A     +   Yiis
  gi|1675801   511 LLAALADPRPLRSPYLDYSDLAKSELGVLErahaIRAQFGARAVRNYIIS 560

                  mataPsDvLAvELLqRECgv............kqtLrvvPLFEkLADLeA
                   + + sD + v LLq+E g+ +++ + ++ + ++ L v+PLFE +ADL+
  gi|1675801   561 HTETVSDLVEVLLLQKETGLfegtlgaphanaRNGLMVIPLFETIADLRN 610

                  APAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkA
                  A   +   F+ +++     +    qevm+GYsDs KD G l   W LY+A
  gi|1675801   611 ASDIMREFFAlpgVGELLAHQGHEQEVMLGYSDSNKDGGFLTSNWELYRA 660

                  qEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRv
                     ++    + G+KL lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R
  gi|1675801   661 ELALVDLFHERGIKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRL 710

                  tvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEWRkLm
                  t qGEvi   F   ++  r L    AAtLE  + P  ++Pk+ P +   m
  gi|1675801   711 TEQGEVIASKFANPEIGRRNLETVVAATLEATLAPHSnAPKqlPAFEAAM 760

                  eemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG
                  + +   A   YR++v+  P F +YF + tP +E   +niGsRPa Rk
  gi|1675801   761 QTLSDAAMASYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASRKLQD 810

                  ....GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiK
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                    ++++ ie LRAiPW F+W q R  L  W G+G A    +d+ ++     K
  gi|1675801   811 pkhrKIEDLRAIPWGFSWGQCRLLLTGWYGFGGAVAAYLDgapdaaERGK 860

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPF
                     +  L+ m k+WPFF   l  ++mv AK D  +A+ y +L+    L+k
  gi|1675801   861 RVALLRKMNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVADKKLrKHV 910

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                     +++ +++  t   L +i G +  L   P L   ++ R +Y+  Ln +q
  gi|1675801   911 FERIVAEWHRTASALAEITGAQARLAANPLLARSIKNRFPYLDPLNHLQV 960

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      +KR R               A +           n   r   G+
  gi|1675801   961 ELIKRHR----------------AGDT----------N--ARLRRGIH-- 980

                    LiLtmKGiAAGmqntG<-*
                      Lt+ GiAAG+ ntG
  gi|1675801   981 --LTINGIAAGLRNTG    994

gi|225870168|ref|YP_002746115.1|: domain 1 of 1, from 1 to 927: score 298.4, E = 1.6e-86
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            ++ L        e + e  A+L +    i   + G++    +
  gi|2258701     1    ---MSVKKLESYNNQ--EIIAEEVAILKEILESITRRMIGDEAFARI 42

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E  +ls     K+D   Le L ak+      D   + + ++ +  L n+
  gi|2258701    43 EEIIDLSE----KQDYVLLEQLIAKISN---KDMEFISRYFSILPLLINI 85

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiE.EtlKkLvlklnKsPeE
                     E+v+lAy    +     D+      t  s  E+E  K L  +
  gi|2258701    86 SEDVDLAYEINRQNNTNQDYLGKLALTIASAAEkENAKELLERV------ 129

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                            +v  vltAHPtq  R+ +L     i n L         v  +
  gi|2258701   130 --------TVVPVLTAHPTQVQRKTVLELTNSIHNLLRRYRDVKAGVMNQ 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                          L R i     tD iR  +   + E+   m Y+   + + +
  gi|2258701   172 NKWYSELYRYIDILMQTDIIREKKLKVKNEITNVMQYYNSSLIQAITALT 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                     +  t  K  Gi   l  +   i    W+GGDRDG nP vt E  R
  gi|2258701   222 SKYKTLAKDKGI---LLDNPKPINMGMWIGGDRDG-NPFVTAETLRLSAT 267

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    +   +   +Yi+++  L   +s+    + L     E+ r a        Y
  gi|2258701   268 VQSEVILRFYIDKLSALYQTFSL---SSALTKTSPEVERLASLSSDQSIY 314

                    iE........FWKqvPPtEPYRviLGd.vRDKLYntRERaRHLLAtGise
                     E+++ ++   + q   t     ++G++  D+L      +   L  G+
  gi|2258701   315 REnepyrrafHYIQARLTQTLQELIGQpASDQLASRMPATVGSLQSGVTS 364

                    isEeA......vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqv
                    i  + ++++ + y     F   L +  +sL   GD  + +G L ++L  v
  gi|2258701   365 IVTNSsdqqapAYKTAAAFKADLVMIEQSLIAAGDSSLVEGDLQEVLQAV 414

                    stFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLla
                      FG  L  +D+Rq+s  q   +  + +  +i   Y   sEe++ E Ll
  gi|2258701   415 DIFGFFLASIDLRQDSSVQEACVAELLKNAGIvENYSALSEEQKCEVLLK 464

                    ELkGK.RPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiisma
                    EL   +R L  + + k E ++  l  +    EL ++ + +     iis +
  gi|2258701   465 ELTEDpRTLSSAAVEKSELLEKELAIYTAARELKdklgEEVIKQHIISHT 514

                    taPsDvLAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLFs
                     + sD+    ++ +E g+ ++++  +++vPLFE + DL+ A A + +  s
  gi|2258701   515 ESVSDMFELAIMLKEVGLvdqrQARVQIVPLFETIEDLDNARAIMTQYLS 564

                    iDWYinri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKk
                     D  +  i ++ G qe+m+GYsDs KD G l+  W LYkAq E+ K+  +
  gi|2258701   565 YDIVKSWIatnAGYQEIMLGYSDSNKDGGYLASGWTLYKAQNELTKIGED 614
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                    yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                     G+ ++ FHGRGGtvGRGGGP   Ai sqP   i+  +R t qGE+iE
  gi|2258701   615 NGISITFFHGRGGTVGRGGGPSYEAITSQPFGSIKDRIRLTEQGEIIENK 664

                    FGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEE
                    +G  ++ +  L     A +   +   +    E +++Rk+m+e+
  gi|2258701   665 YGNQDVAYYNLEMLISASINRMVTRMLTNPDEidgFRKIMDEIVEDSNRI 714

                    YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPW
                    YR +v+  P F +YF  A P  E   +niGsRPa Rk    i  LRAiPW
  gi|2258701   715 YRELVFDNPHFYDYFFEASPIKEVSSLNIGSRPAARKTITDISGLRAIPW 764

                    iFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlD
                    +F+W q R  LP W  vG AFK  idK+  nl kL+ mY++WPFF   l
  gi|2258701   765 VFSWSQNRIMLPGWYAVGSAFKRFIDKEEGNLAKLQHMYDKWPFFHSLLS 814

                    LlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGH
                     ++mv  K    iA  y +L  + e+    + + d+++ tk+ +L iA H
  gi|2258701   815 NVDMVLSKSNMNIAFQYAQLAESKEVCEVFHTILDEWQLTKNVILAIAQH 864

                    kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                     +lLE  P LKq l  R +Y   Ln +q   +KR+R
  gi|2258701   865 DELLEETPSLKQSLDFRLPYFNVLNYIQIELIKRLR-------------H 901

                    EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    E  dE+    + L++                  + GiA G+ n G
  gi|2258701   902 EQLDED---YEKLIHTT----------------INGIATGLRNSG    927

gi|15677883|ref|NP_275051.1|: domain 1 of 1, from 1 to 900: score 298.2, E = 1.7e-86
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|1567788     1    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 38

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|1567788    39 ETVKLLSTS----DDSAALIE--KVLPQLDEQQTHDLTLACGLFAQILNI 82

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+   RR i+          +    E  + Et+++L        + v
  gi|1567788    83 AEDVHHERRRQIHEEA-------GRGGAEGSLTETVRRLKAGK-ADGKSV 124

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                       L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|1567788   125 QRQLDNTSVTAVLTAHPTEVQRQTVLSFNRRIRALLPQrerCTNADALAR 174

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|1567788   175 LRREIDTILLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 220

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R+++   +      R+P    ++k   W+GGDRDG nP v  E  R
  gi|1567788   221 LYRKMEHDFQTAYPGVRVP---DILKIGGWIGGDRDG-NPFVSAETLRFA 266

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                              +Y   ++ L  El +    +  Rv+      ta +dk
  gi|1567788   267 FRRHADAVFRFYRGELDKLYRELPL----SIRRVKVNG-DVTALSDKSPD 311

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEeAv
                      i        +EPYR  +  +   +     +aR L+L  G      e
  gi|1567788   312 EEI-----ARAEEPYRRAIAYI---MARAMGKARALgLGMGCKFGFLEP- 352

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y    eFL+ L    +sL + G + +A+G L Dl+R vs FG  ++ LD+
  gi|1567788   353 YASAQEFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPLDL 402

                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    Rq + ++ Dv+  + +H ++  Y    Ee++q  Ll EL+ +RPL+ + +
  gi|1567788   403 RQHAGKHADVVAELFQHAGLEDYNRLNEEQKQTALLRELSHQRPLYSPFI 452

                    PktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAvELLqR
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                      +  +  l  f++ +++  E   D+    iis +  PsD LA  LL +
  gi|1567788   453 TYSDHTRHELAIFNearkIKDEFGEDAVTQSIISNCEQPSDLLALALLLK 502

                   ECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                   E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   ++
  gi|1567788   503 ETGLlavengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDALLES 552

                   K...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                   +++ qe+m+GYsDs KD G +   W LY+A   ++   Kky v++ lFHG
  gi|1567788   553 RgniQEIMLGYSDSNKDGGYVTSSWCLYQAELGLVELFKKYDVRMRLFHG 602

                   RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                   RGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +     r
  gi|1567788   603 RGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQRN 652

                   LqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvE
                   L    AAtLE  + P    k    kLm+ +  v    YR ++   P F++
  gi|1567788   653 LETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDFID 699

                   YFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPv
                   YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  LP
  gi|1567788   700 YFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLMLPA 749

                   WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                   W G+G A     +     l  L+E  +  PFF   l  +E v AK D  +
  gi|1567788   750 WYGFGSAVETLCEDKPETLAALREHAQSNPFFQAMLSNMEQVMAKTDITL 799

                   AaLyDkLLvaEe.LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                   A  y  L  + ++ k     ++++Y   ++ LL +    +lL     L
  gi|1567788   800 AENYAGLSESPDkAKIIFGMIKEEYRRSRKALLDLLQTEELLRDNRSLAR 849

                   rlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkade
                    l LR +Y+  Ln +q   LKR+R                 E+   +
  gi|1567788   850 SLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNPHA 881

                   LvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   L+ +               Lt+ G+A G+ ntG
  gi|1567788   882 LLMVH--------------LTINGVAQGLRNTG    900

gi|254251704|ref|ZP_04945022.1|: domain 1 of 1, from 61 to 1012: score 298.2, E = 1.8e-86
                   *->siDAqLRlLvPGK....vsed.ekLieYDALLlDkFL.DiLqDLHGe
                      ++ A  R  +  K++ +  ed+++ +  D   l + L+D++ +  G+
  gi|2542517    61    AVRAAARTAAAPKsgarTREDkDRPLFEDIRFLGRLLgDVVREQEGD 107

                   dLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHm
                    + ++v      +  +    D +  + L  kL  L P  ++ v +a++
  gi|2542517   108 TVFDVVETIRQTAVKFRREDDNEAAQTLEKKLRKLTPEQTVSVVRAFSYF 157

                   LnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkln
                     LAn+AE+ +   RRRi+ +        +sA     +   l +L   +n
  gi|2542517   158 SHLANIAEDRHHNRRRRIHALA-------GSAPQPGTVAYALEQLKTTGN 200

                   KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                    s            +  vltAHPt   R+s+L  +  i   La    + +
  gi|2542517   201 ASKRLLQRFFDDALIVPVLTAHPTEVQRKSILDAQHDIARLLAE-RDQPL 249

                   tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                   t  ++   +  L   + A + t  +R a+ t  DE+   +sY+  t  +
  gi|2542517   250 TARERAHNEAMLRARVTALWQTRMLRDARLTVGDEIENALSYYRATFLDE 299

                   vPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                    P     ++ AL   G+  R+P      +  sW+GGDRDG nP vt
  gi|2542517   300 LPALYGDIEAALAEHGLPARVP---AFFQMGSWIGGDRDG-NPNVTAATL 345

                   RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk
                    +       +    Y++qv  L  Els+    + L v A +  +  a
  gi|2542517   346 DEAINRQAAVILEHYLEQVHKLGAELSV----SNLLVGASDAVKALAAA- 390

                   vvKyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGisei.
                             q P++  EPYR  L  +  +L      aR  L  G   ++
  gi|2542517   391 -------SPDQSPhrVDEPYRRALIGIYTRLAAS---ARVRLGEGTVPVr 430
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```
                    .......sEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                    + +++ ++  A +y + +eF+  L +   sL e     +A   L  l+R
  gi|2542517   431 sagrgapPVRATpYADADEFVADLKVLTASLDEHHGASLAAPRLAPLVRA 480

                    vstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLl
                       FG  L  +D+Rq s+ +  v+  +    ++ ++Y   +Ee +   Ll
  gi|2542517   481 AEVFGFHLASIDLRQSSDVHEAVVAELFARAGVEAnYAALAEEDKLRVLL 530

                    aELkGKRPLlgsDLPktEEvkDvldafr....vLAELPiDsFGaYiisma
                    a L   RPL  + L      +  l+ f++ ++v A     +   Yiis +
  gi|2542517   531 AALADPRPLRSPYLEYSALAQSELGVFEkardVRAQFGARAVRNYIISHT 580

                    taPsDvLAvELLqREC............gvkqtLrvvPLFEkLADLeAAP
                     + sD + v LLq+E +  +++ ++++++ k++L v+PLFE + DL+ A
  gi|2542517   581 ETVSDLVEVLLLQKETgllegtlgtpgsHAKNALMVIPLFETIPDLRDAS 630

                    AavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqE
                      +   F+ +++D  i +    qevm+GYsDs KD G l   W LY+A
  gi|2542517   631 RIMREYFAlpgVDTLIAHQGAEQEVMLGYSDSNKDGGFLTSNWELYRAEL 680

                    EiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtv
                     ++   ++  + L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t
  gi|2542517   681 ALVDLFRERKITLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTE 730

                    qGEviEfsFGEEnLCFrsLqRFtAAtLEHGm....nPPvsPkPEWRkLme
                    qGEvi   F   ++  r L    AAtLE  +  ++n P +  P +   m+
  gi|2542517   731 QGEVIASKFANPEIGRRNLETVVAATLEASLllqsNAP-AQLPAFEAAMQ 779

                    emAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.
                     +   A   YR++v+  P F +YF + tP +E   +niGsRPa Rk   +
  gi|2542517   780 TLSDAAMAAYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASRKLQDp 829

                    ...GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiKn
                    +++ ie LRAiPW F+W q R  L  W G+G A    +d+ +++    K
  gi|2542517   830 knrRIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVSAYLDgahdeaERTKR 879

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFG
                    l  Lk m k+WPFF   l  ++mv AK D  +A+ y +L+    L+k
  gi|2542517   880 LALLKKMNKTWPFFSNLLSNMDMVLAKTDLAVASRYAQLVADRKLrKHVF 929

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    +++ ++++ t   L +i GH   L   P L   ++ R +Y+  Ln +q
  gi|2542517   930 ERIVAEWERTSRALAEITGHDTRLATNPLLARSIKNRFPYLDPLNHLQVE 979

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     +KR R                A +           n   r   G+
  gi|2542517   980 LIKRHR----------------AGDT----------N--ARLRRGIH--- 998

                    iLtmKGiAAGmqntG<-*
                     Lt+ GiAAG+ ntG
  gi|2542517   999 -LTINGIAAGLRNTG    1012

gi|121595210|ref|YP_987106.1|: domain 1 of 1, from 7 to 949: score 298.0, E = 2e-86
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                         DA        K  +d  Li+ D  Ll + L+D++ +  G    +
  gi|1215952     7    KTDAAAAPAPARKTDKDLPLIQ-DIRLLGRILgDVIREQEGVAAYDL 52

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls  +    D +    L   L +L    ++ v +a+     LAn
  gi|1215952    53 VEQVRKLSVAFRRDADHEADKALKKLLKGLTGDQTVSVIRAFTYFSHLAN 102

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAE+ +   RRR    +       a    E  iE  l +L   +  +P
  gi|1215952   103 LAED-RHHIRRRAVHER-------AGSAQEGSIEVALARLRWAG-IAPRT 143

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL.........aqLs
                    v + L    v  vltAHPt   R+s+L  +  i   L+++++ + +aqL+
  gi|1215952   144 VAQTLATSYVAPVLTAHPTEVQRKSILDAEREIALLLtqrddiqarAQLY 193

                    ..AKD.vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYi
```

```
                    ++AKD++t+ +    +  L   +   + t  +R ++ t  DE+   +sY+
  gi|1215952   194 nsAKDtLTPRELAANEAQLRARVAQLWQTRLLRYSKLTVADEIENALSYY 243

                    HEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknP
                      t  + +PK     +   + +G    +   +  ++   W+GGDRDG nP
  gi|1215952   244 EYTFLHEIPKIYAELE---RELGGSHPV---ASFLRMGQWIGGDRDG-NP 286

                    RvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEly
                     v  +           +A   Y+  v  L  Els+    + + v AE l+
  gi|1215952   287 NVSADTLALALRRQAEVALRHYLTEVHHLGRELSL--SSNLVQVSAEMLQ 334

                    rtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntR......ERaR
                      a++     +           EPYR  L  v  +L  t ++ +++E aR
  gi|1215952   335 LAARSPDTSEH--------RRDEPYRRALTGVYARLAATLrdltggEAAR 376

                    HLLAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlL
                    H +A      + +A y +  +FL  L +   sL      ++    L  l+
  gi|1215952   377 HAVA------PQNA-YARAGDFLADLRVIEASLRSHRGAALVGERLRPLM 419

                    RqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEW
                    R v  FG  L  +D+Rq s+ +  v+  +     + s+Y   +E  R+
  gi|1215952   420 RAVEVFGFHLATVDLRQSSDQHERVVAELLATARVESdYEALPEPARRAL 469

                    LlaELkGKRPLlgsDLPktE....EvkDvldafrvLAE.LPiDsFGaYii
                    Ll  L   RPL     P  E++++Ev+ + ++ r + E+   D+   Yii
  gi|1215952   470 LLRLLCDARPLRVVGAPYSEhttgEVA-IFETARQMRErYGDDAIRHYII 518

                    smataPsDvLAvELLqRECgv.........kqtLrvvPLFEkLADLeAAP
                    s + + sD L v LLq+E g+ +++ +++ +  L vvPLFE + DL+ A
  gi|1215952   519 SHTETVSDLLEVLLLQKEVGLlqgtldtgaRADLIVVPLFETIEDLRNAA 568

                    AavekLFsiDWYinrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqE
                      +   ++i      +  ++  q++m+GYsDs KD G +   W LY+A
  gi|1215952   569 PIMREFYAIPGIAQLVRasgAEQDIMLGYSDSNKDGGIFTSNWELYRAEI 618

                    EiiKv.....AKkyG..vKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtin
                     ++   ++ +A + G +++L +FHGRGGtvGRGGGP   AiL+qPP t+
  gi|1215952   619 ALVALfdemnAAQAGapIQLRMFHGRGGTVGRGGGPSYQAILAQPPGTVR 668

                    GslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHG.mnPPvsPkPEWR
                    G +R t qGEvi   +   ++  r L    AAtLE   ++P  s    +
  gi|1215952   669 GQIRLTEQGEVIASKYANPEIGRRNLETLVAATLEATlLQPTKSATKAFL 718

                    kLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRk
                    +  e++     E YR++v+  P F +YF   tP  E   +niGsRPa Rk
  gi|1215952   719 EAAEQLSQASMEAYRALVYETPGFTDYFFNSTPIREIAELNIGSRPASRK 768

                    PsGGiesLRAiPWiFaWtqtRFHLPvWLGvGA...AFKhAidKDiK.nlq
                     s  ie LRAiPW F+W q R  LP W G+GA  +AF hA  KD K  l
  gi|1215952   769 ASQQIEDLRAIPWGFSWGQCRLMLPGWFGFGAavdAFTHAPGKDPKaQLA 818

                    kLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL..kPFGk
                     L+ mY++WPFFR  l  ++mv AK D  +A+ y +L+    L++k FG
  gi|1215952   819 LLQKMYRQWPFFRTLLSNMDMVLAKSDLALASRYSELVADARLrkKVFG- 867

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                     + ++++ t d L +i G k  L     L   +R R +Yi  L  +q
  gi|1215952   868 VIEAEWQRTADALTRITGEKQRLAANTALARSIRHRFPYIDPLHHLQVEL 917

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    ++R R  +              dE     +  +++
  gi|1215952   918 VRRWRAGQ-------------GDER---VQTGIHIS-------------- 937

                    LtmKGiAAGmqntG<-*
                      + GiAAG+ ntG
  gi|1215952   938 --INGIAAGLRNTG    949

gi|134296608|ref|YP_001120343.1|: domain 1 of 1, from 52 to 997: score 298.0, E = 2.1e-86
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                             +  +  +  +d  L e D   l + L+D++ +  G+ + ++
  gi|1342966    52    KAAGASKPAARTREDKDGPLFE-DIRFLGRLLgDVVREQEGDTVFDV 97
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                vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                v      +  +    D++  + L  kL  L P  ++ v +a++    LAn
gi|1342966    98 VETIRQTAVKFRREDDSQAAQTLEKKLRKLTPEQTVSVVRAFSYFSHLAN 147

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                +AE+ +   RRRi+ +        +sA     +   l +L   +n s
gi|1342966   148 IAEDRHHNRRRRIHALA-------GSAPQPGTVAYALEQLKTSGNASKRV 190

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                         +  vltAHPt   R+s+L  +  i   La    + +t  ++
gi|1342966   191 LQRFFDDALIVPVLTAHPTEVQRKSILDAQHDIARLLAE-RDQPLTARER 239

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   +  L   + A + t  +R a+ t  DE+   +sY+  t  +  P
gi|1342966   240 AYNESMLRARVTALWQTRMLRDARLTVGDEIENALSYYRTTFLDELPALY 289

                RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                  ++ AL   G+  R+P      +  sW+GGDRDG nP vt     +
gi|1342966   290 GDIEAALAEHGLPARVP---AFFQMGSWIGGDRDG-NPNVTAATLDEAIN 335

                LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    +    Y++qv  L  Els+    + L v A +  +  a
gi|1342966   336 RQAAVILEHYLEQVHKLGAELSV----SNLLVGANDAVKALAAA------ 375

                iEFWKqvP..PtEPYRviLGdvRDKLYntRERaRHLLAtGisei......
                     q P++  EPYR  L  +  +L      aR  L  G   +++ +++
gi|1342966   376 --SPDQSPhrVDEPYRRALIGIYTRLAAS---ARVRLGEGTVPVrsagrg 420

                ..sEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFG
                 ++  Av+y + E F+  L +   sL e     +A   L  l+R    FG
gi|1342966   421 apPVRAVpYADSEAFVADLKVLTASLEEHHGASLAAPRLTPLMRAAEVFG 470

                LsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkG
                  L  +D+Rq s+ +  v+  +    ++ ++Y + sE+ +   Lla L
gi|1342966   471 FHLSSIDLRQSSDIHEAVVAELFARAGVHAdYASLSEDDKLIALLAALAD 520

                KRPLlgsDLPktEEvkDvldaf....rvLAELPiDsFGaYiismataPsD
                 RPL  + +      +  l+ f++ ++v A     +   Yiis + + sD
gi|1342966   521 PRPLRSPYIEYSALAQSELGVFekarEVRAQFGPRAVRNYIISHTETVSD 570

                vLAvELLqRECgv.............kqtLrvvPLFEkLADLeAAPAavek
                 + v LLq+E g+ ++  +  +++ ++ L v+PLFE + DL+ A   +
gi|1342966   571 LVEVLLLQKETGLlegafgaahdsaRNGLMVIPLFETIPDLRDAARIMRE 620

                LFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKv
                 F+ ++i+  i +    qevm+GYsDs KD G l   W LY+A   ++
gi|1342966   621 YFAlpgIEALIAHQGAEQEVMLGYSDSNKDGGFLTSNWELYRAELALVDL 670

                AKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEvi
                 ++  + L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGEvi
gi|1342966   671 FRDRKITLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEVI 720

                EfsFGEEnLCFrsLqRFtAAtLEHGmnPPv...sPkPEWRkLmeemAvvA
                   F   ++  r L    AAtLE  + P  + ++  P +   m+ +   A
gi|1342966   721 ASKFANPEIGRRNLETVVAATLEASLLPQSnapAQLPAFEAAMQALSDAA 770

                tEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....Gie
                   YR++v+  P F +YF  AtP +E   +niGsRPa Rk   ++++ ie
gi|1342966   771 MASYRALVYETPGFTDYFFAATPITEIAELNIGSRPASRKLQDpknrRIE 820

                sLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiKnlqkLkE
                 LRAiPW F+W q R  L  W G+G A    +d+ ++     K +  Lk
gi|1342966   821 DLRAIPWGFSWGQCRLLLTGWYGFGSAVSAYLDgapdaaARTKRVALLKK 870

                mYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdk
                m k+WPFF   l  ++mv AK D  +A+ y +L+    L+k   +++ ++
gi|1342966   871 MNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVADRKLrKHVFERIVAE 920

                YvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiR
                ++ t + L +i GH   L   P L   ++ R +Y+  Ln +q   +KR R
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  gi|1342966   921 WERTAQALAEITGHEGRLATNPLLARSIKNRFPYLDPLNHLQVELIKRHR 970

                   DPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKG
                                A +           n   r   G+     Lt+ G
  gi|1342966   971 ----------------AGDT----------N--ARLRRGIH----LTING 988

                   iAAGmqntG<-*
                   iAAG+ ntG
  gi|1342966   989 IAAGLRNTG    997

gi|251782035|ref|YP_002996337.1|: domain 1 of 1, from 22 to 943: score 297.9, E = 2.2e-86
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           L+ L          + e  A+L D    i   + G++    +
  gi|2517820    22    --SLSLKKLESSNNQ--AIIAEEVAILKDMLEKITRRMIGDEAFATI 64

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        ls     K+D   Le   + + s+   D  ++ + ++ +  L n+
  gi|2517820    65 ETIVALSE----KQDYVGLE---TIIASISNQDMDVISRYFSILPLLINI 107

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    E+v+lAy    +     D+      t ++         v       e
  gi|2517820   108 SEDVDLAYEINYQNNANKDYLGKLALTIDA---------VAEK----ENA 144

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    + L    v  vltAHPtq  R+ +L   + i   L +       v  ++
  gi|2517820   145 KDILEQVNVVPVLTAHPTQVQRKTILELTTHIHDLLRKYRDVKAGVVNQE 194

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                        L R i     tD iR  +   + E+   m Y+   + + v K
  gi|2517820   195 KWHNELYRYIEIIMQTDIIREKKLKVKNEITNVMQYYNGSLIQAVTK--- 241

                   RvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRDvCL
                      t  Kn+     l    P +i    W+GGDRDG nP vt E  R
  gi|2517820   242 -LTTEYKNLAQKRGLDLVNPNpITMGMWIGGDRDG-NPFVTAETLRLSAT 289

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   +   +  n Yi+++  L   +s+    + L     E+ r a   +    Y
  gi|2517820   290 VQSEVILNYYIEKLAALYRTFSL---SSTLIQPSAEVERLASLSQDQSIY 336

                   iEFWKqvPPtEPYRviLGdvRDKLYntRER..............aRHLLA
                    E       +EPYR     v+ +L  tR   ++++++++++ +  R
  gi|2517820   337 RE-------NEPYRRAFHYVKSRLVQTRTQltgdqdttgqsltaGRLTRQ 379

                   tGiseisEe..AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                     + +  E + A y   E+F   L    +sL   GD ++ DG L +++
  gi|2517820   380 LAMQDQLEGpiAAYVSPEDFKADLMAIEQSLLSNGDVALVDGDLREVMQA 429

                   vstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLl
                   v  FG  L  +D+Rq+s  q   +  + +  +i  +Y + sE  + + L+
  gi|2517820   430 VDIFGFFLASIDMRQDSSVQEACVAELLKGANIVEdYSSLSETEKCDLLV 479

                   aELkGK.RPLlgsDLPktEEvkDvldafrvLAELPiDsFG.....aYiis
                     L   +R L  + + k + ++  l  +    EL  D  G++  +  iis
  gi|2517820   480 KQLTEDpRTLSSAAVAKSDLLEKELAIYAAAREL-KDKLGdevikQHIIS 528

                   mataPsDvLAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekL
                    + + sD+    ++ +E g+ +++k  +++vPLFE + DL+ A   +
  gi|2517820   529 HTESVSDMFELAIMLKEVGLidqhKARVQIVPLFETIEDLDNARDIMTTY 578

                   FsiDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvA
                    s D  +  i   ++ qe+m+GYsDs KD G l+  W LYkAq E+  +
  gi|2517820   579 LSYDMVKSWIAANhnyQEIMLGYSDSNKDGGYLASGWTLYKAQNELTAIG 628

                   KkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviE
                    + GvK++ FHGRGGtvGRGGGP   Ai sqP   i+  +R t qGE+iE
  gi|2517820   629 EENGVKITFFHGRGGTVGRGGGPSYDAITSQPFGSIKDRIRLTEQGEIIE 678

                   fsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAt
                     +G  ++ +  L     A +   +   +    E +++R++m+ +
  gi|2517820   679 NKYGNKDVAYYHLEMLISASINRMVTQMLTNPNEidgFREVMDGIVADSN 728
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                    EEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAi
                      YR +v+  P F +YF  A P  E   +niGsRPa Rk    i+ LRAi
  gi|2517820   729 KIYRQLVFDNPHFYDYFFEASPIKEVSSLNIGSRPAARKTITEITGLRAI 778

                    PWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvt
                    PW+F+W q R   P W GvG AFKh id+   nl +L+ mY++WPFF
  gi|2517820   779 PWVFSWSQNRIMFPGWYGVGSAFKHYIDQAEGNLERLQHMYQTWPFFHSL 828

                    lDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiA
                    l  ++mv  K    iA  y +L  + e++   + + d+++ tk+ +L i
  gi|2517820   829 LSNVDMVLSKSNMNIAFQYAQLADSQEVRDVFHVILDEWQLTKNVILAIE 878

                    GHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhl
                    GH +lLE  P LKq l  R +Y   Ln +q   +KR+R  + +
  gi|2517820   879 GHEELLEDNPSLKQSLAFRLPYFNVLNYIQIELIKRLRNHQLR------- 921

                    sKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                         +E+    + L++                  + GiA G+ n G
  gi|2517820   922 -----EED----EKLIHTT----------------INGIATGLRNSG    943

gi|161507563|ref|YP_001577517.1|: domain 1 of 1, from 1 to 912: score 297.6, E = 2.7e-86
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                            ++ L     s d +++  +  +l   L++    L G++L
  gi|1615075     1    ---MTVKKL---ENSSDVNVVTEEVKILTNLLnESTEQLIGKELFTK 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +q    +sA+       k  +EL  ++ sLd  + i+vA+ +  +  L n
  gi|1615075    42 IQNLIKISAD-------KNYQELEDQIASLDNREMIVVARYFATLPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+velA +  +      D+    + t +         +v +  K  +E
  gi|1615075    85 ISEDVELASKVNVLNNTNQDYLGKLNDTID---------IVAQK-KNAKE 124

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + e +    v  vltAHPtq  R+ +L    +i   L         +  +
  gi|1615075   125 ILEKV---NVVPVLTAHPTQVQRKTVLELTDKIHKLLRNYREVKNGIITR 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     E  E L   i     tD iR  +     E+   + Y+   +   + KF
  gi|1615075   172 VEWTEELRACIEILMQTDIIRSHKLKVSNEITNVLTYYPKSLIPAITKFT 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                     R     K  G+   +P   P i    W+GGDRDG nP vt +  +
  gi|1615075   222 ARYKELAKKHGLD--IPDATP-ITMGMWIGGDRDG-NPYVTADTLKLSAT 267

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L   +    Yi q+  L   +s+              y  +  +  v +
  gi|1615075   268 LQGQVIFEYYIKQINQLYRSISL-----------STSYMKPSTE--VMHL 304

                    iEFWKqvPP...tEPYRvi.......LGdvRDKLYntRERaRHLLAtGis
                     E      P +++EPYR      +++L     KL n       L    +
  gi|1615075   305 SELSNDDSPfrtNEPYRRAfyyiesrLVRSEQKLLNITNQHSFLKERDLE 354

                    eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                     +     y +  eF   LE+  +sL e  D+++      ++L  +  FG
  gi|1615075   355 HLDQIPAYEDAQEFKADLEVIKRSLEENRDQAVVKSYFTEILEAIDVFGF 404

                    sLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK
                     L  +D+Rq+s  +   +  + +  ei + Y e sE  +   Ll EL
  gi|1615075   405 HLATIDMRQDSSVNEACVAELLKSAEICdHYSELSEKEKVSLLLNELNND 454

                    .RPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsD
                    +R L     Pk E ++  l  ++   +L ++ + D     iis + + sD
  gi|1615075   455 pRNLHTNNKPKSELLQKELKIYKTARDLKdrlgEDLIKQHIISHTESVSD 504

                    vLAvELLqRECgvkqt....LrvvPLFEkLADLeAAPAavekLFsiD...
                    +L   ++ +E  +   ++ +++vvPLFE + DL+ A   ++    +D  +
  gi|1615075   505 MLEQAIMLKEYDLLDNqsarVQVVPLFETVEDLNNARDIIKEYLNLDivk 554

                    .WYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvK
                    +W + + +  qevm+GYsDs KD G l+  W LYkAq ++  +  + G+K
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```
  gi|1615075   555 kWLVSQHN-YQEVMLGYSDSNKDGGYLASCWNLYKAQKDLTAIGEELGIK 603

                   LvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEE
                   ++  HGRGGtvGRGGGP   Ai +qP   in  +R+t qGE+i   +G
  gi|1615075   604 ITYMHGRGGTVGRGGGPSYEAITAQPFNSINDRIRMTEQGEIIQNKYGNK 653

                   nLCFrsLqRFtAAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsv
                   +  +  L     At++      +   +   ++R  m+++     E Y+ +
  gi|1615075   654 DAAYYNLEMLVSATVDRIASKQIVSEeyiADFRSSMDKIVTESNEIYKKL 703

                   vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaW
                   v+  P F +YF  AtP  E   +niGsRPa Rk      sLRAiPW+F+W
  gi|1615075   704 VFENPNFLDYFLQATPIKEISNLNIGSRPASRKKLSDFSSLRAIPWVFSW 753

                   tqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEm
                    q R   P W GvG AFKh id D Knlq L+ mY+ WPFF   l   +m
  gi|1615075   754 SQSRVMFPGWYGVGSAFKHFIDADKKNLQELQHMYQGWPFFHALLSNADM 803

                   vFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlL
                   v  K    iA  y +L   E  k   + + ++++ tk+++L+i GH DlL
  gi|1615075   804 VLSKSNMEIAKQYAELCQDEKTKSVFDIIYQEWKLTKQIILQIEGHDDLL 853

                   EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                      P LK  l  R +Y   Ln +q   +KR R+ + k   +  +
  gi|1615075   854 SDAPNLKNSLASRMPYFNILNYIQLEMIKRDREDEIKGVFQSII------ 897

                   EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +       + +n                 G+A G+ n G
  gi|1615075   898 -P-------ITIN-----------------GVASGLRNSG    912

gi|254181387|ref|ZP_04887984.1|: domain 1 of 1, from 53 to 994: score 297.1, E = 3.8e-86
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      s   q R     +  +d  L e D   l + L+D++ +  G+ + ++
  gi|2541813    53    SAKPQGRT----REDKDRPLFE-DIRYLGRLLgDVVREQEGDAVFDV 94

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v      +  +    D    + L   L  L P  ++ v +a++    LAn
  gi|2541813    95 VETIRQTAVKFRREDDKAAAQTLEKMLRKLTPEQTVSVVRAFSYFSHLAN 144

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE+ +   RRRi+ +        +sA     +   l kL   ++ s +
  gi|2541813   145 IAEDRHHNRRRRIHALA-------GSAAQAGTVAYALDKLKQAGDASSKT 187

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   + +      +  vltAHPt   R+s+L  +  i    a L A    +
  gi|2541813   188 IKQFFEGALIVPVLTAHPTEVQRKSILDAQHDI----ARLLAERDQPLTA 233

                   kEL..DEALHRE.iqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                   +EL + EAL R ++   + t  +R a+ t  DE+   +sY+  t  +  P
  gi|2541813   234 RELahNEALLRArVTTLWQTRMLRDARLTVADEIENALSYYRATFLDELP 283

                   KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                        ++ AL   G+  R+P      +  sW+GGDRDG nP vt     +
  gi|2541813   284 ALYADIEEALAEHGLRARVP---AFFQMGSWIGGDRDG-NPNVTAATLDE 329

                   vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                          +    Y++qv  L  Els+    + L v A +  +  a
  gi|2541813   330 AISRQAAVIFEHYLEQVHKLGAELSV----SNLLVGASDALKALAAA--- 372

                   KyYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER....aRHLLAtGis
                           q P++  EPYR  L  v  +L  + R R ++++  +   G
  gi|2541813   373 -----SPDQSPhrVDEPYRRALIGVYTRLAAsARVRlgegTVPVRSAGRG 417

                   eisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFG
                     +  A +y + EeF   L +   sL       +A   L  l+R    FG
  gi|2541813   418 AAPVRATpYADAEEFAADLRVLTDSLALHHGESLATPRLAPLMRAAEVFG 467

                   LsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkG
                     L  +D+Rq s+ +  v+  +    ++ ++Y   +E  +   Lla L
  gi|2541813   468 FHLASIDLRQSSDIHEAVVAELLARGGVEAdYAALPEADKLRVLLAALAD 517
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                    KRPLlgsDLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsD
                     RPL  + L   +  k  l+ +++ + + A     +   Yiis + + sD
  gi|2541813   518 PRPLRSPYLDYSDLAKSELGVLErahaIRAQFGARAVRNYIISHTETVSD 567

                    vLAvELLqRECgv.............kqtLrvvPLFEkLADLeAAPAavek
                     + v LLq+E g+ +++ ++++ + ++ L v+PLFE +ADL+ A   +
  gi|2541813   568 LVEVLLLQKETGLfegtlgtphanaRNGLMVIPLFETIADLRNASDIMRA 617

                    LFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKv
                     F+ +++     +    qevm+GYsDs KD G l   W LY+A   ++
  gi|2541813   618 FFAlpgVGELLAHQGHEQEVMLGYSDSNKDGGFLTSNWELYRAELALVDL 667

                    AKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEvi
                      + G+KL lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGEvi
  gi|2541813   668 FDERGIKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEVI 717

                    EfsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEWRkLmeemAvvA
                       F   ++  r L    AAtLE  + P  ++Pk+ P +   m+ +   A
  gi|2541813   718 ASKFANPEIGRRNLETVVAATLEATLAPHSnAPKqlPAFEAAMQTLSDAA 767

                    tEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....Gie
                       YR++v+  P F +YF + tP +E   +niGsRPa Rk   ++++ ie
  gi|2541813   768 MASYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASRKLQDpknrKIE 817

                    sLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiKnlqkLkE
                     LRAiPW F+W q R  L  W G+G A    +d+ ++     K +  Lk
  gi|2541813   818 DLRAIPWGFSWGQCRLLLTGWYGFGSAVAAYLDgapdaaERGKRVALLKK 867

                    mYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdk
                    m k+WPFF   l  ++mv AK D  +A+ y +L+    L+k   +++ ++
  gi|2541813   868 MNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVADKKLrKHVFERIVAE 917

                    YvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiR
                    +  t d L +i G +  L   P L   ++ R +Y+  Ln +q   +KR R
  gi|2541813   918 WHRTADALAEITGAHARLAANPLLARSIKNRFPYLDPLNHLQVELIKRHR 967

                    DPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKG
                                A +           n   r   G+     Lt+ G
  gi|2541813   968 ----------------AGDT----------N--ARLRRGIH----LTING 985

                    iAAGmqntG<-*
                    iAAG+ ntG
  gi|2541813   986 IAAGLRNTG    994

gi|167918035|ref|ZP_02505126.1|: domain 1 of 1, from 53 to 994: score 297.1, E = 3.8e-86
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       s   q R     +  +d  L e D   l + L+D++ +  G+ + ++
  gi|1679180    53    SAKPQGRT----REDKDRPLFE-DIRYLGRLLgDVVREQEGDAVFDV 94

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      +  +    D    + L   L  L P  ++ v +a++    LAn
  gi|1679180    95 VETIRQTAVKFRREDDKAAAQTLEKMLRKLTPEQTVSVVRAFSYFSHLAN 144

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+ +   RRRi+ +        +sA     +   l kL   ++ s +
  gi|1679180   145 IAEDRHHNRRRRIHALA-------GSAAQAGTVAYALDKLKQAGDASSKT 187

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + +      +  vltAHPt   R+s+L  +  i    a L A    +
  gi|1679180   188 IKQFFEGALIVPVLTAHPTEVQRKSILDAQHDI----ARLLAERDQPLTA 233

                    kEL..DEALHRE.iqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                    +EL + EAL R ++   + t  +R a+ t  DE+   +sY+  t  +  P
  gi|1679180   234 RELahNEALLRArVTTLWQTRMLRDARLTVADEIENALSYYRATFLDELP 283

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                         ++ AL   G+  R+P      +  sW+GGDRDG nP vt     +
  gi|1679180   284 ALYADIEEALAEHGLRARVP---AFFQMGSWIGGDRDG-NPNVTAATLDE 329

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                           +    Y++qv  L  Els+    + L v A +  +  a
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  gi|1679180   330 AISRQAAVIFEHYLEQVHKLGAELSV----SNLLVGASDALKALAAA--- 372

                    KyYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER....aRHLLAtGis
                            q P++  EPYR  L  v  +L  + R R ++++  +   G
  gi|1679180   373 -----SPDQSPhrVDEPYRRALIGVYTRLAAsARVRlgegTVPVRSAGRG 417

                    eisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFG
                      +  A +y + EeF   L +   sL       +A   L  l+R    FG
  gi|1679180   418 AAPVRATpYADAEEFAADLRVLTDSLALHHGESLATPRLAPLMRAAEVFG 467

                    LsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkG
                      L  +D+Rq s+ +  v+  +    ++ ++Y   +E  +   Lla L
  gi|1679180   468 FHLASIDLRQSSDIHEAVVAELLARGGVEAdYAALPEADKLRVLLAALAD 517

                    KRPLlgsDLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsD
                     RPL  + L   +  k  l+ +++ + + A     +   Yiis + + sD
  gi|1679180   518 PRPLRSPYLDYSDLAKSELGVLErahaIRAQFGARAVRNYIISHTETVSD 567

                    vLAvELLqRECgv.............kqtLrvvPLFEkLADLeAAPAavek
                     + v LLq+E g+ +++ ++++ + ++ L v+PLFE +ADL+ A   +
  gi|1679180   568 LVEVLLLQKETGLfegtlgtphanaRNGLMVIPLFETIADLRNASDIMRA 617

                    LFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKv
                     F+ +++     +    qevm+GYsDs KD G l   W LY+A   ++
  gi|1679180   618 FFAlpgVGELLAHQGHEQEVMLGYSDSNKDGGFLTSNWELYRAELALVDL 667

                    AKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEvi
                      + G+KL lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGEvi
  gi|1679180   668 FDERGIKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEVI 717

                    EfsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEWRkLmeemAvvA
                       F   ++  r L    AAtLE  + P  ++Pk+ P +   m+ +   A
  gi|1679180   718 ASKFANPEIGRRNLETVVAATLEATLAPHSnAPKqlPAFEAAMQTLSDAA 767

                    tEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....Gie
                       YR++v+  P F +YF + tP +E   +niGsRPa Rk   ++++ ie
  gi|1679180   768 MASYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASRKLQDpknrKIE 817

                    sLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiKnlqkLkE
                     LRAiPW F+W q R  L  W G+G A    +d+ ++     K +  Lk
  gi|1679180   818 DLRAIPWGFSWGQCRLLLTGWYGFGSAVAAYLDgapdaaERGKRVALLKK 867

                    mYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdk
                    m k+WPFF   l  ++mv AK D  +A+ y +L+    L+k   +++ ++
  gi|1679180   868 MNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVADKKLrKHVFERIVAE 917

                    YvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiR
                    +  t d L +i G +  L   P L   ++ R +Y+  Ln +q   +KR R
  gi|1679180   918 WHRTADALAEITGAHARLAANPLLARSIKNRFPYLDPLNHLQVELIKRHR 967

                    DPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKG
                                   A +           n   r   G+     Lt+ G
  gi|1679180   968 ----------------AGDT----------N--ARLRRGIH----LTING 985

                    iAAGmqntG<-*
                    iAAG+ ntG
  gi|1679180   986 IAAGLRNTG    994

gi|241759416|ref|ZP_04757520.1|: domain 1 of 1, from 1 to 900: score 296.9, E = 4.4e-86
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2417594     1    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 38

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2417594    39 ETVKLLSTS----DDSAALIE--KVLPQLDEQQTHDLTLACGLFAQILNI 82

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+   RR i+    G  + E+s t      Et++kL        + v
  gi|2417594    83 AEDVHHERRRQIHEEA-GHNSAEGSLT------ETVRKLKAGK-VNGKAV 124
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                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     + L n  v  vltAHPt   R  +L  n RiR  L q   +   +e
  gi|2417594   125 QQQLDNTVVTAVLTAHPTEVQRQTVLSFNRRIRALLPQ-RERCTNPEALA 173

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     L   +   +   + t E RR +    DE+  G+s +    ++  PK  R
  gi|2417594   174 QLRREIDTVLLGLWQTSETRRHKLSVNDEINNGVSIFPMSFFEALPKLYR 223

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     ++   +      R+P    ++k   W+GGDRDG nP v  E  R
  gi|2417594   224 TMERDFQTAYPGVRVP---NILKIGGWIGGDRDG-NPFVSAETLRFAFRR 269

                    aRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkvvKy
                           +Y   ++ L  E +ls+ R      v A    +
  gi|2417594   270 HADAVFRFYRGELDKLYRElpLSIRRVKVNDDVMALAALSPDEEI----- 314

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEeAvy
                              +EPYR  +  +   +     +aR L+L  G      e  y
  gi|2417594   315 -------ARTEEPYRRAIAYI---MARAMGKARSLgLGMGCKFGFLEP-Y 353

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                      vEeFL  L    +sL e G + +A+G L  ++R vs FG  ++ LD+R
  gi|2417594   354 ATVEEFLTDLKKLQRSLHENGSQLLAEGRLANIIRSVSVFGFHMMPLDLR 403

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    q + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL+ +RPL+ + +
  gi|2417594   404 QHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELSHQRPLYSPFIT 453

                    ktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAvELLqRE
                      +  +  l  f++ +++  E   D+    iis +  PsD LA  LL +E
  gi|2417594   454 YSDHTRHELAIFNearkIKDEFGEDAVTQSIISNCEQPSDLLALALLLKE 503

                    Cgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK
                     g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   ++ +
  gi|2417594   504 SGLlvvengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDALLESR 553

                    ...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    ++ qe+m+GYsDs KD G +   W LY+A   ++   Kky v++ lFHGR
  gi|2417594   554 gniQEIMLGYSDSNKDGGYVTSSWCLYQAELGLVELFKKYDVRMRLFHGR 603

                    GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                    GG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +     r L
  gi|2417594   604 GGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQRNL 653

                    qRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEY
                        AAtLE  + P    k    kLm+++  v    YR ++   P F++Y
  gi|2417594   654 ETLVAATLEASILP--DKKDPDAKLMQDLSEVSFKYYRELITH-PDFIDY 700

                    FRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvW
                    F    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  LP W
  gi|2417594   701 FLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLMLPAW 750

                    LGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiA
                     G+G A     +     l  L+E  +  PFF   l  +E v AK D  +A
  gi|2417594   751 YGFGSAVETLCEGNPDTLAALREHAQSNPFFQAMLSNMEQVMAKTDITLA 800

                    aLyDkLLvaEe.LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                      y  L  + ++ k     ++++Y+  ++ LL +    +lL     L
  gi|2417594   801 ENYAGLSESPDkAKIIFGMIKEEYQRSRKALLDLLQTEELLRDNRSLARS 850

                    lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                    l LR +Y+  Ln +q   LKR+R                  E+   +  L
  gi|2417594   851 LALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNPHAL 882

                    vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    + +              Lt+ G+A G+ ntG
  gi|2417594   883 LMVH--------------LTINGVAQGLRNTG    900

gi|225868820|ref|YP_002744768.1|: domain 1 of 1, from 1 to 927: score 296.6, E = 5.4e-86
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           ++ L        e + e  A+L +    i   + G++    +
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gi|2258688     1    ---MSVKKLESYNNQ--EIIAEEVAILKEILESITRRMIGDEAFARI 42

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E  +ls     K+D   Le L   + ++   D  l+ + ++ +  L n+
gi|2258688    43 EEIIDLSE----KQDYVLLEQL---IAGISNKDMELISRYFSILPLLINI 85

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiE.EtlKkLvlklnKsPeE
                     E+v+lAy    +     D+      t  s  E+E  K L  k
gi|2258688    86 SEDVDLAYEINRQNNTNQDYLGKLALTIASVAEkENAKELLEKV------ 129

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                            +v  vltAHPtq  R+ +L     i n L         v  +
gi|2258688   130 --------TVVPVLTAHPTQVQRKTVLELTNSIHNLLRRYRDVKAGVMNQ 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                          L R i     tD iR  +   + E+   m Y+   + + +
gi|2258688   172 NKWYSELYRYIDILMQTDIIREKKLKVKNEITNVMQYYNSSLIQAITALT 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                     +  t  K  Gi   l  +   i    W+GGDRDG nP vt E  R
gi|2258688   222 SKYKTLAKDKGI---LLDNPKPINMGMWIGGDRDG-NPFVTAETLRLSAT 267

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    +   +   +Yi+++  L   +s+    + L     E+ r a        Y
gi|2258688   268 VQSEVILRFYIDKLSALYQTFSL---SSALTKTSPEVERLASLSSDQSIY 314

                    iE........FWKqvPPtEPYRviLGd.vRDKLYntRERaRHLLAtGise
                     E+++ ++   + qv        ++G++  D+L      +   L  G+
gi|2258688   315 REnepyrrafHYIQVRLAKTLQELVGQpASDQLASRMPATVGSLQSGVTS 364

                    isEeA......vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqv
                    i  + ++++ + y     F   L +  +sL   GD  + +G L ++L  v
gi|2258688   365 IVTNSsdqqapAYKTAAAFKADLVMIEQSLIAAGDSSLVEGDLQEVLQAV 414

                    stFGLsLvKLDiRqEseRqtDvlDAittHLe.iGsYReWsEeKRqEWLla
                      FG  L  +D+Rq+s  q   +  + +  + +  Y   sEe++ E Ll
gi|2258688   415 DIFGFFLASIDLRQDSSVQEACVAELLKNAGmVENYSALSEEQKCEILLK 464

                    ELkGK.RPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiisma
                    EL   +R L  + + k E ++  l  +    EL ++ + +     iis +
gi|2258688   465 ELTEDpRTLSSAAVEKSELLEKELAIYTAARELKdklgEEVIKQHIISHT 514

                    taPsDvLAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLFs
                     + sD+    ++ +E g+ ++++  +++vPLFE + DL+ A A + +  s
gi|2258688   515 ESVSDMFELAIMLKEVGLidqrQARVQIVPLFETIEDLDNARAIMTQYLS 564

                    iDWYinri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKk
                     D  +  i ++ G qe+m+GYsDs KD G l+  W LYkAq E+ K+  +
gi|2258688   565 YDIVKSWIatnAGYQEIMLGYSDSNKDGGYLASGWTLYKAQNELTKIGED 614

                    yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                      v ++ FHGRGGtvGRGGGP   Ai sqP   i+  +R t qGE+iE
gi|2258688   615 NDVSITFFHGRGGTVGRGGGPSYEAITSQPFGSIKDRIRLTEQGEIIENK 664

                    FGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEE
                    +G  ++ +  L     A +   +   +    E +++Rk+m+e+
gi|2258688   665 YGNQDVAYYNLEMLISASINRMVTRMLTNPDEidgFRKIMDEIVEDSKRI 714

                    YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPW
                    YR +v+  P F +YF  A P  E   +niGsRPa Rk    i  LRAiPW
gi|2258688   715 YRELVFDNPHFYDYFFEASPIKEVSSLNIGSRPAARKTITDISGLRAIPW 764

                    iFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlD
                    +F+W q R  LP W  vG AFK  idK+  nl kL+ mY++WPFF   l
gi|2258688   765 VFSWSQNRIMLPGWYAVGSAFKRFIDKEEGNLAKLQHMYDKWPFFHSLLS 814

                    LlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGH
                     ++mv  K    iA  y +L  + e+    + + d+++ tk+ +L iA H
gi|2258688   815 NVDMVLSKSNMNIAFQYAQLAESKEVCEVFHTILDEWQLTKNVILAIAQH 864

                    kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
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                   +lLE  P LKq l  R +Y   Ln +q   +KR+R
  gi|2258688   865 DELLEETPSLKQSLDFRLPYFNVLNYIQIELIKRLR-------------H 901

                   EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   E  dE+    + L++                  + GiA G+ n G
  gi|2258688   902 EQLDED---YEKLIHTT----------------INGIATGLRNSG    927

gi|83719610|ref|YP_441427.1|: domain 1 of 1, from 134 to 1088: score 296.1, E = 7.5e-86
                   *->siDAqLRlLvP.........GKvsed.ekLieYDALLlDkFL.DiLq
                         A  R ++P++  + +++G+  ed+++ +  D   l + L+D++
  gi|8371961   134    --GAAARTIAPtnaasakphGRTREDkDRPLFEDIRYLGRLLgDVVR 178

                   DLHGedLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAk
                   +  G+ + ++v      +  +    D    + L   L  L P  ++ v +
  gi|8371961   179 EQEGDAVFDVVETIRQTAVKFRREDDKTAAQTLEKMLRKLTPEQTVSVVR 228

                   ailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkL
                   a++    LAn+AE+ +   RRRi+ +        +sA     +   l kL
  gi|8371961   229 AFSYFSHLANIAEDRHHNRRRRIHALA-------GSAPQAGTVAYALDKL 271

                   vlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL
                      ++ s + + +      +  vltAHPt   R+s+L  +  i   La
  gi|8371961   272 RQAGDASSKTIKQFFEGALIVPVLTAHPTEVQRKSILDAQHDIARLLAE- 320

                   sAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHE
                     + +t  ++   +  L   +   + t  +R a+ t  DE+   +sY+
  gi|8371961   321 RDQPLTARERAHNEALLRARVTTLWQTRMLRDARLTVADEIENALSYYRA 370

                   tvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRv
                   t  +  P     ++ AL   G+  R+P      +  sW+GGDRDG nP v
  gi|8371961   371 TFLDELPALYTDIEEALAEHGLPARVP---AFFQMGSWIGGDRDG-NPNV 416

                   tPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrt
                   t     +       +     Y++qv  L  Els+    + L v A +  +
  gi|8371961   417 TAATLDEAINRQAAVIFEHYLEQVHKLGAELSV----SNLLVGASDALKA 462

                   aardkvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER....aRH
                    a             q P++  EPYR  L  v  +L  + R R +++a
  gi|8371961   463 LAAA--------SPDQSPhrVDEPYRRALIGVYTRLAAsARVRlgegAVP 504

                   LLAtGiseisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlL
                   +   G    +  A +y + EeF+  L +   sL       +A   L  l+
  gi|8371961   505 VRSAGRGAAPVRATpYADAEEFVADLRVLTDSLAVHHGESLATPRLAPLM 554

                   RqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEW
                   R    +G  L  +D+Rq s+ +  v+  +    ++ + Y   +E  +
  gi|8371961   555 RAAEVYGFHLASIDLRQSSDIHEAVIAELLARGGVEpDYAALPEADKLRV 604

                   LlaELkGKRPLlgsDLPktEEvkDvldafr....vLAELPiDsFGaYiis
                   Lla L   RPL  + L   +  k  l+ +++ + + A     +   Yiis
  gi|8371961   605 LLAALADPRPLRSPYLDYSDLAKSELGVLErahaIRAQFGARAVRNYIIS 654

                   mataPsDvLAvELLqRECgv............kqtLrvvPLFEkLADLeA
                    + + sD + v LLq+E g+ +++ + ++ + ++ L v+PLFE +ADL+
  gi|8371961   655 HTETVSDLVEVLLLQKETGLfegtlgaphanaRNGLMVIPLFETIADLRN 704

                   APAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkA
                   A   +   F+ +++     +    qevm+GYsDs KD G l   W LY+A
  gi|8371961   705 ASDIMREFFAlpgVGELLAHQGHEQEVMLGYSDSNKDGGFLTSNWELYRA 754

                   qEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRv
                      ++    + G+KL lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R
  gi|8371961   755 ELALVDLFHERGIKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRL 804

                   tvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEWRkLm
                   t qGEvi   F   ++  r L    AAtLE  + P  ++Pk+ P +   m
  gi|8371961   805 TEQGEVIASKFANPEIGRRNLETVVAATLEATLAPHSnAPKqlPAFEAAM 854

                   eemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG
                   + +   A   YR++v+  P F +YF + tP +E   +niGsRPa Rk
  gi|8371961   855 QTLSDAAMASYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASRKLQD 904
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                    ....GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......KDiK
                    ++++ ie LRAiPW F+W q R  L  W G+G A    +d+ ++     K
  gi|8371961   905 pkhrKIEDLRAIPWGFSWGQCRLLLTGWYGFGGAVAAYLDgapdaaERGK 954

                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPF
                     +  L+ m k+WPFF   l  ++mv AK D  +A+ y +L+    L+k
  gi|8371961   955 RVALLRKMNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVADKKLrKHV 1004

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA
                     +++ +++  t   L +i G +  L   P L   ++ R +Y+  Ln +q
  gi|8371961  1005 FERIVAEWHRTASALAEITGAQARLAANPLLARSIKNRFPYLDPLNHLQV 1054

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                      +KR R                A +           n   r   G+
  gi|8371961  1055 ELIKRHR----------------AGDT----------N--ARLRRGIH-- 1074

                    LiLtmKGiAAGmqntG<-*
                      Lt+ GiAAG+ ntG
  gi|8371961  1075 --LTINGIAAGLRNTG    1088

gi|116627590|ref|YP_820209.1|: domain 1 of 1, from 1 to 940: score 296.1, E = 7.8e-86
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                              +      s+++++i  +  +l   L+D    + Ge+
  gi|1166275     1    ------MAFNKLESSNNQEIISEEVGILKELLdDATRGIAGEQGLTT 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +q   El        D    e L   +  +   D ++  + ++ +  L n
  gi|1166275    42 IQHLVEL-------YDEGDYEALTQAISEMTNDDMVVASRYFSLLPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    k        DE+     s   Et+  +v       +
  gi|1166275    85 ISEDVDLAYEVNRKNNI-----DESYLGKLS---ETFD-VVAES----DN 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLs.AKD.vtve
                      + L n  v  vltAHPtq  R+ +L     i   L +  + KD++
  gi|1166275   122 ARDILENVNVVPVLTAHPTQVQRKTMLELTNHIHELLRKHRdVKDgLINK 171

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    DK   D  L R +    +tD iR  +   + E+   m Y+   + k + K
  gi|1166275   172 DKWYAD--LRRYVEIMMKTDIIREKKLKVKNEITNVMEYYNSSLIKAITK 219

                    FLRRvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRD
                             K + +   +  d P +i    W+GGDRDG nP vt E  +
  gi|1166275   220 ----LSHEFKRLAVEKGIELDNPTpITMGMWIGGDRDG-NPFVTAETLKL 264

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                       L   +  n Yi++v+ L   +s+    + L    E +   a+    +
  gi|1166275   265 SATLQSEVILNYYIEKVDNLYRSFSL---SSRLTEVSETVAEMAKLSPDT 311

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYnt.........RERaRHLLAt
                      Y E       +EPYR     +  KL  t    + ++ + ERa   L
  gi|1166275   312 SVYRE-------NEPYRRAFSYIQSKLIQTllffkagnfsNERAAKRLSE 354

                    Gi.......seisEeAv.................ytkvEeFLEPLELCY
                     ++ ++ ++ e+  + v+++ +++ +  ++++++ y   E F + L
  gi|1166275   355 NVrlgsvstGEVVADFVhdrlsqslqavsqqttefYETAEAFHDDLLAIK 404

                    ksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAit
                     sL e  D v+  G   +lL  v  FG  L  +D+Rq+s  +   +  +
  gi|1166275   405 NSLLENDDSVLISGDFEELLQAVEVFGFYLATIDMRQDSSVHEACVAELL 454

                    tHLei.GsYReWsEeKRqEWLlaELkGK.RPLlgsDLPktEEvkDvldaf
                    +  +i   Y e  E  +   Ll EL+  +R L    + k E ++  l  f
  gi|1166275   455 KSANIvDNYSELTEVEKVAVLLKELQEDpRTLSSTNVSKSETLEKELAIF 504

                    rvLAELPiDsFG.....aYiismataPsDvLAvELLqRECgv....kqtL
                    r  A L  D  G++  +  iis + + sD+    +L +E g+ ++++  +
  gi|1166275   505 RT-ARLLKDYLGeevikQHIISHTESVSDMFELAILLKEVGLvdteRARV 553

                    rvvPLFEkLADLeAAPAavekLFsiDWYinri...dGKqevmvGYsDsGK
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                    ++vPLFE + DLe     +++    D  +  i++++  qe+m+GYsDs K
  gi|1166275   554 QIVPLFETIEDLENSNEIMKQYLGYDIVKRWIknsNNYQEIMLGYSDSNK 603

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    D G ls  W LYkAq E+ K+  + G+K++ FHGRGGtvGRGGGP   Ai
  gi|1166275   604 DGGYLSSGWTLYKAQNELTKIGEERGIKITFFHGRGGTVGRGGGPSYDAI 653

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                     sqP  ti+  +R t qGEvi   +G  +  +  L     AtL+  +
  gi|1166275   654 TSQPFGTIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLVSATLDRMVTRQ 703

                    vsPkPE...WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGk
                    +    E  ++R++m+ +       YR +v+    F +YF  A P  E
  gi|1166275   704 ITDPDElvdFREIMDSIVQDSNGIYRDLVFGNEHFYDYFFEASPIKEVSS 753

                    mniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid
                    +niGsRPa Rk    i  LRAiPW+F+W q R  LP W GvG AF h i+
  gi|1166275   754 LNIGSRPAARKTITDISGLRAIPWVFSWSQNRIMLPGWYGVGSAFNHYIE 803

                    KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL
                     +  nl kL+ m+++WPFFR  l  ++mv  K D  iA  y +L  +Ee+
  gi|1166275   804 AEEGNLEKLQHMFETWPFFRSLLSNVDMVLSKSDMNIAFHYAQLAESEEV 853

                    kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnv
                    +   + + d+++ tk+ +L i  H D LE  P LK  l  R +Y   Ln
  gi|1166275   854 RSVFNIILDEWQLTKNVILAIEKHDDFLEESPSLKASLGFRLPYFNVLNY 903

                    fqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGL
                    +q   +KR+R  +              dE       L+++
  gi|1166275   904 IQIELIKRLRNNNLT-----------DDEI-----SLIHIT--------- 928

                    EDtLiLtmKGiAAGmqntG<-*
                           + GiA G+ n G
  gi|1166275   929 -------INGIATGLRNSG    940

gi|261379952|ref|ZP_05984525.1|: domain 1 of 1, from 1 to 900: score 295.4, E = 1.2e-85
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2613799     1    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 38

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2613799    39 ETVKLLSTS----DDSAALIE--KVLPQLDEQQTHDLTLACGLFAQILNI 82

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+   RR i+    G  + E+s t      Et++kL        +
  gi|2613799    83 AEDVHHERRRQIHEDA-GHNSAEGSLT------ETVRKLKAGK-VNGKAL 124

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     + L n  v  vltAHPt   R  +L  n RiR  L q   +   ++
  gi|2613799   125 QQQLDNTVVTAVLTAHPTEVQRQTVLSFNRRIRALLPQ-RERCTNPDALA 173

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     L   +   + t E RR +    DE+  G+s +    ++  PK  R
  gi|2613799   174 QLRREIDTVLLGLWQTSETRRHKLSVNDEINNGVSIFPMSFFEALPKLYR 223

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     ++   +      R+P    ++k   W+GGDRDG nP v  E  R
  gi|2613799   224 TMERDFQTAYPGVRVP---NILKIGGWIGGDRDG-NPFVSAETLRFAFRR 269

                    aRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkvvKy
                           +Y   ++ L  E +ls+ R      v A    +
  gi|2613799   270 HADAVFRFYRGELDKLYRElpLSIRRVKVNDDVMALAALSPDEEI----- 314

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEeAvy
                              +EPYR  +  +   +     +aR L+L  G      e  y
  gi|2613799   315 -------ARTEEPYRRAIAYI---MARAMGKARSLgLGMGCKFGFLEP-Y 353

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                      vEeFL  L    +sL e G + +A+G L D++R vs FG  ++ LD+R
  gi|2613799   354 ATVEEFLNDLKKLQRSLHENGSQLLAEGRLADIIRSVSVFGFHMMPLDLR 403
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                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    q + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL  +RPL+ + +
  gi|2613799   404 QHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELGHQRPLYSPFIT 453

                    ktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAvELLqRE
                      +  +  l  f++ +++  E   D+    iis +  PsD LA  LL +E
  gi|2613799   454 YSDHTRHELAIFNearkIKDEFGEDAVTQSIISNCEQPSDLLALALLLKE 503

                    Cgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK
                     g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   ++ +
  gi|2613799   504 SGLlvvengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDALLESR 553

                    ...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    ++ qe+m+GYsDs KD G +   W LY+A   ++   Kky v++ lFHGR
  gi|2613799   554 gniQEIMLGYSDSNKDGGYVTSSWCLYQAELGLVELFKKYDVRMRLFHGR 603

                    GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                    GG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +     r L
  gi|2613799   604 GGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQRNL 653

                    qRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEY
                        AAtLE  + P    k    kLm+++  v    YR ++   P F++Y
  gi|2613799   654 ETLVAATLEASILP--DKKDPDDKLMQDLSDVSFKYYRELITH-PDFIDY 700

                    FRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvW
                    F    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  LP W
  gi|2613799   701 FLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLMLPAW 750

                    LGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiA
                     G+G A     +     l  L+E  +  PFF   l  +E v AK D  +A
  gi|2613799   751 YGFGSAVETLCEGNPDTLTALREHAQSNPFFQAMLSNMEQVMAKTDITLA 800

                    aLyDkLLvaEe.LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                      y  L  + ++ k     ++++Y+  ++ LL +    +lL     L
  gi|2613799   801 ENYAGLSESPDkAKVIFGMIKEEYQRSRKALLDLLQTEELLRDNRSLARS 850

                    lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                    l LR +Y+  Ln +q   LKR+R                 E+   +  L
  gi|2613799   851 LALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNPHAL 882

                    vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    + +               Lt+ G+A G+ ntG
  gi|2613799   883 LMVH--------------LTINGVAQGLRNTG    900

gi|239814380|ref|YP_002943290.1|: domain 1 of 1, from 1 to 947: score 295.3, E = 1.3e-85
                    *->siDAqLRlLvPGK..vsedekLieYDALLlDkFL.DiLqDLHGedLk
                        + A  +  +P K++ +ed+ Li+ D  Ll + L+D++ +  Ge+
  gi|2398143     1    -MKAS-KTPAPPKrrQAEDQPLID-DIRLLGRILgDVIREQEGEESY 44

                    EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                      v     ls  +    D      L   L +L  a+++ v +a+     L
  gi|2398143    45 ALVEKIRTLSVAFRRDADQAADRALKNLLKGLSAAETVRVIRAFTYFSHL 94

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                    AnLAE+ +l  RRR +  + G+ aD        D+   l ++   +   P
  gi|2398143    95 ANLAEDRHLI-RRRTEAERAGESAD-------GDLQTALARIRKAG-VKP 135

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLa.....qLs..
                    +Ev   L    v  vltAHPt   R+s+L  +  i   L+++++ +L ++
  gi|2398143   136 DEVVASLARSYVSPVLTAHPTEVQRKSILDAERAIAQLLTtrdeiKLRqs 185

                    ....AKD.vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGms
                       +AKD +t+ +  E +  +   +   + t  +R ++ t  DE+   +s
  gi|2398143   186 ayagAKDaLTPLEFAENETQMRIRVTQIWQTRLLRFSKLTVADEIENALS 235

                    YiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGk
                    Y+  t  + +P+     + AL   G+   lP  +P ++   W+GGDRDG
  gi|2398143   236 YYEATFLREIPRVYADLEKALGQGGV---LPSVAPFLRMGQWIGGDRDG- 281

                    nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEE
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                    nP vt E           +A   Y+  v  L  Els+      L     E
  gi|2398143   282 NPNVTAETLEYALRRQAELALRHYLTEVHYLGGELSL---SATLVDVSVE 328

                    lyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntR......ER
                    ++  aar        E  K     EPYR  L  v  +L  t ++ +++E
  gi|2398143   329 MQALAARS---PDTSEHRK----DEPYRRALTGVYARLAATLrdltggEA 371

                    aRHLLAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLD
                    aRH        ++ +  y k EeFL+ L     sL e    v+A   L
  gi|2398143   372 ARH-------AVPPQNPYAKAEEFLDDLRTVEESLVEKHGSVLAAPRLRP 414

                    lLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRq
                    l+R v  FG  L  +D+Rq s+++  v+  +     i ++Y + +Ee +q
  gi|2398143   415 LIRAVEVFGFHLATVDLRQSSDKHEAVIAELLATARIEpAYASLAEEAKQ 464

                    EWLlaELkGKRPLlgsDL...PktE.EvkDvldafrvLAELPiDsFGaYi
                      Ll  L   RPL  +D + +P   +E++    a    A     +   Yi
  gi|2398143   465 TLLLKLLDDARPLRVPDAeysPLAQsELAIFAAARTARARYGAAAIRHYI 514

                    ismataPsDvLAvELLqRECgvkq.........tLrvvPLFEkLADL.eA
                    is + + sD L   LLq+E g+ ++  +++ +  L vvPLFE + DL++A
  gi|2398143   515 ISHTETVSDLLEALLLQKEVGLLRgamngkatcDLIVVPLFETIEDLrNA 564

                    APA..avekLFsiDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAq
                    AP  +a   L  i   i r    q+vm+GYsDs KD G +   W LY+A
  gi|2398143   565 APIvrAFYALPNIQALIERSGAEQDVMLGYSDSNKDGGIFTSNWELYRAG 614

                    EEiiKvAKkyG......vKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtin
                      ++    +  +++ ++++L +FHGRGGtvGRGGGP   AiL+qPP t+
  gi|2398143   615 IALVALFDELNkkkanpIRLRMFHGRGGTVGRGGGPSYQAILAQPPGTVR 664

                    GslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE.WR
                    G +R t qGEvi   +   ++  r L    AAtLE  + P     P ++
  gi|2398143   665 GQIRLTEQGEVIGSKYANREIGRRNLETLVAATLEATLLPQAKSAPAtFL 714

                    kLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRk
                        e+       YR +v+  P F +YF   tP  E   +niGsRPa R
  gi|2398143   715 SAAGELSTASMSAYRKLVYETPGFGDYFFGSTPIREIAELNIGSRPASRN 764

                    PsGGiesLRAiPWiFaWtqtRFHLPvWLGvG........AAFKhAidKDi
                    Ps  i+ LRA+PW F+W q R  +P W G+G++ ++    A   A  K+
  gi|2398143   765 PSHKIDDLRAVPWSFSWGQCRLTIPGWFGFGsgveqflaSAATPAARKER 814

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF
                      l  L+ mY +WPFFR  l  ++mv AK D  +A+ y +L+    L+
  gi|2398143   815 TAL--LRRMYAQWPFFRTLLSNMDMVLAKSDLALASRYAELVTDRKLRQK 862

                    GksLRd.kYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfq
                      s+ d+++  t d L  i G k  LEG   ++  +R R +Yi  L  +q
  gi|2398143   863 VFSMIDtEWHRTSDALTLITGAKQRLEGNAEMQRSVRHRFPYIDPLHHLQ 912

                    AYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLED
                       ++R R               A E             +er   G+
  gi|2398143   913 VELMRRYR----------------AGEG-----------GERLQRGIH- 933

                    tLiLtmKGiAAGmqntG<-*
                       + + G+AAG+ ntG
  gi|2398143   934 ---ISINGVAAGLRNTG    947

gi|254190787|ref|ZP_04897294.1|: domain 1 of 1, from 37 to 994: score 294.5, E = 2.3e-85
                    *->siD.AqLRlLvP.........GKvsed.ekLieYDALLlDkFL.DiL
                        +D+A  R L+P++  + +++G+  ed+++ +  D   l + L+D++
  gi|2541907    37    KLDgAAARPLAPtnaasakpqGRTREDkDRPLFEDIRYLGRLLgDVV 83

                    qDLHGedLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvA
                     +  G+ + ++v      +  +    D    + L   L  L P  ++ v
  gi|2541907    84 REQEGDAVFDVVETIRQTAVKFRREDDKAAAQTLEKMLRKLTPEQTVSVV 133

                    kailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKk
                    +a++    LAn+AE+ +   RRRi+ +        +sA     +   l k
  gi|2541907   134 RAFSYFSHLANIAEDRHHNRRRRIHALA-------GSAAQAGTVAYALDK 176
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                LvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq
                L   ++ s + + +      +  vltAHPt   R+s+L  +  i    a
gi|2541907   177 LKQAGDASSKTIKQFFEGALIVPVLTAHPTEVQRKSILDAQHDI----AR 222

                LsAKDvtveDKkEL..DEALHRE.iqAAFRtDEiRRaqPtPqDEmRaGms
                L A    +   +EL + EAL R ++   + t  +R a+ t  DE+   +s
gi|2541907   223 LLAERDQPLTARELahNEALLRArVTTLWQTRMLRDARLTVADEIENALS 272

                YiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGk
                Y+  t  +  P     ++ AL   G+  R+P      +  sW+GGDRDG
gi|2541907   273 YYRATFLDELPALYADIEEALAEHGLRARVP---AFFQMGSWIGGDRDG- 318

                nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEE
                nP vt     +       +    Y++qv  L  Els+    + L v A +
gi|2541907   319 NPNVTAATLDEAISRQAAVIFEHYLEQVHKLGAELSV----SNLLVGASD 364

                lyrtaardkvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER...
                  +  a             q P++  EPYR  L  v  +L  + R R ++
gi|2541907   365 ALKALAAA--------SPDQSPhrVDEPYRRALIGVYTRLAAsARVRlge 406

                .aRHLLAtGiseisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsL
                ++  +   G    +  A +y + EeF   L +   sL       +A   L
gi|2541907   407 gTVPVRSAGRGAAPVRATpYADAEEFAADLRVLTDSLALHHGESLATPRL 456

                LDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeK
                  l+R    FG  L  +D+Rq s+ +  v+  +    ++ ++Y   +E
gi|2541907   457 APLMRAAEVFGFHLASIDLRQSSDIHEAVVAELLARGGVEAdYAALPEAD 506

                RqEWLlaELkGKRPLlgsDLPktEEvkDvldafr....vLAELPiDsFGa
                +   Lla L   RPL  + L   +  k  l+ +++ + + A     +
gi|2541907   507 KLRVLLAALADPRPLRSPYLDYSDLAKSELGVLErahaIRAQFGARAVRN 556

                YiismataPsDvLAvELLqRECgv.............kqtLrvvPLFEkLA
                Yiis + + sD + v LLq+E g+ +++ ++++ + ++ L v+PLFE +A
gi|2541907   557 YIISHTETVSDLVEVLLLQKETGLfegtlgtphanaRNGLMVIPLFETIA 606

                DLeAAPAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWq
                DL+ A   +   F+ +++     +    qevm+GYsDs KD G l   W
gi|2541907   607 DLRNASDIMRAFFAlpgVGELLAHQGHEQEVMLGYSDSNKDGGFLTSNWE 656

                LYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinG
                LY+A   ++    +  +KL lFHGRGGtvGRGGGPt  AiLsqPP t+nG
gi|2541907   657 LYRAELALVDLFDERRIKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNG 706

                slRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEW
                 +R t qGEvi   F   ++  r L    AAtLE  + P  ++Pk+ P +
gi|2541907   707 QIRLTEQGEVIASKFANPEIGRRNLETVVAATLEATLAPHSnAPKqlPAF 756

                RkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKR
                   m+ +   A   YR++v+  P F +YF + tP +E   +niGsRPa R
gi|2541907   757 EAAMQTLSDAAMASYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASR 806

                kPsG....GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......
                k   ++++ ie LRAiPW F+W q R  L  W G+G A    +d+ ++
gi|2541907   807 KLQDpknrKIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVAAYLDgapdaa 856

                KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL
                   K +  Lk m k+WPFF   l  ++mv AK D  +A+ y +L+    L
gi|2541907   857 ERGKRVALLKKMNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVADKKL 906

                .kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLn
                +k   +++ +++  t d L +i G +  L   P L   ++ R +Y+  Ln
gi|2541907   907 rKHVFERIVAEWHRTADALAEITGAHARLAANPLLARSIKNRFPYLDPLN 956

                vfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPG
                 +q   +KR R                A +           n   r   G
gi|2541907   957 HLQVELIKRHR----------------AGDT----------N--ARLRRG 978

                LEDtLiLtmKGiAAGmqntG<-*
                +     Lt+ GiAAG+ ntG
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  gi|2541907   979 IH----LTINGIAAGLRNTG    994

gi|226194359|ref|ZP_03789957.1|: domain 1 of 1, from 67 to 1024: score 294.5, E = 2.3e-85
                  *->siD.AqLRlLvP.........GKvsed.ekLieYDALLlDkFL.DiL
                      +D+A  R L+P++  + +++G+  ed+++ +  D   l + L+D++
  gi|2261943    67    KLDgAAARPLAPtnaasakpqGRTREDkDRPLFEDIRYLGRLLgDVV 113

                  qDLHGedLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvA
                   +  G+ + ++v      +  +    D    + L   L  L P  ++ v
  gi|2261943   114 REQEGDAVFDVVETIRQTAVKFRREDDKAAAQTLEKMLRKLTPEQTVSVV 163

                  kailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKk
                  +a++    LAn+AE+ +   RRRi+ +        +sA     +   l k
  gi|2261943   164 RAFSYFSHLANIAEDRHHNRRRRIHALA-------GSAAQAGTVAYALDK 206

                  LvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq
                  L   ++ s + + +      +  vltAHPt   R+s+L  +  i    a
  gi|2261943   207 LKQAGDASSKTIKQFFEGALIVPVLTAHPTEVQRKSILDAQHDI----AR 252

                  LsAKDvtveDKkEL..DEALHRE.iqAAFRtDEiRRaqPtPqDEmRaGms
                  L A    +   +EL + EAL R ++   + t  +R a+ t  DE+   +s
  gi|2261943   253 LLAERDQPLTARELahNEALLRArVTTLWQTRMLRDARLTVADEIENALS 302

                  YiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGk
                  Y+  t  +  P     ++ AL   G+  R+P      +  sW+GGDRDG
  gi|2261943   303 YYRATFLDELPALYADIEEALAEHGLRARVP---AFFQMGSWIGGDRDG- 348

                  nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEE
                  nP vt     +       +    Y++qv  L  Els+    + L v A +
  gi|2261943   349 NPNVTAATLDEAISRQAAVIFEHYLEQVHKLGAELSV----SNLLVGASD 394

                  lyrtaardkvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER...
                    +  a             q P++  EPYR  L  v  +L  + R R ++
  gi|2261943   395 ALKALAAA--------SPDQSPhrVDEPYRRALIGVYTRLAAsARVRlge 436

                  .aRHLLAtGiseisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsL
                  ++  +   G    +  A +y + EeF   L +   sL       +A   L
  gi|2261943   437 gTVPVRSAGRGAAPVRATpYADAEEFAADLRVLTDSLALHHGESLATPRL 486

                  LDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeK
                    l+R    FG  L  +D+Rq s+ +  v+  +    ++ ++Y   +E
  gi|2261943   487 APLMRAAEVFGFHLASIDLRQSSDIHEAVVAELLARGGVEAdYAALPEAD 536

                  RqEWLlaELkGKRPLlgsDLPktEEvkDvldafr....vLAELPiDsFGa
                  +   Lla L   RPL  + L   +  k  l+ +++ + + A     +
  gi|2261943   537 KLRVLLAALADPRPLRSPYLDYSDLAKSELGVLErahaIRAQFGARAVRN 586

                  YiismataPsDvLAvELLqRECgv.............kqtLrvvPLFEkLA
                  Yiis + + sD + v LLq+E g+ +++ ++++ + ++ L v+PLFE +A
  gi|2261943   587 YIISHTETVSDLVEVLLLQKETGLfegtlgtphanaRNGLMVIPLFETIA 636

                  DLeAAPAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWq
                  DL+ A   +   F+ +++     +    qevm+GYsDs KD G l   W
  gi|2261943   637 DLRNASDIMRAFFAlpgVGELLAHQGHEQEVMLGYSDSNKDGGFLTSNWE 686

                  LYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinG
                  LY+A   ++    +  +KL lFHGRGGtvGRGGGPt  AiLsqPP t+nG
  gi|2261943   687 LYRAELALVDLFDERRIKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNG 736

                  slRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEW
                   +R t qGEvi   F   ++  r L    AAtLE  + P  ++Pk+ P +
  gi|2261943   737 QIRLTEQGEVIASKFANPEIGRRNLETVVAATLEATLAPHSnAPKqlPAF 786

                  RkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKR
                     m+ +   A   YR++v+  P F +YF + tP +E   +niGsRPa R
  gi|2261943   787 EAAMQTLSDAAMASYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASR 836

                  kPsG....GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid......
                  k   ++++ ie LRAiPW F+W q R  L  W G+G A    +d+ ++
  gi|2261943   837 KLQDpknrKIEDLRAIPWGFSWGQCRLLLTGWYGFGSAVAAYLDgapdaa 886
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                    KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL
                       K +  Lk m k+WPFF   l  ++mv AK D  +A+ y +L+    L
  gi|2261943   887 ERGKRVALLKKMNKTWPFFANLLSNMDMVLAKTDLAVASRYAQLVADKKL 936

                    .kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLn
                    +k   +++ +++  t d L +i G +  L   P L   ++ R +Y+  Ln
  gi|2261943   937 rKHVFERIVAEWHRTADALAEITGAHARLAANPLLARSIKNRFPYLDPLN 986

                    vfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPG
                     +q   +KR R                A +           n   r   G
  gi|2261943   987 HLQVELIKRHR----------------AGDT----------N--ARLRRG 1008

                    LEDtLiLtmKGiAAGmqntG<-*
                    +     Lt+ GiAAG+ ntG
  gi|2261943  1009 IH----LTINGIAAGLRNTG    1024

gi|55820784|ref|YP_139226.1|: domain 1 of 1, from 1 to 940: score 294.5, E = 2.3e-85
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                              +      s+++++i  +  +l   L+D    + Ge+
  gi|5582078     1    ------MAFNKLESSNNQEIISEEVGILKELLdDATRGMAGEQGLTT 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +q   El        D    e L   +  +   D ++  + ++ +  L n
  gi|5582078    42 IQHLVEL-------YDEGDYEALTQAISEMTNDDMVVASRYFSLLPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    k        DE+     s   Et+  +v       +
  gi|5582078    85 ISEDVDLAYEVNRKNNI-----DESYLGKLS---ETFD-VVAES----DN 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLs.AKD.vtve
                      + L n  v  vltAHPtq  R+ +L     i   L +  + KD++
  gi|5582078   122 ARDILENVNVVPVLTAHPTQVQRKTMLELTNHIHELLRKHRdVKDgLINK 171

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    DK   D  L R +    +tD iR  +   + E+   m Y+   + k + K
  gi|5582078   172 DKWYAD--LRRYVEIMMKTDIIREKKLKVKNEITNVMEYYNSSLIKAITK 219

                    FLRRvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRD
                             K + +   +  d P +i    W+GGDRDG nP vt E  +
  gi|5582078   220 ----LSHEFKRLAVEKGIELDNPTpITMGMWIGGDRDG-NPFVTAETLKL 264

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                       L   +  n Yi++v+ L   +s+    + L    E +   a+    +
  gi|5582078   265 SATLQSEVILNYYIEKVDNLYRSFSL---SSRLTEVSETVAEMAKLSPDT 311

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYnt..........RERaRHLLAt
                      Y E       +EPYR     +  KL  t    + ++ ++ERa   L
  gi|5582078   312 SVYRE-------NEPYRRAFSYIQSKLIQTllffkagnfsKERAAKRLSE 354

                    Gi.......seisEeAv.................ytkvEeFLEPLELCY
                     ++ ++ ++ e+  + v+++ +++ +  ++++++ y   E F + L
  gi|5582078   355 NVrlgsvstGEVVADFVhdrlsqslqavsqqttefYETAEAFHDDLLAIK 404

                    ksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAit
                     sL e  D v+  G   +lL  v  FG  L  +D+Rq+s  +   +  +
  gi|5582078   405 NSLLENDDSVLISGDFEELLQAVEVFGFYLATIDMRQDSSVHEACVAELL 454

                    tHLei.GsYReWsEeKRqEWLlaELkGK.RPLlgsDLPktEEvkDvldaf
                    +  +i   Y e  E  +   Ll EL+  +R L    + k E ++  l  f
  gi|5582078   455 KSANIvDNYSELTEVEKVAVLLKELQEDpRTLSSTNVSKSETLEKELAIF 504

                    rvLAELPiDsFG.....aYiismataPsDvLAvELLqRECgv....kqtL
                    r  A L  D  G++  +  iis + + sD+    +L +E g+ ++++  +
  gi|5582078   505 RT-ARLLKDYLGeevikQHIISHTESVSDMFELAILLKEVGLvdteRARV 553

                    rvvPLFEkLADLeAAPAavekLFsiDWYinri...dGKqevmvGYsDsGK
                    ++vPLFE + DLe     +++    D  +  i++++  qe+m+GYsDs K
  gi|5582078   554 QIVPLFETIEDLENSNEIMKQYLGYDIVKRWIknsNNYQEIMLGYSDSNK 603

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    D G ls  W LYkAq E+  +  + G+K++ FHGRGGtvGRGGGP   Ai
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  gi|5582078   604 DGGYLSSGWTLYKAQNELTNIGEERGIKITFFHGRGGTVGRGGGPSYDAI 653

                   LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                    sqP  ti+  +R t qGEvi   +G  +  +  L     AtL+  +
  gi|5582078   654 TSQPFGTIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLVSATLDRMVTRQ 703

                   vsPkPE...WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGk
                   +    E  ++R++m+ +       YR +v+    F +YF  A P  E
  gi|5582078   704 ITDPDElvdFREIMDSIVQDSNRIYRDLVFGNEHFYDYFFEASPIKEVSS 753

                   mniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid
                   +niGsRPa Rk    i  LRAiPW+F+W q R  LP W GvG AF h i+
  gi|5582078   754 LNIGSRPAARKTITDISGLRAIPWVFSWSQNRIMLPGWYGVGSAFNHYIE 803

                   KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL
                    +  nl kL+ m+++WPFFR  l  ++mv  K D  iA  y +L  +Ee+
  gi|5582078   804 AEEGNLEKLQHMFETWPFFRSLLSNVDMVLSKSDMNIAFHYAQLAESEEV 853

                   kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnv
                   +   + + d+++ tk+ +L i  H D LE  P LK  l  R +Y   Ln
  gi|5582078   854 RSVFNIILDEWQLTKNVILAIEKHDDFLEESPSLKASLGFRLPYFNVLNY 903

                   fqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGL
                   +q   +KR+R  +              dE       L+++
  gi|5582078   904 IQIELIKRLRNNNLT-----------DDEI-----SLIHIT--------- 928

                   EDtLiLtmKGiAAGmqntG<-*
                          + GiA G+ n G
  gi|5582078   929 -------INGIATGLRNSG    940

gi|288905708|ref|YP_003430930.1|: domain 1 of 1, from 1 to 941: score 294.4, E = 2.5e-85
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                           ++ L          +i  +  +l   LD+    + G+++
  gi|2889057     1    ---MTIKKLENNSTQ---SIITEEVKVLKDLLDeTTHQMVGDEVFAK 41

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +q   ElsA  E      KLe L a+Lt     + ++v + ++ +  L n
  gi|2889057    42 IQNIVELSASDE----YVKLEKLVAQLTN---DEMVVVSRYFSILPLLIN 84

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   + E+v+ Ay    +     D+    s t +         +v+      e
  gi|2889057    85 ISEDVDFAYEINYQNNTNQDYLGKLSLTVD---------MVSES----EN 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     e L n  v  vltAHPtq  R+ +L     i   L +       v  +
  gi|2889057   122 SKEILENVNVVPVLTAHPTQVQRKTVLELTNHIHDLLRKYRDVRAGVVNR 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                         L R i     tD iR  +   + E+   m Y+   + + + K
  gi|2889057   172 DKWYTDLRRYIEIIMQTDIIREKKLKVKNEITNVMEYYNTSLIQAITKLT 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                             Gi    P     i    W+GGDRDG nP vt E  R
  gi|2889057   222 SEYKRLAAEKGIDLENPKP---ITMGMWIGGDRDG-NPYVTAETLRLSAT 267

                   LaRmmAanlYisqvEDLm..FElsmWRCn........dEL.....RvRAE
                   +   +  n Yi+++  L ++F ls    n +++ ++  EL+++++  R
  gi|2889057   268 VQSEVIINYYIEKLTGLYrtFSLSTTLTNispeveklAELssdksIYREN 317

                   Elyrta...ardkvvKyYiEFWKqvPPtEPYRv......iLGdvRDKLYn
                   E yr a +  + k+++  iE   +  P    Rv +++++i  dv     n
  gi|2889057   318 EPYRKAfnyIQSKLIQTLIEL--KAGPAISQRVlessnnISSDVYTSTNN 365

                   tRERaRHL...LAtGiseisEeA.vytkvEeFLEPLELCYksLCeCGDkv
                       ++ L+++  +  se+ Ee + y    eF + L +  +sL + GD +
  gi|2889057   366 ASVVTKYLqtkFSKVSSELQEEIpSYKTAKEFKDDLLIIKQSLLDNGDDA 415

                   iADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YR
                   +  G   +lL  v  FG  L  +D+Rq+s  +   +  + + +  +i  +Y
  gi|2889057   416 LLTGDFSELLQAVDVFGFYLATIDMRQDSSVNEACVAELLKSANIVEdYS 465
```

```
                    eWsEeKRqEWLlaELkGK.RPLlgsDLPktEEvk...DvldafrvLAE.L
                      sEe +   Ll EL+  +R L      k E ++++  + ++ r L ++L
  gi|2889057   466 ALSEEEKVKVLLKELQEDpRTLSSTNAEKSEQLQkelAIFQTARYLKDkL 515

                    PiDsFGaYiismataPsDvLAvELLqRECgv....kqtLrvvPLFEkLAD
                      +     iis + + sD+    ++ +E g+ +++k  +++vPLFE + D
  gi|2889057   516 GDEVIKQHIISHTESVSDMFELAIMLKEVGLldnqKARVQIVPLFETIED 565

                    LeAAPAavekLFsiDWYinri...dGKqevmvGYsDsGKDAGRlsAAWqL
                    Le   A +e     D  +  ++ + G qe+m+GYsDs KD G ls  W L
  gi|2889057   566 LENSRAIMEEYLDYDIVRRWVsanKGYQEIMLGYSDSNKDGGYLSSVWTL 615

                    YkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGs
                    YkAq E+ ++  + G+K++  HGRGGtvGRGGGP   Ai sqP   i+
  gi|2889057   616 YKAQNELTRIGSERGIKVTFIHGRGGTVGRGGGPSYEAITSQPFGSIKDR 665

                    lRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WR
                    +R t qGE+iE  +G  ++ +  L     At++  +   +    E +++R
  gi|2889057   666 IRLTEQGEIIENKYGNKDVAYYNLEMLVSATIDRIVTRMITNPDEiddFR 715

                    kLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRk
                      m+ +       YR +v+  P F +YF  AtP  E   +niGsRPa Rk
  gi|2889057   716 ATMDGIVTYSNGVYRDLVFGNPHFYDYFFEATPIKEVSSLNIGSRPAARK 765

                    PsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkE
                        i  LRAiPW+F+W q R   P W GvG AFK  id +  nl kL+
  gi|2889057   766 TITEISGLRAIPWVFSWSQSRIMFPGWYGVGSAFKNFIDAEGGNLAKLQH 815

                    mYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkY
                    mY++WPFF   l  ++mv  K    iA  y +L  +Ee++   + + d++
  gi|2889057   816 MYEKWPFFHSLLSNVDMVLSKSNMNIAFQYAQLAESEEVRDVFNTILDEW 865

                    vEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRD
                    + tk+ +L i  H DlLE  P L+  l  R +Y   Ln +q   +KR+R
  gi|2889057   866 QLTKNVILAIEKHEDLLEENPSLQASLDYRLPYFNVLNYIQIELIKRLR- 914

                    PsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGi
                                E  dE+    + L++                + Gi
  gi|2889057   915 ------------HEELDED---YEKLIHTT----------------INGI 933

                    AAGmqntG<-*
                    A G+ n G
  gi|2889057   934 ATGLRNSG    941

gi|237747682|ref|ZP_04578162.1|: domain 1 of 1, from 16 to 970: score 294.0, E = 3.3e-85
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                            +    P K    e   + D  +l + L+D + +  Ged
  gi|2377476    16    DQHQEMSTNTPSKSQ-TEAPEKEDIRMLGRMLgDTIREKEGEDTFNL 61

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      +  +         + L   L  L    ai v +a++    LAn
  gi|2377476    62 VEKVRRTAVSFRRDPNICSADTLNNLLKNLSRNQAISVVRAFSYFSHLAN 111

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +A + +     R  +         + A     +   l +L   +    +
  gi|2377476   112 IAVDKHANLAYRSALIS-------GAAPEKGSLNYALDRLDAAG-VPGAA 153

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +   L    +  vltAHPt   R+s L  +  i   La      +t+ +
  gi|2377476   154 IKKSLNKTFISPVLTAHPTEVQRKSTLDSEREIARLLAE-HGSSLTPKES 202

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    k   E L   i A + t  +R ++    DE+   +sY+  t  +  P
  gi|2377476   203 KHNTEMLRAQIAALWQTRLLRYTRLSVADEINNALSYYRTTFLRELPELY 252

                    RRvDtALKniGinERlP.....YdvP.....LikFssWmGGDRDGknPRv
                      +        i ER P++ ++  +P+++++ ++  sW+GGDRDG nP v
  gi|2377476   253 HSIQEE-----ISERYPesadgIAAPgskskYLQMGSWIGGDRDG-NPNV 296

                    tPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrt
                      +           +   +Y++ +  L  Els+    + +     El  t
```

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  gi|2377476   297 NADTMLHALERQSHLVMEFYLEEIHNLGAELSISSLLNHVSPELQELANT 346

                   aardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGis
                   +       + ++        EPYR  L ++  +L  t  R   +     s
  gi|2377476   347 SSDT--SLHRVD--------EPYRRALIAIYSRLAAT-ARDYGMTTLPRS 385

                   eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                   e+     y   EeF   L +   sL +     +    L  l   v  FG
  gi|2377476   386 EVGTGEAYATPEEFGADLQIMIDSLNQNAGELLVRIRLGSLKAAVDIFGF 435

                   sLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK
                    L  LD+Rq s+ +  +l  i    ++ + Y + sEeK+ E L+ EL+
  gi|2377476   436 HLATLDMRQSSDIHERILTEIFATAQVEpDYASLSEEKKVELLIHELSQP 485

                   RPLlgsDLPktEEvkDvldafrvLAELPiD....sFGaYiismataPsDv
                   R L+ +     EE    l  +r    +    ++++   Yiis + + sD+
  gi|2377476   486 RLLYSPFAQYSEETTSELRILRTARNIREQygkrAITNYIISHTETVSDI 535

                   LAvELLqRECgvkqt..................LrvvPLFEkLADLeAAP
                   L v LLq+E g+ ++++++++++  + ++ + +L  +PLFE + DL+ A
  gi|2377476   536 LEVYLLQKESGLLRPkrktgsntvldwneaeadLMAIPLFEMIPDLRSAA 585

                   AavekLFsiDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqE
                   A ++   si   +  i  +++ qevm+GYsDs KD G     W LYkA
  gi|2377476   586 AIMKETMSIPLVRELIRKQgdlQEVMLGYSDSNKDGGYTTSNWELYKAEK 635

                   EiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtv
                    ++    + Gv+L lFHGRGGtvGRGGGPt  AiL+qP  t+nG +R t
  gi|2377476   636 QLVELFNQMGVRLRLFHGRGGTVGRGGGPTYEAILAQPHGTVNGQIRLTE 685

                   qGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPEWRkL......
                   qGE+i   F + ++  r L    AAtLE  + P    k    k+++ ++
  gi|2377476   686 QGEMIASKFADPEIGSRNLELLVAATLEASLMPEDENKKYTDKMrdfesa 735

                   meemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs
                   +ee+   A   YR +v+  P F +YF   tP +E   +niGsRPa Rk s
  gi|2377476   736 LEEISALAYQAYRHLVYDTPGFTDYFFQSTPITEIAELNIGSRPASRKSS 785

                   GGiesLRAiPWiFaWtqtRFHLPvWLGvGAAF.KhAidKDi....Knlqk
                     ie LRAiPW F+W q R  LP W G+G A +++  + D + ++K +
  gi|2377476   786 RRIEDLRAIPWSFSWGQCRVLLPGWYGFGSAItQWLDEEDAsvknKKIAL 835

                   LkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk.PFGksL
                   L+ mY+eWPFF   l  ++mv AK D  iA  y +L+   +L++     +
  gi|2377476   836 LQSMYREWPFFESMLSNMDMVLAKSDLAIAYRYSELVTDRNLRdTVFSHI 885

                   RdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLK
                    ++ + t +    i   k+ L   P L   l+ R +Yi  Ln +q   +K
  gi|2377476   886 CAEHQRTLNSFEIITNEKERLVNNPALARALKDRLAYIDPLNHLQVELIK 935

                   RiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLt
                   R R P                En         L    r   G+     L
  gi|2377476   936 RHRNPGNN------------PEN---------LD--ARATRGIH----LS 958

                   mKGiAAGmqntG<-*
                   + GiAAGm ntG
  gi|2377476   959 INGIAAGMRNTG    970

gi|284989422|ref|YP_003407976.1|: domain 1 of 1, from 5 to 939: score 293.2, E = 5.8e-85
                   *->siD.AqLR....lLvPGKvsedekLieYDALLlDkFL.DiLqDLHGe
                       +D A LR+++++   G  + d  L e D  Ll + L++++ +  G+
  gi|2849894     5    TVDvADLRhhggAEEDGADAADAPLRE-DIRLLGRVLgEVIREQSGD 50

                   dLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHm
                   d+   v E   + A +  ++      ++ a+L +Ld   a  v +a++H
  gi|2849894    51 DVLALV-EATRVEA-FRLRRSEVDRADVAARLDGLDVRSANHVIRAFSHF 98

                   LnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkln
                     LAnLAE+v+   RRR +++        +s      +  t+  L
  gi|2849894    99 SLLANLAEDVHHERRRRFHRLE-------GSPPQKGSLAATFELLDAAH- 140
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                    KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                       + v   L    v  v+tAHPt   RR +   +  +   +
  gi|2849894   141 LDADVVARELAGALVSPVVTAHPTEVRRRTISRVQRQVTELIRRRDRSAP 190

                    tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                       D       L R +   + t  +R ++    DE+   + Y+   +++
  gi|2849894   191 GEADDPAWSGELQRAVLTLWQTALLRLSRLRLADEIDEALRYYEMSLFEV 240

                    vPKFLRRvDtALKniGinERlP...YdvPLikFssWmGGDRDGknPRvtP
                    vP        AL       R P+ + d P+++  sW+GGDRDG nP vt
  gi|2849894   241 VPAINAELRRALHA-----RWPsagSDRPVLRPGSWIGGDRDG-NPFVTA 284

                    EvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaa
                    +            A    +s +  L  Elsm    d L     El + aa
  gi|2849894   285 DAVHLASTRQAQTALGHHLSELLALHDELSM---SDRLITPTPELAQLAA 331

                    rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                                     EPYR  L  v  +L  t  R    +   +
  gi|2849894   332 AS-------GDDSRFRADEPYRRALYGVHARLAATAQR----VLGSVPGP 370

                    sEeAv...ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFG
                    +  Av ++y   Ee L  L     sL   G  ++AD  L  l   v  FG
  gi|2849894   371 PPHAVlepYATPEEVLADLATVDASLRAHGAAALADDRLARLREAVEVFG 420

                    LsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkG
                      L  LD+Rq s  + +vl  +    ++ + Y    E +R E L+ EL+
  gi|2849894   421 FHLAGLDMRQNSAVHAEVLAELFAWAGVCpDYAALDEKQRVELLVGELRM 470

                    KRPLlgsDLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsD
                    +RPL+ +D    +  ++E+   l a   +  L  ++   Y+ism+ + sD
  gi|2849894   471 RRPLVRPDAALSDlargELDVLLAAADQVRALGPEAVPNYVISMCESVSD 520

                    vLAvELLqRECgvkq.........tLrvvPLFEkLADLeAAPAavekLFs
                    vL v +L +E g+  ++++++++ ++ + PLFE + DL+ A  ++  +
  gi|2849894   521 VLEVAVLLKEVGLLDpggdggptcPVGISPLFETIGDLQHAAETLTAVLG 570

                    iDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKk
                       Y+  +  +++ qevm+GYsDs KD G l+A W LY+A   ++ vA++
  gi|2849894   571 QPLYRALLRNRgdvQEVMLGYSDSNKDGGYLAANWALYRAELALVEVARR 620

                    yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                     Gv+L lFHGRGGtvGRGGGP   Ai +qPP  + G+lR+t qGEvi
  gi|2849894   621 EGVRLRLFHGRGGTVGRGGGPSYDAIRAQPPGAVAGALRITEQGEVIAAK 670

                    FGEEnLCFrsLqRFtAAtLEHGm..nPPvsPkPE.WRkLmeemAvvAtEE
                    + E +   r L    AAtLE  + +   +    E+   L++++A  A
  gi|2849894   671 YAEPDRARRNLEAMVAATLEASLldTEGLGDDAEpAYALLDDLAARAQQA 720

                    YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPW
                    YR++v   P FvE+FR AtP  E   +niGsRP  Rk +  i  LRAiPW
  gi|2849894   721 YRALVHETPGFVEWFRAATPIGELAELNIGSRPPSRKAGDSIADLRAIPW 770

                    iFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlD
                    +F+W q R  LP W G G A    ++ D   l +L+E+ + WP+FR  l
  gi|2849894   771 VFSWSQARIMLPGWYGTGSALESWVEGDPARLTRLQELHRRWPWFRTMLS 820

                    LlEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAG
                     + mv AK D  +Aa y +L+  E+L+ +  ++L ++ +    +LL + G
  gi|2849894   821 NMGMVLAKTDLDLAARYAELVPDEQLRHrVFDQLTAEHERSCRMLLAVTG 870

                    HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                       lL   P L   +R R +Y+  L  +q   L+R R
  gi|2849894   871 DDRLLADNPALARSIRNRFPYLEPLHHLQVEMLRRRRG------------ 908

                    KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        d +    deLv+ n            + Lt+ GiA  + n G
  gi|2849894   909 ---HDGQDGDDDELVRRN------------IQLTINGIATALRNSG    939

gi|288942679|ref|YP_003444919.1|: domain 1 of 1, from 11 to 930: score 293.1, E = 5.9e-85
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         D qL     G v   e+  +   +++++  D        +L+E
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gi|2889426    11    ERDIQLYTALLGEVL-REHSRKRVLVVVERLRDGF-----MQLRE-- 49

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE            D++  e L  ++ sLdP     v +a+     L n+
gi|2889426    50 QE------------DPELREKLMKRIQSLDPQTLAEVIRAFTLYFGLVNV 87

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEE + A+  R+     G+    +s       ++t+++    +  sP E
gi|2889426    88 AEELN-AHLARMDVIAAGERLWVGS------FDDTVRQFKEDG-VSP-EH 128

                    FeALKnqsvDL.vltAHPtqsvRRsLLqKnaRiRnC...LaqLsAKDvtv
                    F+ L    + L+v+tAHPt + RR +     Ri   +++L  L   +
gi|2889426   129 FQSLLEHLIYLpVFTAHPTEARRRTISETFRRIFLAgqdLHRLKLNEEEL 178

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                    eDK  L E L   iq  ++tDE+R  +P   DE+R G+ ++ E +++ vP
gi|2889426   179 EDK--LQEIL-TQIQILWKTDEVRVHKPQVTDEIRRGLHFFRESLFEAVP 225

                    KFLRRvDtALKn...iGinERlPYdvPLikFssWmGGDRDGknPRvtPEv
                    +  R  + A++ + + G   R+P     i+F sW+GGDRDG nP v PE
gi|2889426   226 RVYRFLEKAVRRnygAGCGIRVP---SFIRFGSWIGGDRDG-NPFVKPET 271

                    tRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaard
                    t    L  Rm A  +    +E L     m    + L             d
gi|2889426   272 TE---LAVRMHAELILEAYLERLQDLSRMLSHSSALCQPSPAFLDSLDAD 318

                    kvvKyYiEFWKqvPPt...EPYRviLGdvRDKLYntRERaRHLLAtGise
                        y++    q       EPYR  L  +  +L    +R R  +  G+s+
gi|2889426   319 --EEYWVGVMGQRQRRflyEPYRRKLTMMGHRLQANLDRIRRRM-EGLSD 365

                    isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                          y    +FL  L L   sL   GD   ADG L Dl+R   tFG
gi|2889426   366 DGLPDGYAGAADFLADLMLIRDSLIHHGDASAADGPLQDLIRLAETFGFH 415

                    LvKLDiRqEseRqtD.vlDAittHLeiGsYReWsEeKRqEWLlaELkGKR
                    Lv LDiRqEs R+t  v +   +  +   Y  + Ee+R   L   +
gi|2889426   416 LVHLDIRQESTRHTQaVTELFARQPGAPFYQAFNEEQRLMALAEAIAHPH 465

                    PLlgsDLPktEEvkDvldafrvL....AELPiDsFGaYiismataPsDvL
                    P +      t E ++ l++f+v+ + +AE+    FG Y+ism+ a s v+
gi|2889426   466 PFIIDKATLTPETRETLETFEVIarmrAEVGERVFGQYVISMTHAASHVM 515

                    AvELLqRECgvk........qtLrvvPLFEkLADLeAAPAavekLFsiDW
                     v LL R  g+ + ++++   tL+v PLFE + DL      +  LF
gi|2889426   516 EVMLLARLAGLVgvdnrgwfCTLQVSPLFETIEDLSHIDRVMSTLFDDPT 565

                    YinridG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGv
                    Y   +  ++++qevm+GYsDs KD G l+  W+L+ Aq  +i  A + Gv
gi|2889426   566 YLALLRAsgnQQEVMLGYSDSCKDGGILASSWKLFEAQKKVIALADDRGV 615

                    KLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGE
                       lFHGRGGtvGRGGGPtH AiL+qP Dt++G ++ t qGEv+ + +
gi|2889426   616 ACRLFHGRGGTVGRGGGPTHEAILAQPVDTVHGQIKFTEQGEVLSYRYAN 665

                    EnLCFrsLqRFtAAtLEHG...mnPPvsPkPEWRkLmeemAvvAtEEYRs
                     +     L       +   +  ++PP   + ++  +m+e+A      YR
gi|2889426   666 PETARYELTMGISGLIKASrclIEPPEPERNDYLAIMDELARHGEAAYRG 715

                    vvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiF
                    +v     F +YF   tP      +niGsRPa Rk + + + s+RAiPW+F
gi|2889426   716 LVRDTEGFLDYFYECTPLDGIALLNIGSRPAHRKKADrSLASIRAIPWVF 765

                    aWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLl
                     W q R  LP W  +G A       D+  l kL+ mY+eWP+FR  l
gi|2889426   766 GWGQARVTLPAWFSIGQAIERYRGHDVERLAKLQRMYQEWPYFRALLSNT 815

                    EmvFAKGDPGiAaLyDkLLvaEeLkPFGksL...RdkYvEtkdlLLkiAG
                     m   K +  iA  y  L  aE+     + L+   ++Y+ t   +L +AG
gi|2889426   816 QMSLFKAEMHIAREY--LRLAEDRERAAQILgliEEEYQRTLVQVLNVAG 863

                    HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
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                     l++  P L+  l  R+ Y+  Ln +q   L R R            s
  gi|2889426   864 LLALMDETPELRHSLARRNLYLDPLNHIQVALLERYR------------S 901

                   KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    E  dE   k +e +             D L+  +  + AGm ntG
  gi|2889426   902 EE--DEA--KREEWL-------------DPLLRSINALSAGMRNTG    930

gi|240114073|ref|ZP_04728563.1|: domain 1 of 1, from 1 to 900: score 293.0, E = 6.5e-85
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2401140     1    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 38

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2401140    39 ETVKLLSTS----DDSAALIE--KVLPQLDERQTYDLTLACGLFAQILNI 82

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AE+v+   RR i+    G  a E+s t      Et+++L        + v
  gi|2401140    83 AEDVHHERRRQIHEDA-GHNAAEGSLT------ETVRRLKAGK-ADGKSV 124

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                      L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|2401140   125 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 174

                   DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|2401140   175 LRREIDTVLLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 220

                   FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     R+++   +      R+P    ++k   W+GGDRDG nP v  E  R
  gi|2401140   221 LYRKMEHDFQTAYPDVRVP---NILKIGGWIGGDRDG-NPFVSGETLRFA 266

                   CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                            +Y s ++ L  E +ls+ R      v A    +
  gi|2401140   267 FRRHADAVFRFYRSELDKLYRElpLSIRRVKVNDDVMALAALSPDEEI-- 314

                   vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                              +EPYR  +  +   +     +aR L+L  G      e
  gi|2401140   315 ----------ARTEEPYRRAIAYI---MARAMGKARSLgLGMGCKFGFLE 351

                   AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                     y    +FL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
  gi|2401140   352 P-YASAQKFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 400

                   DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                   D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL  +RPL+ +
  gi|2401140   401 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELGHQRPLYSP 450

                   DLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                    +   +++++E++   +a ++  E   D+    iis +  P D LA  LL
  gi|2401140   451 FITYSDhtrrELAIFNEARKIKDEFGEDAVTQSIISNCEQPGDLLALALL 500

                   qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                    +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   +
  gi|2401140   501 LKESGLlavengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDALL 550

                   dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                   + +++ qe+m+GYsDs KD G +   W L +A   ++   Kky v++ lF
  gi|2401140   551 ESRgniQEIMLGYSDSNKDGGYVTSSWCLHQAELGLVELFKKYDVRMRLF 600

                   HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                   HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|2401140   601 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 650

                   rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                   r L    AAtLE  + P    k    kLm+ +  v    YR ++   P F
  gi|2401140   651 RNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDF 697

                   vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                   ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
  gi|2401140   698 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 747
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                    PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                    P W G+G A     +   K l  L+   ++ PFF   l  +E v AK D
  gi|2401140   748 PAWYGFGSAVETLCEGSPKTLAALRGHAQNNPFFQAMLSNMEQVMAKTDI 797

                    GiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     +A  y  L  ++E  k     ++++Y   ++ LL +    +lL     L
  gi|2401140   798 TLAENYAGLSESpEKAKVIFGMIKEEYRRSRKALLDLLQTEELLRDNRSL 847

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                       l LR +Y+  Ln +q   LKR+R                  E+   +
  gi|2401140   848 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 879

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      L+ +               Lt+ G+A G+ ntG
  gi|2401140   880 HALLMVH--------------LTINGVAQGLRNTG    900

gi|268600141|ref|ZP_06134308.1|: domain 1 of 1, from 15 to 914: score 293.0, E = 6.5e-85
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2686001    15    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 52

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2686001    53 ETVKLLSTS----DDSAALIE--KVLPQLDERQTYDLTLACGLFAQILNI 96

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+   RR i+    G  a E+s t      Et+++L        + v
  gi|2686001    97 AEDVHHERRRQIHEDA-GHNAAEGSLT------ETVRRLKAGK-ADGKSV 138

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                       L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|2686001   139 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 188

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|2686001   189 LRREIDTVLLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 234

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R+++   +      R+P    ++k   W+GGDRDG nP v  E  R
  gi|2686001   235 LYRKMEHDFQTAYPDVRVP---NILKIGGWIGGDRDG-NPFVSGETLRFA 280

                    CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                              +Y s ++ L  E +ls+ R      v A    +
  gi|2686001   281 FRRHADAVFRFYRSELDKLYRElpLSIRRVKVNDDVMALAALSPDEEI-- 328

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                                 +EPYR  +  +   +     +aR L+L  G      e
  gi|2686001   329 ----------ARTEEPYRRAIAYI---MARAMGKARSLgLGMGCKFGFLE 365

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y    +FL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
  gi|2686001   366 P-YASAQKFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 414

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL  +RPL+ +
  gi|2686001   415 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELGHQRPLYSP 464

                    DLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                     +   +++++E++   +a ++  E   D+    iis +  P D LA  LL
  gi|2686001   465 FITYSDhtrrELAIFNEARKIKDEFGEDAVTQSIISNCEQPGDLLALALL 514

                    qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                     +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   +
  gi|2686001   515 LKESGLlavengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDALL 564

                    dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                    + +++ qe+m+GYsDs KD G +   W L +A   ++   Kky v++ lF
  gi|2686001   565 ESRgniQEIMLGYSDSNKDGGYVTSSWCLHQAELGLVELFKKYDVRMRLF 614

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
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                    HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|2686001   615 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 664

                    rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                    r L    AAtLE  + P    k    kLm+ +  v    YR ++   P F
  gi|2686001   665 RNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDF 711

                    vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                    ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
  gi|2686001   712 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 761

                    PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                    P W G+G A     +   K l  L+   ++ PFF   l  +E v AK D
  gi|2686001   762 PAWYGFGSAVETLCEGSPKTLAALRGHAQNNPFFQAMLSNMEQVMAKTDI 811

                    GiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     +A  y  L  ++E  k     ++++Y   ++ LL +    +lL     L
  gi|2686001   812 TLAENYAGLSESpEKAKVIFGMIKEEYRRSRKALLDLLQTEELLRDNRSL 861

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                       l LR +Y+  Ln +q   LKR+R                 E+   +
  gi|2686001   862 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 893

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      L+ +               Lt+ G+A G+ ntG
  gi|2686001   894 HALLMVH--------------LTINGVAQGLRNTG    914

gi|161869130|ref|YP_001598297.1|: domain 1 of 1, from 18 to 917: score 292.9, E = 7e-85
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|1618691    18    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 55

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|1618691    56 ETVKLLSTS----DDSAALIE--KVLPQLDEQQTHDLTLACGLFAQILNI 99

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+   RR i+          +    E  + Et+++L        + v
  gi|1618691   100 AEDVHHERRRQIHEEA-------GRGGAEGSLTETVRRLKAGK-ADGKSV 141

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                       L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|1618691   142 QRQLDNTSVTAVLTAHPTEVQRQTVLSFNRRIRALLPQrerCTNADALAR 191

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|1618691   192 LRREIDTILLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 237

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R ++   + +     +P    ++k   W+GGDRDG nP v  E  R
  gi|1618691   238 LYRNMEHDFQMVYPDVCVP---NILKIGGWIGGDRDG-NPFVSAETLRFA 283

                    CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                              +Y   ++ L  E +ls+ R      v A    +
  gi|1618691   284 FRRHADAVFRFYRGELDKLYRElpLSIRRVKVNDDVMALAALSPDEEL-- 331

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                                +EPYR  +  +   +     +aR L+L  G      e
  gi|1618691   332 ----------ARTEEPYRRAIAYI---MARAMGKARALgLGMGCKFGFLE 368

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y    eFL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
  gi|1618691   369 P-YASAQEFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 417

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL+ +RPL+ +
  gi|1618691   418 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELSHQRPLYSP 467

                    DLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAvELL
                     +   +  +  l  f++ +++  E   D+    iis +  PsD LA  LL
  gi|1618691   468 FITYSDHTRHELAIFNearkIKDEFGEDAVTQSIISNCEQPSDLLALALL 517
```

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                    qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                     +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   +
  gi|1618691   518 LKESGLlavengkpQSRINIVPLFETIEALENACPVMETMFRLDWYDALL 567

                    dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                    + +++ qe+m+GYsDs KD G +   W LY+A   ++   Kky v++ lF
  gi|1618691   568 ESRgniQEIMLGYSDSNKDGGYVTSSWCLYQAELGLVELFKKYDVRMRLF 617

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|1618691   618 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 667

                    rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                    r L    AAtLE  + P    k    kLm+ +  v    YR ++   P F
  gi|1618691   668 RNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDF 714

                    vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                    ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
  gi|1618691   715 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 764

                    PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                    P W G+G A     +     l  L+E  +  PFF   l  +E v AK D
  gi|1618691   765 PAWYGFGSAVETLCEDKPETLAALREHAQSNPFFQAMLSNMEQVMAKTDI 814

                    GiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     +A  y  L  ++E        ++++Y+  ++ LL +    +lL     L
  gi|1618691   815 TLAENYAGLSESpEKAAVIFGMIKEEYQRSRKALLDLLQTEELLRDNRSL 864

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                       l LR +Y+  Ln +q   LKR+R                  E+   +
  gi|1618691   865 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 896

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      L+ +                Lt+ G+A G+ ntG
  gi|1618691   897 HALLMVH--------------LTINGVAQGLRNTG    917

gi|261393385|emb|CAX51021.1|: domain 1 of 1, from 1 to 900: score 292.6, E = 8.5e-85
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2613933     1    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 38

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2613933    39 ETVKLLSTS----DDSAALIE--KVLPQLDEQQTHDLTLACGLFAQILNI 82

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+   RR i+          +    E  + Et+++L        + v
  gi|2613933    83 AEDVHHERRRQIHEEA-------GRGGAEGSLTETVRRLKAGK-ADGKSV 124

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                       L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|2613933   125 QRQLDNTSVTAVLTAHPTEVQRQTVLSFNRRIRALLPQrerCTNADALAR 174

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|2613933   175 LRREIDTILLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 220

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R ++   + +     +P    ++k   W+GGDRDG nP v  E  R
  gi|2613933   221 LYRNMEHDFQMVYPDVCVP---NILKIGGWIGGDRDG-NPFVSAETLRFA 266

                    CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                              +Y   ++ L  E +ls+ R      v A    +
  gi|2613933   267 FRRHADAVFRFYRGELDKLYRElpLSIRRVKVNDDVMALAALSPDEEI-- 314

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                                +EPYR  +  +   +     +aR L+L  G      e
  gi|2613933   315 ----------ARTEEPYRRAIAYI---MARAMGKARALgLGMGCKFGFLE 351

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
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                     y    eFL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
  gi|2613933   352 P-YASAQEFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 400

                     DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                     D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL+ +RPL+ +
  gi|2613933   401 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELSHQRPLYSP 450

                     DLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAvELL
                      +   +  +  l  f++ +++  E   D+    iis +  PsD LA  LL
  gi|2613933   451 FITYSDHTRHELAIFNearkIKDEFGEDAVTQSIISNCEQPSDLLALALL 500

                     qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                      +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   +
  gi|2613933   501 LKESGLlavengkpRSRINIVPLFETIEALENACPVMETMFRLDWYDALL 550

                     dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                     +  ++ qe+m+GYsDs KD G +   W LY+A   ++   Kky v++ lF
  gi|2613933   551 ESCgniQEIMLGYSDSNKDGGYVTSSWCLYQAELGLVELFKKYDVRMRLF 600

                     HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                     HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|2613933   601 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 650

                     rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                     r L    AAtLE  + P    k    kLm+ +  v    YR ++   P F
  gi|2613933   651 RNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDF 697

                     vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                     ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
  gi|2613933   698 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 747

                     PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                     P W G+G A     +     l  L+E  +  PFF   l  +E v AK D
  gi|2613933   748 PAWYGFGSAVETLCEDKPETLAALREHAQSNPFFQAMLSNMEQVMAKTDI 797

                     GiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                      +A  y  L  ++E        ++++Y+  ++ LL +    +lL     L
  gi|2613933   798 TLAENYAGLSESpEKAAVIFGMIKEEYQRSRKALLDLLQTEELLRDNRSL 847

                     KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                        l LR +Y+  Ln +q   LKR+R                  E+   +
  gi|2613933   848 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 879

                     deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       L+ +               Lt+ G+A G+ ntG
  gi|2613933   880 HALLMVH--------------LTINGVAQGLRNTG    900

gi|288918904|ref|ZP_06413247.1|: domain 1 of 1, from 1 to 944: score 292.5, E = 9.3e-85
                     *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         + A +R L  G     e L + +               G +L + v
  gi|2889189     1    -MRADVRRL--GTLL-GEALTRHE--------------GAELLDLV 28

                     qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          l+      +      EL a+L  +d + ai +A+a++    LAn+
  gi|2889189    29 ERVRLLA------RGEDAGAELAAVLDEVDASRAIPLARAFSAYFQLANI 72

                     AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                      E     +R R    +    +   +A tE  i + +    l     P+Ev
  gi|2889189    73 TEQL---HRSREISDR---SSGRLQALTE-QIADAVADGSLDP-GLPAEV 114

                     FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                        L       v+tAHPt + RRs+L     i   L             +
  gi|2889189   115 MRRLELRP---VFTAHPTEASRRSVLDTLRGIADLLDASDDPRRPGAGDE 161

                     ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                      L   L   +   + tDE+R  +P P DE R    Y+   + +  P  L
  gi|2889189   162 RLARRLAEMVDVLWQTDELRVERPKPADEARSATYYLGSIITEVLPDLLE 211

                     RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                       D AL  iG+   lP  +  + F sW GGDRDG nP vtP vt +v  L
  gi|2889189   212 DLDRALARIGVE--LPVTARPLTFGSWAGGDRDG-NPNVTPAVTLEVLNL 258
```

```
                    aRmmAanlYisqvEDLmFElsm.WRCndELRv..RAEElyrtaardkvvK
                           +    ++ L+ El  + R   E+ ++ RA      aa   v
  gi|2889189   259 QHEFGIRVLTAALDRLVRELTAsTRVVGEIGAglRAALAADRAALPEVYD 308

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                     +i     +  +EPYR     +  +L  tR R    LA G   ++    y
  gi|2889189   309 RFI----RLNAEEPYRLKCSYILARLAATRAR----LAAGSPHVPGKD-Y 349

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     ++ e ++ LEL   sL       +A G LL  +R     GLsL  LDiR
  gi|2889189   350 LRITELVDELELMRASLAASHGELVANGPLLRAIRTANAAGLSLATLDIR 399

                    qEseRqtDvlDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLl...
                      ++ +   l Ai   L+  +  Y +     R   L+aEL G+RPLl+
  gi|2889189   400 EHADAHHATLGAIYDQLGEldVPYASLDRPARLALLVAELAGRRPLLgav 449

                    gsDLP.ktEEvkDvldafrvLAELPiD.sFGaYiismataPsDvLAvELL
                    ++ LP++     + l ++r   +L  D+   +Yi+sm+    D+LAv +L
  gi|2889189   450 PPPLPeRAARTFELLTTVRRALDLYGDgVIESYIVSMTRGVDDILAVVVL 499

                    qRECgvkqt.....................................
                     RE g+  t+++ + ++++++  ++++  ++++  +++++ +++++ +++
  gi|2889189   500 AREAGLVGTgrsagaetgsgtaagtgtaagtgtaagtgtgagtgtgagtg 549

                    .....LrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...qevmvG
                    +   ++  vPLFE + +L+AA   +e+L +   Y+  +  +++ qevm+G
  gi|2889189   550 gawarIGFVPLFETVTELRAAGSLLERLLADPSYRSLVAARgdvQEVMLG 599

                    YsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGG
                    YsDs KDAG  +  W + kAq E+   A+ +Gv L lFHGRGG vGRGGG
  gi|2889189   600 YSDSSKDAGITASQWEIHKAQRELRDTARAHGVVLRLFHGRGGSVGRGGG 649

                    PtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLE
                    P   AiL+qP  t++G ++vt qGEvi   +    L  + L    AA +E
  gi|2889189   650 PSGEAILAQPYGTLDGPIKVTEQGEVISDKYILPSLARQNLEIALAAVVE 699

                    HGmnPPvsPkPE.....WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlA
                      +    s +P++   +W + m  +   A   YRs+v  +P  v +F  A
  gi|2889189   700 ASVLHRTSRQPDqvlagWDDTMAAVSDAAQGAYRSLVA-DPALVPFFLAA 748

                    tPElEYGkmniGsRPaKRkPs..GGiesLRAiPWiFaWtqtRFHLPvWLG
                    tP  E G +niGsRPa R+P+++GG+  LRAiPW+F Wtq R  LP W G
  gi|2889189   749 TPVDELGNLNIGSRPA-RRPGgtGGLADLRAIPWVFGWTQSRILLPGWFG 797

                    vGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaL
                    vG     A  +       L EmY+ W FFR  l  + m  AK D  iA
  gi|2889189   798 VGSGL--AAARAAGAGDELAEMYRSWHFFRTFLGNVQMTLAKADLTIARR 845

                    yDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRL
                    y   Lv        + +R++Y  t   +L + G  +lLE  P L+  l +
  gi|2889189   846 YVSTLVDPAQAGLLDVIRAEYDRTVREVLSVTGQSELLETAPVLRHTLQV 895

                    RdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkL
                    Rd+Y+  L  +q   L R R               A+ +
  gi|2889189   896 RDAYLAPLHALQVSLLARTR----------------AAGD---------- 919

                    nptervaPGLEDtLiLtmKGiAAGmqntG<-*
                           P L   L+Lt+ GiAAG+ ntG
  gi|2889189   920 ----DADPRLRRGLLLTINGIAAGLRNTG    944

gi|240122526|ref|ZP_04735482.1|: domain 1 of 1, from 1 to 900: score 292.3, E = 1e-84
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2401225     1    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 38

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2401225    39 ETVKLLSTS----DDSAALIE--KVLPQLDERQTYDLTLACGLFAQILNI 82

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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                AE+v+   RR i+    G  a E+s t      Et+++L        + v
gi|2401225    83 AEDVHHERRRQIHEDA-GHNAAEGSLT------ETVRRLKAGK-ADGKSV 124

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                   L n sv  vltAHPt   R  +L  n RiR  L q+++    D
gi|2401225   125 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 174

                DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                 ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
gi|2401225   175 LRREIDTVLLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 220

                FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                  R+++   +      R+P    ++k   W+GGDRDG nP v  E  R
gi|2401225   221 LYRKMEHDFQTAYPDVRVP---NILKIGGWIGGDRDG-NPFVSGETLRFA 266

                CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                          +Y s ++ L  E +ls+ R      v A    +
gi|2401225   267 FRRHADAVFRFYRSELDKLYRElpLSIRRVKVNDDVMALAALSPDEEI-- 314

                vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                            +EPYR  +  +   +     +aR L+L  G      e
gi|2401225   315 ----------ARTEEPYRRAIAYI---MARAMGKARSLgLGMGCKFGFLE 351

                AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                  y    +FL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
gi|2401225   352 P-YASAQKFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 400

                DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL+ +RPL+ +
gi|2401225   401 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELSHQRPLYSP 450

                DLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                 +   +++++E++   +a ++  E   D+    iis +  P D LA  LL
gi|2401225   451 FITYSDhtrrELAIFNEARKIKDEFGEDALTQSIISNCEQPGDLLALALL 500

                qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                 +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   +
gi|2401225   501 LKESGLlavengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDALL 550

                dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                + +++ qe+m+GYsDs KD G +   W L +A   ++   Kky v++ lF
gi|2401225   551 ESRgniQEIMLGYSDSNKDGGYVTSSWCLHQAELGLVELFKKYDVRMRLF 600

                HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
gi|2401225   601 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 650

                rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                r L    AAtLE  + P    k    kLm+ +  v    YR ++   P F
gi|2401225   651 RNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDF 697

                vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
gi|2401225   698 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 747

                PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                P W G+G A     +     l  L+   ++ PFF   l  +E v AK D
gi|2401225   748 PAWYGFGSAVETLCEGSPETLAALRGHAQNNPFFQAMLSNMEQVMAKTDI 797

                GiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                 +A  y  L  ++E  k     ++++Y   ++ LL +    +lL     L
gi|2401225   798 TLAENYAGLSESpEKAKVIFGMIKEEYRRSRKALLDLLQTEELLRDNRSL 847

                KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                   l LR +Y+  Ln +q   LKR+R                  E+   +
gi|2401225   848 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 879

                deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                  L+ +               Lt+ G+A G+ ntG
gi|2401225   880 HALLMVH--------------LTINGVAQGLRNTG    900
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gi|268681114|ref|ZP_06147976.1|: domain 1 of 1, from 18 to 917: score 292.3, E = 1e-84
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2686811    18    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 55

                     qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2686811    56 ETVKLLSTS----DDSAALIE--KVLPQLDERQTYDLTLACGLFAQILNI 99

                     AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     AE+v+   RR i+    G  a E+s t      Et+++L        + v
  gi|2686811   100 AEDVHHERRRQIHEDA-GHNAAEGSLT------ETVRRLKAGK-ADGKSV 141

                     FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                        L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|2686811   142 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 191

                     DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                      ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|2686811   192 LRREIDTVLLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 237

                     FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                       R+++   +      R+P    ++k   W+GGDRDG nP v  E  R
  gi|2686811   238 LYRKMEHDFQTAYPDVRVP---NILKIGGWIGGDRDG-NPFVSGETLRFA 283

                     CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                               +Y s ++ L  E +ls+ R      v A    +
  gi|2686811   284 FRRHADAVFRFYRSELDKLYRElpLSIRRVKVNDDVMALAALSPDEEI-- 331

                     vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                                 +EPYR  +  +   +     +aR L+L  G      e
  gi|2686811   332 ----------ARTEEPYRRAIAYI---MARAMGKARSLgLGMGCKFGFLE 368

                     AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                       y    +FL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
  gi|2686811   369 P-YASAQKFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 417

                     DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                     D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL+ +RPL+ +
  gi|2686811   418 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELSHQRPLYSP 467

                     DLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                      +   +++++E++   +a ++  E   D+    iis +  P D LA  LL
  gi|2686811   468 FITYSDhtrrELAIFNEARKIKDEFGEDALTQSIISNCEQPGDLLALALL 517

                     qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                      +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   +
  gi|2686811   518 LKESGLlavengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDALL 567

                     dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                     + +++ qe+m+GYsDs KD G +   W L +A   ++   Kky v++ lF
  gi|2686811   568 ESRgniQEIMLGYSDSNKDGGYVTSSWCLHQAELGLVELFKKYDVRMRLF 617

                     HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                     HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|2686811   618 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 667

                     rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                     r L    AAtLE  + P    k    kLm+ +  v    YR ++   P F
  gi|2686811   668 RNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDF 714

                     vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                     ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
  gi|2686811   715 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 764

                     PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                     P W G+G A     +     l  L+   ++ PFF   l  +E v AK D
  gi|2686811   765 PAWYGFGSAVETLCEGSPETLAALRGHAQNNPFFQAMLSNMEQVMAKTDI 814

                     GiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                      +A  y  L  ++E  k     ++++Y   ++ LL +    +lL     L
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  gi|2686811   815 TLAENYAGLSESpEKAKVIFGMIKEEYRRSRKALLDLLQTEELLRDNRSL 864

                   KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                      l LR +Y+  Ln +q   LKR+R                  E+   +
  gi|2686811   865 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 896

                   deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     L+ +               Lt+ G+A G+ ntG
  gi|2686811   897 HALLMVH--------------LTINGVAQGLRNTG    917

gi|240081793|ref|ZP_04726336.1|: domain 1 of 1, from 1 to 900: score 292.3, E = 1e-84
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2400817     1    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 38

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2400817    39 ETVKLLSTS----DDSAALIE--KVLPQLDERQTYDLTFACGLFAQILNI 82

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AE+v+   RR i+    G  a E+s t      Et+++L        + v
  gi|2400817    83 AEDVHHERRRQIHEDA-GHNAAEGSLT------ETVRRLKAGK-ADGKSV 124

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                      L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|2400817   125 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 174

                   DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|2400817   175 LRREIDTVLLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 220

                   FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     R+++   +      R+P    ++k   W+GGDRDG nP v  E  R
  gi|2400817   221 LYRKMEHDFQTAYPDVRVP---NILKIGGWIGGDRDG-NPFVSGETLRFA 266

                   CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                             +Y s ++ L  E +ls+ R      v A    +
  gi|2400817   267 FRRHADAVFRFYRSELDKLYRElpLSIRRVKVNDDVMALAALSPDEEI-- 314

                   vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                                +EPYR  +  +   +     +aR L+L  G      e
  gi|2400817   315 ----------ARTEEPYRRAIAYI---MARAMGKARSLgLGMGCKFGFLE 351

                   AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                     y    +FL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
  gi|2400817   352 P-YASAQKFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 400

                   DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                   D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL+ +RPL+ +
  gi|2400817   401 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELSHQRPLYSP 450

                   DLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                    +   +++++E++   +a ++  E   D+    iis +  P D LA  LL
  gi|2400817   451 FITYSDhtrrELAIFNEARKIKDEFGEDALTQSIISNCEQPGDLLALALL 500

                   qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                    +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   +
  gi|2400817   501 LKESGLlavengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDALL 550

                   dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                   + +++ qe+m+GYsDs KD G +   W L +A   ++   Kky v++ lF
  gi|2400817   551 ESRgniQEIMLGYSDSNKDGGYVTSSWCLHQAELGLVELFKKYDVRMRLF 600

                   HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                   HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|2400817   601 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 650

                   rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                   r L    AAtLE  + P    k    kLm+ +  v    YR ++   P F
  gi|2400817   651 RNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDF 697
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                    vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                    ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
  gi|2400817   698 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 747

                    PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                    P W G+G A     +     l  L+   ++ PFF   l  +E v AK D
  gi|2400817   748 PAWYGFGSAVETLCEGSPETLAALRGHAQNNPFFQAMLSNMEQVMAKTDI 797

                    GiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     +A  y  L  ++E  k     ++++Y   ++ LL +    +lL     L
  gi|2400817   798 TLAENYAGLSESpEKAKVIFGMIKEEYRRSRKALLDLLQTEELLRDNRSL 847

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                       l LR +Y+  Ln +q   LKR+R                  E+   +
  gi|2400817   848 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 879

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      L+ +               Lt+ G+A G+ ntG
  gi|2400817   880 HALLMVH--------------LTINGVAQGLRNTG    900

gi|268597893|ref|ZP_06132060.1|: domain 1 of 1, from 18 to 917: score 292.3, E = 1e-84
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2685978    18    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 55

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2685978    56 ETVKLLSTS----DDSAALIE--KVLPQLDERQTYDLTFACGLFAQILNI 99

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+   RR i+    G  a E+s t      Et+++L        + v
  gi|2685978   100 AEDVHHERRRQIHEDA-GHNAAEGSLT------ETVRRLKAGK-ADGKSV 141

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                       L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|2685978   142 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 191

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|2685978   192 LRREIDTVLLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 237

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R+++   +      R+P    ++k   W+GGDRDG nP v  E  R
  gi|2685978   238 LYRKMEHDFQTAYPDVRVP---NILKIGGWIGGDRDG-NPFVSGETLRFA 283

                    CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                              +Y s ++ L  E +ls+ R      v A    +
  gi|2685978   284 FRRHADAVFRFYRSELDKLYRElpLSIRRVKVNDDVMALAALSPDEEI-- 331

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                                 +EPYR  +  +   +     +aR L+L  G      e
  gi|2685978   332 ----------ARTEEPYRRAIAYI---MARAMGKARSLgLGMGCKFGFLE 368

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y    +FL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
  gi|2685978   369 P-YASAQKFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 417

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL+ +RPL+ +
  gi|2685978   418 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELSHQRPLYSP 467

                    DLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                     +   +++++E++   +a ++  E   D+    iis +  P D LA  LL
  gi|2685978   468 FITYSDhtrrELAIFNEARKIKDEFGEDALTQSIISNCEQPGDLLALALL 517

                    qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                     +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   +
  gi|2685978   518 LKESGLlavengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDALL 567

                    dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                    + +++ qe+m+GYsDs KD G +   W L +A   ++   Kky v++ lF
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  gi|2685978   568 ESRgniQEIMLGYSDSNKDGGYVTSSWCLHQAELGLVELFKKYDVRMRLF 617

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|2685978   618 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 667

                    rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                    r L    AAtLE  + P    k    kLm+ +  v    YR ++   P F
  gi|2685978   668 RNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDF 714

                    vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                    ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
  gi|2685978   715 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 764

                    PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                    P W G+G A     +     l  L+   ++ PFF   l  +E v AK D
  gi|2685978   765 PAWYGFGSAVETLCEGSPETLAALRGHAQNNPFFQAMLSNMEQVMAKTDI 814

                    GiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     +A  y  L  ++E  k     ++++Y   ++ LL +    +lL     L
  gi|2685978   815 TLAENYAGLSESpEKAKVIFGMIKEEYRRSRKALLDLLQTEELLRDNRSL 864

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                       l LR +Y+  Ln +q   LKR+R                  E+   +
  gi|2685978   865 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 896

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      L+ +               Lt+ G+A G+ ntG
  gi|2685978   897 HALLMVH--------------LTINGVAQGLRNTG    917

gi|291044869|ref|ZP_06570578.1|: domain 1 of 1, from 21 to 920: score 292.3, E = 1e-84
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2910448    21    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 58

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2910448    59 ETVKLLSTS----DDSAALIE--KVLPQLDERQTYDLTFACGLFAQILNI 102

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+   RR i+    G  a E+s t      Et+++L        + v
  gi|2910448   103 AEDVHHERRRQIHEDA-GHNAAEGSLT------ETVRRLKAGK-ADGKSV 144

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                       L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|2910448   145 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 194

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|2910448   195 LRREIDTVLLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 240

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R+++   +      R+P    ++k   W+GGDRDG nP v  E  R
  gi|2910448   241 LYRKMEHDFQTAYPDVRVP---NILKIGGWIGGDRDG-NPFVSGETLRFA 286

                    CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                              +Y s ++ L  E +ls+ R      v A    +
  gi|2910448   287 FRRHADAVFRFYRSELDKLYRElpLSIRRVKVNDDVMALAALSPDEEI-- 334

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                                +EPYR  +  +   +     +aR L+L  G      e
  gi|2910448   335 ----------ARTEEPYRRAIAYI---MARAMGKARSLgLGMGCKFGFLE 371

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y    +FL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
  gi|2910448   372 P-YASAQKFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 420

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL+ +RPL+ +
  gi|2910448   421 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELSHQRPLYSP 470
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                    DLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                     +   +++++E++   +a ++  E   D+    iis +  P D LA  LL
  gi|2910448   471 FITYSDhtrrELAIFNEARKIKDEFGEDALTQSIISNCEQPGDLLALALL 520

                    qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                     +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   +
  gi|2910448   521 LKESGLlavengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDALL 570

                    dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                    + +++ qe+m+GYsDs KD G +   W L +A   ++   Kky v++ lF
  gi|2910448   571 ESRgniQEIMLGYSDSNKDGGYVTSSWCLHQAELGLVELFKKYDVRMRLF 620

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|2910448   621 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 670

                    rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                    r L    AAtLE  + P    k    kLm+ +  v    YR ++   P F
  gi|2910448   671 RNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDF 717

                    vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                    ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
  gi|2910448   718 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 767

                    PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                    P W G+G A     +     l  L+   ++ PFF   l  +E v AK D
  gi|2910448   768 PAWYGFGSAVETLCEGSPETLAALRGHAQNNPFFQAMLSNMEQVMAKTDI 817

                    GiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     +A  y  L  ++E  k     ++++Y   ++ LL +    +lL     L
  gi|2910448   818 TLAENYAGLSESpEKAKVIFGMIKEEYRRSRKALLDLLQTEELLRDNRSL 867

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                       l LR +Y+  Ln +q   LKR+R                  E+   +
  gi|2910448   868 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 899

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      L+ +                Lt+ G+A G+ ntG
  gi|2910448   900 HALLMVH--------------LTINGVAQGLRNTG    920

gi|121635719|ref|YP_975964.1|: domain 1 of 1, from 1 to 900: score 292.3, E = 1.1e-84
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|1216357     1    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 38

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|1216357    39 ETVKLLSTS----DDSAALIE--KVLPQLDEQQTHDLTLACGLFAQILNI 82

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+   RR i+          +    E  + Et+++L        + v
  gi|1216357    83 AEDVHHERRRQIHEEA-------GRGGAEGSLTETVRRLKAGK-ADGKSV 124

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                       L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|1216357   125 QRQLDNTSVTAVLTAHPTEVQRQTVLSFNRRIRALLPQrerCTNADALAR 174

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|1216357   175 LRREIDTILLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 220

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R ++   + +     +P    ++k   W+GGDRDG nP v  E  R
  gi|1216357   221 LYRNMEHDFQMVYPDVCVP---NILKIGGWIGGDRDG-NPFVSAETLRFA 266

                    CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                              +Y   ++ L  E +ls+ R      v A    +
  gi|1216357   267 FRRHADAVFRFYRGELDKLYRElpLSIRRVKVNDDVMALAALSPDEEL-- 314

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                                +EPYR  +  +   +     +aR L+L  G      e
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  gi|1216357   315 ----------ARTEEPYRRAIAYI---MARAMGKARALgLGMGCKFGFLE 351

                   AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                     y    eFL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
  gi|1216357   352 P-YASAQEFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 400

                   DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                   D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL+ +RPL+ +
  gi|1216357   401 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAVLLRELSHQRPLYSP 450

                   DLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAvELL
                    +   +  +  l  f++ +++  E   D+    iis +  PsD LA  LL
  gi|1216357   451 FITYSDHTRHELAIFNearkIKDEFGEDAVTQSIISNCEQPSDLLALALL 500

                   qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                    +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   +
  gi|1216357   501 LKESGLlavengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDALL 550

                   dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                   + +++ qe+m+GYsDs KD G +   W LY+A   ++   Kky v++ lF
  gi|1216357   551 ESRgniQEIMLGYSDSNKDGGYVTSSWCLYQAELGLVELFKKYDVRMRLF 600

                   HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                   HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|1216357   601 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 650

                   rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                   r L    AAtLE  + P    k    kLm+ +  v    YR ++   P F
  gi|1216357   651 RNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDF 697

                   vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                   ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
  gi|1216357   698 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 747

                   PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                   P W G+G A     +     l  L+E  +  PFF   l  +E v AK D
  gi|1216357   748 PAWYGFGSAVETLCEGNPDTLTALREHAQSNPFFQAMLSNMEQVMAKTDI 797

                   GiAaLyDkLLvaEe.LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                    +A  y  L  + ++ k     ++++Y   ++ LL +    +lL     L
  gi|1216357   798 TLAENYAGLSESPDkAKIIFGMIKEEYRRSRKALLDLLQTEELLRDNRSL 847

                   KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                      l LR +Y+  Ln +q   LKR+R                  E+   +
  gi|1216357   848 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 879

                   deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     L+ +               Lt+ G+A G+ ntG
  gi|1216357   880 HALLMVH--------------LTINGVAQGLRNTG    900

gi|289167828|ref|YP_003446097.1|: domain 1 of 1, from 1 to 898: score 292.1, E = 1.2e-84
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           L  L     s +  +++ + L+l   L+Di + +  ++
  gi|2891678     1    ---MSLQKLE--NYS-NKAVVQEEVLILTELLeDITKNMLAPETFAK 41

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   + E  Els +    +D + L+ L   +tsL   +   + + ++ +  L n
  gi|2891678    42 IMELKELSTQ----EDYQGLNQL---VTSLTNDEMAYISRYFSILPLLIN 84

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   + E+v+lAy    +     D+    sAt          k+v       e
  gi|2891678    85 ISEDVDLAYEINHQNNIDQDYLGKLSATI---------KMVAEK----EN 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     e L    v  vltAHPtq  R+s+L     i   L +     +    K
  gi|2891678   122 AVEILEHLNVVPVLTAHPTQVQRKSMLDLTNHIHTLLRKYRDVKLGLINK 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   +     L R i     tD iR  +     E+   m Y+     k vP
  gi|2891678   172 EKWHNDLRRYIEIIMQTDMIREKKLKVTNEITNVMEYYNSSFLKAVPHLT 221
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                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                           K  G+  + P     i    W+GGDRDG nP vt +  +   +
  gi|2891678   222 AEYKRLAKKHGLELKHPKP---ITMGMWIGGDRDG-NPFVTADTLKQSAM 267

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                        +  n Y +++  L  E+s+      +     E+ r ++ +     Y
  gi|2891678   268 TQCEVIMNYYDEKIYQLYREFSLSTSIVNVSKQVREMARQSKDN---SIY 314

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                     E        E YR  L d+  K+  t+          i +    A y
  gi|2891678   315 RE-------KELYRRALFDIQSKIQATK-------TYLIEDKEVGARYET 350

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      +F   L     sL e    ++  G  ++l+  v  FG  L  +D+Rq+
  gi|2891678   351 ANDFYKDLITIRDSLLENKGEALISGDFVELIQAVEIFGFYLASIDMRQD 400

                    seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK.RPLlgsDLP
                    s  +   +  + +  +i s+Y e sEe +   Ll EL+  +R L    +
  gi|2891678   401 SSVHEACVAELLKSAGIHSrYSELSEEEKCQLLLKELEEDpRILSATHVE 450

                    ktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRE
                    k E  ++E++    a +    L  D     iis at+ sD+L   +L +E
  gi|2891678   451 KSEflekELAIFKAARKLKDKLGDDVIRQTIISHATSVSDMLELAILLKE 500

                    Cgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri...dGKq
                     g+ ++++  +++vPLFE + DL+    ++    s+   +  i +++  q
  gi|2891678   501 VGLvdkeRSRVQIVPLFETIEDLDHSEETMREYLSLPLAKKWIasrNNYQ 550

                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                    e+m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGRGGtv
  gi|2891678   551 EIMLGYSDSNKDGGYLSSCWTLYKAQQQLTAIGDEFGVKVTFFHGRGGTV 600

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                    GRGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
  gi|2891678   601 GRGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLV 650

                    AAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                     A +   +    s  +++  +  +m+++     + YR +v+    F +YF
  gi|2891678   651 SAAINRMITQWKSDTntsNRYEAIMDQVVDRSYDIYRDLVFGNDYFYDYF 700

                    RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                        P       niGsRPa Rk    i  LRAiPW+F+W q R   P W
  gi|2891678   701 FESSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWY 750

                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    GvG  FK  id+   n+  L++mYk+WPFF   l  ++mv  K    iA
  gi|2891678   751 GVGSSFKEFIDQNPENIEILRDMYKNWPFFQSLLSNVDMVLSKSNMNIAF 800

                    LyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                     y kL   +++k   + + d+++ tk+ +L+i G  +lL   PYLK  l
  gi|2891678   801 EYAKLCEDDQVKAIYDTILDEWQLTKNVILEIEGYDELLAENPYLKASLD 850

                    LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                     R +Y   Ln +q   +KR R        r +ls +  +E       L++
  gi|2891678   851 YRMPYFNILNYIQLELIKRQR--------RGELSSD--QEK------LIH 884

                    LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                      + GiA G+ n G
  gi|2891678   885 TT----------------INGIATGLRNSG    898

gi|167569217|ref|ZP_02362091.1|: domain 1 of 1, from 4 to 952: score 291.1, E = 2.5e-84
                    *->siDAqLRlLvP.GKvsed.ekLieYDALLlDkFL.DiLqDLHGedLk
                       +  A      P+G+  ed+++ +  D   l + L+D++ +  G+ +
  gi|1675692     4    ARPASAAPAKPhGRTREDkDRPLFEDIRYLGRLLgDVVREQEGDAVF 50

                    EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                     +v      +  +    D+   + L   L  L P  ++ v +a++    L
  gi|1675692    51 HVVETIRQTAVKFRREDDSAAAQTLEKMLRKLTPEQTVSVVRAFSYFSHL 100

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                    An+AE+ +   RRRi+ +        +sA     +   l kL   ++ s
```

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gi|1675692   101 ANIAEDRHHNRRRRIHALA-------GSAPQAGTVAYALDKLKEAGDASS 143

                  eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                  + +        +  vltAHPt   R+s+L  +  i   La    + +t
gi|1675692   144 KVIKRFFEGALIVPVLTAHPTEVQRKSILDAQHDIAHLLAE-RDQPLTAR 192

                  DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                  +    +  L   +   + t  +R a+ t  DE+   +sY+  t  +  P
gi|1675692   193 EFAHNEALLRARVTTLWQTRMLRDARLTVADEIENALSYYRATFLDELPA 242

                  FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      ++ AL   G+  R+P      +  sW+GGDRDG nP vt     +
gi|1675692   243 LYADIEEALAEHGLPARVP---AFFQMGSWIGGDRDG-NPNVTAATLDEA 288

                  CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                        +    Y++qv  L  Els+    + L v A +  +  a
gi|1675692   289 INRQAAVIFEHYLEQVHKLGAELSV----SNLLVGANDALKALAAA---- 330

                  yYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER....aRHLLAtGise
                         q P++  EPYR  L  v  +L  + R R +++a  +   G
gi|1675692   331 ----SPDQSPhrVDEPYRRALIGVYTRLAAsARVRlgegAVPVRSAGRGA 376

                  isEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                   +  A +y + EeF   L +   sL       +A   L  l+R    FG
gi|1675692   377 APVRATpYADAEEFAADLRVLTDSLALHHGESLATPRLAPLMRAAEVFGF 426

                  sLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK
                   L  +D+Rq s+ +  v+  +    ++ + Y   +E  +   Lla L
gi|1675692   427 HLASIDLRQSSDIHEAVIAELLARGGVEpDYAALAEADKLRVLLAALADP 476

                  RPLlgsDLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDv
                  RPL  + L   +  k  l+ +++ + + A     +   Yiis + + sD
gi|1675692   477 RPLRSPYLDYSDLAKSELGVLErahaIRAQFGPRAVRNYIISHTETVSDL 526

                  LAvELLqRECgv............kqtLrvvPLFEkLADLeAAPAavekL
                  + v LLq+E g+ +++ ++++ + ++ L  +PLFE +ADL+ AP  +
gi|1675692   527 VEVLLLQKETGLfegtlgtphanaRNGLMAIPLFETIADLRNAPDIMREF 576

                  Fs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvA
                  F+ +++   + +    qevm+GYsDs KD G l   W LY+A   ++
gi|1675692   577 FAlpgVGELVAHQGHEQEVMLGYSDSNKDGGFLTSNWELYRAELALVDLF 626

                  KkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviE
                   + G+KL lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGEvi
gi|1675692   627 SERGIKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEVIA 676

                  fsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEWRkLmeemAvvAt
                    F   ++  r L    AAtLE  + P  ++Pk+ P +   m+ +   A
gi|1675692   677 SKFANPEIGRRNLETVVAATLEATLLPHRnAPKqlPAFEAAMQALSDAAM 726

                  EEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....Gies
                    YR++v+  P F +YF + tP +E   +niGsRPa Rk   ++++ ie
gi|1675692   727 ASYRALVYETPGFTDYFFSSTPITEIAELNIGSRPASRKLQDpknrKIED 776

                  LRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid..KD....iKnlqkLkEm
                  LRAiPW F+W q R  L  W G+G A    +d++KD  ++ K +  Lk m
gi|1675692   777 LRAIPWGFSWGQCRLLLTGWYGFGSAVAAFLDgtKDaaerAKRVALLKKM 826

                  YkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkY
                   k+WPFF   l  ++mv AK D  +A+ y +L+    L+k   +++  ++
gi|1675692   827 NKTWPFFAHLLSNMDMVLAKTDLAVASRYAQLVADKKLrKHVFERIVSEW 876

                  vEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRD
                    t d L +i G    L   P L   ++ R +Y+  Ln +q   +KR R
gi|1675692   877 HRTSDALAEITGSDARLAANPLLARSIKNRFPYLDPLNHLQVELIKRHRS 926

                  PsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGi
                                 d n        +L             + Lt+ Gi
gi|1675692   927 ---------------GDTN-------ARLR----------RGIHLTINGI 944

                  AAGmqntG<-*
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                  AAG+ ntG
  gi|1675692   945 AAGLRNTG    952

gi|171780080|ref|ZP_02920984.1|: domain 1 of 1, from 3 to 943: score 290.9, E = 2.9e-84
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                     s+  q +l      s    +i  +  +l   LD+    + G+++
  gi|1717800     3    SVTIQ-KLENNDTQS----IITEEVKVLKSLLDeTTHQMVGDEVFAK 44

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  +q    lsA  E      KLeEL a+Lt     + ++v + ++ +  L n
  gi|1717800    45 IQNIVKLSASDE----YGKLEELVAQLTN---EEMVVVSRYFSILPLLIN 87

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  + E+v+ Ay    +     D+    s t +         +v+      e
  gi|1717800    88 ISEDVDFAYEINYQNNTNQDYLGKLSMTVD---------MVSES----EN 124

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    e L n  v  vltAHPtq  R+ +L     i   L +       v  +
  gi|1717800   125 SKEILENVNVVPVLTAHPTQVQRKTVLELTNHIHDLLRKYRDVKAGVVNR 174

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                        L R i     tD iR  +   + E+   m Y+   + + + K
  gi|1717800   175 DKWYTDLRRYIEIIMQTDIIREKKLKVKNEITNVMEYYNGSLIQAITKLT 224

                  RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                            Gi    P     i    W+GGDRDG nP vt E  R
  gi|1717800   225 SEYKRLAAEKGIDLTNPKP---ITMGMWIGGDRDG-NPYVTAETLRLSAT 270

                  LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                  +   +  n Yi+++  L   +s+      +    E l   +  +     Y
  gi|1717800   271 VQSEVIINYYIEKLTGLYRTFSLSTTLTKISPEVERLAELSSDK---SIY 317

                  iEFWKqvPPtEPYRviLGdvRDKLYntRER.......aRH..........
                   E       +EPYR     +  KL  t    + +++ +RH  ++++ +++
  gi|1717800   318 RE-------NEPYRKAFNYIQSKLIQTLIElkagptiSRHafensklgsd 360

                  .........LLAtGi........seisEeA.vytkvEeFLEPLELCYksL
                     ++++ +++A+ ++++ ++ +se+ +e + y    eF + L +  +sL
  gi|1717800   361 vyantnnasVIAKYLqnkvnkvsSELQDEIpSYKTAKEFKDDLLIIKQSL 410

                  CeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHL
                   + GD ++  G   +lL  v  FG  L  +D+Rq+s  +   +  + +
  gi|1717800   411 LDNGDDALLTGDFSELLQAVDVFGFYLATIDMRQDSSVNEACVAELLKSA 460

                  ei.GsYReWsEeKRqEWLlaELkGK.RPLlgsDLPktEEvk...Dvldaf
                  +i   Y   sEe +   Ll EL+  +R L      k E ++++  + ++
  gi|1717800   461 NIvDDYSALSEEEKVKVLLKELQEDpRTLSSTNAEKSEQLQkelAIFQTA 510

                  rvLAE.LPiDsFGaYiismataPsDvLAvELLqRECgv....kqtLrvvP
                  r L ++L  +     iis + + sD+    ++ +E g+ +++k  +++vP
  gi|1717800   511 RYLKDkLGDEVIKQHIISHTESVSDMFELAIMLKEVGLldnqKARVQIVP 560

                  LFEkLADLeAAPAavekLFsiDWYinri...dGKqevmvGYsDsGKDAGR
                  LFE + DLe     +e     D  +  ++ + G qe+m+GYsDs KD G
  gi|1717800   561 LFETIKDLENSRGIMEEFLDYDIVRRWVtanKGYQEIMLGYSDSNKDGGY 610

                  lsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqP
                  ls  W LYkAq E+ ++  + G+K++  HGRGGtvGRGGGP   Ai sqP
  gi|1717800   611 LSSVWTLYKAQNELTRIGSERGIKVTFIHGRGGTVGRGGGPSYEAITSQP 660

                  PDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPk
                     i+  +R t qGE+iE  +G  ++ +  L     At+   +   +
  gi|1717800   661 FGSIKERIRLTEQGEIIENKYGNKDVAYYNLEMLLSATVGRIVTRMITNP 710

                  PE...WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                   E +++R+ m+ +       YR +v+  P F +YF  AtP  E   +niG
  gi|1717800   711 DEidtFRETMDGIVTYSNGVYRDLVFGNPHFYDYFFEATPIKEVSSLNIG 760

                  sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK
                  sRPa Rk    i  LRAiPW+F+W q R   P W GvG AFKh id +
  gi|1717800   761 SRPAARKTITEISGLRAIPWVFSWSQSRIMFPGWYGVGSAFKHFIDAEEG 810
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                    nlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFG
                    nl kL+ mY++WPFF   l  ++mv  K    iA  y kL  +Ee++
  gi|1717800   811 NLEKLQHMYEKWPFFHSLLSNVDMVLSKTNMNIAFQYSKLAESEEVRNVF 860

                    ksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                    + + d+++ tkd +L i  H  lLE  P L+  l  R +Y   Ln +q
  gi|1717800   861 NVILDEWQLTKDVILAIEKHDNLLEENPSLRASLDYRIPYFNVLNYIQIE 910

                    tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                     +KR+R  +              dE+    + L++
  gi|1717800   911 LIKRLRHDEL-------------DED---YEKLIHTT------------- 931

                    iLtmKGiAAGmqntG<-*
                       + GiA G+ n G
  gi|1717800   932 ---INGIATGLRNSG    943

gi|121605982|ref|YP_983311.1|: domain 1 of 1, from 38 to 982: score 290.8, E = 2.9e-84
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                             R  v  K    e+ +  D  Ll + L+D++ D  G    E
  gi|1216059    38    ETGKPARPSVRAKNN--ERPLVEDIRLLGRILgDVIRDQEGVAAYEL 82

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls  +    D +    L a L  L    ++ v +a+     LAn
  gi|1216059    83 IEQVRTLSVAFRRDADQEADKALKALLKDLSGDQTVSVIRAFTYFSHLAN 132

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAE+ +   RR i+ +  GD       t E  iE  l +L   +  +P+
  gi|1216059   133 LAEDRHHIRRRAIHERA-GD-------TQEGSIEVALARLRWAG-IAPKA 173

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL..........
                    + + L    v  vltAHPt   R+s+L  +  i   L+  ++ +
  gi|1216059   174 ISDTLARSFVSPVLTAHPTEVQRKSILDAERGIAQLLTARdsikamalav 223

                    .sAKDvtveDKkELDEA.LHREiqAAFRtDEiRRaqPtPqDEmRaGmsYi
                    +sAKD          EA+L   +   + t  +R ++ t  DE+   +sY+
  gi|1216059   224 sSAKDALSPRELAANEAqLRARVMQLWQTRLLRFSKLTVADEIENALSYY 273

                    HEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknP
                      t  + +PK     +  L n  +          ++   W+GGDRDG nP
  gi|1216059   274 EATFLRQIPKIYANLERELGNQPVHS-------FLRMGQWIGGDRDG-NP 315

                    RvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsm....WRCndELRvRA
                     v  +           +A   Y+  v  L  Elsm+     C  E+ + A
  gi|1216059   316 NVNADTLNYALGRQADVALRHYLTEVHLLGAELSMsailVECSAEMQALA 365

                    EElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntR......
                    E    t                    EPYR  L  v  +L  t +  +++
  gi|1216059   366 ESSPDTNEHR--------------QDEPYRRALTGVYARLAATLkaltgg 401

                    ERaRHLLAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsL
                    E aRH +A        +  y + E+FL  L     sL      ++    L
  gi|1216059   402 EAARHAVAP-------QNPYGRAEDFLADLRTLEASLKSHHGEALTAQRL 444

                    LDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeK
                      l+R v  FG  L  +D+Rq s+++ +v+  +     i + Y +  E
  gi|1216059   445 HPLIRAVEVFGFHLATVDLRQSSDKHEEVVAELLAVARIEpGYASLDEAA 494

                    RqEWLlaELkGKRPL..lgsDLPktEEvkDvl..dafrvLAELPiDsFGa
                    ++  Ll  L   RPL+ lg        ++  + + a    A    ++
  gi|1216059   495 KRALLLKMLNDARPLrvLGHVYSGLAQIELAIfeAARTARARFGKEAIRH 544

                    YiismataPsDvLAvELLqRECgvkq..............tLrvvPLFEk
                    Yiis + + sD L v LLq+E g+ ++  ++ +++ +++  L vvPLFE
  gi|1216059   545 YIISHTETVSDLLEVLLLQKEVGLMHglldaqdqigsscDLIVVPLFET 594

                    LADLeAAPAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAA
                    + DL+ A   +   ++ +++   + r    q++m+GYsDs KD G +
  gi|1216059   595 IEDLRNAAPIMREFYAlpgVAALVQRSGAEQDIMLGYSDSNKDGGIFTSN 644

                    WqLYkAqEEii....KvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqP
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                    W LY+A   +++  ++ A  +G+ L +FHGRGGtvGRGGGP   AiL+qP
  gi|1216059   645 WELYRAEIALVelfdQLAVSHGITLRMFHGRGGTVGRGGGPSYEAILAQP 694

                    PDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPk
                    P t+ G +R t qGEvi   +   ++  r L    AAtLE  +  P  P
  gi|1216059   695 PGTVRGQIRLTEQGEVIGSKYANPEIGRRNLETLVAATLEATLLQPTKPA 744

                    .PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    +P + +  +++       YR++v+  P F EYF +AtP  E   +niGsR
  gi|1216059   745 tPAFLQAADQLSQASMAAYRALVYETPGFTEYFFSATPIREIAELNIGSR 794

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAi......d
                    Pa RkPs  ie LRAiPW F+W q R  LP W G+G A    ++++++++
  gi|1216059   795 PASRKPSQKIEDLRAIPWGFSWGQCRLTLPGWYGFGSAIEQFLgqggspE 844

                    KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL
                         l  Lk mY++WPFFR  l  ++mv AK D  +A+ y +L+    L
  gi|1216059   845 SRKDALAVLKKMYRQWPFFRTLLSNMDMVLAKSDLALASRYSELVADAKL 894

                    .kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLn
                    +k     + +++  t + L  i G k  L G   L+  +R R +Yi  L
  gi|1216059   895 rKKIFTAIDAEWHKTAQALSLITGEKQRLAGNAALQRSIRHRFPYIDPLH 944

                    vfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPG
                     +q   ++R R                A    ++ +  +++
  gi|1216059   945 HLQVELVRRYR----------------AGQTDQRVQTGIHIS-------- 970

                    LEDtLiLtmKGiAAGmqntG<-*
                            + GiAAG+ ntG
  gi|1216059   971 --------INGIAAGLRNTG    982

gi|270292890|ref|ZP_06199101.1|: domain 1 of 1, from 1 to 898: score 290.7, E = 3.1e-84
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                            L  L     s +  +++ + L+l   L+Di + +  ++  +
  gi|2702928     1    ---MSLQKLE--NYS-NKAVVQEEVLILTELLeDITKNMLAPETFDK 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +    +ls        ++  + L   +tsL   + i + + ++ +  L n
  gi|2702928    42 IMQLKDLST-------SENYQGLNKLVTSLSNEEMIYISRYFSILPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+    s t          k+v       e
  gi|2702928    85 ISEDVDLAYEINHQNNVDQDYLGKLSTTI---------KMVAEK----EN 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                        L    v  vltAHPtq  R+s+L     i   L +     +    K
  gi|2702928   122 AAAILEQLNVVPVLTAHPTQVQRKSMLDLTNHIHTLLRKYRDVKLGLINK 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +     L R i     tD iR  +     E+   m Y+     + vP+
  gi|2702928   172 EKWHMDLRRYIEIIMQTDMIREKKLKVTNEITNVMEYYQSSFLNAVPRLT 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                           K  Gi    P     i    W+GGDRDG nP vt E      L
  gi|2702928   222 AEYKKLAKEQGIELEHPKP---ITMGMWIGGDRDG-NPFVTAETLNKSAL 267

                    LaRmmAanlYisqvEDLm..FElsmWRCndELRvRAEElyrtaardkvvK
                        +  n Y +++  L ++F ls    n   +vR   l++   +
  gi|2702928   268 TQCKVIMNYYDEKIYNLYreFSLSTSIVNVSDKVREMALKSQDNSI---- 313

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                     Y E        E YR  L d+  K+  t+       A  i +   +  y
  gi|2702928   314 -YRE-------KELYRRALFDIQAKMQATK-------AYLIEDKDIQPRY 348

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                       +eF   L     sL e     +  G  ++l+  v  FG  L  +D+R
  gi|2702928   349 ATADEFYQDLLAIRDSLLENKGEYLISGEFVELMQAVEIFGFYLASIDMR 398

                    qEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    q+s  +   +  +    +i+  Y + sE+ +   Ll EL+    +l +
  gi|2702928   399 QDSSVHEACVAELLASAGInDHYSDLSEDEKCTLLLKELEEDPRILSATH 448
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                    PktEEvkD....vldafrvLAE.LPiDsFGaYiismataPsDvLAvELLq
                        E+ +++ ++  a r L ++L        iis at+ sD+L   ++
  gi|2702928   449 AEKSELLEkelsIFKAARKLKDkLGENVIRQTIISHATSVSDMLELAIML 498

                    RECgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK..
                    +E g+ + +k  +++vPLFE + DL+    ++ + Fs+   +  i  K++
  gi|2702928   499 KEVGLvdaqKARVQIVPLFETIEDLDHSEETMRRYFSLPLAKKWIASKdn 548

                    .qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                     qe+m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGRGG
  gi|2702928   549 yQEIMLGYSDSNKDGGYLSSCWTLYKAQQQLTAIGDEFGVKVTFFHGRGG 598

                    tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                    tvGRGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
  gi|2702928   599 TVGRGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNLEM 648

                    FtAAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFvE
                       A +   +    s  +++  +  +m+++     + YR +v+    F +
  gi|2702928   649 LVSAAINRMITKKKSDTntsNRYEAIMDQVVDRSYDIYRDLVFGNEHFYD 698

                    YFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPv
                    YF    P       niGsRPa Rk    i  LRAiPW+F+W q R   P
  gi|2702928   699 YFFESSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPG 748

                    WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                    W GvG  FK  id+D Kn+  L++mY++WPFF   l  ++mv  K    i
  gi|2702928   749 WYGVGSSFKEFIDQDPKNIEILRDMYQNWPFFQSLLSNVDMVLSKSNMNI 798

                    AaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                    A  y kL   Ee++     + d+++ tk+ +L i G  +lL    YLK
  gi|2702928   799 AFEYAKLCEDEEVQAIYYTILDEWQLTKNVILAIEGYDELLAENSYLKDS 848

                    lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                    l  R +Y   Ln +q   +KR R        r +ls   AdE+      L
  gi|2702928   849 LNYRMPYFNILNYIQLELIKRQR--------RGELS---ADEE-----KL 882

                    vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    ++                 + GiA G+ n G
  gi|2702928   883 IHTT----------------INGIATGLRNSG    898

gi|197104620|ref|YP_002129997.1|: domain 1 of 1, from 4 to 898: score 290.7, E = 3.1e-84
                    *->siDAqLRlLvP..GKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                       s+  qLR+ v   G+v   + +   D + +  F  i      ed++
  gi|1971046     4    SVPDQLRAAVRflGRVL-GDVIRAQDGVAV--FNQI------EDIRQ 41

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    a      +    EG  ++ +L  +  +L sL   D++  A+++   L +
  gi|1971046    42 A-----SVGFHREGTPEAARL--MAERLGSLSLEDTVRFAHSFACFLQIT 84

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE+ ++  RRRi   +    a Ea   t   +   ++ L   +    +
  gi|1971046    85 NIAED-QI-QRRRI---R----AGEARPDT---LAGAVRALAADG-VERK 121

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    Ev + L    +  v+tAHP    R+s+L +++ i   L     +  t  +
  gi|1971046   122 EVEDLLAGALIAPVITAHPSEVRRKSVLDRQSAIARGLEAFD-RARTDAE 170

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    ++  +  L RE+   +Rt  +R  +    DE+   +sY+        P+
  gi|1971046   171 REAAEQELVREVSIFWRTRLLRHVKIAVGDEIENAVSYFERSFLAALPRL 220

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                      R    L   G  E l   +  ++  sW+GGDRDG nP vt  v R
  gi|1971046   221 YARWRHVL---GQDEAL---ASFLRVGSWVGGDRDG-NPFVTAQVMRQAL 263

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                          A  lY++qv  L  Els+    ++L     El+  a +     +
  gi|1971046   264 ARQSRAALRLYLDQVHALGAELSI---SSDLAGVTPELQALADKA----H 306

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
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                      +     EPYR  L  v  +L  t       L tG  e +     t
  gi|1971046   307 DASPHRT---DEPYRRALTGVYARLAAT-----YPLLTG--EAPPRPAST 346

                  kvEeFLEP......LELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                    E + +P++ + +L     sL      + ADG L Dl+R v  FG  L
  gi|1971046   347 PGEPYEDPqtlradLQTVLDSLLRMHGEAFADGPLPDLIRAVDVFGFHLA 396

                  KLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPL
                   LD+Rq s  +  v   + +  ++ ++Y    E  R   Ll+EL+  R L
  gi|1971046   397 TLDMRQNSAVHARVAAELLRTAGVCAdYEALDEAGRCQLLLSELRHGRLL 446

                  lgsDLPktEEvkDvldafrvLAELPi....DsFGaYiismataPsDvLAv
                    +     EE +  l+ +   AE+  + ++Ds  aYi+s +t+ sD L v
  gi|1971046   447 ASPFATYSEETARELEILATAAEIKRrygpDSIRAYIVSNTTSVSDLLEV 496

                  ELLqRECgvkqt.......LrvvPLFEkLADLeAAPAavekLFsiDWYin
                   LL +E g+ +++ +++ ++   PLFE + DL+AAP ++++  ++
  gi|1971046   497 YLLLKEVGLFRPgapptaeILAEPLFETIEDLRAAPKTMARYLALPQIHD 546

                  ridGK..qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                   + G + qevm+GYsDs KD   l   W L k    ++ v    G +L l
  gi|1971046   547 LLAGHglQEVMIGYSDSNKDGSYLTSTWELHKTSRALASVVGGAGLRLQL 596

                  FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                  FHGRGG vGRGGG    A+++qP  t+ G +R+t qGEv+   + + +L
  gi|1971046   597 FHGRGGAVGRGGGSSFEALVAQPRGTVGGRIRITEQGEVVANKYADPELA 646

                  FrsLqRFtAAtLEHGmnPPvsP..kPEWRkLmeemAvvAtEEYRsvvvKE
                   +sL   tA  +   +    s +      k m+ +A  A   YRs+v+
  gi|1971046   647 GQSLETLTAGVVLASLRRHASEdlAAPQTKAMDALARHAMQAYRSLVYET 696

                  PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
                  P Fv+YF  AtP  E   +niGsRP+ R+ s  i+ LRAiPW+F+W q R
  gi|1971046   697 PGFVDYFFAATPIAEIADLNIGSRPTSRQASRSIQGLRAIPWVFSWSQSR 746

                  FHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAK
                    LP W G+G     A+      + +L+E+++ WPFF  tl  +Emv AK
  gi|1971046   747 AMLPGWYGFGS----AVANGGVPMAQLRELFESWPFFATTLANMEMVLAK 792

                  GDPGiAaLyDkLLvaEeLk..PFGksLRdkYvEtkdlLLkiAGHkDlLEG
                  GD  iA+ y  L+    L ++ FG ++R++++ t + LL+i G   lLE
  gi|1971046   793 GDLAIAGRYAGLVEDQALAetVFG-QIRAEWERTTEALLEITGQSALLEH 841

                  DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                   P L   +R R +Yi  Ln +q   ++R R
  gi|1971046   842 NPDLAAVIRSRLPYIDPLNHLQIELIRRRR---------------------- 871

                  skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                  s   +e v+              + Lt+ G+AAG+ ntG
  gi|1971046   872 SGDDQEAVRQG-----------IHLTINGVAAGLRNTG    898

gi|55822687|ref|YP_141128.1|: domain 1 of 1, from 1 to 940: score 290.7, E = 3.2e-84
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                          +      s+++++i  +  +l   L+D    + Ge+
  gi|5582268     1    ------MAFNKLESSNNQEIISEEVGILKELLdDATRGMAGEQGLTT 41

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  +q   El        D    e L   +  +   D +   + ++ +  L n
  gi|5582268     42 IQHLVEL-------YDEGDYEALTQAISEMTNDDMVFASRYFSLLPLLIN 84

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  + E+v+lAy    k        DE+     s   Et+  +v       +
  gi|5582268     85 ISEDVDLAYEVNRKNNI-----DESYLGKLS---ETFD-VVAES----DN 121

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLs.AKD.vtve
                    + L n  v  vltAHPtq  R+ +L     i   L +  + KD++
  gi|5582268    122 ARDILENVNVVPVLTAHPTQVQRKTMLELTNHIHELLRKHRdVKDgLINK 171

                  DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                  DK   D  L R +    +tD iR  +   + E+   m Y+   + k + K
  gi|5582268    172 DKWYAD--LRRYVEIMMKTDIIREKKLKVKNEITNVMEYYNSSLIKAITK 219
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                    FLRRvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRD
                             K + +   +  d P +i    W+GGDRDG nP vt E  +
  gi|5582268   220 ----LSHEFKRLAVEKGIELDNPTpITMGMWIGGDRDG-NPFVTAETLKL 264

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                       L   +  n Yi++v+ L   +s+    + L    E +   a+    +
  gi|5582268   265 SATLQSEVILNYYIEKVDNLYRSFSL---SSRLTEVSETVAEMAKLSPDT 311

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYnt..........RERaRHLLAt
                      Y E       +EPYR     +  KL  t    + ++ + ERa   L
  gi|5582268   312 SVYRE-------NEPYRRAFSYIQSKLIQTllffkagnfsNERAAKRLSE 354

                    Gi.......seisEeAv.................ytkvEeFLEPLELCY
                     ++ ++ ++ e+  + v+++ +++ +  ++++++ y   E F + L
  gi|5582268   355 NVrlgsvstGEVVADFVhdrlsqslqavsqqttefYETAEAFHDDLLAIK 404

                    ksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAit
                     sL e  D v+  G   +lL  v  FG  L  +D+Rq+s  +   +  +
  gi|5582268   405 NSLLENDDSVLISGDFEELLQAVEVFGFYLATIDMRQDSSVHEACVAELL 454

                    tHLei.GsYReWsEeKRqEWLlaELkGK.RPLlgsDLPktEEvkDvldaf
                    +  +i   Y e  E  +   Ll EL+  +R L    + k E ++  l  f
  gi|5582268   455 KSANIvDNYSELTEVEKVAVLLKELQEDpRTLSSTNVSKSETLEKELAIF 504

                    rvLAELPiDsFG.....aYiismataPsDvLAvELLqRECgv....kqtL
                    r  A L  D  G++  +  iis + + sD+    +L +E g+ ++++  +
  gi|5582268   505 RT-ARLLKDYLGeevikQHIISHTESVSDMFELAILLKEVGLvdteRARV 553

                    rvvPLFEkLADLeAAPAavekLFsiDWYinri...dGKqevmvGYsDsGK
                    ++vPLFE + DLe     +++    D  +  i++++  qe+m+GYsDs K
  gi|5582268   554 QIVPLFETIEDLENSNEIMKQYLGYDIVKRWIknsNNYQEIMLGYSDSNK 603

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    D G ls  W LYkAq E+  +  + G+K++ FHGRGGtvGRGGGP   Ai
  gi|5582268   604 DGGYLSSGWTLYKAQNELTNIGEERGIKITFFHGRGGTVGRGGGPSYDAI 653

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP
                     sqP  ti+  +R t qGEvi   +G  +  +  L     AtL+  +
  gi|5582268   654 TSQPFGTIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLVSATLDRMVTRQ 703

                    vsPkPE...WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGk
                    +    E  ++R++m+ +       YR +v+    F +YF  A P  E
  gi|5582268   704 ITDPDElvdFREIMDSIVQDSNRIYRDLVFGNEHFYDYFFEASPIKEVSS 753

                    mniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid
                    +niGsRPa Rk    i  LRAiPW+F+W q R  LP W GvG AF h i+
  gi|5582268   754 LNIGSRPAARKTITDISGLRAIPWVFSWSQNRIMLPGWYGVGSAFNHYIE 803

                    KDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL
                     +  nl kL+ m+++WPFFR  l  ++mv  K D  iA  y +L  +Ee+
  gi|5582268   804 AEEGNLEKLQHMFETWPFFRSLLSNVDMVLSKSDMNIAFHYAQLAESEEV 853

                    kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnv
                    +   + + d+++ tk+ +L i  H D LE  P LK  l  R +Y   Ln
  gi|5582268   854 RSVFNIILDEWQLTKNVILAIEKHDDFLEESPSLKASLGFRLPYFNVLNY 903

                    fqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGL
                    +q   +KR+R  +              dE       L+++
  gi|5582268   904 IQIELIKRLRNNNLT-----------DDEI-----SLIHIT--------- 928

                    EDtLiLtmKGiAAGmqntG<-*
                           + GiA G+ n G
  gi|5582268   929 -------INGIATGLRNSG    940

gi|116513617|ref|YP_812523.1|: domain 1 of 1, from 50 to 967: score 290.4, E = 4e-84
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           + +l+v  K  e++        ++   + iL DL  e+ +  v
  gi|1165136    50    YFKRKRKLIVTAKKLENNS----NHAVIAEEVKILTDLLDESTRHLV 92

                    .qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
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                + E +           ++    L +++  L   + i+vA+ +  +  L n
gi|1165136    93 gDEEFAKIKGLVKIAASSDHSQLESQIACLSNQEMIIVARYFATLPLLIN 142

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                + E+v+lA    + ++            t+ D    l   v +     +
gi|1165136   143 ITEDVDLA--TEVNLLN----------NTDKDYLGKLESTVDLV-AEKDN 179

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  e L    v  vltAHPtq  R+ +L    +i   L            +
gi|1165136   180 AAEILSHVNVVPVLTAHPTQVQRKTILELTNKIHDQLRRHRDVKASTINR 229

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                kE    L R i     tD iR  +     E++  m Y+   +   + K
gi|1165136   230 KEWINQLRRYIEIIMQTDIIREKKLKVSNEIKNVMVYYPGSLIPAITKLT 279

                RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                 R     +  G+n  +    P i    W+GGDRDG nP vt E  R
gi|1165136   280 ARYKELAREKGLN--VDGATP-ITMGMWIGGDRDG-NPYVTAETLRLSAT 325

                LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                +   +    Y+  + DL   +s         v    ++ t+    + K
gi|1165136   326 IQSEVIFEYYVKALNDLYRTVS---------VSTSYVQPTPEVAELAKLS 366

                iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA....
                 +       +EPYR        +L  t      +  +      E A + +
gi|1165136   367 ADN-SPFRENEPYRRAFYYLESRLVHTEMELLDVFSKEAVVKKEAAlkap 415

                vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                vy +  eF   LE   +sL +  D+++  G    lL  +  FG  L  +D
gi|1165136   416 VYKDAYEFKKDLEAIKRSLIQNHDRAVTGGHFDALLEAIDVFGFHLATID 465

                iRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK.RPLlg
                +Rq+s  +   +  + + +   i + Y +  Ee +   Ll+EL   +R L
gi|1165136   466 MRQDSSVNEACVAELLKSARICdNYSDLDEEEKIQILLSELNNDpRSLHS 515

                sDLPktEEvkDvldafrvLAELPiDsFG.....aYiismataPsDvLAvE
                s  Pk E ++  l  ++  A L  D+ G++  +  iis + + sD+L
gi|1165136   516 SNSPKSELLQRELKIYHT-ARLLKDTLGenvikQHIISHTESISDMLEQA 564

                LLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                ++ +E g+ +++k  ++vvPLFE + DL+     +++  s D  +  +
gi|1165136   565 IMLKEYGLldseKARVQVVPLFETVEDLQNSREIMKRYLSFDIVKRWVAS 614

                K...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                K++ qe+m+GYsDs KD G l+  W LYkAq E+  +  + G+K++  HG
gi|1165136   615 KgnyQEIMLGYSDSNKDGGYLASCWNLYKAQTELTAIGEEQGIKITFMHG 664

                RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                RGGtvGRGGGP   Ai sqP   i+  +R t qGE+i   +G  +  +
gi|1165136   665 RGGTVGRGGGPSYEAITSQPFGSIKDRIRTTEQGEIIQNKYGNKDAAYYN 714

                LqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEE...YRsvvvKEPR
                L     A ++  +      +    +    m  +  + ++ YR +v+  P
gi|1165136   715 LEMLVSAAVDRIVSKQKVSQDHIQDFTASMDGIVEDSnrvYRELVFDNPH 764

                FvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFH
                F +YF  AtP  E   +niGsRPa Rk    +  LRAiPW+F+W q R
gi|1165136   765 FHDYFFQATPIKEVSSLNIGSRPAARKKITELSGLRAIPWVFSWSQSRVM 814

                LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                 P W GvG AFKh id D  nl+ L+EmY+ WPFF   l  ++mv  K
gi|1165136   815 FPGWYGVGSAFKHFIDADPNNLKELQEMYQGWPFFHSLLSNVDMVLSKSN 864

                PGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                  iA  y +L   E  +   + ++ +++ tk+ +L+i GH  lLE  P L
gi|1165136   865 MEIAEKYADLCEDEATRSVFDIIKKEWELTKEVILQIEGHSKLLEDNPSL 914

                KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                   l  R +Y   Ln +q   +KR R        + +ls  y  E
gi|1165136   915 ERSLDYRLPYFNVLNYVQLEMIKRGR--------QEKLSGIY--ES---- 950
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                  deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    ++++                 + G+A G+ n G
  gi|1165136   951 --IIHIT----------------INGVASGLRNSG    967

gi|194690202|gb|ACF79185.1|: domain 1 of 1, from 1 to 383: score 289.5, E = 7.4e-84
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1946902     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1946902     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1946902     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1946902     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1946902     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1946902     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                                                           d
  gi|1946902     1 ----------------------------------------MD------- 2

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1946902     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1946902     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1946902     - ---------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1946902     - ---------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                              ri GKq+vmvGYsDsGKDAG
  gi|1946902     3 ------------------------------RIKGKQQVMVGYSDSGKDAG 22

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLY+AqEE+++vAK+yGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1946902    23 RLSAAWQLYRAQEEMAQVAKRYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 72

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGs+RvtvqGEviEf FGEE+LCF++LqRFtAAtLEHGm+PPvsP
  gi|1946902    73 PPDTINGSIRVTVQGEVIEFCFGEEHLCFQTLQRFTAATLEHGMHPPVSP 122

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWRkLm+emAvvAtEEYRsvvvKE RFvEYFR+AtPE+EYG+mniGsR
  gi|1946902   123 KPEWRKLMDEMAVVATEEYRSVVVKEARFVEYFRSATPETEYGRMNIGSR 172

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+AidKD++n+
  gi|1946902   173 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKFAIDKDVRNF 222

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q LkEmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLvaEeLkPFGk+
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  gi|1946902   223 QVLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVAEELKPFGKQ 272

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LRdkYvEt++lLL+iAGHkD+LEGDP+LKq+l LR++YittLnvfqAYtL
  gi|1946902   273 LRDKYVETQQLLLQIAGHKDILEGDPFLKQGLVLRNPYITTLNVFQAYTL 322

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP++kvt++P+lsKE+AdEn  k+++LvkLnp+++++PGLEDtLiL
  gi|1946902   323 KRIRDPNFKVTPQPPLSKEFADEN--KPAGLVKLNPASEYPPGLEDTLIL 370

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|1946902   371 TMKGIAAGMQNTG    383

gi|83814357|ref|YP_444246.1|: domain 1 of 1, from 6 to 957: score 289.4, E = 7.8e-84
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        D  L     G +s   k +     L+   L+ i  +  Ge L E
  gi|8381435     6    --DLDLETEGTG-IS---KPLSRQVNLVGSMLgHIAEEQSGEALFEH 46

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     l    E    ++K eE   ++ +Ld      + + +     L n
  gi|8381435    47 VEGLRALCKAAEQEDAPEKREEAAERIAALDQDTLERLLHVYTTFFHLVN 96

                   LAEEvelAyRRRikkkk...........hGDFaDEasAttEsDiEEtlKk
                    AE  e+    R + +++++++ + +++ G  aD a+    s i+  +
  gi|8381435    97 QAEQQEIIRINRERARQsgpsewplgpgDGPGADGAEPRPQS-IDAAVAD 145

                   LvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq
                   L   +  + +Ev    +   +   ltAHPt + RRs+L K+  i   L+
  gi|8381435   146 LKAEG-YTADEVVAFFRQLDIQPTLTAHPTEARRRSVLRKEQHIADLLST 194

                   LsAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiH
                   L   D t++++ E  + L   +     tDE+R  +Pt  +E+  G  ++H
  gi|8381435   195 LRRPDATPDERAETLDRLYSQVAFLLGTDEVRAERPTVREEVEQGHYFLH 244

                   EtvWkGvPKFLRRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknP
                     +W+ +P   R v  AL++       lP     +++ sW+G DRDG nP
  gi|8381435   245 GSIWDTIPAIHRDVQQALrRHYDATAELP---AFLQYRSWIGSDRDG-NP 290

                   RvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsm....WRCndELRvRA
                    vt +vtR      R      Y++ +++L  +ls+++++    d L +
  gi|8381435   291 NVTADVTRWTVARQRRTTLEHYLDEIDELRDDLSIstrqLTVSDALEASL 340

                   E.ElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRH
                   E +    a  d v + Y          EPYR        KL    ER R
  gi|8381435   341 EaDAEEIALPDDVRRQY--------QREPYRL-------KLCYIEERLRG 375

                   LLAt.GiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlL
                   LL      +++  A     ++ L  L+L   sL   G    A    L  L
  gi|8381435   376 LLDRiDATDVAAMAGAYAADDLLADLDLIAESLQGHGFEDAAQSGQLHRL 425

                   R.qvstFGLsLvKLDiRqEseRqtDvlDAittHLe.iGsYReWsEeKRqE
                   R+ v tFG  L  LD+Rq s  + D + A+    + +  Y   sEe + E
  gi|8381435   426 RsLVKTFGFHLAALDVRQHSRVHEDTVAALLDAGDvVDDYGALSEEEKLE 475

                   WLlaELkGKRPLlg..sDLPk.tEEvkDvldafrvLAELPiDsFGaYiis
                    L  EL+  RPL+ +++DLP +  E+ +v + +r +  +  D  G+Y++s
  gi|8381435   476 VLSRELQNPRPLVSrhADLPAdAAELMEVFGVLRAMHAVDPDIVGSYVVS 525

                   mataPsDvLAvELLqRECgv.........kqtLrvvPLFEkLADLeAAPAa
                   m+ + sD L   LL +E g++   +++ + +L vvPLFE + DL+AA
  gi|8381435   526 MTHTVSDLLEPMLLAKEAGLgavvdgsyRCPLDVVPLFETIEDLDAADDR 575

                   vekLFsiDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEi
                   +e LF    Y  +++G+++ qe+m+GYsDs KD G   A W L kA   +
  gi|8381435   576 METLFTHPVYAAQLEGRdgfQEIMLGYSDSNKDGGYWMANWALHKAIHAL 625

                   iKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqG
                     v  ++ v L lFHGRGGtvGRGGG t  Ai + PP   nG +R+t qG
  gi|8381435   626 GVVCDEHDVDLRLFHGRGGTVGRGGGHTSQAIRALPPVVHNGRIRMTEQG 675
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                    EviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE.............
                    E+i f +   ++  r +     AtL         P PE++   ++ + ++
  gi|8381435   676 EIISFRYALPDIARRHVEQIVNATLTATARAQNTPAPEnplladkvsmes 725

                    .WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPa
                    +   Lm+++A      YR  +  +P    ++  AtP     ++ i sRP
  gi|8381435   726 dVVALMDRLAEEGMSAYREFI-DDPEGWQWYTAATPIEHISRLPIASRPV 774

                    KRkPsG...GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                     R   G++   e LRAiPW+FaWtqtR+  P W G G      ++ +
  gi|8381435   775 SRASEGeqvEFENLRAIPWVFAWTQTRYIAPGWYGTGQGLATLLENEPDA 824

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                       L+++Y++WPFFR  lD      A+    iA  yD L  aE    F
  gi|8381435   825 RDTLRDLYENWPFFRTVLDSAQREMARARLPIAERYDAL--AEVETSFHA 872

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                     + d+Y+  +  +L+i     l +G P LK+ + LR++Y   Ln +q
  gi|8381435   873 PIVDDYERAESAILEITDQAALFDGNPVLKKSIELRNPYTDVLNLIQIEL 922

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    LKR R            s + A+ +                 L + +
  gi|8381435   923 LKRYRA-----------STDDAEQE-----------------ALREAIF 943

                    LtmKGiAAGmqntG<-*
                    L + G+AA mq tG
  gi|8381435   944 LSINGVAAAMQSTG    957

gi|161572971|ref|YP_209040.2|: domain 1 of 1, from 1 to 900: score 289.3, E = 8.5e-84
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|1615729     1    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 38

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|1615729    39 ETVKLLSTS----DDSAALIE--KVLPQLDERQTYDLTLACGLFAQILNI 82

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+   RR i+    G  a E+s t      Et+++L        + v
  gi|1615729    83 AEDVHHERRRQIHEDA-GHNAAEGSLT------ETVRRLKAGK-ADGKSV 124

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                       L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|1615729   125 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 174

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|1615729   175 LRREIDTVLLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 220

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R+++   +      R+P    ++k   W+GGDRDG nP v  E  R
  gi|1615729   221 LYRKMEHDFQTAYPDVRVP---NILKIGGWIGGDRDG-NPFVSGETLRFA 266

                    CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                              +Y s ++ L  E +ls+ R      v A    +
  gi|1615729   267 FRRHADAVFRFYRSELDKLYRElpLSIRRVKVNDDVMALAALSPDEEI-- 314

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                                +EPYR  +  +   +     +aR L+L  G      e
  gi|1615729   315 ----------ARTEEPYRRAIAYI---MARAMGKARSLgLGMGCKFGFLE 351

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y    +FL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
  gi|1615729   352 P-YASAQKFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 400

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL  +RPL+ +
  gi|1615729   401 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELGHQRPLYSP 450

                    DLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                     +   +++++E++   +a ++  E   D+    iis +  P D LA  LL
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  gi|1615729   451 FITYSDhtrrELAIFNEARKIKDEFGEDAVTQSIISNCEQPGDLLALALL 500

                   qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                    +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   +
  gi|1615729   501 LKESGLlavengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDALL 550

                   dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                   + +++ qe+m+GYsDs KD G +   W L +A   ++   Kky v++ lF
  gi|1615729   551 ESRgniQEIMLGYSDSNKDGGYVTSSWCLHQAELGLVELFKKYDVRMRLF 600

                   HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                   HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|1615729   601 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 650

                   rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                   r L    AAtLE  + P    k    kLm+ +  v    YR ++   P F
  gi|1615729   651 RNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDF 697

                   vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                   ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
  gi|1615729   698 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 747

                   PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                   P W G+G A     +     l  L+   ++ PFF   l  +E v AK D
  gi|1615729   748 PAWYGFGSAVETLCEGSPETLAALRGHAQNNPFFQAMLSNMEQVMAKTDI 797

                   GiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                    +A  y  L  ++E  k     ++++Y   ++ LL +    +lL     L
  gi|1615729   798 TLAENYAGLSESpEKAKVIFGMIKEEYRRSRKALLDLLQTEELLRDNRSL 847

                   KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                      l LR +Y+  Ln +q   LKR+R                  E+   +
  gi|1615729   848 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 879

                   deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     L+ +               Lt+ G+A G+ ntG
  gi|1615729   880 HALLMVH--------------LTINGVAQGLRNTG    900

gi|268602565|ref|ZP_06136732.1|: domain 1 of 1, from 18 to 917: score 289.3, E = 8.5e-84
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2686025    18    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 55

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2686025    56 ETVKLLSTS----DDSAALIE--KVLPQLDERQTYDLTLACGLFAQILNI 99

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AE+v+   RR i+    G  a E+s t      Et+++L        + v
  gi|2686025   100 AEDVHHERRRQIHEDA-GHNAAEGSLT------ETVRRLKAGK-ADGKSV 141

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                      L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|2686025   142 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 191

                   DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|2686025   192 LRREIDTVLLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 237

                   FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     R+++   +      R+P    ++k   W+GGDRDG nP v  E  R
  gi|2686025   238 LYRKMEHDFQTAYPDVRVP---NILKIGGWIGGDRDG-NPFVSGETLRFA 283

                   CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                            +Y s ++ L  E +ls+ R      v A    +
  gi|2686025   284 FRRHADAVFRFYRSELDKLYRElpLSIRRVKVNDDVMALAALSPDEEI-- 331

                   vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                                +EPYR  +  +   +     +aR L+L  G      e
  gi|2686025   332 ----------ARTEEPYRRAIAYI---MARAMGKARSLgLGMGCKFGFLE 368
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                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y    +FL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
  gi|2686025   369 P-YASAQKFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 417

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL  +RPL+ +
  gi|2686025   418 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELGHQRPLYSP 467

                    DLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                     +   +++++E++   +a ++  E   D+    iis +  P D LA  LL
  gi|2686025   468 FITYSDhtrrELAIFNEARKIKDEFGEDAVTQSIISNCEQPGDLLALALL 517

                    qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                     +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   +
  gi|2686025   518 LKESGLlavengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDALL 567

                    dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                    + +++ qe+m+GYsDs KD G +   W L +A   ++   Kky v++ lF
  gi|2686025   568 ESRgniQEIMLGYSDSNKDGGYVTSSWCLHQAELGLVELFKKYDVRMRLF 617

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|2686025   618 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 667

                    rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                    r L    AAtLE  + P    k    kLm+ +  v    YR ++   P F
  gi|2686025   668 RNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDF 714

                    vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                    ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
  gi|2686025   715 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 764

                    PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                    P W G+G A     +     l  L+   ++ PFF   l  +E v AK D
  gi|2686025   765 PAWYGFGSAVETLCEGSPETLAALRGHAQNNPFFQAMLSNMEQVMAKTDI 814

                    GiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     +A  y  L  ++E  k     ++++Y   ++ LL +    +lL     L
  gi|2686025   815 TLAENYAGLSESpEKAKVIFGMIKEEYRRSRKALLDLLQTEELLRDNRSL 864

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                       l LR +Y+  Ln +q   LKR+R                  E+   +
  gi|2686025   865 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 896

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      L+ +               Lt+ G+A G+ ntG
  gi|2686025   897 HALLMVH--------------LTINGVAQGLRNTG    917

gi|194099706|ref|YP_002002841.1|: domain 1 of 1, from 24 to 923: score 289.3, E = 8.5e-84
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|1940997    24    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 61

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|1940997    62 ETVKLLSTS----DDSAALIE--KVLPQLDERQTYDLTLACGLFAQILNI 105

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+   RR i+    G  a E+s t      Et+++L        + v
  gi|1940997   106 AEDVHHERRRQIHEDA-GHNAAEGSLT------ETVRRLKAGK-ADGKSV 147

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                       L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|1940997   148 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 197

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|1940997   198 LRREIDTVLLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 243

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R+++   +      R+P    ++k   W+GGDRDG nP v  E  R
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  gi|1940997   244 LYRKMEHDFQTAYPDVRVP---NILKIGGWIGGDRDG-NPFVSGETLRFA 289

                    CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                              +Y s ++ L  E +ls+ R      v A    +
  gi|1940997   290 FRRHADAVFRFYRSELDKLYRElpLSIRRVKVNDDVMALAALSPDEEI-- 337

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                                +EPYR  +  +   +     +aR L+L  G      e
  gi|1940997   338 ----------ARTEEPYRRAIAYI---MARAMGKARSLgLGMGCKFGFLE 374

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y    +FL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
  gi|1940997   375 P-YASAQKFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 423

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL  +RPL+ +
  gi|1940997   424 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELGHQRPLYSP 473

                    DLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                     +   +++++E++   +a ++  E   D+    iis +  P D LA  LL
  gi|1940997   474 FITYSDhtrrELAIFNEARKIKDEFGEDAVTQSIISNCEQPGDLLALALL 523

                    qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                     +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   +
  gi|1940997   524 LKESGLlavengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDALL 573

                    dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                    + +++ qe+m+GYsDs KD G +   W L +A   ++   Kky v++ lF
  gi|1940997   574 ESRgniQEIMLGYSDSNKDGGYVTSSWCLHQAELGLVELFKKYDVRMRLF 623

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|1940997   624 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 673

                    rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                    r L    AAtLE  + P    k    kLm+ +  v    YR ++   P F
  gi|1940997   674 RNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDF 720

                    vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                    ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
  gi|1940997   721 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 770

                    PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                    P W G+G A     +     l  L+   ++ PFF   l  +E v AK D
  gi|1940997   771 PAWYGFGSAVETLCEGSPETLAALRGHAQNNPFFQAMLSNMEQVMAKTDI 820

                    GiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     +A  y  L  ++E  k     ++++Y   ++ LL +    +lL     L
  gi|1940997   821 TLAENYAGLSESpEKAKVIFGMIKEEYRRSRKALLDLLQTEELLRDNRSL 870

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                       l LR +Y+  Ln +q   LKR+R                 E+   +
  gi|1940997   871 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 902

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      L+ +               Lt+ G+A G+ ntG
  gi|1940997   903 HALLMVH--------------LTINGVAQGLRNTG    923

gi|293397945|ref|ZP_06642151.1|: domain 1 of 1, from 21 to 920: score 289.3, E = 8.5e-84
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2933979    21    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 58

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2933979    59 ETVKLLSTS----DDSAALIE--KVLPQLDERQTYDLTLACGLFAQILNI 102

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+   RR i+    G  a E+s t      Et+++L        + v
  gi|2933979   103 AEDVHHERRRQIHEDA-GHNAAEGSLT------ETVRRLKAGK-ADGKSV 144
```

```
                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                       L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|2933979   145 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 194

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|2933979   195 LRREIDTVLLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 240

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R+++   +      R+P    ++k   W+GGDRDG nP v  E  R
  gi|2933979   241 LYRKMEHDFQTAYPDVRVP---NILKIGGWIGGDRDG-NPFVSGETLRFA 286

                    CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                              +Y s ++ L  E +ls+ R      v A    +
  gi|2933979   287 FRRHADAVFRFYRSELDKLYRElpLSIRRVKVNDDVMALAALSPDEEI-- 334

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                                 +EPYR  +  +   +     +aR L+L  G      e
  gi|2933979   335 ----------ARTEEPYRRAIAYI---MARAMGKARSLgLGMGCKFGFLE 371

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y    +FL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
  gi|2933979   372 P-YASAQKFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 420

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL  +RPL+ +
  gi|2933979   421 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELGHQRPLYSP 470

                    DLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                     +   +++++E++   +a ++  E   D+    iis +  P D LA  LL
  gi|2933979   471 FITYSDhtrrELAIFNEARKIKDEFGEDAVTQSIISNCEQPGDLLALALL 520

                    qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                     +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   +
  gi|2933979   521 LKESGLlavengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDALL 570

                    dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                    + +++ qe+m+GYsDs KD G +   W L +A   ++   Kky v++ lF
  gi|2933979   571 ESRgniQEIMLGYSDSNKDGGYVTSSWCLHQAELGLVELFKKYDVRMRLF 620

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|2933979   621 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 670

                    rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                    r L    AAtLE  + P    k    kLm+ +  v    YR ++   P F
  gi|2933979   671 RNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDF 717

                    vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                    ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
  gi|2933979   718 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 767

                    PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                    P W G+G A     +     l  L+   ++ PFF   l  +E v AK D
  gi|2933979   768 PAWYGFGSAVETLCEGSPETLAALRGHAQNNPFFQAMLSNMEQVMAKTDI 817

                    GiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     +A  y  L  ++E  k     ++++Y   ++ LL +    +lL     L
  gi|2933979   818 TLAENYAGLSESpEKAKVIFGMIKEEYRRSRKALLDLLQTEELLRDNRSL 867

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                       l LR +Y+  Ln +q   LKR+R                  E+   +
  gi|2933979   868 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 899

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      L+ +               Lt+ G+A G+ ntG
  gi|2933979   900 HALLMVH--------------LTINGVAQGLRNTG    920

gi|254492745|ref|ZP_05105916.1|: domain 1 of 1, from 18 to 917: score 289.1, E = 9.5e-84
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
```

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gi|2544927    18    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 55

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
gi|2544927    56 ETVKLLSTS----DDSAALIE--KVLPQLDERQTYDLTLACGLFAQILNI 99

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+   RR i+    G  a E+s t      Et+++L        + v
gi|2544927   100 AEDVHHERRRQIHEDA-GHNAAEGSLT------ETVRRLKAGK-ADGKSV 141

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                       L n sv  vltAHPt   R  +L  n RiR  L q+++    D
gi|2544927   142 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 191

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
gi|2544927   192 LRREIDTVLLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 237

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R+++   +      R+P    ++k   W+GGDRDG nP v  E  R
gi|2544927   238 LYRKMEHDFQTAYPDVRVP---NILKIGGWIGGDRDG-NPFVSGETLRFA 283

                    CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                              +Y s ++ L  E +ls+ R      v A    +
gi|2544927   284 FRRHADAVFRFYRSELDKLYRElpLSIRRVKVNDDVMALAALSPDEEI-- 331

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                                +EPYR  +  +   +     +aR L+L  G      e
gi|2544927   332 ----------ARTEEPYRRAIAYI---MARAMGKARSLgLGMGCKFGFLE 368

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y    +FL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
gi|2544927   369 P-YASAQKFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 417

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL  +RPL+ +
gi|2544927   418 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELGHQRPLYSP 467

                    DLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                     +   +++ +E++   +a ++  E   D+    iis +  P D LA  LL
gi|2544927   468 FITYSDhtcrELAIFNEARKIKDEFGEDAVTQSIISNCEQPGDLLALALL 517

                    qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                     +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   +
gi|2544927   518 LKESGLlavengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDALL 567

                    dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                    + +++ qe+m+GYsDs KD G +   W L +A   ++   Kky v++ lF
gi|2544927   568 ESRgniQEIMLGYSDSNKDGGYVTSSWCLHQAELGLVELFKKYDVRMRLF 617

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
gi|2544927   618 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 667

                    rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                    r L    AAtLE  + P    k    kLm+ +  v    YR ++   P F
gi|2544927   668 RNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDF 714

                    vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                    ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
gi|2544927   715 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 764

                    PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                    P W G+G A     +     l  L+   ++ PFF   l  +E v AK D
gi|2544927   765 PAWYGFGSAVETLCEGSPETLAALRGHAQNNPFFQAMLSNMEQVMAKTDI 814

                    GiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     +A  y  L  ++E  k     ++++Y   ++ LL +    +lL     L
gi|2544927   815 TLAENYAGLSESpEKAKVIFGMIKEEYRRSRKALLDLLQTEELLRDNRSL 864

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
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                     l LR +Y+  Ln +q   LKR+R                  E+   +
  gi|2544927   865 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 896

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      L+ +               Lt+ G+A G+ ntG
  gi|2544927   897 HALLMVH--------------LTINGVAQGLRNTG    917

gi|239999896|ref|ZP_04719820.1|: domain 1 of 1, from 1 to 900: score 289.1, E = 9.5e-84
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2399998     1    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 38

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2399998    39 ETVKLLSTS----DDSAALIE--KVLPQLDERQTYDLTLACGLFAQILNI 82

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+   RR i+    G  a E+s t      Et+++L        + v
  gi|2399998    83 AEDVHHERRRQIHEDA-GHNAAEGSLT------ETVRRLKAGK-ADGKSV 124

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                       L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|2399998   125 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 174

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|2399998   175 LRREIDTVLLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 220

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R+++   +      R+P    ++k   W+GGDRDG nP v  E  R
  gi|2399998   221 LYRKMEHDFQTAYPDVRVP---NILKIGGWIGGDRDG-NPFVSGETLRFA 266

                    CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                              +Y s ++ L  E +ls+ R      v A    +
  gi|2399998   267 FRRHADAVFRFYRSELDKLYRElpLSIRRVKVNDDVMALAALSPDEEI-- 314

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                                +EPYR  +  +   +     +aR L+L  G      e
  gi|2399998   315 ----------ARTEEPYRRAIAYI---MARAMGKARSLgLGMGCKFGFLE 351

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y    +FL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
  gi|2399998   352 P-YASAQKFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 400

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL  +RPL+ +
  gi|2399998   401 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELGHQRPLYSP 450

                    DLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                     +   +++ +E++   +a ++  E   D+    iis +  P D LA  LL
  gi|2399998   451 FITYSDhtcrELAIFNEARKIKDEFGEDAVTQSIISNCEQPGDLLALALL 500

                    qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                     +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   +
  gi|2399998   501 LKESGLlavengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDALL 550

                    dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                    + +++ qe+m+GYsDs KD G +   W L +A   ++   Kky v++ lF
  gi|2399998   551 ESRgniQEIMLGYSDSNKDGGYVTSSWCLHQAELGLVELFKKYDVRMRLF 600

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|2399998   601 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 650

                    rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                    r L    AAtLE  + P    k    kLm+ +  v    YR ++   P F
  gi|2399998   651 RNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDF 697

                    vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                    ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
  gi|2399998   698 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 747
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                    PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                    P W G+G A     +     l  L+   ++ PFF   l  +E v AK D
  gi|2399998   748 PAWYGFGSAVETLCEGSPETLAALRGHAQNNPFFQAMLSNMEQVMAKTDI 797

                    GiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     +A  y  L  ++E  k     ++++Y   ++ LL +    +lL     L
  gi|2399998   798 TLAENYAGLSESpEKAKVIFGMIKEEYRRSRKALLDLLQTEELLRDNRSL 847

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                       l LR +Y+  Ln +q   LKR+R                  E+   +
  gi|2399998   848 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 879

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      L+ +               Lt+ G+A G+ ntG
  gi|2399998   880 HALLMVH--------------LTINGVAQGLRNTG    900

gi|94265456|ref|ZP_01289207.1|: domain 1 of 1, from 12 to 947: score 288.8, E = 1.2e-83
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                              + +PG        +     L+ + L+ ++qDL G+++ E
  gi|9426545    12    CAGDEPGAQAPGPLP-----LAGQIKLVGRILgKVIQDLRGPQVYEQ 53

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v E   l       k +   + +  ++  Ld  + + v +a+     L n
  gi|9426545    54 VEELRLLCKRAAVEKRPDLRQRVQQRIADLDCREIVEVLQAYTVFFHLVN 103

                    LAEEvel..AyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                      E +e+++A RR +           +       i+E +  L  ++
  gi|9426545   104 KVEQMEIsrADRRHNPGPV-------GHVPRRESIDEAVADLKAQG-AGI 145

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    + v   L    +   ltAHPt + RRs+L K+ Ri   L  Ls +D   +
  gi|9426545   146 DRVLGLLGKLDIQPTLTAHPTEARRRSILYKQKRIAALLEELSRRDNGLD 195

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    +++ L   L  Ei     tD+iR  +Pt  DE+  G+ ++   +W+ vP+
  gi|9426545   196 EQEALLAELEGEIGLLLATDDIRLVRPTVEDEVESGLYFVRNAIWQTVPQ 245

                    FLRRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRD
                           AL+        P   P  ++F sW+G DRDG nP vt  v R
  gi|9426545   246 IYQDLRAALQR--HYGECPAALPaFLRFRSWIGSDRDG-NPYVTAAVSRH 292

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                      L  R +A  lY++ +  L  Els+    +        +   aa
  gi|9426545   293 TWLYQRRVALRLYLEELRQLRRELSLSGRQQPPAGLLKSIEEDAAEL--- 339

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                        E  +     EPYR  +     +L              G  +    A
  gi|9426545   340 -TLSENRRRRYRYEPYRLKISYLMARLKQLEADIDAGRFPGGGDPYGAA- 387

                    ytkvEeFLEPLELCYksLCeCG.DkviADGsLLDlLRqvstFGLsLvKLD
                         e L  L L   sL   G  + +  G L  +L qv  FGL Lv LD
  gi|9426545   388 -----ELLADLQLLADSLQAQGfSRLVSHGRLGRMLLQVRSFGLHLVALD 432

                    iRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgs
                     Rq s  + + +  + +  ++ + Y   +Ee+R   L  EL   RPLl+
  gi|9426545   433 FRQHSRVHEEGVALLLRLAGVCdDYAALAEEQRLALLEGELANPRPLLPR 482

                    DLPktEEvkDvldafrvLAELPiD...sFGaYiismataPsDvLAvELLq
                          Ev + l +fr +AE+   ++ + GaYiism+ aPsD L v LL
  gi|9426545   483 NRELPPEVDELLASFRLIAEIQQHdpaALGAYIISMTHAPSDLLEVLLLA 532

                    RECg........vkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                    +E g  ++++++v  +L  vPL E + DL+ A A + ++     Y+ ++
  gi|9426545   533 KETGlwerrdgrVVSALDLVPLLETIEDLDQAGALLRQILENPVYRAQLT 582

                    GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                     +++ qevm+GYsDs KD G   A W L +AqEE+  v ++yG+ L lFH
  gi|9426545   583 ARshfQEVMLGYSDSNKDGGYWMANWALHRAQEELGEVSREYGIELRLFH 632

                    GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
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                    GRGGtvGRGGG    AiL+ P    nG +R t qGEvi f +   ++  r
  gi|9426545   633 GRGGTVGRGGGRANQAILALPEQVHNGRIRFTEQGEVITFRYAFSDIARR 682

                    sLq.......RFtAAtLEHGmn.......PPvsPkP.EWRkLmeemAvvA
                     L +  +   R tAA    G+ + +  ++P  +P  +E  + + ++A
  gi|9426545   683 HLEqivnamlRTTAAAESAGLAgadaaggPAAAPAVsEENRFLARIAAAG 732

                    tEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLR
                     E YR +v  +P F  ++   tP     ++ i sRP  R  +   +e LR
  gi|9426545   733 MEAYRELV-HDPDFWAWYTRITPIEQISRLPIASRPVSRSAGEvDLEGLR 781

                    AiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFR
                    AiPW+FaWtqtR+ +P W G GAA   A+  +    q L+E+Y+  PFF
  gi|9426545   782 AIPWVFAWTQTRYIVPGWFGTGAALN-AVLAEPGGRQYLRELYRRDPFFQ 830

                    vtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLk
                    + +D      A+  P iAa yD L  aE    F +++ ++ +   + L +
  gi|9426545   831 MVVDNARREMARVRPEIAAEYDAL--AEVPARFHQRITADLEMALQALPE 878

                    iAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrP
                      G  +lL   P ++  +RLR++Y   +n +q   L+R  D
  gi|9426545   879 FTGESELLARNPAVQRSIRLRNPYTDVINLLQVELLRRYHD--------- 919

                    hlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<
                                          + +    L D L L + GiAA mq tG
  gi|9426545   920 ----------------------SGGEEREALRDALFLSVNGIAAAMQSTG  947

                    -*

  gi|9426545     -    -

gi|225021380|ref|ZP_03710572.1|: domain 1 of 1, from 1 to 922: score 288.3, E = 1.7e-83
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +  qL+           k i+    Ll k   ++ +  G+++   v
  gi|2250213     1    -MKNQLK-----------KDIRHLGKLLGK---VIAEQEGDEVYRQV 32

                    qECYElsAeYE.GKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                         ls +  +G  D + L +L    t     D + +A+a+ H   LAn
  gi|2250213    33 EAARALSFDIArGTSDISALVDLFRNNTT---RDFLPIARAFNHFALLAN 79

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkL.vlklnKsPe
                    L E+    +   +         + +    +s +E t  kL+  k + sP+
  gi|2250213    80 LVEDL---HDNANYIAD----REAGLPAPDSTLEATAAKLsAAKAEISPD 122

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq....LsA..K
                     + + LKn  v  vltAHPt   RR +   +  i   L  +++ L A++
  gi|2250213   123 NITQLLKNAQVAPVLTAHPTETRRRTVFDAQEHITALLVDrhriLNApeN 172

                    DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvW
                     +t      +D  + R +   + t  iR a+P   DE+  G+ Y+   +
  gi|2250213   173 ALTKTRLDNIDQQITRWLTTLWQTALIRVARPRIEDEIEVGLRYYKLSLL 222

                    kGvPKFLRRvDtALKn.iGinERlPYdvPLikFssWmGGDRDGknPRvtP
                    k +P     v   L  + G n     +  +i+  sW+GGD DG nP vt
  gi|2250213   223 KAIPDINQTVSQVLADtFGTNT----QTAIIQPGSWIGGDHDG-NPYVTA 267

                    EvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaa
                             a       Y + +  L  Els+    d L    +El   a
  gi|2250213   268 STLEYATSRAAETVLKYYEQELHQLEHELSL---SDRLAHVTDELRELAE 314

                    rdkvvKyYiEFWKqvPP..tEPYRviLGdvRDKLYntRERaRHLLAtGis
                    +             +P +  EPYR  +  +R ++   t        A
  gi|2250213   315 QG---------HNNIPArvDEPYRRAVHGIRGRIIATLAALIGDDAVEGT 355

                    eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                         A y    + L  L +   sL    D++iAD  L  +     tFG
  gi|2250213   356 WYTNHAPYQTPNQVLADLAIIDESLRANHDHIIADDRLRRIRTALITFGF 405

                    sLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK
                     L  +D+Rq se   D l  i  H  + + YR+  E  +   L aEL
  gi|2250213   406 HLYSMDLRQNSESYEDFLTEIFAHAHVHpDYRSLDEAEKVALLTAELTSP 455
```

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                    RPLlgsD.LPktEEvkDvldafrvLAELPiDsFGaY.....iismataPs
                    RPL+  D  P  E  +  ld +   A   +D FG+   +++iisma + s
  gi|2250213   456 RPLIAHDaAPFSEATQRELDLIAA-AKQAVDNFGPRmvphsIISMAQSVS 504

                    DvLAvELLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFs
                    D L   +L +E g+ + +++++++t+ v+PLFE + DL+A    +e+L++
  gi|2250213   505 DLLEAMVLLKEFGLIHadgdhptgTVDVIPLFETIEDLQAGAHIIEQLWA 554

                    iDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKk
                    i  Y+n +  +++ qe+m+GYsDs KD G ++A W LY A  +++  A++
  gi|2250213   555 IPLYRNYLKQRgdvQEIMLGYSDSNKDGGYFAANWALYDAELDLVATAQN 604

                    yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                    + + L lFHGRGGtvGRGGGP   AiL+qP   ++G++R+t qGE+i
  gi|2250213   605 HNIALRLFHGRGGTVGRGGGPSYDAILAQPEGAVHGAVRITEQGEIISAK 654

                    FGEEnLCFrsLqRFtAAtLEHGmnPPvsPk..PEWR.kLmeemAvvAtEE
                    +G  +   r L    AAt+E  +      +++PE    +m e+
  gi|2250213   655 YGTPETARRNLEALVAATIEASLLKVEQWQtdPEQAyAIMREISELSQTK 704

                    YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPW
                    Y  +v  +P F+EYF + tP  E G +niGsRPa Rk    i  LRAiPW
  gi|2250213   705 YADLVHNDPGFIEYFTSSTPLAEIGDLNIGSRPASRKQTTAISDLRAIPW 754

                    iFaWtqtRFHLPvWLGvGAAFKhAidKDiKn....lqkLkEmYkeWPFFR
                    + +W q R  LP W G+G A    ++    n++++l +L+E+Y++WPFF
  gi|2250213   755 VLSWSQSRVMLPGWYGMGTALHQWVHAPGENpddrLARLRELYETWPFFN 804

                    vtlDLlEmvFAKGDPGiAaLyDkLLv.aEeLkPFGksLRdkYvEtkdlLL
                      l  +  v  K +  +A+Ly +L+ + E  +   +++R+++  t  +
  gi|2250213   805 SVLSNMAQVMSKAEITLAGLYADLVAdKEAAHRIYHNIREEFDLTTRMFF 854

                    kiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlr
                     i G   lL   P L   +R R +Y+  Lnv+q   L+R R
  gi|2250213   855 AITGVDSLLADNPSLARSVRRRYPYLLPLNVIQLELLRRYR--------- 895

                    PhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG
                         E  d++      Lv               + Ltm G+A  + n G
  gi|2250213   896 -----EGTDDP------LVGHG------------IRLTMNGLATALRNSG 922

                    <-*

  gi|2250213     -     -

gi|269213946|ref|ZP_05983221.2|: domain 1 of 1, from 19 to 918: score 287.7, E = 2.6e-83
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2692139    19    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 56

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2692139    57 ETVKLLSTS----DDSAALIE--KVLPQLDEQQTHDLTLACGLFAQILNI 100

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+  + RR +        D +s   E  + Et++kL        + v
  gi|2692139   101 AEDVH--HERRRQVYE-----DAGSSGAEGSLAETVRKLKAGK-INGKTV 142

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL...aqLsAKDvtve
                     + L n +v  vltAHPt   R  +L  n  iR  L+++      D
  gi|2692139   143 QQQLDNTAVTAVLTAHPTEVQRQTVLSFNRHIRALLprrERCANADALTA 192

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++E+D  L    q    t E R  +    DE+  G+s +    ++  PK
  gi|2692139   193 LRREIDTILLGLWQ----TSETRHHKLSVNDEINNGVSIFPMSFFEALPK 238

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R ++   +       +P    ++k   W+GGDRDG nP v  E  R
  gi|2692139   239 LYRNMERDFQTAYPDVDVP---DILKIGGWIGGDRDG-NPFVSAETLRFA 284

                    CLLaRmmAanlYisqvEDLmFE..lsmWR..CndELRvRAEElyrtaard
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                          +Y s ++ L  E +ls+ R + n ++ +  +E
  gi|2692139   285 FRRHADAVFRFYRSELDKLYRElpLSIRRvkVNGDVMALSDESPDEEIAR 334

                   kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseis
                                 +EPYR  +  +   +     +aR L+L  G
  gi|2692139   335 --------------TEEPYRRAIAYI---MARALGKARALgLGMGCKFGF 367

                   EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                    e  y    eFL+ L    +sL + G + +A+G L Dl+R vs FG  ++
  gi|2692139   368 LEP-YASAQEFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMM 416

                   KLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLl
                    LD+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL+ +RPL+
  gi|2692139   417 PLDLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELSHQRPLY 466

                   gsDLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAvE
                    + +   +  +  l  f++ +++  E   D+    iis +  PsD LA
  gi|2692139   467 SPFITYSDHTRHELAIFNearkIKDEFGEDAVTQSIISNCEQPSDLLALA 516

                   LLqRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYin
                   LL +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY
  gi|2692139   517 LLLKESGLlvvedgkpRSRINIVPLFETIEALENACPVMETMFRLDWYDA 566

                   ridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                    ++ +++ qe+m+GYsDs KD G +   W LY+A   ++   Kky v++
  gi|2692139   567 LLESRgniQEIMLGYSDSNKDGGYVTSSWCLYQAELGLVELFKKYDVRMR 616

                   lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                   lFHGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|2692139   617 LFHGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGN 666

                   CFrsLqRFtAAtLEHGmnPPv.sPkPEWRkLmeemAvvAtEEYRsvvvKE
                     r L    AAtLE  + P  + P P    Lm+ +  v    YR ++
  gi|2692139   667 AVRNLETLVAATLEASLLPDQkDPEP---ALMQALSDVSFKYYRELITH- 712

                   PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
                   P F++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R
  gi|2692139   713 PDFIDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNR 762

                   FHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAK
                     LP W G+G A     +     l  L+E  ++ PFF   l  +E v AK
  gi|2692139   763 LMLPAWYGFGSAVETLCEGKPETLAALREHAQNNPFFQAMLSNMEQVMAK 812

                   GDPGiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                    D  +A  y  L  ++E        ++++Y+  ++ LL +    +lL
  gi|2692139   813 TDITLAENYAGLSESpEKAAVIFGMIKEEYQRSRKALLDLLQTEELLRDN 862

                   PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                     L   l LR +Y+  Ln +q   LKR+R                  E+
  gi|2692139   863 RSLARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP- 894

                   kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     +  L+ +               Lt+ G+A G+ ntG
  gi|2692139   895 DNPHALLMVH--------------LTINGVAQGLRNTG    918

gi|254804129|ref|YP_003082350.1|: domain 1 of 1, from 18 to 917: score 286.8, E = 4.8e-83
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2548041    18    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 55

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2548041    56 ETVKLLSTS----DDSAALIE--KVLPQLDEQQTHDLTLACGLFAQILNI 99

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AE+v+   RR i+          +    E  + Et+++L        + v
  gi|2548041   100 AEDVHHERRRQIHEEA-------GRGGAEGSLTETVRRLKAGK-ADGKSV 141

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                      L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|2548041   142 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 191
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                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++E+D  L     q     t E RR +    DE+  G+s +    ++  PK
  gi|2548041   192 LRREIDTILLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 237

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R ++   + +     +P    ++k   W+GGDRDG nP v  E  R
  gi|2548041   238 LYRNMEHDFQMVYPDVCVP---NILKIGGWIGGDRDG-NPFVSAETLRFA 283

                    CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                              +Y   ++ L  E +ls+ R      v A    +
  gi|2548041   284 FRRHADAVFRFYRGELDKLYRElpLSIRRVKVNDDVMALAALSPDEEL-- 331

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                                +EPYR  +  +   +     +aR L+L  G      e
  gi|2548041   332 ----------ARTEEPYRRAIAYI---MARAMGKARALgLGMGCKFGFLE 368

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y    eFL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
  gi|2548041   369 P-YASAQEFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 417

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL  +RPL+ +
  gi|2548041   418 DLRQHAGKHADVVAELFQHAGLEDYNSLDEEQKQAALLRELGHQRPLYSP 467

                    DLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                     +   +++++E++   +a ++  E   D+    iis +  P D LA  LL
  gi|2548041   468 FITYSDhtrrELAIFNEARKIKDEFGEDAVTQSIISNCEQPGDLLALALL 517

                    qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                     +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   +
  gi|2548041   518 LKESGLlavengkpRSRINIVPLFETIEALENACPVMETMFRLDWYDALL 567

                    dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                    + +++ qe+m+GYsDs KD G +   W LY+A   ++   Kky v++ lF
  gi|2548041   568 ESRgniQEIMLGYSDSNKDGGYVTSSWCLYQAELGLVELFKKYDVRMRLF 617

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|2548041   618 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 667

                    rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                    r L    AAtLE  + P    k    kLm+ +  v    YR ++   P F
  gi|2548041   668 RNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDF 714

                    vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                    ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
  gi|2548041   715 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 764

                    PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                    P W G+G A     +     l  L+E  +  PFF   l  +E v AK D
  gi|2548041   765 PAWYGFGSAVETLCEDKPETLAALREHAQSNPFFQAMLSNMEQVMAKTDI 814

                    GiAaLyDkLLvaEe.LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     +A  y  L  + ++ k     ++++Y   ++ LL +    +lL     L
  gi|2548041   815 TLAENYAGLSESPDkAKIIFGMIKEEYRRSRKALLDLLQTEELLRDNRSL 864

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                       l LR +Y+  Ln +q   LKR+R                 E+   +
  gi|2548041   865 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 896

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      L+ +              Lt+ G+A G+ ntG
  gi|2548041   897 HALLMVH--------------LTINGVAQGLRNTG    917

gi|240015599|ref|ZP_04722139.1|: domain 1 of 1, from 1 to 904: score 286.3, E = 6.7e-83
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2400155     1    ---MQLHILNNPKDA----ALAADAEFLKQSLFNL--LHEEASPLVV 38

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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                    ls       D+  L E   +L  Ld   +  +  a      + n+
gi|2400155    39 ETVKLLSTS----DDSAALIE--KVLPQLDERQTYDLTFACGLFAQILNI 82

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AE+v+   RR i+    G  a E+s t      Et+++L        + v
gi|2400155    83 AEDVHHERRRQIHEDA-GHNAAEGSLT------ETVRRLKAGK-ADGKSV 124

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                      L n sv  vltAHPt   R  +L  n RiR  L q+++    D
gi|2400155   125 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 174

                   DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
gi|2400155   175 LRREIDTVLLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 220

                   FLRRvDtALKniGinERlPYdvPLi..kFssWmGGDRDGknPRvtPEvtR
                     R+++   +      R+P ++  i++    W+GGDRDG nP v  E  R
gi|2400155   221 LYRKMEHDFQTAYPDVRVP-NILKIggWIGGWIGGDRDG-NPFVSGETLR 268

                   DvCLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaard
                              +Y s ++ L  E +ls+ R      v A    +
gi|2400155   269 FAFRRHADAVFRFYRSELDKLYRElpLSIRRVKVNDDVMALAALSPDEEI 318

                   kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseis
                                 +EPYR  +  +   +     +aR L+L  G
gi|2400155   319 ------------ARTEEPYRRAIAYI---MARAMGKARSLgLGMGCKFGF 353

                   EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                    e  y    +FL+ L    +sL + G + +A+G L Dl+R vs FG  ++
gi|2400155   354 LEP-YASAQKFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMM 402

                   KLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLl
                    LD+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL+ +RPL+
gi|2400155   403 PLDLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELSHQRPLY 452

                   gsDLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvE
                    + +   +++++E++   +a ++  E   D+    iis +  P D LA
gi|2400155   453 SPFITYSDhtrrELAIFNEARKIKDEFGEDALTQSIISNCEQPGDLLALA 502

                   LLqRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYin
                   LL +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY
gi|2400155   503 LLLKESGLlavengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDA 552

                   ridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                    ++ +++ qe+m+GYsDs KD G +   W L +A   ++   Kky v++
gi|2400155   553 LLESRgniQEIMLGYSDSNKDGGYVTSSWCLHQAELGLVELFKKYDVRMR 602

                   lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                   lFHGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
gi|2400155   603 LFHGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGN 652

                   CFrsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEP
                     r L    AAtLE  + P    k    kLm+ +  v    YR ++   P
gi|2400155   653 AQRNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-P 699

                   RFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRF
                    F++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R
gi|2400155   700 DFIDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRL 749

                   HLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                    LP W G+G A     +     l  L+   ++ PFF   l  +E v AK
gi|2400155   750 MLPAWYGFGSAVETLCEGSPETLAALRGHAQNNPFFQAMLSNMEQVMAKT 799

                   DPGiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDP
                   D  +A  y  L  ++E  k     ++++Y   ++ LL +    +lL
gi|2400155   800 DITLAENYAGLSESpEKAKVIFGMIKEEYRRSRKALLDLLQTEELLRDNR 849

                   YLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnsk
                    L   l LR +Y+  Ln +q   LKR+R                 E+
gi|2400155   850 SLARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-D 881
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```
                    kadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     +  L+ +               Lt+ G+A G+ ntG
  gi|2400155   882 NPHALLMVH--------------LTINGVAQGLRNTG    904

gi|20196784|emb|CAC86364.1|: domain 1 of 1, from 1 to 396: score 285.2, E = 1.5e-82
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2019678     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2019678     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2019678     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                           +v+Lv+tAHPtqs+RRsLLqK+aRiRnCL+qL+AKD+  +DKk
  gi|2019678     1 -------TVELVFTAHPTQSIRRSLLQKHARIRNCLTQLYAKDISEDDKK 43

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL REiqA FRtDEiRRaqPtPqDEmR+GmsY+HEt+WkGvPKFLR
  gi|2019678    44 ELDEALQREIQACFRTDEIRRAQPTPQDEMRYGMSYFHETIWKGVPKFLR 93

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGi ERlPY+vPLikFssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2019678    94 RVDTALKNIGIDERLPYNVPLIKFSSWMGGDRDG-NPRVTPEVTRDVCLL 142

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAan+Y+sq+E+LmFElsmWRCndELR+RA Ely  a ++k+ K+Yi
  gi|2019678   143 ARMMAANMYFSQIEELMFELSMWRCNDELRARAGELY--ASSQKISKHYI 190

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFW+q+P +EPYRv+LG vRDKLYntRER+RHLL  G+s+i+E+  +t v
  gi|2019678   191 EFWRQIPANEPYRVVLGYVRDKLYNTRERSRHLLTSGFSDIPEDSAFTSV 240

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCYksLC+ GDk iADGsLLD++RqvstFGLsLvKLDiRqEs
  gi|2019678   241 EQFLEPLELCYKSLCDSGDKTIADGSLLDFMRQVSTFGLSLVKLDIRQES 290

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+tDv+DAittHL+iGsYReWsEeKRqEWL++ELkGKRPLl +D+P+tE
  gi|2019678   291 ERHTDVIDAITTHLGIGSYREWSEEKRQEWLISELKGKRPLLSPDMPQTE 340

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvl+ f+vLAELP  sFG+YiismataPsDv AvELLqREC+vkq+L
  gi|2019678   341 EIADVLGCFQVLAELPRGSFGPYIISMATAPSDVFAVELLQRECHVKQPL 390

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLF
  gi|2019678   391 PVVPLF---------------------------------------------- 396

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|2019678     - ---------------------------------------------- -

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

  gi|2019678     - ---------------------------------------------- -

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|2019678     - ---------------------------------------------- -

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|2019678     - ---------------------------------------------- -

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
```

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  gi|2019678     - ------------------------------------------------ -

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|2019678     - ------------------------------------------------ -

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|2019678     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|2019678     - -------------    -

gi|241766972|ref|ZP_04764768.1|: domain 1 of 1, from 2 to 929: score 284.6, E = 2.2e-82
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                    K s+ ++ +  D  Ll + L+D++ +  G +  E
  gi|2417669     2    ------------KRSDKDQPLIDDIRLLGRILgDVIREQEGVEAYEL 36

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v     ls  +    D +    L   L sL    ++ v +a+     LAn
  gi|2417669    37 VEQVRKLSVAFRRDADQEADRALKKLLKSLSGDQTVSVIRAFTYFSHLAN 86

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   LAE+ +   RRR    + GD       t E  iE  l +L   +  +P+
  gi|2417669    87 LAED-RHHIRRRAVHERAGD-------TQEGSIEVALSRLRWAG-IAPKT 127

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL.........aqLs
                   + + L    v  vltAHPt   R+s+L  +  i   L+++++ + +aqL+
  gi|2417669   128 IAQTLASSYVAPVLTAHPTEVQRKSILDAERDIAQLLstrddiqvrAQLY 177

                   ..AKDvtveDKkELDEALHRE.iqAAFRtDEiRRaqPtPqDEmRaGmsYi
                   ++AKD          EAL R ++   + t  +R ++ t  DE+   +sY+
  gi|2417669   178 nsAKDALTPRELAANEALLRArVAQLWQTRLLRYSKLTVADEIENALSYY 227

                   HEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknP
                     t  + +PK     +  L    +          ++   W+GGDRDG nP
  gi|2417669   228 ESTFLREIPKIYADLERELGQYPVHS-------FLRMGQWIGGDRDG-NP 269

                   RvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEly
                    vt             mA   Y+  v  L  Els       L +R   +
  gi|2417669   270 NVTAQTLQHALRSQADMALRHYLTEVHYLGGELS-------LSARLVTVS 312

                   rtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtG
                          +        +q    EPYR  L  +  +L  t        A
  gi|2417669   313 PAMEALALRSPDTSEHRQ---DEPYRRALTGIYARLAATLKELTGGDAAR 359

                   iseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstF
                    +  + +A y    eFL  L +   sL     k++A   L  l+R v  F
  gi|2417669   360 HAVAPQNA-YAGAAEFLADLRVIEASLESHHGKALAAERLHPLIRAVEVF 408

                   GLsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELk
                   G  L  +D+Rq s+++ +v+  +     i + Y +  E  ++  L+  L
  gi|2417669   409 GFHLATVDLRQSSDKHEEVVAELLATARIEpNYSSLQEAAKRALLIKLLN 458

                   GKRPL..lgsDL.PktEEvkDvldafrvLAE.LPiDsFGaYiismataPs
                     RPL+ +g++ +  t     + ++ rv+ E+   ++   Yiis + + s
  gi|2417669   459 DARPLrvVGAEYsAHTQGELAIFETARVMRErFGHEAIRHYIISHTETVS 508

                   DvLAvELLqRECgv.........kqtLrvvPLFEkLADLeAAPAavekLF
                   D L v LLq+E g+ +++ ++++++ L vvPLFE + DL+ A   +   +
  gi|2417669   509 DLLEVLLLQKEVGLvrgtldeesHNDLIVVPLFETIEDLRNAAPIMREFY 558

                   s...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                   + +++   + r  G q++m+GYsDs KD G +   W LY+A   ++
  gi|2417669   559 AlpgVAALVQRSGGEQDIMLGYSDSNKDGGIFTSNWELYRAEIALVELFD 608

                   k....yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGE
                   + ++++G++L +FHGRGGtvGRGGGP   AiL+qPP t+ G +R t qGE
  gi|2417669   609 EldtsHGIQLRMFHGRGGTVGRGGGPSYQAILAQPPGTVRGQIRLTEQGE 658
```

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                  viEfsFGEEnLCFrsLqRFtAAtLEHG.mnPPvsPkPEWRkLmeemAvvA
                  vi   +   ++  r L    AAtLE   ++P  s    + +   ++
  gi|2417669   659 VIASKYANPEIGRRNLETLVAATLEATlLQPTKSATKAFLDAAARLSQAS 708

                  tEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRA
                     YR++v+  P F +YF   tP  E   +niGsRPa Rk s  ie LRA
  gi|2417669   709 MGAYRALVYETPGFTDYFFNSTPIREIAELNIGSRPASRKASQKIEDLRA 758

                  iPWiFaWtqtRFHLPvWLGvGA...AFKhAidKDiK.nlqkLkEmYkeWP
                  iPW F+W q R  LP W G+GA  +AF  A  KD K  l  L+ mY++WP
  gi|2417669   759 IPWGFSWGQCRLTLPGWFGFGAaveAFVNAEGKDPKaQLALLQKMYRQWP 808

                  FFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtkd
                  FFR  l  ++mv AK D  +A+ y +L+    L+k     + +++  t d
  gi|2417669   809 FFRTLLSNMDMVLAKSDLALASRYSELVTDTRLrKKVFSTIEAEWHRTVD 858

                  lLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykv
                   L +i G k  L     L   ++ R +Yi  L  +q   ++R R  +
  gi|2417669   859 ALTRITGDKQRLTHNTALARSIKHRFPYIDPLHHLQVELVRRWRAGQ--- 905

                  tlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmq
                            dE     +  +++                + GiAAG+
  gi|2417669   906 ----------GDER---VQTGIHIS----------------INGIAAGLR 926

                  ntG<-*
                  ntG
  gi|2417669   927 NTG    929

gi|270494458|ref|ZP_06211504.1|: domain 1 of 1, from 11 to 951: score 283.2, E = 5.6e-82
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      +     +  PG+ ++ ++ +  D  Ll + L+D++ +  G    +
  gi|2704944    11    PVSEPQAAPSPGRRADKDQPLIQDIRLLGRILgDVIREQEGVAAYDL 57

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v     ls  +    D +    L   L +L    ++ v +a+     LAn
  gi|2704944    58 VEQVRKLSVAFRRDADQEADKALKKLLKGLSGDQTVSVIRAFTYFSHLAN 107

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  LAE+ +   RRR    +       a  t E  iE  l +L   +  +P
  gi|2704944   108 LAED-RHHIRRRTVHER-------AGSTQEGSIEVALARLRWAG-IAPRT 148

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL..........
                  v + L    v  vltAHPt   R+s+L  +  i   La  ++ + ++
  gi|2704944   149 VAQTLARSYVSPVLTAHPTEVQRKSILDAERDIAELLAERdeiqarglfy 198

                  .sAKD.vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYi
                  +sA+D +t+ +    +  L   +   + t  +R ++ t  DE+   +sY+
  gi|2704944   199 kSARDaLTPRELAANEARLRARVAQLWQTRLLRYSKLTVADEIENALSYY 248

                  HEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknP
                    t  + +P+     + AL    +       +  ++   W+GGDRDG nP
  gi|2704944   249 ESTFLREIPRLYEDLERALGSQPV-------ASFLRMGQWIGGDRDG-NP 290

                  RvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEly
                   v  E           +A   Y+  v  L  Els+      + v  E  +
  gi|2704944   291 NVSAETLALALRRQAEVALRHYLTEVHYLGGELSL--SARLVQVSPEMEQ 338

                  rtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntR......ERaR
                     ++     +     +q    EPYR  L  +  +L  t ++ +++E aR
  gi|2704944   339 LAERSPDTSEH-----RQ---DEPYRRALTGIYARLAATLreltggEAAR 380

                  HLLAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlL
                  H +A        +  y +  eFL  L +   sL       +A   L  l+
  gi|2704944   381 HAVAP-------QNPYGDASEFLADLRVIEASLRSHRGAPLAAQRLHPLV 423

                  RqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEW
                  R v  FG  L  +D+Rq s+ +  v+  +     i  +Y   +E+ Rq
  gi|2704944   424 RAVEVFGFHLATVDLRQSSDQHERVVAELLATARIETdYAALPEDARQAL 473

                  LlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGa.....Yii
                  L+  L   RPL        E  +  +  f+  A    D +Ga+  ++Yii
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  gi|2704944   474 LVRLLCDARPLRVVGAEYSEHTRGEIAIFET-ARRMRDRYGAqairhYII 522

                   smataPsDvLAvELLqRECgvkq..........tLrvvPLFEkLADLeAA
                   s + + sD L v LLq+E g+ +++ ++ + +  L vvPLFE + DL+ A
  gi|2704944   523 SHTETVSDLLEVLLLQKEVGLMHgtldgadaraDLIVVPLFETIGDLRNA 572

                   PAavekLFsiDWYinrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAq
                      +  L+ +  +   +++++  q++m+GYsDs KD G +   W LY+A
  gi|2704944   573 QPIMRALYEVPGFAAMVQrggAEQDIMLGYSDSNKDGGIFTSNWELYRAE 622

                   EEiiK....vAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGs
                     ++   +    ++ ++L lFHGRGGtvGRGGGP   AiL+qPP t+ G
  gi|2704944   623 IALVElfdvLEARHRIRLRLFHGRGGTVGRGGGPSYQAILAQPPGTVRGQ 672

                   lRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE.WRkL
                   +R t qGEvi   +   ++  r L    AAtLE  +  P  P    + +
  gi|2704944   673 IRLTEQGEVIASKYANPEIGRRNLETLVAATLEATLLQPTKPATKaFHEA 722

                   meemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs
                     e+       YR++v+  P F +YF   tP  E   +niGsRPa RkPs
  gi|2704944   723 AAELSQASMAAYRALVYDTPGFADYFFNSTPIREIAELNIGSRPASRKPS 772

                   GGiesLRAiPWiFaWtqtRFHLPvWLGvGA...AFKhAidKDiKn.lqkL
                     ie LRAiPW F+W q R  LP W G+G   +AF  A d D K ++  L
  gi|2704944   773 QKIEDLRAIPWGFSWGQCRLTLPGWYGFGSaveAFVKAADEDPKArMALL 822

                   kEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL..kPFGksL
                   + mY++WPFFR  l  ++mv AK D  +A+ y +L+    L++k FG  +
  gi|2704944   823 QKMYRQWPFFRTLLSNMDMVLAKSDLALASRYSELVADARLrrKVFG-AI 871

                   RdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLK
                    ++++ t d L +i G +  L     L   +R R +Yi  L  +q   ++
  gi|2704944   872 EAEWQRTVDALARITGDRQRLAHNTALARSIRHRFPYIDPLHHLQVELVR 921

                   RiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLt
                   R R               A E s + +  +++
  gi|2704944   922 RWR----------------AGEGSERVQTGIHIC---------------- 939

                   mKGiAAGmqntG<-*
                   + GiAAG+ ntG
  gi|2704944   940 INGIAAGLRNTG    951

gi|252126365|ref|ZP_04836407.1|: domain 1 of 1, from 1 to 922: score 283.1, E = 6.3e-82
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       +  qL+           k i+    Ll k   ++ +  G+++   v
  gi|2521263     1    -MKNQLK-----------KDIRHLGKLLGK---VIAEQEGDEVYRQV 32

                   qECYElsAeYE.GKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                        ls +  +G  D + L +L    t     D + +A+a+ H   LAn
  gi|2521263    33 EAARALSFDIArGTSDISALVDLFRNNTT---RDFLPIARAFNHFALLAN 79

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkL.vlklnKsPe
                   L E+    +   +         + +    +s +E t  kL+  k + sP+
  gi|2521263    80 LVEDL---HDNANYIAD----REAGLPAPDSTLEATAAKLsAAKAEISPD 122

                   EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq....LsA..K
                    + + LKn  v  vltAHPt   RR +   +  i   L  +++ L A++
  gi|2521263   123 NITQLLKNAQVAPVLTAHPTETRRRTVFDAQEHITALLVDrhriLNApeN 172

                   DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvW
                    +t      +D  + R +   + t  iR a+P   DE+  G+ Y+   +
  gi|2521263   173 ALTKTRLDNIDQQITRWLTTLWQTALIRVARPRIEDEIEVGLRYYKLSLL 222

                   kGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPE
                   k +P     v   L           +  +i+  sW+GGD DG nP vt
  gi|2521263   223 KAIPDINQTVSQVLADTFDTNT---QTAIIQPGSWIGGDHDG-NPYVTAS 268

                   vtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaar
                           a       Y + +  L  Els+    d L    +El   a +
  gi|2521263   269 TLEYATSRAAETVLKYYEQELHQLEHELSL---SDRLAHVTDELRELAEQ 315
```

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                    dkvvKyYiEFWKqvPP..tEPYRviLGdvRDKLYntRERaRHLLAtGise
                                +P +  EPYR  +  +R ++  t        A
  gi|2521263   316 G---------HNNIPArvDEPYRRAVHGIRGRIIATLAALIGDDAVEGTW 356

                    isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                        A y   ++ L  L +   sL    D++iAD  L  +     tFG
  gi|2521263   357 YTNHAPYQTPDQVLADLAIIDESLRANHDHIIADDRLRRIRTALITFGFH 406

                    LvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKR
                    L  +D+Rq se   D l  i  H  + + YR+  E  +   L aEL   R
  gi|2521263   407 LYSMDLRQNSESYEDFLTEIFAHAHVHpDYRSLDEAEKVALLTAELTSPR 456

                    PLlgsD.LPktEEvkDvldafrvLAELPiDsFGaY.....iismataPsD
                    PL+  D  P  E  +  ld +   A   +D FG+   +++iisma + sD
  gi|2521263   457 PLIAHDaAPFSEATQRELDLIAA-AKQAVDDFGPRmvphsIISMAQSVSD 505

                    vLAvELLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsi
                     L   +L +E g+ + +++++++t+ v+PLFE + DL+A    +e+L++i
  gi|2521263   506 LLEAMVLLKEFGLIHadgdhptgTVDVIPLFETIEDLQAGAHIIEQLWAI 555

                    DWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKky
                      Y+n +  +++ qe+m+GYsDs KD G ++A W LY A  +++  A+++
  gi|2521263   556 PLYRNYLKQRgdvQEIMLGYSDSNKDGGYFAANWALYDAELDLVATAQNH 605

                    GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF
                     + L lFHGRGGtvGRGGGP   AiL+qP   ++G++R+t qGE+i   +
  gi|2521263   606 NIALRLFHGRGGTVGRGGGPSYDAILAQPEGAVHGAVRITEQGEIISAKY 655

                    GEEnLCFrsLqRFtAAtLEHGmnPPvsPk..PEWR.kLmeemAvvAtEEY
                    G  +   r L    AAt+E  +      +++PE    +m e+       Y
  gi|2521263   656 GTPETARRNLEALVAATIEASLLKVEQWQtdPEQAyAIMREISELSQTKY 705

                    RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWi
                      +v  +P F+EYF + tP  E G +niGsRPa Rk    i  LRAiPW+
  gi|2521263   706 ADLVHNDPGFIEYFTSSTPLAEIGDLNIGSRPASRKQTTAISDLRAIPWV 755

                    FaWtqtRFHLPvWLGvGAAFKhAidKDiKn....lqkLkEmYkeWPFFRv
                     +W q R  LP W G+G A    ++    n++++l +L+E+Y++WPFF
  gi|2521263   756 LSWSQSRVMLPGWYGMGTALHQWVHAPGENpddrLARLRELYETWPFFNS 805

                    tlDLlEmvFAKGDPGiAaLyDkLLv.aEeLkPFGksLRdkYvEtkdlLLk
                     l  +  v  K +  +A+Ly +L+ + E  +   +++R+++  t  +
  gi|2521263   806 VLSNMAQVMSKAEITLAGLYADLVAdKEAAHRIYHNIREEFDLTTRMFFT 855

                    iAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrP
                    i G   lL   P L   +R R +Y+  Lnv+q   L+R R
  gi|2521263   856 ITGVDSLLADNPSLARSVRRRYPYLLPLNVIQLELLRRYR---------- 895

                    hlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<
                        E  d++      Lv               + Ltm G+A  + n G
  gi|2521263   896 ----EGTDDP------LVGHG-----------IRLTMNGLATALRNSG  922

                    -*

  gi|2521263     -    -

gi|262196990|ref|YP_003268199.1|: domain 1 of 1, from 1 to 907: score 282.9, E = 7.2e-82
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                              +    +s  ++L    ALL ++   ++ ++ G+d    v
  gi|2621969     1    --------MTAETIS-MDRLDADVALLNERLDAVIAEIAGDDALALV 38

                    qECY.ElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    q   +E  A  EG  +  + +   a++ + d  +  l+A+ +     L n
  gi|2621969    39 QGLVgEAIAMREGTLEGGR-DAFAARMQAFDLDELALIARVFTLWFHLVN 87

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     AEE    +R R+ + +     D a+   +  +    + L       PeE
  gi|2621969    88 AAEE---QHRTRVLRAR-----DTAESAPDGSLAAAARELAQSS-ADPEE 128

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                        L    +  vltAHPt + RR +L   + i   L  L    +   ++
```

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  gi|2621969   129 LRALLGRLFIMPVLTAHPTEARRRTVLEHLGVIASVLDELDRATLGNRER 178

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + L + LH  i   F t+E R  +PtP DE+  G+  +  t+ +  P
  gi|2621969   179 QHLIDSLHGAILSLFGTEEARAVKPTPRDEVASGLDVFRATLLDVTPGMY 228

                    RRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDvC
                    R  + AL        l  dvP+ +++  W+GGDRDG nP vt + tR v
  gi|2621969   229 RTFEEALAAAFPGQSL--DVPsFMRWGTWIGGDRDG-NPFVTSDTTRWVL 275

                    LLaRmmAanlYisqvEDLmFElsm..WRCndELRvRAEElyrtaardkvv
                       R+     Y+   EDLm Els++  R  d     A E    + r+
  gi|2621969   276 EQQRVCVLKRYLRDAEDLMRELSVsaRRVKDPGGLAALEASLAPNRE-SL 324

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                       +   +     EP+       R+K++  R R    L  G      +A
  gi|2621969   325 PEVMAKAQRYATHEPW-------REKVWYIRRRLEDTLTRG------DAA 361

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y + E++L+ L +    L +CG   +A+GsL D +R    FG  L  LD+
  gi|2621969   362 YARAEDYLDDLRVLRDTLQDCGFARLAEGSLHDAIRRAEVFGFHLASLDL 411

                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    Rq s  +   +  + +H +   Y +  E+ R   Ll+EL       +s
  gi|2621969   412 RQHSAVHERAVAELLRHSGKDGYEQMDEDARVA-LLTELLDHADFEPSAR 460

                    P.....ktEEvkDvldaf.rvLAELPiDsFGaYiismataPsDvLAvELL
                    P + +  t E+   ld ++r   E    +   Yi+s +  PsD L v  L
  gi|2621969   461 PaklsaETREILATLDMVgRARREQGPRACERYIVSFTSQPSDLLEVLFL 510

                    qRECgvk.qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevm
                    qR  ++ +  Lr vPL E+L DL+ A    + +  +   +  + G  evm
  gi|2621969   511 QRAAHLApGELRPVPLLEQLEDLDHADVMADAMLTVRPIRAALRGELEVM 560

                    vGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRG
                    +GYsD+GK  G ++AA  L +Aq  +++ A k+Gv L++FHGRGGt+GRG
  gi|2621969   561 IGYSDAGKQIGYFAAAVALRRAQLTLARAADKHGVPLTIFHGRGGTIGRG 610

                    GGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAt
                    GGP    i +qP   + G +Rvt qGE i   +G  ++  r L     A
  gi|2621969   611 GGPANQTIRAQPSQALRGRIRVTEQGETITARYGRSEIASRDLEQMVHAV 660

                    L.....EHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                    L  + +E     P +      +L +     A E Y  +         Y
  gi|2621969   661 LvatadEKRERLPGAELEARNELFDAAGDAAREAYGGLLADPDLLARYAV 710

                    lAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG
                     AtP     k+ iGsRPa R+P+   + LRAiPW+F+W q R  LP W G
  gi|2621969   711 AATPIQQVTKLPIGSRPASRRPGLSFDDLRAIPWVFSWNQSRHGLPGWFG 760

                    vGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaL
                    +G A  + i++  K l   + +Y+e PFFR  +    +   + D  +A
  gi|2621969   761 LGTALGFIIER--KGLDYARSLYRESPFFRALINNAQLALSRSDIDVARC 808

                    yDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRL
                    y   L  E+ +    ++ ++Y  t + +L++   ++lL   P L   ++
  gi|2621969   809 YAA-LADEDARQIFARIEAEYARTLEHVLEVVERQELLGNRPHLVGTIKR 857

                    RdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkL
                    R++++  L   q   L+R+R  +             dE+  + + L+ +
  gi|2621969   858 RNPFVDVLSHAQIELLQRLRRSE--------------DED--ERERLLAI 891

                    nptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                  +t+ GiAAG+q  G
  gi|2621969   892 L-------------FITINGIAAGLQTAG    907

gi|104773626|ref|YP_618606.1|: domain 1 of 1, from 1 to 909: score 280.8, E = 3.1e-81
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           +L       v  +e  i  D  LlD   +    L G++    +
  gi|1047736     1    MTAKKLENNSNHAVTAEEVKILTD--LLD---ESTRHLVGDEEFAKI 42
```

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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                +    ++A      D ++Le   +++  L   + i+vA+ +  +  L n+
gi|1047736    43 KGLVKIAAS----SDHSQLE---SQIACLSNQEMIIVARYFATLPLLINI 85

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                 E+v+lA    + ++            t+ D    l   v +     +
gi|1047736    86 TEDVDLA--TEVNLLN----------NTDKDYLGKLESTVDLV-AEKDNA 122

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                 e L    v  vltAHPtq  R+ +L    +i   L            +k
gi|1047736   123 AEILSHVNVVPVLTAHPTQVQRKTILELTNKIHDQLRRHRDVKASTINRK 172

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                E    L R i     tD iR  +     E++  m Y+   +   + K
gi|1047736   173 EWTNQLRRYIEIIMQTDIIREKKLKVSNEIKNVMVYYPGSLIPAITKLTA 222

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                R     +  G+n  +    P i    W+GGDRDG nP vt E  R    +
gi|1047736   223 RYKELAREKGLN--VDGATP-ITMGMWIGGDRDG-NPYVTAETLRLSATI 268

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   +    Y+  + DL   +s         v    ++ t+    + K
gi|1047736   269 QSEVIFEYYVKALNDLYRTVS---------VSTSYVQPTPEVAELAKLSA 309

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA....v
                +       +EPYR        +L  t      +  +      E A + +v
gi|1047736   310 DN-SPFRENEPYRRAFYYLESRLAHTEMELLDVFSKEAVVKKEAAlkapV 358

                ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                y +  eF   LE   +sL +  D+++  G    lL  +  FG  L  +D+
gi|1047736   359 YKDAYEFKKDLEAIKRSLIQNHDRAVTGGHFDALLEAIDVFGFHLATIDM 408

                RqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK.RPLlgs
                Rq+s  +   +  + +   i + Y +  Ee +   Ll+EL   +R L  s
gi|1047736   409 RQDSSVNEACVAELLKSARICdNYSDLDEEEKIQILLSELNNDpRSLHSS 458

                DLPktEEvkDvldafrvLAELPiDsFG.....aYiismataPsDvLAvEL
                  Pk E ++  l  ++  A L  D+ G++  +  iis + + sD+L   +
gi|1047736   459 NSPKSELLQRELKIYHT-ARLLKDTLGenvikQHIISHTESISDMLEQAI 507

                LqRECgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK
                + +E g+ +++k  ++vvPLFE + DL+     +++  s D  +  +  K
gi|1047736   508 MLKEYGLldseKARVQVVPLFETVEDLQNSREIMKRYLSFDIVKRWVASK 557

                ...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                ++ qe+m+GYsDs KD G l+  W LYkAq E+  +  + G+K++  HGR
gi|1047736   558 gnyQEIMLGYSDSNKDGGYLASCWNLYKAQTELTAIGEEQGIKITFMHGR 607

                GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                GGtvGRGGGP   Ai sqP   i+  +R t qGE+i   +G  +  +  L
gi|1047736   608 GGTVGRGGGPSYEAITSQPFGSIKDRIRTTEQGEIIQNKYGNKDAAYYNL 657

                qRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEE...YRsvvvKEPRF
                     A ++  +      +    +    m  +  + ++ YR +v+  P F
gi|1047736   658 EMLVSAAVDRMVSKQKVSQDHIQDFTASMDGIVEDSnrvYRELVFDNPHF 707

                vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                 +YF  AtP  E   +niGsRPa Rk    +  LRAiPW+F+W q R
gi|1047736   708 HDYFFQATPIKEVSSLNIGSRPAARKKITELSGLRAIPWVFSWSQSRVMF 757

                PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                P W GvG AFKh id D  nl+ L+EmY+ WPFF   l  ++mv  K
gi|1047736   758 PGWYGVGSAFKHFIDADPNNLKELQEMYQGWPFFHSLLSNVDMVLSKSNM 807

                GiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLK
                 iA  y +L   E  +   + ++ +++ tk+ +L+i GH  lLE  P L
gi|1047736   808 EIAEKYADLCEDEATRSVFDIIKKEWELTKEVILQIEGHSKLLEDNPSLE 857

                qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                  l  R +Y   Ln +q   +KR R        + +ls  y  E
gi|1047736   858 RSLDYRLPYFNVLNYVQLEMIKRGR--------QEKLSGIY--ES----- 892
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                  eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   ++++                + G+A G+ n G
  gi|1047736   893 -IIHIT---------------INGVASGLRNSG    909

gi|20196776|emb|CAC86360.1|: domain 1 of 1, from 1 to 387: score 280.1, E = 5e-81
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2019677     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2019677     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2019677     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                              +tAHPtqs+RRsLLqKnaRiRnCL+qLsAKD t+eDKk
  gi|2019677     1 ------------FTAHPTQSARRSLLQKNARIRNCLTQLSAKDTTPEDKK 38

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                  ELDEAL REiqAAFRtDEiRRaqPtPqDEmR+GmsYiHEtvWkGvPKFLR
  gi|2019677    39 ELDEALQREIQAAFRTDEIRRAQPTPQDEMRYGMSYIHETVWKGVPKFLR 88

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                  RvDtALKniGinERlPY+vPLikF+sWmGGDRDG nPRvtPEvtRDvCLL
  gi|2019677    89 RVDTALKNIGINERLPYNVPLIKFCSWMGGDRDG-NPRVTPEVTRDVCLL 137

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                  +RmmAanlYi+qvEDLmFElsmWR n+ELR+RA+El +t+a++kv+KyYi
  gi|2019677   138 SRMMAANLYIDQVEDLMFELSMWRANEELRARADELLSTPASKKVTKYYI 187

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                  EFWKq+PP+EPYRviLG+vRDKLYntRERaRHLLAtG+s+is + ++t +
  gi|2019677   188 EFWKQIPPNEPYRVILGAVRDKLYNTRERARHLLATGFSDISVDSIFTSI 237

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                  E+ LEPLELCYksL +CGDk iADGsLLDlLRqv+tFGLsLvKLDiRqEs
  gi|2019677   238 EQILEPLELCYKSLVDCGDKTIADGSLLDLLRQVYTFGLSLVKLDIRQES 287

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  eR+tDv+DAittHL+iGsYR+W+E+KR E+L++ELkGKRPLl++DLP+tE
  gi|2019677   288 ERHTDVIDAITTHLGIGSYRSWPEDKRVEFLVTELKGKRPLLPADLPMTE 337

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++Dv++a++v+AELP+DsFG+Yiism+taPsDvLAvELLqRECg+kqtL
  gi|2019677   338 EIADVIGAMKVIAELPSDSFGPYIISMCTAPSDVLAVELLQRECGIKQTL 387

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG

  gi|2019677     - ---------------------------------------------- -

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|2019677     - ---------------------------------------------- -

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

  gi|2019677     - ---------------------------------------------- -

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|2019677     - ---------------------------------------------- -

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|2019677     - ---------------------------------------------- -

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
```

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  gi|2019677     - ------------------------------------------------- -

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|2019677     - ------------------------------------------------- -

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|2019677     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|2019677     - -------------    -

gi|227881566|ref|ZP_03999428.1|: domain 1 of 1, from 1 to 897: score 280.0, E = 5.3e-81
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                              L    v    ++ e  ALL     D+L      +    v
  gi|2278815     1    ------MELHTRDVR--RDVRELGALL----GDVLESQSSTQSFQTV 35

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    +    + +Y  K D     EL  ++ +L P    +vA+a+     L nL
  gi|2278815    36 EDIRTAAIDYR-KGDLDSRTELLQVIDGLSPDGESVVARAFTTYFELINL 84

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEE e     R   +  GD  D   At  s            +   Pe v
  gi|2278815    85 AEERERVRTIREASQA-GDLEDGLVATVKS---------FAGGGADPETV 124

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      L    ++  +tAHPt + R+ +  K   i   +  +  + +t  +++
  gi|2278815   125 QRVLDDVLIEPTFTAHPTEARRKTVKAKLRSIASRIEEMDERNLTDRERQ 174

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    L   +  E+   + t  +R  +P PqDE R    Y+   +++ v
  gi|2278815   175 QLWREVDAEVTSLWQTSQVRGRRPEPQDEARNVQWYLESILFDVVGE--- 221

                   RvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDvCL
                    v      +   E    dvP+L +F sW G DRDG nP vtPEvt D
  gi|2278815   222 -VYSEFEDVLAEEYPEVDVPkLFEFRSWAGSDRDG-NPFVTPEVTEDTLA 269

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                     R +    Y + +  L   ls     + + v AE   +  a
  gi|2278815   270 RQRSVVLEKYSDALKRLSGVLS--QDGSRIDVGAEFERSLIADRERLPVV 317

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                    E      P+EPY       R KL   RER R      i ++  +  y
  gi|2278815   318 AEETEERYPEEPY-------RQKLKLMRERIRR-----IEDVRPDG-YAA 354

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     e LE LE+  +sL + G  v+AD  +  l+Rqv tFG  L  LD+R
  gi|2278815   355 HHELLEDLEIIDQSLRDNGADVVADEYVSPLMRQVDTFGFTLASLDLRDH 404

                   seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    e +t+ +       +i  Y +  E+ R   L   +    PL+  DL
  gi|2278815   405 RENHTEAVHEALAREGI-DYYDRDEDGRVAVLTEAILQDEPLV--DLSNR 451

                   EEvkD....vldafrvLA....ELPiDsFGaYiismataPsDvLAvELLq
                   E++ D+ ++vl  f+ L + ++E  + +   Y ism+  Ps vL v  L
  gi|2278815   452 EDLSDtadrVLTRFEKLGewqrEYGVGAIDTYCISMTEEPSHVLEVLFLA 501

                   RECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri...d
                      gv + +++  L vvPL E    L+ A   +  LF  + Y   +  ++
  gi|2278815   502 DQAGVvslpdHCGLDVVPLLETESALNGARRIMGSLFENEAYEQVLaarN 551

                   GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRG
                   G qe+m+GYsDs K+ G l+A W LYk q  ++ +  ++ vK+ lFHGRG
  gi|2278815   552 GVQEIMLGYSDSNKENGYLAANWDLYKNQRRLAAICDDFDVKMRLFHGRG 601

                   GtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLq
                   G + RGGGP   A+L+ P +t+ G ++ t qGE i   +   ++  r L
  gi|2278815   602 GSISRGGGPMNEAMLALPNETVTGQIKFTEQGEAIAEKYANPHIAERNLE 651
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                    RFtAAtL...EHGmnPPvsPkPE.WRkLmeemAvvAtEEYRsvvvKEPRF
                        A ++ +   ++ P    PE W + m+ mA  A  EYR +   E  F
  gi|2278815   652 QMLNAQVrarHEAIQEPEEDVPEaWIDAMDTMAAAARQEYRNLLESEG-F 700

                    vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                    v YF  AtP +    +n+GsRPa R     +e LRAiPW+F+Wtq R  +
  gi|2278815   701 VSYFEQATPITVIEDLNLGSRPASRSGERTVEDLRAIPWVFSWTQSRCII 750

                    PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                      W  +G   +  +d        L+EmY+eWPFFR tlD   +  A+ +
  gi|2278815   751 TGWYALGTGLQTYLDEGGDR-ATLREMYDEWPFFRTTLDNASLALARTEF 799

                    GiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLK
                    GiA  y  L   +    F  +L ++Y+  +dl+L + G   lL    +L
  gi|2278815   800 GIAEHYAALADDDLREAFYPRLFEEYERAHDLVLDVIGRESLLKRQ-WLD 848

                    qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                      lR R++Y+  Ln +q   L                s+ +  E+
  gi|2278815   849 ESLRRRNPYVDPLNLLQTHLL----------------SQTHRTED----- 877

                    eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                 E tL Lt+KGiAAGm+ntG
  gi|2278815   878 -----E---------ERTLRLTVKGIAAGMKNTG    897

gi|256389410|ref|YP_003110974.1|: domain 1 of 1, from 20 to 940: score 279.7, E = 6.6e-81
                    *->siDAqLRlLv...PGKvsedekLieYDALLlDkFLDiLqDLHGedLk
                       s  A     ++++P + ++d +L      L D     L   HG++L
  gi|2563894    20    SPTARANDTAndnPPRTADDAELRAAIRRLGDLLGQTLVRQHGPELL 66

                    EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                    E v     l     GK+ +  + EL   L ++dP  ai + +a+    nL
  gi|2563894    67 EQVEAIRAL-----GKQGAD-VSEL---LAAVDPEQAIKLVRAFTAYFNL 107

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                    An AE v   +R R              A   s +   + ++   +
  gi|2563894   108 ANTAEQV---HRGRELAAT--------RAAEGSWLGQAVDRIQAAG--LA 144

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                        eA+   sv  v+tAHPt ++RR +L K  ++    a L     t
  gi|2563894   145 GTAAEAVSHLSVRPVFTAHPTEAARRTVLAKLRKV----AELLEAPQTAY 190

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                      + L E +    q    tDEiR ++P P DE R  + Y+ E   +  P
  gi|2563894   191 NERRLAETVEQLWQ----TDEIRITRPEPVDEARNAVYYLDELAAHAAPE 236

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     L      L+ +G+   lP  +  + F sW+GGDRDG nP vtP +t Dv
  gi|2563894   237 VLEELAVELRRLGVE--LPLSARPLSFGSWIGGDRDG-NPNVTPQMTLDV 283

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      L    A    +  ++ L   ls     + + +  E l      d
  gi|2563894   284 LELQHEHAIRTALASMDALREILS---TSERIAAPTEALRASLDAD--LE 328

                    yYiEF...WKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                       E +++++ +  +EPYR     +R KL ntR R    +A G    +
  gi|2563894   329 ALPEIpnrYRRLNAEEPYRLKATTIRQKLLNTRTR----IAEGRQHDPRR 374

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y    e L  L L   sL       iA G L   +R +  FGL    L
  gi|2563894   375 D-YLGTSELLRDLSLMRDSLYADRGELIATGELETAIRTIAAFGLHHAVL 423

                    DiRqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPL.
                    D+R  ++ +  vl  +   L+   +R ++ + + R   L  EL   RPL+
  gi|2563894   424 DVREHADAHHHVLAQLFDRLGDQPWRysDLPRDYRTRLLAKELASSRPLs 473

                    ....lgsD.LPktEEvkD..vldafrvLAE.LPiDsFGaYiismataPsD
                      +++++D+L     vk  +v  a+r   E+   D   +Yi+sm+    D
  gi|2563894   474 algqVPADtLLDAAGVKSfgVFTAIRTAFEkYGPDVIESYIVSMTRGVDD 523

                    vLAvELLqRECgv......kqtLrvvPLFEkLADLeAAPAavekLFsiDW
```

```
                    A  +L RE g+ + + +  ++  vPL E   +L+ A   ++ + s
  gi|2563894   524 LFAAVVLAREAGLvdvhahTAAIGFVPLLETPDELKIAGSILDEMLSDPS 573

                    Yinrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGv
                    Y   +  ++G qevm+GYsDs K  G     W + +Aq E+   A ++G+
  gi|2563894   574 YAAIVAargGVQEVMLGYSDSNKMGGISTSQWEIHRAQRELRDTALRHGI 623

                    KLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGE
                    ++ lFHGRGG vGRGGGP H AiL+qP  t++G ++vt qGEvi   +
  gi|2563894   624 RIRLFHGRGGSVGRGGGPSHDAILAQPWGTLDGEIKVTEQGEVISDKYAI 673

                    EnLCFrsLqRFtAAtLEHGm...nPPvsPk..PEWRkLmeemAvvAtEEY
                      L    L    AAtLE  + ++ P  s  +   W   me +     + Y
  gi|2563894   674 PALARENLELTLAATLEATVlhrAPRQSAEdlATWSATMEGVSSAGQDRY 723

                    RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKR.kPsGGiesLRAiPW
                    R +v   P    YF   tP    G + +GsRP++R+  s Gi+ LRAiPW
  gi|2563894   724 RELV-EHPDLPAYFFASTPVDLLGDLHLGSRPSRRpDTSAGIDGLRAIPW 772

                    iFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlD
                    +F Wtq R  +P W GvG     A +         ++mY+ W FFR  l
  gi|2563894   773 VFGWTQSRQIVPGWFGVGTGLAAARQNPAFAGTDWQDMYERWHFFRNFLG 822

                    LlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGH
                     + m  AK D  iA  y + Lv  eL+ F + + ++Y+ t   +L+i G
  gi|2563894   823 NVSMTLAKTDLRIARHYVETLVPRELHHFFDTITEEYERTVAEVLRITGE 872

                    kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                     +lL     L   lR+Rd Y+  +  +q   LKR R+
  gi|2563894   873 SELLGRNETLARTLRVRDMYLDPISYMQVSLLKRQRE------------- 909

                    EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      A               +  v P L   L+L + GiAAG++ntG
  gi|2563894   910 --ATKA------------GLPVDPDLARALLLSVNGIAAGLKNTG    940

gi|94264993|ref|ZP_01288763.1|: domain 1 of 1, from 18 to 947: score 278.9, E = 1.1e-80
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                          Aq    +PG        +     L+ + L+ ++qDL G+++ E
  gi|9426499    18    --GAQ----APGPLP-----LAGQIKLVGRILgKVIQDLRGPQVYEQ 53

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v E   l       k +   + +  ++  Ld  + + v +a+     L n
  gi|9426499    54 VEELRLLLCKRAAVEKRPDLRQRVQQRIADLDCREIVEVLQAYTVFFHLVN 103

                    LAEEvel..AyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                      E +e+++A RR +           +       i+E +  L  ++
  gi|9426499   104 KVEQMEIsrADRRHNPGPV-------GHVPRRESIDEAVADLKAQG-AGI 145

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    + v   L    +   ltAHPt + RRs+L K+ Ri   L  Ls +D   +
  gi|9426499   146 DRVLGLLGKLDIQPTLTAHPTEARRRSILYKQKRIAALLEELSRRDNGLD 195

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    +++ L   L  Ei     tD+iR  +Pt  DE+  G+ ++   +W+ vP+
  gi|9426499   196 EQEALLAELEGEIGLLLATDDIRLVRPTVEDEVESGLYFVRNAIWQTVPQ 245

                    FLRRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRD
                           AL+        P   P  ++F sW+G DRDG nP vt  v R
  gi|9426499   246 IYQDLRAALQR--HYGECPAALPaFLRFRSWIGSDRDG-NPYVTAAVSRY 292

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                      L  R +A  lY++ +  L  Els+    +        +   aa
  gi|9426499   293 TWLYQRRVALRLYLEELRQLRRELSLSGRQQPPAGLLKSIEEDAAEL--- 339

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                        E  +     EPYR  +     +L             G  +    A
  gi|9426499   340 -TLSENRRRRYRYEPYRLKISYLMARLKQLEADIDAGRFPGGGDPYGAA- 387

                    ytkvEeFLEPLELCYksLCeCG.DkviADGsLLDlLRqvstFGLsLvKLD
                         e L  L L   sL   G  + +  G L  +L qv  FGL Lv LD
  gi|9426499   388 -----ELLADLQLLADSLQAQGfSRLVSHGRLGRMLLQVRSFGLHLVALD 432
```

```
                    iRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgs
                     Rq s  + + +  + +  ++ + Y   +Ee+R   L  EL   RPLl+
  gi|9426499   433 FRQHSRVHEEGVALLLRLAGVCdDYAALAEEQRLALLEGELANPRPLLPR 482

                    DLPktEEvkDvldafrvLAELPiD...sFGaYiismataPsDvLAvELLq
                          Ev + l +fr +AE+   ++ + GaYiism+ a sD L v LL
  gi|9426499   483 NRELPPEVDELLASFRLIAEIQQHdpaALGAYIISMTHATSDLLEVLLLA 532

                    RECg........vkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                    +E g  ++++++v  +L  vPL E + DL+ A   + ++     Y+ ++
  gi|9426499   533 KETGlwerrdgrVVSALDLVPLLETIEDLDQAGELLRQILENPVYRDQLT 582

                    GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                     +++ qevm+GYsDs KD G   A W L +AqEE+  v ++yG+ L lFH
  gi|9426499   583 ARshfQEVMLGYSDSNKDGGYWMANWALHRAQEELGEVSREYGIELRLFH 632

                    GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                    GRGGtvGRGGG    AiL+ P    nG +R t qGEvi f +   ++  r
  gi|9426499   633 GRGGTVGRGGGRANQAILALPEQVHNGRIRFTEQGEVITFRYAFSDIARR 682

                    sLq.......RFtAAtLEHGmn.......PPvsPkP.EWRkLmeemAvvA
                     L +  +   R tAA    G+ + +  ++P  +P  +E  + + ++A
  gi|9426499   683 HLEqivnamlRTTAAAESAGLAgadaaggPAAAPAVsEENRFLARIAAAG 732

                    tEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLR
                     E YR +v  +P F  ++   tP     ++ i sRP  R  +   +e LR
  gi|9426499   733 MEAYRELV-HDPDFWAWYTRITPIEQISRLPIASRPVSRSAGEvDLEGLR 781

                    AiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFR
                    AiPW+FaWtqtR+ +P W G GAA   A+  +    q L+E+Y+  PFF
  gi|9426499   782 AIPWVFAWTQTRYIVPGWFGTGAALN-AVLAEPGGRQYLRELYRRDPFFQ 830

                    vtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLk
                    + +D      A+  P iAa yD L  aE    F +++ ++ +   + L +
  gi|9426499   831 MVVDNARREMARVRPEIAAEYDAL--AEVPARFHQRITADLEMALQALPE 878

                    iAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrP
                      G  +lL   P ++  +RLR++Y   +n +q   L+R  D
  gi|9426499   879 FTGESELLARNPAVQRSIRLRNPYTDVINLLQVELLRRYHD--------- 919

                    hlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<
                                          + +    L D L L + GiAA mq tG
  gi|9426499   920 ----------------------SGGEEREALRDALFLSVNGIAAAMQSTG  947

                    -*

  gi|9426499     -    -

gi|56807908|ref|ZP_00365735.1|: domain 1 of 1, from 10 to 932: score 277.9, E = 2.2e-80
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                         D  L  L     s+++ +i  +  Ll   L+ i   + G+d   +
  gi|5680790    10    --DGHL-PLKKLESSNNQAIIAEEVALLKEMLgNITRRMIGDDAFTV 53

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls     K+D   Le    ++  +   +  ++ + ++ +  L n
  gi|5680790    54 IESIMVLSE----KQDYIELEK---VIANISNQEMEVISRYFSILPLLIN 96

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+           +  t+K L  k
  gi|5680790    97 ISEDVDLAYEINHQNNTDTDYLGK--------LALTIKDLAGKD-----N 133

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      + L    v  vltAHPtq  R+ +L   + i   L +       v
  gi|5680790   134 GKDILEQVNVVPVLTAHPTQVQRKTILELTTHIHKLLRKYRDAKAGVINL 183

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +     L R i     tD iR  +   + E++  m Y+   + + v K
  gi|5680790   184 EKWRQELYRYIEMIMQTDIIREKKLQVKNEIKNVMQYYDGSLIQAVTK-- 231

                    RRvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRDvC
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                      t  Kn+     l  d P +i    W+GGDRDG nP vt E
  gi|5680790   232 --LTTEYKNLAQKHGLELDNPKpITMGMWIGGDRDG-NPFVTAETLCLSA 278

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    +   +  n Yi+++  L   +s+    + L     E+ r a   +
  gi|5680790   279 TVQSEVILNYYIDKLAALYRTFSL---SSTLVQPNSEVERLASLSQDQSI 325

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRER......aRHLLAtGi..se
                   Y         +EPYR     +  +L  t    ++++ aR     G+++s
  gi|5680790   326 Y-------RGNEPYRRAFHYIQSRLKQTQIQltnqpaARMSSSVGLntSA 368

                   isEeA.......vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                    +  A+ +++   y    +F   L    +sL + G  ++ +G L +++
  gi|5680790   369 WPSPAslenpilAYDSPVDFKADLKAIEQSLLDNGNSALIEGDLREVMQA 418

                   vstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLl
                   v  FG  L  +D+Rq+s  q   +  + +  +i   Y + sE  + + L+
  gi|5680790   419 VDIFGFFLASIDMRQDSSVQEACVAELLKGANIvDDYSSLSETEKCDVLV 468

                   aELkGK.RPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiism
                     L   +R L  + + k + ++  l  +    EL ++ + +     iis
  gi|5680790   469 QQLMEEpRTLSSAAVAKSDLLEKELAIYTTARELKdklgEEVIKQHIISH 518

                   ataPsDvLAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLF
                   + + sD+    ++ +E g+ ++++  +++vPLFE + DL+ A   ++
  gi|5680790   519 TESVSDMFELAIMLKEVGLvdqqRARVQIVPLFETIEDLDNARDIMAAYI 568

                   siDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                   s D  +  i   ++ qe+m+GYsDs KD G l+  W LYkAq E+  +
  gi|5680790   569 SHDIVRSWIATNrdyQEIMLGYSDSNKDGGYLASGWTLYKAQNELTAIGE 618

                   kyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf
                   ++GvK++ FHGRGGtvGRGGGP   Ai sqP   i+  +R t qGE+iE
  gi|5680790   619 EHGVKITFFHGRGGTVGRGGGPSYDAITSQPFGSIKDRIRLTEQGEIIEN 668

                   sFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtE
                    +G  ++ +  L     A +   +   +    E +++R++m+ +
  gi|5680790   669 KYGNKDVAYYHLEMLISASINRMVTQMITDPNEidsFREIMDSIVADSNT 718

                   EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                    YR +v+  P F +YF  A P  E   +niGsRPa Rk    i+ LRAiP
  gi|5680790   719 IYRKLVFDNPHFYDYFFEASPIKEVSSLNIGSRPAARKTITEITGLRAIP 768

                   WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                   W+F+W q R   P W GvG AFK  id+   nl +L+ mY++WPFF   l
  gi|5680790   769 WVFSWSQNRIMFPGWYGVGSAFKRYIDRAQGNLERLQHMYQTWPFFHSLL 818

                   DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                     ++mv  K    iA  y +L  + +++    ++ d+++ tk+ +L i
  gi|5680790   819 SNVDMVLSKSNMNIAFQYAQLAESQDVRDVFYEILDEWQLTKNVILAIQD 868

                   HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                   H DlLE  P LK  l+ R +Y   Ln +q   +KR R  +
  gi|5680790   869 HDDLLEDNPSLKHSLKSRLPYFNVLNYIQIELIKRWRNNQL--------- 909

                   KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       dEn    + L++                 + GiA G+ n G
  gi|5680790   910 ----DEN---DEKLIHTT----------------INGIATGLRNSG    932

gi|94990008|ref|YP_598108.1|: domain 1 of 1, from 15 to 937: score 277.7, E = 2.6e-80
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                        D  L  L     s+++ +i  +  Ll   L++i   + G+d   +
  gi|9499000    15    --DGHL-PLKKLESSNNQAIIAEEVALLKEMLEnITRRMIGDDAFTV 58

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +     ls     K+D   Le    ++  +   +  ++ + ++ +  L n
  gi|9499000    59 IESIVVLSE----KQDYIELEK---VVANISNQEMEVISRYFSILPLLIN 101

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   + E+v+lAy    +     D+           +  t+K L  k
  gi|9499000   102 ISEDVDLAYEINHQNNTDTDYLGK--------LALTIKDLAGKD-----N 138
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                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      + L    v  vltAHPtq  R+ +L   + i   L +       v
  gi|9499000   139 GKDILEQVNVVPVLTAHPTQVQRKTILELTTHIHKLLRKYRDAKAGVINL 188

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +     L R i     tD iR  +   + E++  m Y+   + + v K
  gi|9499000   189 EKWRQELYRYIEMIMQTDIIREKKLQVKNEIKNVMQYYDGSLIQAVTK-- 236

                    RRvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRDvC
                        t  Kn+     l  d P +i    W+GGDRDG nP vt E
  gi|9499000   237 --LTTEYKNLAQKHGLELDNPKpITMGMWIGGDRDG-NPFVTAETLCLSA 283

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     +   +  n Yi+++  L   +s+    + L     E+ r a   +
  gi|9499000   284 TVQSEVILNYYIDKLAALYRTFSL---SSTLVQPNSEVERLASLSQDQSI 330

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRER......aRHLLAtGiseis
                    Y         +EPYR     +  +L  t    ++++ aR     G+s  +
  gi|9499000   331 Y-------RGNEPYRRAFHYIQSRLKQTQIQltnqpaARMSSSVGLSTSA 373

                    .......EeAv..ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                     +++ + E+ +  y    +F   L    +sL + G  ++ +G L +++
  gi|9499000   374 wsspaslENPIlaYDSPVDFKADLKAIEQSLLDNGNSALIEGDLREVMQA 423

                    vstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLl
                    v  FG  L  +D+Rq+s  q   +  + +  +i   Y + sE  + + L+
  gi|9499000   424 VDIFGFFLASIDMRQDSSVQEACVAELLKGANIvDDYSSLSETEKCDVLV 473

                    aELkGK.RPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiism
                      L   +R L  + + k + ++  l  +    EL ++ + +     iis
  gi|9499000   474 QQLMEEpRTLSSAAVAKSDLLEKELAIYTTARELKdklgEEVIKQHIISH 523

                    ataPsDvLAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLF
                    + + sD+    ++ +E g+ ++++  +++vPLFE + DL+ A   ++
  gi|9499000   524 TESVSDMFELAIMLKEVGLvdqqRARVQIVPLFETIEDLDNARDIMAAYL 573

                    siDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                    s D  +  i   ++ qe+m+GYsDs KD G l+  W LYkAq E+  +
  gi|9499000   574 SHDIVKSWIATNrnyQEIMLGYSDSNKDGGYLASGWTLYKAQNELTAIGE 623

                    kyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf
                    ++GvK++ FHGRGGtvGRGGGP   Ai sqP   i+  +R t qGE+iE
  gi|9499000   624 EHGVKITFFHGRGGTVGRGGGPSYDAITSQPFGSIKDRIRLTEQGEIIEN 673

                    sFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtE
                     +G  ++ +  L     A +   +   +    E +++R++m+ +
  gi|9499000   674 KYGNKDVAYYHLEMLISASINRMVTQMITDPNEidsFREIMDSIVADSNT 723

                    EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                     YR +v+  P F +YF  A P  E   +niGsRPa Rk    i+ LRAiP
  gi|9499000   724 IYRKLVFDNPHFYDYFFEASPIKEVSSLNIGSRPAARKTITEITGLRAIP 773

                    WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                    W+F+W q R   P W GvG AFK  id+   nl +L+ mY++WPFF   l
  gi|9499000   774 WVFSWSQNRIMFPGWYGVGSAFKRYIDRAQGNLERLQHMYQTWPFFHSLL 823

                    DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                      ++mv  K    iA  y +L  + +++    ++ d+++ tk+ +L i
  gi|9499000   824 SNVDMVLSKSNMNIAFQYAQLAESQDVRDVFYEILDEWQLTKNVILAIQD 873

                    HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                    H DlLE  P LK  l+ R +Y   Ln +q   +KR R  +
  gi|9499000   874 HDDLLEDNPSLKHSLKSRLPYFNVLNYIQIELIKRWRNNQL--------- 914

                    KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        dEn    + L++                  + GiA G+ n G
  gi|9499000   915 ----DEN---DEKLIHTT----------------INGIATGLRNSG    937

gi|94988126|ref|YP_596227.1|: domain 1 of 1, from 15 to 937: score 277.7, E = 2.6e-80
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
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                  D  L  L     s+++ +i  +  Ll   L++i   + G+d   +
gi|9498812    15    --DGHL-PLKKLESSNNQAIIAEEVALLKEMLEnITRRMIGDDAFTV 58

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  +     ls     K+D   Le    ++  +   +  ++ + ++ +  L n
gi|9498812    59 IESIMVLSE----KQDYIELEK---VVANISNQEMEVISRYFSILPLLIN 101

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  + E+v+lAy    +     D+           +  t+K L  k
gi|9498812   102 ISEDVDLAYEINYQNNTDTDYLGK--------LALTIKDLAGKD-----N 138

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + L    v  vltAHPtq  R+ +L   + i   L +       v
gi|9498812   139 GKDILEQVNVVPVLTAHPTQVQRKTILELTTHIHKLLRKYRDAKAGVINL 188

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  +     L R i     tD iR  +   + E++  m Y+   + + v K
gi|9498812   189 EKWRQELYRYIEMIMQTDIIREKKLQVKNEIKNVMQYYDGSLIQAVTK-- 236

                  RRvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRDvC
                      t  Kn+     l  d P +i    W+GGDRDG nP vt E
gi|9498812   237 --LTTEYKNLAQKHGLELDNPKpITMGMWIGGDRDG-NPFVTAETLCLSA 283

                  LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                   +   +  n Yi+++  L   +s+    + L     E+ r a   +
gi|9498812   284 TVQSEVILNYYIDKLAALYRTFSL---SSTLVQPNSEVERLASLSQDQSI 330

                  YiEFWKqvPPtEPYRviLGdvRDKLYntRER......aRHLLAtGi..se
                  Y         +EPYR     +  +L  t    ++++ aR     G+++s
gi|9498812   331 Y-------RGNEPYRRAFHYIQSRLKQTQNQltnqpaARMSSSVGLntSA 373

                  isEeA.......vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                   s  A+ +++   y    +F   L    +sL + G  ++ +G L +++
gi|9498812   374 WSSPAslenpilAYDSPVDFKADLKAIEQSLLDNGNSALIEGDLREVMQA 423

                  vstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLl
                  v  FG  L  +D+Rq+s  q   +  + +  +i   Y + sE  + + Ll
gi|9498812   424 VDIFGFFLASIDMRQDSSVQEACVAELLKGANIvDDYSSLSETEKCDVLL 473

                  aELkGK.RPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiism
                    L   +R L  + + k + ++  l  +    EL ++ + +     iis
gi|9498812   474 QQLMEEpRTLSSAAVAKSDLLEKELAIYTTARELKdklgEEVIKQHIISH 523

                  ataPsDvLAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLF
                  + + sD+    ++ +E g+ ++++  +++vPLFE + DL+ A   ++
gi|9498812   524 TESVSDMFELAIMLKEVGLvdqqRARVQIVPLFETIEDLDNARDIMAAYL 573

                  siDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                  s D  +  i   ++ qe+m+GYsDs KD G l+  W LYkAq E+  +
gi|9498812   574 SHDIVKSWIATNrnyQEIMLGYSDSNKDGGYLASGWTLYKAQNELTAIGE 623

                  kyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf
                  ++GvK++ FHGRGGtvGRGGGP   Ai sqP   i+  +R t qGE+iE
gi|9498812   624 EHGVKITFFHGRGGTVGRGGGPSYDAITSQPFGSIKDRIRLTEQGEIIEN 673

                  sFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtE
                   +G  ++ +  L     A +   +   +    E +++R++m+ +
gi|9498812   674 KYGNKDVAYYHLEMLISASINRMVTQMITDPNEidsFREIMDSIVADSNT 723

                  EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                   YR +v+  P F +YF  A P  E   +niGsRPa Rk    i+ LRAiP
gi|9498812   724 IYRKLVFDNPHFYDYFFEASPIKEVSSLNIGSRPAARKTITEITGLRAIP 773

                  WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                  W+F+W q R   P W GvG AFK  id+   nl +L+ mY++WPFF   l
gi|9498812   774 WVFSWSQNRIMFPGWYGVGSAFKRYIDRAQGNLERLQHMYQTWPFFHSLL 823

                  DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                    ++mv  K    iA  y +L  + +++    ++ d+++ tk+ +L i
gi|9498812   824 SNVDMVLSKSNMNIAFQYAQLAESQDVRDVFYEILDEWQLTKNVILAIQD 873
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                    HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                    H DlLE  P LK  l+ R +Y   Ln +q   +KR R  +
  gi|9498812   874 HDDLLEDNPSLKHSLKSRLPYFNVLNYIQIELIKRWRNNQL--------- 914

                    KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        dEn    + L++                  + GiA G+ n G
  gi|9498812   915 ----DEN---DEKLIHTT----------------INGIATGLRNSG    937

gi|71903150|ref|YP_279953.1|: domain 1 of 1, from 15 to 937: score 277.6, E = 2.8e-80
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                         D  L  L     s+++ +i  +  Ll   L++i   + G+d   +
  gi|7190315    15    --DGHL-PLKKLESSNNQAIIAEEVALLKEMLEnITRRMIGDDAFAV 58

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls     K+D   Le    ++  +   +  ++ + ++ +  L n
  gi|7190315    59 IESIMVLSE----KQDYIELEK---VVANISNQEMEVISRYFSILPLLIN 101

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+           +  t+K L  k
  gi|7190315   102 ISEDVDLAYEINYQNNTDTDYLGK--------LALTIKDLAGKD-----N 138

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      + L    v  vltAHPtq  R+ +L   + i   L +       v
  gi|7190315   139 GKDILEQVNVVPVLTAHPTQVQRKTILELTTHIHKLLRKYRDAKAGVINL 188

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +     L R i     tD iR  +   + E++  m Y+   + + v K
  gi|7190315   189 EKWRQELYRYIEMIMQTDIIREKKLQVKNEIKNVMQYYDGSLIQAVTK-- 236

                    RRvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRDvC
                        t  Kn+     l  d P +i    W+GGDRDG nP vt E
  gi|7190315   237 --LTTEYKNLAQKHGLELDNPKpITMGMWIGGDRDG-NPFVTAETLCLSA 283

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     +   +  n Yi+++  L   +s+    + L     E+ r a   +
  gi|7190315   284 TVQSEVILNYYIDKLAALYRTFSL---SSTLVQPNSEVERLASLSQDQSI 330

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRER......aRHLLAtGiseis
                    Y         +EPYR     +  +L  t    ++++ aR     G+s  +
  gi|7190315   331 Y-------RGNEPYRRAFHYIQSRLKQTQIQltnqpaARMSSSVGLSTSA 373

                    .......EeAv..ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                     +++ + E+ +  y    +F   L    +sL + G  ++ +G L +++
  gi|7190315   374 wsspaslENPIlaYDSPVDFKADLKAIEQSLLDNGNSALIEGDLREVMQA 423

                    vstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLl
                    v  FG  L  +D+Rq+s  q   +  + +  +i   Y + sE  + + Ll
  gi|7190315   424 VDIFGFFLASIDMRQDSSVQESCVAELLKGANIvDDYSSLSETEKCDVLL 473

                    aELkGK.RPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiism
                      L   +R L  + + k + ++  l  +    EL ++ + +     iis
  gi|7190315   474 QQLMEEpRTLSSAAVAKSDLLEKELAIYTTARELKdklgEEVIKQHIISH 523

                    ataPsDvLAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLF
                    + + sD+    ++ +E g+ ++++  +++vPLFE + DL+ A   ++
  gi|7190315   524 TESVSDMFELAIMLKEVGLvdqqRARVQIVPLFETIEDLDNARDIMAAYL 573

                    siDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                    s D  +  i   ++ qe+m+GYsDs KD G l+  W LYkAq E+  +
  gi|7190315   574 SHDIVKSWIATNrnyQEIMLGYSDSNKDGGYLASGWTLYKAQNELTAIGE 623

                    kyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf
                    ++GvK++ FHGRGGtvGRGGGP   Ai sqP   i+  +R t qGE+iE
  gi|7190315   624 EHGVKITFFHGRGGTVGRGGGPSYDAITSQPFGSIKDRIRLTEQGEIIEN 673

                    sFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtE
                     +G  ++ +  L     A +   +   +    E +++R++m+ +
  gi|7190315   674 KYGNKDVAYYHLEMLISASINRMVTQMITDPNEidsFREIMDSIVADSNT 723

                    EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                     YR +v+  P F +YF  A P  E   +niGsRPa Rk    i+ LRAiP
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  gi|7190315   724 IYRKLVFDNPHFYDYFFEASPIKEVSSLNIGSRPAARKTITEITGLRAIP 773

                   WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                   W+F+W q R   P W GvG AFK  id+   nl +L+ mY++WPFF   l
  gi|7190315   774 WVFSWSQNRIMFPGWYGVGSAFKRYIDRAQGNLERLQHMYQTWPFFHSLL 823

                   DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                     ++mv  K    iA  y +L  + +++    ++ d+++ tk+ +L i
  gi|7190315   824 SNVDMVLSKSNMNIAFQYAQLAESQDVRDVFYEILDEWQLTKNVILAIQD 873

                   HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                   H DlLE  P LK  l+ R +Y   Ln +q   +KR R  +
  gi|7190315   874 HDDLLEDNPSLKHSLKSRLPYFNVLNYIQIELIKRWRNNQL--------- 914

                   KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       dEn    + L++                  + GiA G+ n G
  gi|7190315   915 ----DEN---DEKLIHTT----------------INGIATGLRNSG    937

gi|197103239|ref|YP_002128617.1|: domain 1 of 1, from 1 to 888: score 277.0, E = 4.2e-80
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           + +  PG v       e  ALL     D   D       Eav
  gi|1971032     1    -----MSATPPGDVR--SATQEVGALLGQIIRD--EDPSAFARIEAV 38

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        ++  + G       +EL a L +L   +a  v + +   L  An
  gi|1971032    39 RR-LAVARHFQGAA-----GELPALLDGLSADEAFKVVHGFACFLQAANA 82

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AE+   A  RR ++          +A    D+   l  L   +  + + v
  gi|1971032    83 AEDAMQA--RRASLGE--------DAIRLDDV---LDALAKEG-VTEDQV 118

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      L    +  vltAHP    RRs+L     +R  L  L   D  + D +
  gi|1971032   119 RALLGKGLIVPVLTAHPSEVRRRSVLEHAQAMRETLGALAHPDCGP-DAE 167

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    L E L RE    + t  +R  +PtP DE+   ++ +   +   +P
  gi|1971032   168 TLSEILLRETALLWGTRLLRSVKPTPEDEVDNTVAVMRASLLSAIPAVYE 217

                   RvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDvCL
                                  Rl  + P+ ++  sW+GGDRDG nP vt Ev R
  gi|1971032   218 ---------AWERRLGPELPgFLRLGSWVGGDRDG-NPFVTGEVLRRA-- 255

                   LaRmmAanl..YisqvEDLmFElsmWRCnd....ELRvRAEElyrtaard
                   LaR   a l++Y++ v  L   ls+     ++++EL++ A+ l   +a +
  gi|1971032   256 LARQAEAVLghYLEEVHRLGVSLSLAEDLApptpELKAFADSLADPPAHQ 305

                   kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                                  EPYR  L  +  +L  t        A  ++
  gi|1971032   306 --------------AREPYRRALTLIYARLAATYQALVGRPAPRLAAARA 341

                   eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                   +  y   +  +  LE    sL     ++   G L  l+R v  FG  L
  gi|1971032   342 DP-YASPDALVADLERLLSSLRRTNARAFSRGPLPNLVRAVRVFGFHLAS 390

                   LDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLl
                   LD+Rq +  +  v+  +    +  + Y    E  Rq  LlaEL  +RPL+
  gi|1971032   391 LDLRQNAAVHERVVAELLAKAGACdDYLALDEAGRQRILLAELAHRRPLV 440

                   gsDLPktEEvkDvldafrvLAELPi....DsFGaYiismataPsDvLAvE
                    + +   EE +  l+ fr  AE   + ++ + GaYi+s a a sD L
  gi|1971032   441 SPIVCYSEETARELGVFRAAAEARArfgpAALGAYIVSNAGAVSDLLEPY 490

                   LLqRECgv......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                   +L +E g+ ++ ++  +Lrv PLFE +ADL+AAP  ++    +      +
  gi|1971032   491 VLMKEAGLfdpiepSAPLRVEPLFETIADLRAAPEVLAAYLETPLIAGLM 540

                   dG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                    G +  qevm+GYsDs KD   l   WqL +    +   A   Gv+L lF
  gi|1971032   541 RGanaHQEVMIGYSDSSKDGSYLTSSWQLHRTSAALSALADAKGVRLQLF 590
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                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGG vGRGGG    Ai++qPP  + G +R t qGEvi   + +  L
  gi|1971032   591 HGRGGAVGRGGGSSFEAIVAQPPGVLRGRMRLTEQGEVIANKYADAALAR 640

                    rsLqRFtAAtLEHGmnPPvs.PkPEWRkLmeemAvvAtEEYRsvvvKEPR
                    rsL   +   +   + P  ++      + m+ +A      YR +v+  P
  gi|1971032   641 RSLETLACGVIAASLRPAFAdVSAADVEAMDALAETSRRAYRGLVYETPG 690

                    FvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFH
                    F ++F + tP  E   +ni sRP  R+ +  iesLRAiPW+F+W q R
  gi|1971032   691 FADFFFSSTPIAELSELNIASRPVARQAARTIESLRAIPWVFSWSQARLM 740

                    LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                    LP W G+GAA K A       l +L+  ++ WPFFR tl  +Emv AK D
  gi|1971032   741 LPGWYGFGAATKEA------DLERLRAWWRGWPFFRATLRNMEMVLAKAD 784

                    PGiAaLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLkiAGHkDlLEGDP
                      i a y +L+   +L+   FG+ +R+++  t d LL i G   lLE +P
  gi|1971032   785 LAIGARYAELVADVDLRAviFGR-IRAEWDRTVDRLLAITGQTQLLEHEP 833

                    YLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnsk
                     L   ++ R +Yi  Ln +q   L+R R               A E+
  gi|1971032   834 RLAEAIKGRLPYIEPLNHLQVELLRRRR---------------AGED-- 865

                    kadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                  P L + L++t+ GiA G+ n G
  gi|1971032   866 --------------DPKLHEALLMTLNGIASGLRNSG    888

gi|209559064|ref|YP_002285536.1|: domain 1 of 1, from 10 to 932: score 276.8, E = 4.9e-80
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                         D  L  L     s+++ +i  +  Ll   L+ i   + G+d   +
  gi|2095590    10    --DGHL-PLKKLESSNNQAIIAEEVALLKEMLgNITRRMIGDDAFTV 53

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls     K+D   Le    ++  +   +  ++ + ++ +  L n
  gi|2095590    54 IESIMVLSE----KQDYIELEK---VIANISNQEMEVISRYFSILPLLIN 96

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+           +  t+K L  k
  gi|2095590    97 ISEDVDLAYEINHQNNTDTDYLGK--------LALTIKDLAGKD-----N 133

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      + L    v  vltAHPtq  R+ +L   + i   L +       v
  gi|2095590   134 GKDILEQVNVVPVLTAHPTQVQRKTILELTTHIHKLLRKYRDAKAGVINL 183

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +     L R i     tD iR  +   + E++  m Y+   + + v K
  gi|2095590   184 EKWRQELYRYIEMIMQTDIIREKKLQVKNEIKNVMQYYDGSLIQAVTK-- 231

                    RRvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRDvC
                        t  Kn+     l  d P +i    W+GGDRDG nP vt E
  gi|2095590   232 --LTTEYKNLAQKHGLELDNPKpITMGMWIGGDRDG-NPFVTAETLCLSA 278

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     +   +  n Yi+++  L   +s+    + L     E+ r a   +
  gi|2095590   279 TVQSEVILNYYIDKLAALYRTFSL---SSTLVQPNSEVERLASLSQDQSI 325

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRER......aRHLLAtGi..se
                    Y         +EPYR     +  +L  t    ++++ aR     G+++s
  gi|2095590   326 Y-------RGNEPYRRAFHYIQSRLKQTQIQltnqpaARMSSSVGLntSA 368

                    isEeA.......vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                     +  A+ +++   y    +F   L    +sL + G  ++ +G L +++
  gi|2095590   369 WPSPAslenpilAYDSPVDFKADLKAIEQSLLDNGNSALIEGDLREVMQA 418

                    vstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLl
                    v  FG  L  +D+Rq+s  q   +  + +  +i   Y + sE  + + L+
  gi|2095590   419 VDIFGFFLASIDMRQDSSVQEACVAELLKGANIvDDYSSLSETEKCDVLV 468

                    aELkGK.RPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiism
                      L   +R L  + + k + ++  l  +    EL ++ + +     iis
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  gi|2095590   469 QQLMEEpRTLSSAAVAKSDLLEKELAIYTTARELKdklgEEVIKQHIISH 518

                   ataPsDvLAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLF
                   + + sD+    ++ +E g+ ++++  +++vPLFE + DL+ A   ++
  gi|2095590   519 TESVSDMFELAIMLKEVGLvdqqRARVQIVPLFETIEDLDNARDIMAAYL 568

                   siDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                   s D  +  i   ++ qe+m+GYsDs KD G l+  W LYkAq E+  +
  gi|2095590   569 SHDIVKSWIATNrnyQEIMLGYSDSNKDGGYLASGWTLYKAQNELTAIGE 618

                   kyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf
                   ++GvK++ FHGRGGtvGRGGGP   Ai sqP   i+  +R t qGE+iE
  gi|2095590   619 EHGVKITFFHGRGGTVGRGGGPSYDAITSQPFGSIKDRIRLTEQGEIIEN 668

                   sFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtE
                    +G  ++ +  L     A +   +   +    E +++R++m+ +
  gi|2095590   669 KYGNKDVAYYHLEMLISASINRMVTQMITDPNEidsFREIMDSIVADSNT 718

                   EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                    YR +v+  P F +YF  A P  E   +niGsRPa Rk    i+ LRAiP
  gi|2095590   719 IYRKLVFDNPHFYDYFFEASPIKEVSSLNIGSRPAARKTITEITGLRAIP 768

                   WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                   W+F+W q R   P W GvG AFK  id+   nl +L+ mY++WPFF   l
  gi|2095590   769 WVFSWSQNRIMFPGWYGVGSAFKRYIDRAQGNLERLQHMYQTWPFFHSLL 818

                   DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                     ++mv  K    iA  y +L  + +++    ++ d+++ tk+ +L i
  gi|2095590   819 SNVDMVLSKSNMNIAFQYAQLAESQDVRDVFYEILDEWQLTKNVILAIQD 868

                   HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                   H DlLE  P LK  l+ R +Y   Ln +q   +KR R  +
  gi|2095590   869 HDDLLEDNPSLKHSLKSRLPYFNVLNYIQIELIKRWRNNQL--------- 909

                   KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       dEn    + L++                  + GiA G+ n G
  gi|2095590   910 ----DEN---DEKLIHTT----------------INGIATGLRNSG    932

gi|293168120|ref|ZP_06606869.1|: domain 1 of 1, from 7 to 930: score 276.2, E = 7.5e-80
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        D       P  v  +e++++ D   +   L+  L    G++L +
  gi|2931681     7    HADRLPEQNLPADVP-QEEVLRSDVRRVADLLgQTLVRQEGQELFDL 52

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDail.vAkailHmLnLA
                   v     ls   +    ++    + a L  L P+D++ ++ +a++   nLA
  gi|2931681    53 VERVRVLSRRRDDEGAAEDRATVHALLDEL-PTDTVAsLVRAFSVYFNLA 101

                   nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                   n+AE v    R R    +               ++  +  +v      P
  gi|2931681   102 NVAEQVA---RVREVVDR---------PYGTGWLDRAVAEIVEDQ--GPG 137

                   EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                      eA     +  v+tAHPt   RRs L K  Ri   L   s  D
  gi|2931681   138 ALAEAFASLDIRTVFTAHPTEVSRRSTLTKIRRIADILGEPSDDDTVLRR 187

                   KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                   ++  D  L   i   + tD +RR +PtP DE R  + Y+ + + + +P
  gi|2931681   188 RQ--DANLAQLIDLIWQTDPVRRNRPTPLDEARHAVYYLQDILDETMPTL 235

                   LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                          L   Gi  R    +  + F sW+GGDRDG nP vtPE+tR+v
  gi|2931681   236 SADLADTLAVHGI--RPAATARPLSFGSWIGGDRDG-NPNVTPEITREVL 282

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    L   +A  +    ++ L+ Els     d + v  + l +      v
  gi|2931681   283 RLQHRIANRVVTASLDVLIRELST--SVDLVGVGDDLLASLEVDLEVLTD 330

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                          v   EPYR  L  +R KL  t +R    +A G + ++    y
  gi|2931681   331 LDPRLLSVNAAEPYRLKLSCMRLKLEHTADR----IAAGAAHVPGHD-YA 375
```

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                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  e L  L L   sL   G  ++AD  + D +R  s  GL L  LD+R
  gi|2931681   376 DRSELLADLALVDGSLRAHGGEIVADRMVADTIRTASLVGLHLATLDVRE 425

                    EseRqtDvlDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLlgsDL
                     ++ +   +  +   ++ ++ +Y +     R   L  EL  +RPL +
  gi|2931681   426 HADAHHHAVGLLVDRVGEqpVAYADLDRAARHRLLSVELGSRRPLSPQPP 475

                    PktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvELLq
                       E  +   + f+v+ E+    FG++  ++Yi+sm+    DvLA  +L
  gi|2931681   476 ALDEAAARTYGVFEVIREM-HGVFGPevvesYIVSMSQGADDVLAAAVLA 524

                    RECg...vkqtLrv.....vPLFEkLADLeAAPAavekLFsiDWYinrid
                    RE g  +++ + +v + + vPL E + +++ A   ++ L     Y+  +
  gi|2931681   525 REVGlvdLHSPEPVarigfVPLLETIEEIRRAGDVLDDLLGDPVYRRIVS 574

                    GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                     +++ qe+m+GYsDs K+ G     W L +Aq  +  vA ++Gv L lFH
  gi|2931681   575 LRgevQEIMLGYSDSNKEGGITTSQWELHQAQRSLRDVAARHGVTLRLFH 624

                    GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF.....GEE
                    GRGGtvGRGGGPt  AiL+qP   + G ++ t qGEvi   +  +    E
  gi|2931681   625 GRGGTVGRGGGPTYDAILAQPWGVLAGDIKFTEQGEVISDKYalpvlARE 674

                    nLCFrsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvK
                    nL        tA  L      P     +W   me +   A   YR +v
  gi|2931681   675 NLELSMAAVLTASSLHTESRQPAETLTDWDTTMELVSGRAYAAYRELV-E 723

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGG.iesLRAiPWiFaWtq
                    +P   +YF   tP    G +niGsRPa+R  sGG+i  LRAiPW+F Wtq
  gi|2931681   724 DPSLFDYFLASTPVDQLGGLNIGSRPARRPDSGGdISGLRAIPWVFGWTQ 773

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     R  +P W GvG   + A  ++      L  m ++W FF   +  +Em
  gi|2931681   774 SRQIVPGWFGVGSGLRAA--REAGHEAALAQMLEQWHFFGTFISNVEMTL 821

                    AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                    AK D  +A+ y   Lv ++L+   + +R++   t + +L++ G + lL+
  gi|2931681   822 AKTDLAVASHYVSALVPDDLQHVFDLIRAEHAITVEEVLRVTGEQRLLDH 871

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiR.DPsykvtlrPhlsKEyAdE
                     P L+  l +Rd Y+  +   q   L R R+DP            +  dE
  gi|2931681   872 QPALRRTLEIRDTYLQPISYAQVDLLARSRqDP------------DSTDE 909

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                        L   L+Lt+ GiAAG+ ntG
  gi|2931681   910 H-------------------LRRALLLTVNGIAAGLRNTG    930

gi|21909966|ref|NP_664234.1|: domain 1 of 1, from 10 to 932: score 276.1, E = 8.1e-80
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                         D  L  L     s+++ +i  +  Ll   L++i   + G+d   +
  gi|2190996    10    --DGHL-PLKKLESSNNQTIIAEEVALLKEMLEnITRRMIGDDAFTV 53

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls     K+D   Le    ++  +   +  ++ + ++ +  L n
  gi|2190996    54 IESIMVLSE----KQDYIELEK---VVANISNQEMEVISRYFSILPLLIN 96

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+           +  t+K L  k
  gi|2190996    97 ISEDVDLAYEINHQNNTDTDYLGK--------LALTIKDLAGKD-----N 133

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      + L    v  vltAHPtq  R+ +L   + i   L +       v
  gi|2190996   134 GKDILEQVNVVPVLTAHPTQVQRKTILELTTHIHKLLRKYRDAKAGVINL 183

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +     L R i     tD iR  +   + E++  m Y+   + + v K
  gi|2190996   184 EKWRQELYRYIEMIMQTDIIREKKLQVKNEIKNVMQYYDGSLIQAVTK-- 231

                    RRvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRDvC
                        t  Kn+     l  d P +i    W+GGDRDG nP vt E
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  gi|2190996   232 --LTTEYKNLAQKHGLELDNPKpITMGMWIGGDRDG-NPFVTAETLCLSA 278

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     +   +  n Yi+++  L   +s+    + L     E+ r a   +
  gi|2190996   279 TVQSEVILNYYIDKLAALYRTFSL---SSTLVQPNSEVERLASLSQDQSI 325

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRER......aRHLLAtGi..se
                    Y         +EPYR     +  +L  t    ++++ aR     G+++s
  gi|2190996   326 Y-------RGNEPYRRAFHYIQSRLKQTQIQltnqpaARMSSSVGLntSA 368

                    isEeA.......vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                     s  A+ +++   y    +F   L    +sL + G  ++ +G L +++
  gi|2190996   369 WSSPAslenpilAYDSPVDFKADLKAIEQSLLDNGNSALIEGDLREVMQA 418

                    vstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLl
                    v  FG  L  +D+Rq+s  q   +  + +  +i   Y + sE  + + Ll
  gi|2190996   419 VDIFGFFLASIDMRQDSSVQEACVAELLKGANIvDDYSSLSETEKCDVLL 468

                    aELkGK.RPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiism
                      L   +R L  + + k + ++  l  +    EL ++ + +     iis
  gi|2190996   469 QQLMEEpRTLSSAAVAKSDLLEKELAIYTTARELKdklgEEVIKQHIISH 518

                    ataPsDvLAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLF
                    + + sD+    ++ +E g+ ++++  +++vPLFE + DL+ A   ++
  gi|2190996   519 TESVSDMFELAIMLKEVGLvdqqRARVQIVPLFETIEDLDNARDIMAAYL 568

                    siDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                    s D  +  i   ++ qe+m+GYsDs KD G l+  W LYkAq E+  +
  gi|2190996   569 SHDIVKSWIATNrnyQEIMLGYSDSNKDGGYLASGWTLYKAQNELTAIGE 618

                    kyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf
                    ++GvK++ FHGRGGtvGRGGGP   Ai sqP   i+  +R t qGE+iE
  gi|2190996   619 EHGVKITFFHGRGGTVGRGGGPSYDAITSQPFGSIKDRIRLTEQGEIIEN 668

                    sFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtE
                     +G  ++ +  L     A +   +   +    E +++R++m+ +
  gi|2190996   669 KYGNKDVAYYHLEMLISASINRMVTQMITDPNEidsFREIMDSIVADSNT 718

                    EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                     YR +v+  P F +YF  A P  E   +niGsRPa Rk    i+ LRAiP
  gi|2190996   719 IYRKLVFDNPHFYDYFFEASPIKEVSSLNIGSRPAARKTITEITGLRAIP 768

                    WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                    W+F+W q R   P W GvG AFK  id+   nl +L+ mY++WPFF   l
  gi|2190996   769 WVFSWSQNRIMFPGWYGVGSAFKRYIDRAQGNLERLQHMYQTWPFFHSLL 818

                    DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                      ++mv  K    iA  y +L  + +++    ++ d+++ tk+ +L i
  gi|2190996   819 SNVDMVLSKSNMNIAFQYAQLAESQDVRDVFYEILDEWQLTKNVILAIQD 868

                    HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                    H DlLE  P LK  l+ R +Y   Ln +q   +KR R  +
  gi|2190996   869 HDDLLEDNPSLKHSLKSRLPYFNVLNYIQIELIKRWRNNQL--------- 909

                    KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        dEn    + L++                  + GiA G+ n G
  gi|2190996   910 ----DEN---DEKLIHTT----------------INGIATGLRNSG    932

gi|50913872|ref|YP_059844.1|: domain 1 of 1, from 15 to 937: score 275.9, E = 9.3e-80
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                         D  L  L     s+++ +i  +  Ll   L++i   + G+d   +
  gi|5091387    15    --DGHL-PLKKLESSNNQAIIAEEVALLKEMLEnITRRMIGDDAFTV 58

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls     K+D   Le    ++  +   +  ++ + ++ +  L n
  gi|5091387    59 IESIMVLSE----KQDYIELEK---VVANISNQEMEVISRYFSILPLLIN 101

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+           +  t+K L  k
  gi|5091387   102 ISEDVDLAYEINYQNNTDTDYLGK--------LALTIKDLAGKD-----N 138
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                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      + L    v  vltAHPtq  R+ +L   + i   L +       v
  gi|5091387   139 GKDILEQVNVVPVLTAHPTQVQRKTILELTTHIHKLLRKYRDAKAGVISL 188

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +     L R i     tD iR  +   + E++  m Y+   + + v K
  gi|5091387   189 EKWRQELYRYIEMIMQTDIIREKKLQVKNEIKNVMQYYDGSLIQAVTK-- 236

                    RRvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRDvC
                        t  Kn+     l  d P +i    W+GGDRDG nP vt E
  gi|5091387   237 --LTTEYKNLAQKHGLELDNPKpITMGMWIGGDRDG-NPFVTAETLCLSA 283

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     +   +  n Yi+++  L   +s+    + L     E+ r a   +
  gi|5091387   284 TVQSEVILNYYIDKLAALYRTFSL---SSTLVQPNSEVERLASLSQDQSI 330

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRER......aRHLLAtGiseis
                    Y         +EPYR     +  +L  t    ++++ aR     G+s  +
  gi|5091387   331 Y-------RGNEPYRRAFHYIQSRLKQTQIQltnqpaARMSSSVGLSTSA 373

                    .......EeAv..ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                     +++ + E+ +  y    +F   L    +sL + G  ++ +G L +++
  gi|5091387   374 wsspaslENPIlaYDSPVDFKADLKAIEQSLLDNGNSALIEGDLREVMQA 423

                    vstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLl
                    v  FG  L  +D+Rq+s  q   +  + +  +i   Y + sE  + + L+
  gi|5091387   424 VDIFGFFLASIDMRQDSSVQEACVAELLKGANIvDDYSSLSETEKCDVLV 473

                    aELkGK.RPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiism
                      L   +R L  + + k + ++  l  +    EL ++ + +     iis
  gi|5091387   474 QQLMEEpRTLSSAAVAKSDLLEKELAIYTTARELKdklgEEVIKQHIISH 523

                    ataPsDvLAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLF
                    + + sD+    ++ +E g+ ++++  +++vPLFE + DL+ A   ++
  gi|5091387   524 TESVSDMFELAIMLKEVGLvdqqRARVQIVPLFETIEDLDNARDIMAAYL 573

                    siDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                    s D  +  i   ++ qe+m+GYsDs KD G l+  W LYkAq E+  +
  gi|5091387   574 SHDIVKSWIATNrnyQEIMLGYSDSNKDGGYLASGWTLYKAQNELTAIGE 623

                    kyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf
                    ++GvK++ FHGRGGtvGRGGGP   Ai sqP   i+  +R t qGE+iE
  gi|5091387   624 EHGVKITFFHGRGGTVGRGGGPSYDAITSQPFGSIKDRIRLTEQGEIIEN 673

                    sFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtE
                     +G  ++ +  L     A +   +   +    E +++R++m+ +
  gi|5091387   674 KYGNKDVAYYHLEMLISASINRMVTQMITDPNEidsFREIMDSIVADSNI 723

                    EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                     YR +v+  P F +YF  A P  E   +niGsRPa Rk    i+ LRAiP
  gi|5091387   724 IYRKLVFDNPHFYDYFFEASPIKEVSSLNIGSRPAARKTITEITGLRAIP 773

                    WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                    W+F+W q R   P W GvG AFK  id+   nl +L+ mY++WPFF   l
  gi|5091387   774 WVFSWSQNRIMFPGWYGVGSAFKRYIDRAQGNLERLQHMYQTWPFFHSLL 823

                    DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                      ++mv  K    iA  y +L  + +++    ++ d+++ tk+ +L i
  gi|5091387   824 SNVDMVLSKSNMNIAFQYAQLAESQDVRDVFYEILDEWQLTKNVILAIQD 873

                    HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                    H DlLE  P LK  l+ R +Y   Ln +q   +KR R  +
  gi|5091387   874 HDDLLEDNPSLKHSLKSRLPYFNVLNYIQIELIKRWRNNQL--------- 914

                    KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        dEn    + L++                 + GiA G+ n G
  gi|5091387   915 ----DEN---DEKLIHTT----------------INGIATGLRNSG    937

gi|120610680|ref|YP_970358.1|: domain 1 of 1, from 11 to 951: score 275.8, E = 9.7e-80
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                PG+ ++ ++ +  D  Ll + L+D++ +  G    +
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gi|1206106    11    TAPEPQASPSPGRRADKDQPLIQDIRLLGRILgDVIREQEGVAAYDL 57

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls  +    D +    L   L +L    ++ v +a+     LAn
gi|1206106    58 VEQVRKLSVAFRRDADQEADKALKKLLKGLSGDQTVSVIRAFTYFSHLAN 107

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAE+ +   RRR    +       a  t E  iE  l +L   +  +P
gi|1206106   108 LAED-RHHIRRRTVHER-------AGSTQEGSIEVALARLRWAG-IAPRA 148

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL..........
                    v + L    v  vltAHPt   R+s+L  +  i   La  ++ + ++
gi|1206106   149 VAQTLARSYVSPVLTAHPTEVQRKSILDAERDIAELLAERdeiqarglfy 198

                    .sAKD.vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYi
                    +sA+D +t+ +    +  L   +   + t  +R ++ t  DE+   +sY+
gi|1206106   199 kSARDaLTPRELAANEARLRARVAQLWQTRLLRYSKLTVADEIENALSYY 248

                    HEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknP
                      t  + +P+     + AL    +       +  ++   W+GGDRDG nP
gi|1206106   249 ESTFLREIPRLYEDLERALGSQPV-------ASFLRMGQWIGGDRDG-NP 290

                    RvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEly
                     v  +           +A   Y+  v  L  Els+      L     E++
gi|1206106   291 NVSADTLALALRRQAEVALRHYLTEVHYLGGELSL---SARLVQVSPEMQ 337

                    rtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntR......ERaR
                    + a r           +q    EPYR  L  +  +L  t ++ +++E aR
gi|1206106   338 QLAERS----PDTSEHRQ---DEPYRRALTGIYARLAATLreltggEAAR 380

                    HLLAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlL
                    H +A        +  y +  eFL  L +   sL       +A   L  l+
gi|1206106   381 HAVAP-------QNPYGDASEFLADLRVIEASLRSHRGAPLAAQRLHPLV 423

                    RqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEW
                    R v  FG  L  +D+Rq s+ +  v+  +     i ++Y   +E+ Rq
gi|1206106   424 RAVEVFGFHLATVDLRQSSDQHERVVAELLATARIEAdYAALPEDARQAL 473

                    LlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGa.....Yii
                    L+  L   RPL        E  +  +  f+  A    D +Ga+  ++Yii
gi|1206106   474 LVRLLCDARPLRVVGAEYSEHTRGEIAIFET-ARRMRDRYGAqairhYII 522

                    smataPsDvLAvELLqRECgvkq.........tLrvvPLFEkLADLeAA
                    s + + sD L v LLq+E g+ +++ ++ + +  L vvPLFE + DL+ A
gi|1206106   523 SHTETVSDLLEVLLLQKEVGLMHgtldgadaraDLIVVPLFETIGDLRNA 572

                    PAavekLFsiDWYinrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAq
                       +  L+ +  +   +++++  q++m+GYsDs KD G +   W LY+A
gi|1206106   573 QPIMRALYEVPGFAAMVQrggAEQDIMLGYSDSNKDGGIFTSNWELYRAE 622

                    EEiiK....vAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGs
                      ++   +    ++ ++L lFHGRGGtvGRGGGP   AiL+qPP t+ G
gi|1206106   623 IALVElfdaLEARHRIRLRLFHGRGGTVGRGGGPSYQAILAQPPGTVRGQ 672

                    lRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE.WRkL
                    +R t qGEvi   +   ++  r L    AAtLE  +  P  P    + +
gi|1206106   673 IRLTEQGEVIASKYANPEIGRRNLETLVAATLEATLLQPTKPATKaFHEA 722

                    meemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs
                      e+       YR++v+  P F +YF   tP  E   +niGsRPa RkPs
gi|1206106   723 AAELSQASMAAYRALVYETPGFADYFFNSTPIREIAELNIGSRPASRKPS 772

                    GGiesLRAiPWiFaWtqtRFHLPvWLGvGA...AFKhAidKDiKn.lqkL
                      ie LRAiPW F+W q R  LP W G+G   +AF  A   D K ++  L
gi|1206106   773 QKIEDLRAIPWGFSWGQCRLTLPGWYGFGSaveAFVKAAGEDPKArMALL 822

                    kEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL..kPFGksL
                    + mY++WPFFR  l  ++mv AK D  +A+ y +L+    L++k FG  +
gi|1206106   823 QKMYRQWPFFRTLLSNMDMVLAKSDLALASRYSELVADARLrrKVFG-AI 871

                    RdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLK
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                    ++++ t d L +i G +  L     L   +R R +Yi  L  +q   ++
  gi|1206106   872 EAEWQRTVDALARITGDRQRLAHNTALARSIRHRFPYIDPLHHLQVELVR 921

                    RiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLt
                    R R               A E s + +  +++
  gi|1206106   922 RWR----------------AGEGSERVQTGIHIC---------------- 939

                    mKGiAAGmqntG<-*
                    + GiAAG+ ntG
  gi|1206106   940 INGIAAGLRNTG    951

gi|261365408|ref|ZP_05978291.1|: domain 1 of 1, from 1 to 900: score 275.6, E = 1.1e-79
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2613654     1    ---MQLHILNNPKDA----ALAADAEFLKQSLYKL--LHEEASPLVV 38

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls       D+  L E   +L  Ld   +  +  a      + n+
  gi|2613654    39 ETVKLLSTS----DDSAALIE--KVLPQLDEQQTHDLTLACGLFAQILNI 82

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+   RR i+          +    E  + Et++kL        + v
  gi|2613654    83 AEDVHHERRRQIHEEA-------GHGGAEGSLAETVRKLKAAK-IGGKAV 124

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL...aqLsAKDvtve
                       L    v  vltAHPt   R  +L  n RiR  L+++      D   e
  gi|2613654   125 QKQLNTTNVTAVLTAHPTEVQRQTVLNFNRRIRALLprrERCTHADALAE 174

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++E+D  L    q    t E R  +    DE+  G+s +    ++  PK
  gi|2613654   175 LRREIDTILLGLWQ----TSETRHHKISVNDEINNGVSIFPMSFFEALPK 220

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R ++   +       +P    ++k   W+GGDRDG nP v  E  R
  gi|2613654   221 LYRSMEREFQTTYPDVDVP---DILKIGGWIGGDRDG-NPFVSAETLRFA 266

                    CLLaRmmAanlYisqvEDLmFE..lsmWR..CndELRvRAEElyrtaard
                              +Y   ++ L  E +ls+ R + nd++ +  +E
  gi|2613654   267 FGRHADAVFRFYRGELDKLYRElpLSVRRvkVNDDVMALSDESPDEEIAR 316

                    kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseis
                                  +EPYR  +  +  ++     +aR L+L  G
  gi|2613654   317 --------------TEEPYRRAIAYIMARVMG---KARSLgLGMG-CKFG 348

                    EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                        y    eF + L    +sLC+ G   + +G L Dl+R vs FG  ++
  gi|2613654   349 FMMPYASAQEFSDDLYKLQRSLCDNGSALLGEGRLADLIRSVSVFGFHMM 398

                    KLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLl
                     LD+Rq +e++ Dv+  + +H ++  Y + sE  +q  Ll ELk +RPL
  gi|2613654   399 PLDLRQHAEKHADVVAELFKHAGLEDYASLSETEKQTVLLRELKHQRPLS 448

                    gsDLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvE
                     + +   E++++E++   +a ++  E    +    iis +  PsD LA
  gi|2613654   449 SPFITYSEhtrrEMAIFNEARKIKDEFGENAVTQSIISNCEQPSDLLALA 498

                    LLqRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYin
                    LL +E g+ + ++++++  + +vPLFE +  Le A   +e +Fs +WY+
  gi|2613654   499 LLLKESGLltvengkpQSRINIVPLFETIEALENACPVMETMFSNEWYRD 548

                    ridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                     ++ +++ qe+m+GYsDs KD G +   W LY+A   ++   Kky v++
  gi|2613654   549 LLQSRdniQEIMLGYSDSNKDGGYVTSSWCLYQAELGLVELFKKYDVRMR 598

                    lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                    lFHGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|2613654   599 LFHGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGN 648

                    CFrsLqRFtAAtLEHGmnPPv.sPkPEWRkLmeemAvvAtEEYRsvvvKE
                      r L    AAtLE  + P  + P P    Lm+ +  v    YR ++
  gi|2613654   649 AVRNLETLVAATLEASLLPDQkDPEP---ALMQALSDVSFKYYRELITH- 694
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                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
                    P F++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R
  gi|2613654   695 PDFIDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNR 744

                    FHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAK
                      LP W G+G A     +     l  L+   +  PFF   l  +E v AK
  gi|2613654   745 LMLPAWYGFGSAVESLCEGKPETLAALQAHAQHNPFFQAMLSNMEQVMAK 794

                    GDPGiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                     D  +A  y  L  ++E        ++++Y+  ++ LL +    +lL
  gi|2613654   795 TDITLAENYAGLSESpEKAAVIFGMIKEEYQRSRKALLDLLQTDELLRDN 844

                    PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                      L   l LR +Y+  Ln +q   LKR+R                  ++
  gi|2613654   845 RSLARSLALRIPYLNALNGLQVAMLKRLR-----------------KDP- 876

                    kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    + +  L+ +               Lt+ G+A G+ ntG
  gi|2613654   877 HDPHTLLMVH--------------LTINGVAQGLRNTG    900

gi|16588669|gb|AAL26863.1|AF314923_1: domain 1 of 1, from 1 to 391: score 275.1, E = 1.6e-79
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1658866     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1658866     - ------------------------------------------------ -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1658866     - ------------------------------------------------ -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1658866     - ------------------------------------------------ -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1658866     - ------------------------------------------------ -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1658866     - ------------------------------------------------ -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1658866     - ------------------------------------------------ -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1658866     - ------------------------------------------------ -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1658866     - ------------------------------------------------ -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1658866     - ------------------------------------------------ -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1658866     - ------------------------------------------------ -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                        LFs+DW + ri+GKqevm+GYsDsGKDAG
  gi|1658866     1 --------------------LFSVDWHRDRINGKQEVMIGYSDSGKDAG 29

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
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                    RlsAAW LYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1658866     30 RLSAAWALYKAQEELIKVAKDFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 79

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtv GEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PPv+P
  gi|1658866     80 PPDTIHGSLRVTVEGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVAP 129

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAv+AtEEYRs+v++EPRFvEYFR AtPElEYG+mniGsR
  gi|1658866    130 KPEWRALMDEMAVIATEEYRSIVFQEPRFVEYFRCATPELEYGRMNIGSR 179

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+h ++KD Knl
  gi|1658866    180 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHVVKKDPKNL 229

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+L++mY++WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+EeL+ FG++
  gi|1658866    230 QMLQDMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVTEELWSFGER 279

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR  Y+Etk lLL++AGH+DlLEGDPYLKqrlRLRdsY ttLnv+qAYtL
  gi|1658866    280 LRSMYEETKRLLLQVAGHRDLLEGDPYLKQRLRLRDSYTTTLNVLQAYTL 329

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+v l+PhlsK+y  E s +a+eLvkLnpt+++aPGLEDtLiL
  gi|1658866    330 KRIRDPDYHVNLKPHLSKDYM-ESSNPAAELVKLNPTSEYAPGLEDTLIL 378

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|1658866    379 TMKGIAAGMQNTG    391

gi|221633046|ref|YP_002522271.1|: domain 1 of 1, from 6 to 928: score 275.0, E = 1.7e-79
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       ++D    + +       e L +   LL     D+L +  G +L + v
  gi|2216330      6    ALDDERSAKALRAEP-IEGLRNEVNLLGALLGDVLREQGGTELFDLV 51

                    qECYElsAeYEGKkDtk.KLeELGakLtsLdPaDailvAkailHmLnLAn
                          s         ++    L a+L      +   + +a+     L n
  gi|2216330     52 EWARLQSITGRTVGNMSdAFRGLLARLEEASDEEIFGLVRAFGIFFHLIN 101

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAE     +R R  +++         A  Es +EE +  L  ++   P+
  gi|2216330    102 LAEQ---HHRVRTLRQR----ERQERALHES-LEEAFLTLRDRG-VEPDR 142

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v e L       vltAHP    RR +Lq+ a +   + qL    + + ++
  gi|2216330    143 VKELLDDLLLFPVLTAHPSETRRRTVLQRLAALGQLIQQLDDTRLSPRER 192

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L + L  Ei   + t E R a+PtP DE+R  ++ +   +++ vP F
  gi|2216330    193 DWLFDRLREEITLLWQTAETRLARPTPLDEVRSTIAILAGPIYDVVPFFR 242

                    RRvDtALKni..GinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    R    A+    + +     ++   i+  sW+GGDRDG nP vt  vt
  gi|2216330    243 RALRRAILRAypELTSEALWNRLPIRIGSWVGGDRDG-NPAVTAAVTEAT 291

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      L R      Y++ v DL   ls+      LR   +El  t  ++   +
  gi|2216330    292 ARLMREAILRRYLEEVVDLRRALSV---SARLRGASDELMATIDQE---R 335

                    yYiEFW.KqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                      + F +      EPYR +LG + ++L  t ER             E+
  gi|2216330    336 ERLGFApVRAWADEPYRRMLGLIEERLRRT-ERG-----------EQGG 372

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y   EeF   L +   sL +   + iADG L Dl+  v  FG  L  L+i
  gi|2216330    373 YAGPEEFATHLKVMADSLRQHEGHWIADGRLADLIARVDVFGFHLAELEI 422

                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaEL.kGKRPLlgsD
                    Rq++ R  + l  +   ++   Y   + + R   +l+ L++G   L
  gi|2216330    423 RQDAARYREALAELFALVGCAGYEAMPSDEREHLVLTRLeQGVFGLPRGA 472
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                    L.PktEEvkDvldafrvLAELPiD.sFGaYiismataPsDvLAvELLqRE
                    L+P t Ev    da+  +  L  +++    i+sm+  P+DvL   +L RE
  gi|2216330   473 LsPDTREVLATFDAIGRIQRLSGErACHTVIVSMTREPADVLGTVVLARE 522

                    Cg.........vkqt.LrvvPLFEkLADLeAAPAavekLFsiDWYin..r
                     g  +  +++ v++ ++ vvPLFE++A+L+     +++L +   Y+   r
  gi|2216330   523 AGlidfatdgaVRHCrIDVVPLFEQIAELDRCDQILARLLANPIYRTvvR 572

                    idG.KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                    + G++qevm+GYsDs KD G +s  W +Y+AqE ++ vA+++G +L lF
  gi|2216330   573 LRGnQQEVMLGYSDSNKDGGYVSSNWRIYRAQERLAEVARQFGAQLRLFY 622

                    GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                    GRGG +GRGGGP   Ai + P       l+ t qGEvi   + +  +  r
  gi|2216330   623 GRGGAIGRGGGPMGRAIRARPAAARRPVLKTTEQGEVIFARYSDPAIALR 672

                    sLqRFtAAtL.EHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                         t A ++  G +P  s    W ++me++A    E Y  +v  EP F
  gi|2216330   673 HWEQMTHASIgSLGSDPDPSMPESWYRMMEQLATWSQEAYERLVKDEPTF 722

                    vEYFRlAtPElEYGkmniGsRPaKRk..PsGGi..esLRAiPWiFaWtqt
                    v +F +AtP  E   +n+ sRP  R+++P  G+    LRAiPW+F+Wtqt
  gi|2216330   723 VRFFTSATPFPELASLNLASRPVARRgsPESGLcfADLRAIPWVFSWTQT 772

                    RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                    R  LP W G+G A   A+         L+EmY  WPFF + lD   +  A
  gi|2216330   773 RVNLPGWYGLGTALERALAAGEES--TLREMYYRWPFFEMLLDNAQISLA 820

                    KGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                      D  iA  y  L  a +     +++ ++Y+     +L + G  +lLE
  gi|2216330   821 TADMLIAECYATL--AGDDGWIAERIAEEYQRAVRTILAVTGQCELLERS 868

                    PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                    P L   +RLR++Y+  L  +q   L+R R                A
  gi|2216330   869 PILARLVRLRNPYVDVLHACQIVLLRRYR----------------AGAG- 901

                    kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     k +   +L           D +   +  iAAG+q tG
  gi|2216330   902 -KGERQSRLL----------DAIHHSINAIAAGLQTTG    928

gi|94993920|ref|YP_602018.1|: domain 1 of 1, from 15 to 937: score 274.6, E = 2.3e-79
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                         D  L  L     s+++ +i  +  Ll   L++i   + G+d   +
  gi|9499392    15    --DGHL-PLKKLESSNNQTIIAEEVALLKEMLEnITRRMIGDDAFTV 58

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls     K+D   Le    ++  +   +  ++ + ++ +  L n
  gi|9499392    59 IESIMVLSE----KQDYIELEK---VVANISNQEMEVISRYFSILPLLIN 101

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+           +  t+K L  k
  gi|9499392   102 ISEDVDLAYEINHQNNTDTDYLGK--------LALTIKDLAGKD-----N 138

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      + L    v  vltAHPtq  R+ +L   + i   L +       v
  gi|9499392   139 GKDILEQVNVVPVLTAHPTQVQRKTILELTTHIHKLLRKYRDAKTGVINL 188

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +     L R i     tD iR  +   + E++  m Y+   + + v K
  gi|9499392   189 EKWRQELYRYIEMIMQTDIIREKKLQVKNEIKNVMQYYDGSLIQAVTK-- 236

                    RRvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRDvC
                        t  Kn+     l  d P +i    W+GGDRDG nP vt E
  gi|9499392   237 --LTTEYKNLAQKHGLELDNPKpITMGMWIGGDRDG-NPFVTAETLCLSA 283

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     +   +  n Yi+++  L   +s+    + L     E+ r a   +
  gi|9499392   284 TVQSEVILNYYIDKLAALYRTFSL---SSTLVQPNSEVERLASLSQDQSI 330

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRER......aRHLLAtGi..se
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                    Y         +EPYR     +  +L  t    ++++ aR     G+++s
  gi|9499392   331 Y-------RGNEPYRRAFHYIQSRLKQTQIQltnqpaARMSSSVGLntSA 373

                    isEeA.......vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                     s  A+ +++   y    +F   L    +sL + G  ++ +G L +++
  gi|9499392   374 WSSPAslenpilAYDSPVDFKADLKAIEQSLLDNGNFALIEGDLREVMQA 423

                    vstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLl
                    v  FG  L  +D+Rq+s  q   +  + +  +i   Y + sE  + + Ll
  gi|9499392   424 VDIFGFFLASIDMRQDSSVQEACVAELLKGANIvDDYSSLSETEKCDVLL 473

                    aELkGK.RPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiism
                      L   +R L  + + k + ++  l  +    EL ++ + +     iis
  gi|9499392   474 QQLMEEpRTLSSAAVAKSDLLEKELAIYTTARELKdklgEEVIKQHIISH 523

                    ataPsDvLAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLF
                    + + sD+    ++ +E g+ ++++  +++vPLFE + DL+ A   ++
  gi|9499392   524 TESVSDMFELAIMLKEVGLvdqqRARVQIVPLFETIEDLDNARDIMAAYL 573

                    siDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                    s D  +  i   ++ qe+m+GYsDs KD G l+  W LYkAq E+  +
  gi|9499392   574 SHDIVKSWIATNrnyQEIMLGYSDSNKDGGYLASGWTLYKAQNELTAIGE 623

                    kyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf
                    ++GvK++ FHGRGGtvGRGGGP   Ai sqP   i+  +R t qGE+iE
  gi|9499392   624 EHGVKITFFHGRGGTVGRGGGPSYDAITSQPFGSIKDRIRLTEQGEIIEN 673

                    sFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtE
                     +G  ++ +  L     A +   +   +    E +++R++m+ +
  gi|9499392   674 KYGNKDVAYYHLEMLISASINRMVTQMITDPNEidsFREIMDSIVADSNT 723

                    EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                     YR +v+  P F +YF  A P  E   +niGsRPa Rk    i+ LRAiP
  gi|9499392   724 IYRKLVFDNPHFYDYFFEASPIKEVSSLNIGSRPAARKTITEITGLRAIP 773

                    WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                    W+F+W q R   P W GvG AFK  id+   nl +L+ mY++WPFF   l
  gi|9499392   774 WVFSWSQNRIMFPGWYGVGSAFKRYIDRAQGNLERLQHMYQTWPFFHSLL 823

                    DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                      ++mv  K    iA  y +L  + +++    ++ d+++ tk+ +L i
  gi|9499392   824 SNVDMVLSKSNMNIAFQYAQLAESQDVRDVFYEILDEWQLTKNVILAIQD 873

                    HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                    H DlLE  P LK  l+ R +Y   Ln +q   +KR R  +
  gi|9499392   874 HDDLLEDNPSLKHSLKSRLPYFNVLNYIQIELIKRWRNNQL--------- 914

                    KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        dEn    + L++                  + GiA G+ n G
  gi|9499392   915 ----DEN---DEKLIHTT---------------INGIATGLRNSG    937

gi|94970716|ref|YP_592764.1|: domain 1 of 1, from 13 to 900: score 274.4, E = 2.5e-79
                    *->siDAqLRlLvPGKvsed...ekLieYDALLlDkFL.DiLqDLHGedL
                       + D   RlL      +d+++e  ++ D   l   L+ +L +  G++
  gi|9497071    13    AADQHERLLELTAATDDprkEIPLRRDVRSLGILLgRVLVEQAGPQT 59

                    kEavqECYElsAeYEGKkDtkK.....LeELGakLtsLdPaDailvAkai
                      av     +      +   + ++++ LeE    + sLd a    + ka+
  gi|9497071    60 FNAVETLRNVLIKHRERTRIESgtgtlLEEAQEFVASLDLATMYRISKAF 109

                    lHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvl
                         L nLAE  +   RRR ++++      E  A   s    tl++L
  gi|9497071   110 GTYFELTNLAETNHRKRRRRASQLH-----AEQPALPGS-FRGTLQHLRE 153

                    klnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsA
                        s e v +AL    v  v+tAHPt   RR  L K  +i   L  L
  gi|9497071   154 TA-ISSEQVLQALSELQVVPVFTAHPTEITRRTTLLKRRKIAETLERLDV 202

                    KDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtv
                      +   D +E +  L  Ei A +  DE+R  +Pt  DE+R G+ Y+   +
  gi|9497071   203 LPLSEMDAEEHEARLMAEITALWQSDEVRLHRPTVDDEIRGGIRYFNLSL 252
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                    WkGvPKFLRRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvt
                    +  +P     +  AL+     E  P d P +++F sW+GGDRDG nP vt
  gi|9497071   253 FAAIPELYEEIGAALRATLEVEIEPTDLPiMLRFGSWIGGDRDG-NPLVT 301

                    PEvtRDvCLLaRmmAanlYisqvEDLmFElsm....WRCndELRvRAEEl
                       t D   LaR      Y++q   +   ls+++++    d LR+  E+
  gi|9497071   302 AKETTDAAELAREAVLHHYVEQARVIGRALSIsehqVGISDNLRALVEDY 351

                    yrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAt
                     +   +          +   P  E YR               Ra  L+A
  gi|9497071   352 EKLIPQR------ASEYERTPKPEYYR---------------RALLLMAM 380

                    GiseisEe....AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLR
                     +s  s e+++ A y +  eF   L L   sLCe     +    L  lL
  gi|9497071   381 RLSLASREpdhaAAYRDAFEFEKDLRLLHASLCEHNGARLSRQRLDALLL 430

                    qvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLl
                    +v t G  L  LDiRq +  + +v
  gi|9497071   431 KVRTHGFRLHTLDIRQHARVHNEV------------------------- 454

                    aELkGKRPLlgsDLPktEEvkDvldafrvLAELPi...DsFGaYiismat
                      L+G           t + + v++++r +  L  + +D    Y+is a
  gi|9497071   455 --LSG----------ETNDAQQVIETLRTVSSLKQrfgDIVRQYVISGAE 492

                    aPsDvLAvELLqRECgvkqt.......LrvvPLFEkLADLeAAPAavekL
                    + sD L v  L    gv   +++++++L  vPLFE +  L+   A +  +
  gi|9497071   493 TASDLLGVCELANRAGVSTVggdtdsgLMPVPLFESIDALRKSAAVMREV 542

                    FsiDWYinrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvA
                    ++   Y+  +d+ +G qevm+GYsDs KD G l   W +Y A   +   A
  gi|9497071   543 WADRAYRKLVDswgGWQEVMLGYSDSNKDGGMLTSMWEIYNAHHALHDAA 592

                    KkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviE
                    ++ GvKL lFHGRGGtvGRGGGPtH AiL+qP     G +R+t qGEv+
  gi|9497071   593 REAGVKLRLFHGRGGTVGRGGGPTHSAILAQPAGDFTGQIRITEQGEVLN 642

                    fsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEY
                      + +  L    L    AA LE  + P  +P+  W   m+em   A   Y
  gi|9497071   643 WKYADPLLAEWNLEVVLAAALEARLRPTSAPQAAWMAAMDEMSREAFSFY 692

                    RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWi
                    R  +  +P   EYF lAtP  E      GsRPa+R  s  ++ LRAiPW+
  gi|9497071   693 RQHIAEDPALLEYFELATPVNELEFARAGSRPARRSSSRSLNDLRAIPWV 742

                    FaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDL
                    F W q R  +P W GvG AF             L+Em   +P F   +
  gi|9497071   743 FGWMQSRHAVPAWFGVGHAFET-----FGQTELLREMLGGFPLFLDMVQN 787

                    lEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGH
                    +E+  AK D  iA Ly  L+    L+ +  ++L d+++ t+  +L +
  gi|9497071   788 VELAMAKADLSIAKLYSALVPDRSLRErIFDKLADEFERTRRQILSLKQQ 837

                    kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                     +lLE  P L   +RLR++Y+  L  +q   L+R R
  gi|9497071   838 SELLEKNPVLLRSIRLRNPYVDPLSLVQVELLRRKRS------------- 874

                    EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        E+         Ln    +a G       tm GiAAG+ ntG
  gi|9497071   875 GMESEE---------LN----YALG------STMNGIAAGLHNTG    900

gi|68536075|ref|YP_250780.1|: domain 1 of 1, from 10 to 948: score 274.0, E = 3.5e-79
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +i      ++   +s     ++ D   l + L++++ +  G+
  gi|6853607    10    AIPVAPEEIAHPEIS---PTVRDDTRYLGRILgEVIREQEGDYTFNL 53

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +      sA ++ +     +eEL  +   L    a+ v +a++H   +An
  gi|6853607    54 IENTR--SAAFDLRYGEMPIEELAEQFNKLPTEKALPVIRAFSHFALMAN 101

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
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                LAE+    y  R++ +      D ++    s +  t + L  +     e
gi|6853607   102 LAEDL---YVERVRDLE----EDRGNTAPRSTLAYTWQELHNRE-VPGEK 143

                vFeALKnqsvDLvltAHPtqsvRRsL......LqKnaRiRn.CLaqLsAK
                v e + n  v  vltAHPt   RR + + ++++ K  R R + L  L
gi|6853607   144 VAETMANALVAPVLTAHPTETRRRTVfdvqtdIMKMMRRRArVLKELKLN 193

                DvtveDKkELDE...ALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHE
                   v   + L E +  + R +   + t  i   +P   DE++ G+ Y+
gi|6853607   194 PDSVRSARQLAEielVIRRRMTLLWQTSLIGSVRPRIEDEIKVGLRYYGI 243

                tvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRv
                 +   +P   RRv   +K     + +P  + +++  sW+GGD DG nP v
gi|6853607   244 SLLSEIPAINRRVNEHMKE-QYGDVVPRTA-VVRPGSWIGGDHDG-NPYV 290

                tPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrt
                t E        a       Y   +  L  Els+    +      E l +
gi|6853607   291 TAETVGIATTFAARTIFDHYQKTIYALEHELSL---SSKFIDTTEALEQL 337

                aardkvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERa..RHLLA
                a r             vP++  EP+R  L  +R ++  t   + +  ++
gi|6853607   338 ADRG---------RNDVPsrVDEPFRRALHGMRGRVAATAKHTlgEPVVS 378

                tGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvs
                 Gi    E   y +  e L  ++    +L    D  +AD  L Dl   v
gi|6853607   379 GGIHKGHEP--YANPAELLADIDTVDEALRHSMDDLLADHTLADLREAVE 426

                tFGLsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaE
                tFG  L  LD+Rq se    vl  +    ++ + Y e  E+ + E Ll+E
gi|6853607   427 TFGFNLYSLDLRQNSESFENVLTEVFARAGVAeNYAELDEDAKVELLLTE 476

                LkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGa.....Yiismat
                L   RPL  ++    EE +  l+ fr  A      FGa+  ++ iisma
gi|6853607   477 LASPRPLADPEAEWSEETARELGIFRAAAK-AAKKFGAevvphCIISMAS 525

                aPsDvLAvELLqRECgvkqt........LrvvPLFEkLADLeAAPAavek
                + sDv+   +L +E g+ q++++++++++ ++PLFE + DL      + +
gi|6853607   526 SVSDVIEPMILLKEVGLIQAngehpqgsVDIIPLFETIDDLAGGADIMRQ 575

                LFsiDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKv
                L+ +  Y+n + G+++ qe+m+GYsDs KD G ++A W LY A   ++
gi|6853607   576 LWQLPLYRNYVAGRgdiQEIMLGYSDSNKDGGYFAANWALYDAELALVEA 625

                AKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEvi
                 ++ G  L lFHGRGGtvGRGGGP   AiL+qP   ++G++R+t qGE+i
gi|6853607   626 SREAGLFLRLFHGRGGTVGRGGGPSYDAILAQPKGAVQGAVRITEQGEII 675

                EfsFGEEnLCFrsLqRFtAAtLEHGmnPP..vsPkPEWRkLmeemAvvAt
                   +G+     r L    AAtLE  + P +++       + m ++A
gi|6853607   676 SAKYGDPANASRNLEALVAATLEASLLPVddLDDPDVAFETMRQIAEESR 725

                EEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAi
                  Y +++  +P F+EYF   tP  E G +niGsRP+ Rk    +  LRAi
gi|6853607   726 KAYSALMHEDPGFIEYFTTSTPLAEIGSLNIGSRPSSRKQTTAVSDLRAI 775

                PWiFaWtqtRFHLPvWLGvGAAFKhAidKDi.......KnlqkLkEmYke
                PW+ +W q R  LP W GvG A K  i+  ++ +++ +  l  L+E+ +
gi|6853607   776 PWVLSWSQSRVMLPGWFGVGSALKRWIEDGSsvsgdatSRLNYLRELHRR 825

                WPFFRvtlDLlEmvFAKGDPGiAaLyDkLLv.aEeLkPFGksLRdkYvEt
                WPFF   l  +  v  K D  iA Ly +L+ + E      + + ++Y+ t
gi|6853607   826 WPFFDSVLSNMAQVMSKADLSIAQLYSELVGdREAAERIFDVIVEEYKLT 875

                kdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsy
                 ++ L+i     lL   P L   +R R +Y+  Ln +q   L+R R
gi|6853607   876 VEMFLQITERETLLADNPELVSSVRNRFPYLVPLNLLQVELLRRFR---- 921

                kvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAG
                            A ++            ++ v  G+     Ltm G+A
gi|6853607   922 ------------AGDD------------SDSVRSGIQ----LTMNGLATA 943
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                    mqntG<-*
                    + n G
  gi|6853607   944 LRNSG    948

gi|73540405|ref|YP_294925.1|: domain 1 of 1, from 52 to 1006: score 273.9, E = 3.7e-79
                    *->siDAqLRlLv.PGKvsedekLi..eYDALLlDkFL.DiLqDLHGedL
                        + A   l ++P + s  +k ++ + D   l + L++ L +  G+
  gi|7354040    52    VVPANGALNAsPARRSATDKDVplREDIRFLGRLLgECLREQEGDAT 98

                    kEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLn
                     E+v      +  +    D     EL   L  L    +  v +a++
  gi|7354040    99 FEVVETIRQTAVRFRRENDRAAGTELDRLLKRLSRDQTNQVVRAFSYFSH 148

                    LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                    LAn+AE+ +   RRRi+ +        +s   +  +   l k+   +  +
  gi|7354040   149 LANIAEDQHHNRRRRIHALA-------GSPPQDGSLQHALEKIDAAG-VT 190

                    PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                     +     L    +  vltAHPt   R+s+L  +  i   La      +t
  gi|7354040   191 GKQLRKFLDEALIVPVLTAHPTEVQRKSILDAEREIARLLAE-RDLPMTA 239

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                     ++      L   +   + t  +R ++ t  DE+   +sY+  t  +G+P
  gi|7354040   240 RERDRNTAQLRAKVTTLWQTRMLRDSRLTVADEIDNALSYYRTTFLHGIP 289

                    KFLRRvDtALKni........GinERlPYdvPLikFssWmGGDRDGknPR
                    + +   +  +  i + +++++G        +P ++  sW+GGDRDG nP
  gi|7354040   290 QLMSELEEDIAAIfpasrktkGAAAEAAPLAPFMQMGSWIGGDRDG-NPN 338

                    vtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE.Ely
                    vt E           m    Y++ v  L  Elsm    + L v A +El
  gi|7354040   339 VTAETLDHAATQQSRMILGWYLDEVHALGAELSM----STLMVDASpELL 384

                    rtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtG
                      a       +          EPYR  L  +  +L  t   ++ L  +G
  gi|7354040   385 ALAEAS--PDHSAH-----RADEPYRRALIGIYARLAAT---SKMLTGQG 424

                    ise..isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvs
                       +++++   y   E F   + +   sL     +++    +  l+R +
  gi|7354040   425 APRhpVADAEPYSSAEAFAADVQIVIDSLRAHHGRALTSTRIDALVRAIA 474

                    tFGLsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaE
                     FG  L  +D+Rq s+ +  v+  +    ++ + Y   +E ++ E LlaE
  gi|7354040   475 VFGFHLASVDMRQVSDVHEAVVAELFAAAGVEkDYAALPESRKLELLLAE 524

                    LkGKRPLlgsDLPktEEvkDvldafrvLAELPi....DsFGaYiismata
                    L+  R L  +     E  +  l  +    EL  + ++     Yiis + +
  gi|7354040   525 LRQPRLLTLPYHEYSEQTRNELAILATARELRArygqRVARNYIISHTET 574

                    PsDvLAvELLqRECgv.............kqtLrvvPLFEkLADLeAAPAa
                     sD + v LLq+E g+ +++ ++++++ +  L v+PLFE + DL+ A
  gi|7354040   575 LSDLVEVMLLQKEAGMlkgtlgsktdpaRMELMVIPLFETIEDLQNAAGI 624

                    vekLFsi...DWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEi
                    ++ L  +++ D  i +    qevm+GYsDs KD G l   W LYkA   +
  gi|7354040   625 MQSLLDLpgfDSVIEHHGVEQEVMLGYSDSNKDGGFLTSNWELYKAELAL 674

                    iKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqG
                    ++   +  vKL lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qG
  gi|7354040   675 VQLFEQRKVKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQG 724

                    EviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemA
                    E+i   F   ++  r L    AAtLE  + P      E +++  +m+++
  gi|7354040   725 EIINSKFANAEIGRRNLETVIAATLEASLLPQQNAPKElstFEGIMQQLS 774

                    vvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....
                      A   YR +v+  P F +YF   tP +E   +n+GsRPa Rk   ++++
  gi|7354040   775 DRAFGAYRNLVYETPGFKDYFFATTPITEIADLNLGSRPASRKLMDkknr 824

                    GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidK..DiK....nlqk
                     ie LRAiPW F+W q R  LP W G+G A K  +d  +D K ++  +
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  gi|7354040   825 RIEDLRAIPWGFSWGQCRLLLPGWYGFGSAVKSLLDTapDEKarkaAVAT 874

                   LkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksL
                   L+ m k+WPFF   l  ++mv AK D  +A+ y +L     L+k    ++
  gi|7354040   875 LRKMVKTWPFFSTLLSNMDMVLAKTDLAVASRYAQLCDDAALrKNVFARI 924

                   RdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLK
                     ++  t ++L  + GH++ L   P L   ++ R +Y+  Ln +q   LK
  gi|7354040   925 SKEWHLTCEMLALVTGHQERLADNPLLARSIKNRFAYLDPLNHLQVELLK 974

                   RiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLt
                   R R                   s k  + +++             + Lt
  gi|7354040   975 RYR-------------------SGKDGDDIRVR----------RGIHLT 994

                   mKGiAAGmqntG<-*
                   + G+AAG+ ntG
  gi|7354040   995 INGVAAGLRNTG    1006

gi|91789513|ref|YP_550465.1|: domain 1 of 1, from 18 to 970: score 273.8, E = 3.8e-79
                   *->siDAqLRlL.......vPGKvs....edekLieYDALLlDkFL.DiL
                       i A  R ++++ +++ PGK  ++ +++e+ +  D  Ll + L+D++
  gi|9178951    18    VISARARKVsenakdgTPGKTGtrarDNERPLVEDIRLLGRILgDVI 64

                   qDLHGedLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvA
                    +  G    E +     ls  +    D +    L   L +L    ++ v
  gi|9178951    65 REQEGVTAYELIEQVRKLSVAFRRDADQEADKALKKLLKGLSGEQTVSVI 114

                   kailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKk
                   +a+     LAnLAE+ +   RRR    + GD       t E  iE  l +
  gi|9178951   115 RAFTYFSHLANLAED-RHHIRRRAVHERAGD-------TQEGSIEVALAR 156

                   LvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq
                   L   +  sP+ +   L    v  vltAHPt   R+s+L  +  i   L+
  gi|9178951   157 LRWAG-ISPKTIATTLAHSFVSPVLTAHPTEVQRKSILDAERDIAQLLTA 205

                   L...........sAKD.vtveDKkELDEALHREiqAAFRtDEiRRaqPtP
                    ++ +     ++ AKD +t+ +    +  L   +   + t  +R ++ t
  gi|9178951   206 RddikalalatnAAKDaLTPRELAANEAQLRARVMQLWQTRLLRFSKLTV 255

                   qDEmRaGmsYiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFss
                    DE+   +sY+  t  + +PK     +  L n  +          ++
  gi|9178951   256 ADEIENALSYYEATFLREIPKLYANLERELGNQPVHS-------FLRMGQ 298

                   WmGGDRDGknPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCn
                   W+GGDRDG nP v  +           +A   Y+  v  L  Els+
  gi|9178951   299 WIGGDRDG-NPNVSADTLNYALARQAEVALRHYLTEVHYLGGELSL---S 344

                   dELRvRAEElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYnt
                     L +    ++  a +        E  K     EPYR  L  v  +L  t
  gi|9178951   345 AMLVAVSPGMQALAESS---PDTNEHRK----DEPYRRALTGVYARLAAT 387

                   R......ERaRHLLAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDk
                    ++ +++E aRH +A      + +A y + E+FL  L     sL
  gi|9178951   388 LkeltggEAARHAVA------PQNA-YARAEDFLADLRTIETSLRSNHGE 430

                   viADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiG.sY
                   ++    L  l+R v  FG  L  +D+Rq s+++ +v+  +     i + Y
  gi|9178951   431 ALIAQRLHPLIRAVEVFGFHLATVDLRQSSDKHEEVVAELLAVARIEpRY 480

                   ReWsEeKRqEWLlaELkGKRPL.lgsDLPktE...EvkDvldafrvLAEL
                    +  E  ++  L+  L   RPL++ s +     ++E++    a    A
  gi|9178951   481 PSLDEAAKRALLIRLLNDARPLrVISTIYSAHaqsELAIFEAARTARARF 530

                   PiDsFGaYiismataPsDvLAvELLqRECgvkqt.........LrvvPLF
                     ++   Yiis + + sD L v LLq+E g+ + + +++ +++L vvPLF
  gi|9178951   531 GKEAIRHYIISHTETVSDLLEVLLLQKEVGLMHRtlddkatndLIVVPLF 580

                   EkLADLeAAPAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRls
                   E + DL+ A   +   ++ ++i   + r    q++m+GYsDs KD G +
  gi|9178951   581 ETIEDLRNAAPIMREYYAlpgIAQLVQRSGAEQDIMLGYSDSNKDGGIFT 630
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                    AAWqLYkAqEEii....KvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                      W LY+A   +++  ++ A  + ++L +FHGRGGtvGRGGGP   AiL+
  gi|9178951   631 SNWELYRAEIALVelfdQLANSHNIQLRMFHGRGGTVGRGGGPSYQAILA 680

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                    qPP t+ G +R t qGEvi   +   ++  r L    AAtLE  +  P
  gi|9178951   681 QPPGTVRGQIRLTEQGEVIGSKYANPEIGRRNLETLVAATLEATLLQPTK 730

                    PkPE.WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniG
                    P    + +   e+       YR++v+  P F EYF  AtP  E   +niG
  gi|9178951   731 PATKaFLQAAAELSQASMAAYRALVYDTPGFNEYFFGATPIREIAELNIG 780

                    sRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidK...
                    sRPa Rk s  ie LRAiPW F+W q R  LP W G+GAA    +d +++
  gi|9178951   781 SRPASRKASQKIEDLRAIPWGFSWGQCRLTLPGWYGFGAAIEKMLDAggt 830

                    ...DiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaE
                    + +    l  L+ mYk+WPFFR  l  ++mv AK D  +A+ y +L+
  gi|9178951   831 patRKEALALLQKMYKQWPFFRTLLSNMDMVLAKSDLALASRYAELVADA 880

                    eL.kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYitt
                     L+k     + +++  t + L  i G k  L G   L+  +R R +Yi
  gi|9178951   881 RLrKKVFTAIEAEWHRTAEALTLITGEKQRLAGNAALQRSIRHRFPYIDP 930

                    LnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpterva
                    L  +q   ++R R                  E   kad+ v+
  gi|9178951   931 LHHLQVELVRRYR-----------------EG--KADQKVQTG------ 954

                    PGLEDtLiLtmKGiAAGmqntG<-*
                          + + + GiAAG+ ntG
  gi|9178951   955 ------IHISINGIAAGLRNTG    970

gi|73920189|sp|Q8K873.2|CAPP_STRP3: domain 1 of 1, from 1 to 920: score 273.8, E = 4e-79
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                            L+ L     s+++ +i  +  Ll   L++i   + G+d   +
  gi|7392018     1    ---MPLKKL---ESSNNQTIIAEEVALLKEMLEnITRRMIGDDAFTV 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls     K+D   Le    ++  +   +  ++ + ++ +  L n
  gi|7392018    42 IESIMVLSE----KQDYIELEK---VVANISNQEMEVISRYFSILPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+           +  t+K L  k
  gi|7392018    85 ISEDVDLAYEINHQNNTDTDYLGK--------LALTIKDLAGKD-----N 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      + L    v  vltAHPtq  R+ +L   + i   L +       v
  gi|7392018   122 GKDILEQVNVVPVLTAHPTQVQRKTILELTTHIHKLLRKYRDAKAGVINL 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +     L R i     tD iR  +   + E++  m Y+   + + v K
  gi|7392018   172 EKWRQELYRYIEMIMQTDIIREKKLQVKNEIKNVMQYYDGSLIQAVTK-- 219

                    RRvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRDvC
                        t  Kn+     l  d P +i    W+GGDRDG nP vt E
  gi|7392018   220 --LTTEYKNLAQKHGLELDNPKpITMGMWIGGDRDG-NPFVTAETLCLSA 266

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     +   +  n Yi+++  L   +s+    + L     E+ r a   +
  gi|7392018   267 TVQSEVILNYYIDKLAALYRTFSL---SSTLVQPNSEVERLASLSQDQSI 313

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRER......aRHLLAtGi..se
                    Y         +EPYR     +  +L  t    ++++ aR     G+++s
  gi|7392018   314 Y-------RGNEPYRRAFHYIQSRLKQTQIQltnqpaARMSSSVGLntSA 356

                    isEeA.......vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                     s  A+ +++   y    +F   L    +sL + G  ++ +G L +++
  gi|7392018   357 WSSPAslenpilAYDSPVDFKADLKAIEQSLLDNGNSALIEGDLREVMQA 406

                    vstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLl
                    v  FG  L  +D+Rq+s  q   +  + +  +i   Y + sE  + + Ll
```

```
  gi|7392018   407 VDIFGFFLASIDMRQDSSVQEACVAELLKGANIvDDYSSLSETEKCDVLL 456

                   aELkGK.RPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiism
                     L   +R L  + + k + ++  l  +    EL ++ + +     iis
  gi|7392018   457 QQLMEEpRTLSSAAVAKSDLLEKELAIYTTARELKdklgEEVIKQHIISH 506

                   ataPsDvLAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLF
                   + + sD+    ++ +E g+ ++++  +++vPLFE + DL+ A   ++
  gi|7392018   507 TESVSDMFELAIMLKEVGLvdqqRARVQIVPLFETIEDLDNARDIMAAYL 556

                   siDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                   s D  +  i   ++ qe+m+GYsDs KD G l+  W LYkAq E+  +
  gi|7392018   557 SHDIVKSWIATNrnyQEIMLGYSDSNKDGGYLASGWTLYKAQNELTAIGE 606

                   kyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf
                   ++GvK++ FHGRGGtvGRGGGP   Ai sqP   i+  +R t qGE+iE
  gi|7392018   607 EHGVKITFFHGRGGTVGRGGGPSYDAITSQPFGSIKDRIRLTEQGEIIEN 656

                   sFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtE
                    +G  ++ +  L     A +   +   +    E +++R++m+ +
  gi|7392018   657 KYGNKDVAYYHLEMLISASINRMVTQMITDPNEidsFREIMDSIVADSNT 706

                   EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                    YR +v+  P F +YF  A P  E   +niGsRPa Rk    i+ LRAiP
  gi|7392018   707 IYRKLVFDNPHFYDYFFEASPIKEVSSLNIGSRPAARKTITEITGLRAIP 756

                   WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                   W+F+W q R   P W GvG AFK  id+   nl +L+ mY++WPFF   l
  gi|7392018   757 WVFSWSQNRIMFPGWYGVGSAFKRYIDRAQGNLERLQHMYQTWPFFHSLL 806

                   DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                     ++mv  K    iA  y +L  + +++    ++ d+++ tk+ +L i
  gi|7392018   807 SNVDMVLSKSNMNIAFQYAQLAESQDVRDVFYEILDEWQLTKNVILAIQD 856

                   HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                   H DlLE  P LK  l+ R +Y   Ln +q   +KR R  +
  gi|7392018   857 HDDLLEDNPSLKHSLKSRLPYFNVLNYIQIELIKRWRNNQL--------- 897

                   KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       dEn    + L++                  + GiA G+ n G
  gi|7392018   898 ----DEN---DEKLIHTT----------------INGIATGLRNSG    920

gi|260578770|ref|ZP_05846677.1|: domain 1 of 1, from 10 to 948: score 273.6, E = 4.5e-79
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      +i      ++   +s     ++ D   l + L++++ +  G+
  gi|2605787    10    AIPVAPEEIAHPEIS---PTVRDDTRYLGRILgEVIREQEGDYTFNL 53

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +      sA ++ +     +eEL  +   L    a+ v +a++H   +An
  gi|2605787    54 IENTR--SAAFDLRYGEMPIEELAEQFNKLPTEKALPVIRAFSHFALMAN 101

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   LAE+    y  R++ +      D ++    s +  t + L  +     e
  gi|2605787   102 LAEDL---YVERVRDLE----EDRGNTAPRSTLAYTWQELHNRE-VPGEK 143

                   vFeALKnqsvDLvltAHPtqsvRRsL......LqKnaRiRn.CLaqLsAK
                   v e + n  v  vltAHPt   RR + + ++++ K  R R + L  L
  gi|2605787   144 VAETMANALVAPVLTAHPTETRRRTVfdvqtdIMKMMRRRArVLKELKLN 193

                   DvtveDKkELDE...ALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHE
                      v   + L E +  + R +   + t  iR  +P   DE++ G+ Y+
  gi|2605787   194 PDSVRSARQLAEielVIRRRMTLLWQTSLIRSVRPRIEDEIKVGLRYYGI 243

                   tvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRv
                    +   +P   RRv   +K     + +P  + +++  sW+GGD DG nP v
  gi|2605787   244 SLLSEIPAINRRVNEHMKE-QYGDVVPRTA-VVRPGSWIGGDHDG-NPYV 290

                   tPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrt
                   t E        a       Y   +  L  Els+    +      E l +
  gi|2605787   291 TAETVGIATTFAARTIFDHYQKTIYALEHELSL---SSKFIDTTEALEQL 337
```

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                    aardkvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYntRERa..RHLLA
                    a r             vP++  EP+R  L  +R ++  t   + +  ++
  gi|2605787   338 ADRG---------RNDVPsrVDEPFRRALHGMRGRVAATAKHTlgEPVVS 378

                    tGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvs
                     Gi    E   y +  e L  ++    +L    D  +AD  L Dl   v
  gi|2605787   379 GGIHKGHEP--YANPAELLADIDTVDEALRHSMDDLLADHTLADLREAVE 426

                    tFGLsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaE
                    tFG  L  LD+Rq se    vl  +    ++ + Y e  E+ + E Ll+E
  gi|2605787   427 TFGFNLYSLDLRQNSESFENVLTEVFARAGVAeNYAELDEDAKVELLLTE 476

                    LkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGa.....Yiismat
                    L    PL  ++    EE +  l+ fr  A      FGa+  ++ iisma
  gi|2605787   477 LASPLPLADPEAEWSEETARELGIFRAAAK-AAKKFGAevvphCIISMAS 525

                    aPsDvLAvELLqRECgvkqt........LrvvPLFEkLADLeAAPAavek
                    + sDv+   +L +E g+ q++++++++++ ++PLFE + DL      + +
  gi|2605787   526 SVSDVIEPMILLKEVGLIQAngehpqgsVDIIPLFETIDDLAGGADIMRQ 575

                    LFsiDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKv
                    L+ +  Y+n + G+++ qe+m+GYsDs KD G ++A W LY A   ++
  gi|2605787   576 LWQLPLYRNYVAGRgdiQEIMLGYSDSNKDGGYFAANWALYDAELALVEA 625

                    AKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEvi
                     ++ G  L lFHGRGGtvGRGGGP   AiL+qP   ++G++R+t qGE+i
  gi|2605787   626 SREAGLFLRLFHGRGGTVGRGGGPSYDAILAQPKGAVQGAVRITEQGEII 675

                    EfsFGEEnLCFrsLqRFtAAtLEHGmnPP..vsPkPEWRkLmeemAvvAt
                       +G+     r L    AAtLE  + P +++       + m ++A
  gi|2605787   676 SAKYGDPANASRNLEALVAATLEASLLPVddLDDPDVAFETMRQIAEESR 725

                    EEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAi
                      Y +++  +P F+EYF   tP  E G +niGsRP+ Rk    +  LRAi
  gi|2605787   726 KAYSALMHEDPGFIEYFTTSTPLAEIGSLNIGSRPSSRKQTTAVSDLRAI 775

                    PWiFaWtqtRFHLPvWLGvGAAFKhAidKDi.......KnlqkLkEmYke
                    PW+ +W q R  LP W GvG A K  i+  ++ +++ +  l  L+E+ +
  gi|2605787   776 PWVLSWSQSRVMLPGWFGVGSALKRWIEDGSsvsgdatSRLNYLRELHRR 825

                    WPFFRvtlDLlEmvFAKGDPGiAaLyDkLLv.aEeLkPFGksLRdkYvEt
                    WPFF   l  +  v  K D  iA Ly +L+ + E      + + ++Y+ t
  gi|2605787   826 WPFFDSVLSNMAQVMSKADLSIAQLYSELVGdREAAERIFDVIVEEYKLT 875

                    kdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsy
                     ++ L+i     lL   P L   +R R +Y+  Ln +q   L+R R
  gi|2605787   876 VEMFLQITERETLLADNPELVSSVRNRFPYLVPLNLLQVELLRRFR---- 921

                    kvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAG
                                A ++            ++ v  G+     Ltm G+A
  gi|2605787   922 ------------AGDD------------SDSVRSGIQ----LTMNGLATA 943

                    mqntG<-*
                    + n G
  gi|2605787   944 LRNSG    948

gi|139474183|ref|YP_001128899.1|: domain 1 of 1, from 1 to 920: score 273.6, E = 4.5e-79
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                           L+ L     s+++ +i  +  Ll   L++i   + G+d   +
  gi|1394741     1    ---MPLKKL---ESSNNQAIIAEEVALLKEMLEnITRRMIGDDAFTV 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls     K+D   Le    ++  +   +  ++ + ++ +  L n
  gi|1394741    42 IESIMVLSE----KQDYIELEK---VVANISNQEMEVISRYFSILPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+           +  t+K L  k
  gi|1394741    85 ISEDVDLAYEINYQNNTDTDYLGK--------LALTIKDLAGKD-----N 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      + L    v  vltAHPtq  R+ +L   + i   L +       v
```

```
  gi|1394741   122 GKDILEQVNVVPVLTAHPTQVQRKTILELTTHIHKLLRKYRDAKAGVISL 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +     L R i     tD iR  +   + E++  m Y+   + + v K
  gi|1394741   172 EKWRQELYRYIEMIMQTDIIREKKLQVKNEIKNVMQYYDGSLIQAVTK-- 219

                    RRvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRDvC
                        t  Kn+     l  d P +i    W+GGDRDG nP vt E
  gi|1394741   220 --LTTEYKNLAQKHGLELDNPKpITMGMWIGGDRDG-NPFVTAETLCLSA 266

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     +   +  n Yi+++  L   +s+    + L     E+ r a   +
  gi|1394741   267 TVQSEVILNYYIDKLAALYRTFSL---SSTLVQPNSEVERLASLSQDQSI 313

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRER......aRHLLAtGiseis
                    Y         +EPYR     +  +L  t    ++++ aR     G+s  +
  gi|1394741   314 Y-------RGNEPYRRAFHYIQSRLKQTQIQltnqpaARMSSSVGLSTSA 356

                    .......EeAv..ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                     +++ + E+ +  y    +F   L    +sL + G  ++ +G L +++
  gi|1394741   357 wsspaslENPIlaYDSPVDFKADLKAIEQSLLDNGNSALIEGDLREVMQA 406

                    vstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLl
                    v  FG  L  +D+Rq+s  q   +  + +  +i   Y + sE  + + L+
  gi|1394741   407 VDIFGFFLASIDMRQDSSVQEACVAELLKGANIvDDYSSLSETEKCDVLV 456

                    aELkGK.RPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiism
                      L   +R L  + + k + ++  l  +    EL ++ + +     iis
  gi|1394741   457 QQLMEEpRTLSSAAVAKSDLLEKELAIYTTARELKdklgEEVIKQHIISH 506

                    ataPsDvLAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLF
                    + + sD+    ++ +E g+ ++++  +++vPLFE + DL+ A   ++
  gi|1394741   507 TESVSDMFELAIMLKEVGLvdqqRARVQIVPLFETIEDLDNARDIMAAYL 556

                    siDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                    s D  +  i   ++ qe+m+GYsDs KD G l+  W LYkAq E+  +
  gi|1394741   557 SHDIVKSWIATNrnyQEIMLGYSDSNKDGGYLASGWTLYKAQNELTAIGE 606

                    kyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf
                    ++GvK++ FHGRGGtvGRGGGP   Ai sqP   i+  +R t qGE+iE
  gi|1394741   607 EHGVKITFFHGRGGTVGRGGGPSYDAITSQPFGSIKDRIRLTEQGEIIEN 656

                    sFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtE
                     +G  ++ +  L     A +   +   +    E +++R++m+ +
  gi|1394741   657 KYGNKDVAYYHLEMLISASINRMVTQMITDPNEidsFREIMDSIVADSNI 706

                    EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                     YR +v+  P F +YF  A P  E   +niGsRPa Rk    i+ LRAiP
  gi|1394741   707 IYRKLVFDNPHFYDYFFEASPIKEVSSLNIGSRPAARKTITEITGLRAIP 756

                    WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                    W+F+W q R   P W GvG AFK  id+   nl +L+ mY++WPFF   l
  gi|1394741   757 WVFSWSQNRIMFPGWYGVGSAFKRYIDRAQGNLERLQHMYQTWPFFHSLL 806

                    DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                      ++mv  K    iA  y +L  + +++    ++ d+++ tk+ +L i
  gi|1394741   807 SNVDMVLSKSNMNIAFQYAQLAESQDVRDVFYEILDEWQLTKNVILAIQD 856

                    HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                    H DlLE  P LK  l+ R +Y   Ln +q   +KR R  +
  gi|1394741   857 HDDLLEDNPSLKHSLKSRLPYFNVLNYIQIELIKRWRNNQL--------- 897

                    KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        dEn    + L++                  + GiA G+ n G
  gi|1394741   898 ----DEN---DEKLIHTT----------------INGIATGLRNSG    920

gi|255067797|ref|ZP_05319652.1|: domain 1 of 1, from 1 to 900: score 272.7, E = 8.2e-79
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL +L   K +     +  DA  l + L  L  LH e    +v
  gi|2550677     1    ---MQLHILNNPKDA----ALAADAEFLKQSLYKL--LHEEASPLVV 38
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     ls       D+  L E   +L  Ld   +  +  a      + n+
gi|2550677    39 ETVKLLSTS----DDSAALIE--KVLPQLDEQQTHDLTLACGLFAQILNI 82

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AE+v+   RR i+          +    E  + Et++kL        + v
gi|2550677    83 AEDVHHERRRQIHEEA-------GHGGAEGSLAETVRKLKAAK-IGGKAV 124

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL...aqLsAKDvtve
                   L    v  vltAHPt   R  +L  n RiR  L+++      D   e
gi|2550677   125 QKQLNTTNVTAVLTAHPTEVQRQTVLNFNRRIRALLprrERCTHADALAE 174

                DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                 ++E+D  L    q    t E R  +    DE+  G+s +    ++  PK
gi|2550677   175 LRREIDTILLGLWQ----TSETRHHKLSVNDEINNGVSIFPMSFFEALPK 220

                FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                  R ++   +       +P    ++k   W+GGDRDG nP v  E  R
gi|2550677   221 LYRSMEREFQTTYPDVDVP---DILKIGGWIGGDRDG-NPFVSAETLRFA 266

                CLLaRmmAanlYisqvEDLmFE..lsmWR..CndELRvRAEElyrtaard
                          +Y   ++ L  E +ls+ R + nd++ +  +E
gi|2550677   267 FRRHADAVFRFYRGELDKLYRElpLSVRRvkVNDDVMALSDESPDEEIAR 316

                kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseis
                                +EPYR  +  +  ++     +aR L+L  G
gi|2550677   317 --------------TEEPYRRAIAYIMARVMG---KARSLgLGMG-CKFG 348

                EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                    y    eF + L    +sL + G   + +G L Dl+R vs FG  ++
gi|2550677   349 FMMPYASAQEFSDDLHKLQRSLRDNGSALLGEGRLADLIRSVSVFGFHMM 398

                KLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLl
                 LD+Rq +e++ Dv+  + +H ++  Y + sE  +q  Ll ELk +RPL
gi|2550677   399 PLDLRQHAEKHADVVAELFKHAGLEDYGSLSETEKQTVLLRELKHQRPLS 448

                gsDLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvE
                 + +   E++++E++   +a ++  E    +    iis +  PsD LA
gi|2550677   449 SPFITYSEhtrrEMAIFNEARNIKDEFGENAVTQSIISNCEQPSDLLALA 498

                LLqRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYin
                LL +E g+ + ++++++  + +vPLFE +  Le A   +e +Fs +WY+
gi|2550677   499 LLLKESGLltvengkpQSRINIVPLFETIEALENACPVMETMFSNEWYRD 548

                ridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                 ++ +++ qe+m+GYsDs KD G +   W LY+A   ++   Kky v++
gi|2550677   549 LLQSRdniQEIMLGYSDSNKDGGYVTSSWCLYQAELGLVELFKKYDVRMR 598

                lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                lFHGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
gi|2550677   599 LFHGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGN 648

                CFrsLqRFtAAtLEHGmnPPv.sPkPEWRkLmeemAvvAtEEYRsvvvKE
                  r L    AAtLE  + P  + P P    Lm+ +  v    YR ++
gi|2550677   649 AVRNLETLVAATLEASLLPDQkDPEP---ALMQALSDVSFKYYRELITH- 694

                PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
                P F++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R
gi|2550677   695 PDFIDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNR 744

                FHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAK
                  LP W G+G A     +     l  L+E  +  PFF   l  +E v AK
gi|2550677   745 LMLPAWYGFGSAVESLCEGKPETLAALREHAQHNPFFQAMLSNMEQVMAK 794

                GDPGiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                 D  +A  y  L  ++E        ++++Y+  ++ LL +    +lL
gi|2550677   795 TDITLAENYAGLSESpEKAAVIFGMIKEEYQRSRKALLDLLQTDELLRDN 844

                PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                  L   l LR +Y+  Ln +q   LKR+R                 ++
gi|2550677   845 RSLARSLALRIPYLNALNGLQVAMLKRLR-----------------KDP- 876
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                  kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                  + +  L+ +               Lt+ G+A G+ ntG
  gi|2550677   877 HDPHTLLMVH--------------LTINGVAQGLRNTG    900

gi|229824131|ref|ZP_04450200.1|: domain 1 of 1, from 2 to 895: score 272.2, E = 1.2e-78
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      i+ q+        s          LL D        +  ++ +
  gi|2298241     2    NIENQIQQSQVAHLS---------QLLTDALERAFTSMTSPQQQALL 39

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         A      D        a +  L+  D  lvA+ ++ +  L n+
  gi|2298241    40 -------AKLKHLADQGDYAAYVAAIQPLAEEDLALVARYFSALPLLINI 82

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AE+velA   ++k+ +h D   E  At  + i    K  vl+
  gi|2298241    83 AEDVELASQIKMKRCRHADLEGELPATLAA-IKQAGKGQVLQR------- 124

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                         +++ vltAHPtq  R+s+L    ++   L+          D++
  gi|2298241   125 -----PMTIEPVLTAHPTQVQRKSMLDLMDKLYGLLTDYRNTRPEFLDRQ 169

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                       L   i     tD iR  +     E+   m Y+   + + +
  gi|2298241   170 AWQHELEAVIEIILGTDLIREQKLQVANEIANVMTYYQKSLIESITDITL 219

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                      AL  + i      +v  i    W+GGDRDG nP vt E  R    +
  gi|2298241   220 NYRQALSDLEIESQ---QVLPITMGMWIGGDRDG-NPYVTAETLRLTASI 265

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                     +    Y+s ++ L    s     ++L +   El   a
  gi|2298241   266 QSQVILDYYLSSLDQLYRRYSF---SSDLVAVTPELAALAEES------- 305

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                  E +      EPYR  L  ++ +L      a   L  G +   E   y +
  gi|2298241   306 EDYSIFRQKEPYRKALNTIKNRLC-----ASKALILGEACQVEAQAYPDA 350

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                  E F   L L   +L   G        L  l+     FG  L  +D+Rq+s
  gi|2298241   351 ESFKADLVLVSEALKADGKESHTLAPLESLIVCLEIFGFHLASIDLRQDS 400

                  e.RqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                     +t v + + +     +Y +  E  +   Ll  L      l s L +
  gi|2298241   401 SiNETCVAELLAQAKVEEAYSQLDEASKVQCLLHQLTQEPRRLSSALNQA 450

                  EEv.kDvldafrvLAELP....iDsFGaYiismataPsDvLAvELLqREC
                    +    l  ++ +A+L ++ +       iis +t+ sD L   LL +E
  gi|2298241   451 SAIlTRELAIYQAVADLQkrlgHRIIKRHIISHTTSVSDLLELALLFKEV 500

                  gvkqt....LrvvPLFEkLADLeAAPAave...kLFsiDWYinridGKqe
                  g+  ++  +++ vPLFE + DLe A   + +  +L  +  +    d  qe
  gi|2298241   501 GLVGPdfahVQLVPLFETIEDLEEALEVMTtylRLPLVQKWLASQDWCQE 550

                  vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                  +m+GYsDs KD G l+  W LY Aq  + +  K+ G+ +  FHGRGGtvG
  gi|2298241   551 IMLGYSDSNKDGGYLASGWALYLAQNKLTRLGKQEGITISFFHGRGGTVG 600

                  RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                  RGGGP   Ai+sqP  tin  +Rvt qGEvi   +G  +  +  L
  gi|2298241   601 RGGGPSYEAIMSQPIGTINRLMRVTEQGEVIGTKYGNPDTAYYQLENMLV 650

                  AtLEHG.mnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlA
                  A L H  +   v     +  +m+++       YR +v+  P F E+F  A
  gi|2298241   651 ASLSHVlLAHEVHDSSPYEAVMNRLVDWSYQAYRQLVFATPGFSEFFFQA 700

                  tPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvG
                  tP  E  ++niGsRPa Rk    i+ LRAiPW+F+W q R   P W GvG
  gi|2298241   701 TPIKEVSQLNIGSRPASRKKVTDIDGLRAIPWVFSWSQSRMMFPGWYGVG 750

                  AAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyD
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                     AF+  i+ D   l  L+EmY eWPFFR  l  ++mv AK D  +A+ y
  gi|2298241   751 TAFQRFIEEDPSHLALLQEMYAEWPFFRALLSNVDMVLAKSDMEVASYYS 800

                    kLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRd
                    +L+   e +   ++L ++++ tkdlLL+i G   lL    YL+  l +R
  gi|2298241   801 QLVEEPEGQAIFQKLEAEWQRTKDLLLQIEGEEQLLAQNNYLRDSLAMRL 850

                    sYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnp
                    +Y   Ln +q   ++R R                 +E          L
  gi|2298241   851 PYFNALNYLQVELIRRSR----------------QEA---------LS- 873

                    tervaPGLEDtLiLtmKGiAAGmqntG<-*
                         P     L +t+ GiA G+ n G
  gi|2298241   874 -----PLASKILHITINGIATGLRNSG    895

gi|257455375|ref|ZP_05620610.1|: domain 1 of 1, from 31 to 956: score 271.0, E = 2.7e-78
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s  A + l+   K s    L+    LL    + ++     e +k  +
  gi|2574553    31    SNTALVELIDSDKDS---PLLADTQLLSRVLITVVEQQTSEPVKQTI 74

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                                 +D++  + + a L  L+      + +a      + n+
  gi|2574553    75 NKLLN-------GEDPQ--QTIQAILPTLNHQQRKNLIRACGLFAQVFNI 115

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+++   RRR    +     DE+     s     +  L +++    +E
  gi|2574553   116 AEDMH-HERRRLAHEQ-----DESAS--KSSFAHVIDELKSQG-IDSDEL 156

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L    +  vltAHPt   R  +L     iR  L q          ++
  gi|2574553   157 QAQLDDTYISAVLTAHPTEVQRQTILSLRRQIRALLEQYHT--AIGYQRQ 204

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     ++  L   +   + t E R  + t +DE+  G++Y+    ++  P   R
  gi|2574553   205 RIEQQLEATLLSQWQTNETRHFKITVKDEIDNGIAYFDLSFFEALPSLYR 254

                    RvDtALKniGinERlP.YdvP.LikFssWmGGDRDGknPRvtPEvtRDvC
                    + D  LK     ER P+ d P+L+    W+GGDRDG nP v  +  R
  gi|2574553   255 KLDYQLK-----ERFPdTDMPnLLNIGGWIGGDRDG-NPFVSADTLRYA- 297

                    LLaRmmAanlYi..sqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                       R  A+ +Y+ ++q+  L  El +      +      l   ++ d +
  gi|2574553   298 -FKRQAATVFYFyrDQLGKLYQELPLSIRHVKVSDAVLALSEQSKEDNIS 346

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                    +           +EPYR  +G +  +L  t   +  L       +sE
  gi|2574553   347 RE----------EEPYRRAIGFISSRLVAT-SHTFDLSYGCRFGLSEP-- 383

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y + +eFL+ L + Y+sL + G   +A   L D++R v  FG  L+ LD+
  gi|2574553   384 YADCDEFLDDLYVVYQSLVDNGSELLANERLTDIIRAVEVFGFYLMPLDL 433

                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    Rq s  + + +  + +H ++  Y + sE  Rq  Ll EL   RPL+ + +
  gi|2574553   434 RQFSGIHAETVHDLFKHADLEDYLSLSESARQRVLLRELATARPLYNPYI 483

                    PktEEvkDvldafrvLAELPi....DsFGaYiismataPsDvLAvELLqR
                          +  l+ f+  A++  + ++ +    iis a   sD LA  LL +
  gi|2574553   484 TYEPQTQRELEIFQAAADIKNrfgdKAITQSIISNAEQVSDLLALALLLK 533

                    ECg...vkqtLrv.....vPLFEkLADLeAAPAavekLFsiDWYinri..
                    E g   vk  ++v++ + vPLFE +  L+     +  L    WY+  + +
  gi|2574553   534 ESGlllVKDGVPVsriniVPLFETIEALQNSTRIMSELLDKPWYKSVLas 583

                    .dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                    +d  qe+m+GYsDs KD G +   W LY+A   ++ +A ky ++L lFHG
  gi|2574553   584 rDNLQEIMLGYSDSNKDGGYVTSQWSLYQAEIQLVEMAEKYAIQLRLFHG 633

                    RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                    RGG vGRGGGP   AiL+qP   ++G +R+t qGEvi   + +     r
  gi|2574553   634 RGGSVGRGGGPSFEAILAQPEGSVDGQIRITEQGEVITAKYADAGNAERN 683
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                    LqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvE
                    L    AAtL   + P  s  P+  +Lm+++   A   YR+++ + P F++
  gi|2574553   684 LETLIAATLKASLLPSHSESPD-SDLMNQLSHEAFNCYRALITQ-PYFID 731

                    YFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPv
                    YF       E   +niGsRPa Rk    i+ LRAiPW+F+W q R  LP
  gi|2574553   732 YFLQTSLVKEIASLNIGSRPASRKSLARIQDLRAIPWVFSWMQNRLMLPA 781

                    WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                    W G+G A    i     nl kL+   +   F    l  +  v AK D  i
  gi|2574553   782 WYGFGTAVEKLIADNPENLAKLQHNAQHSAFMQAMLSNMAQVMAKTDIEI 831

                    AaLyDkLLv.aEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                    A  y +L  +a e       + ++Y    + LL +     lL+    L
  gi|2574553   832 AQAYVELANdATEANAIFALITAEYHRSLKALLTLTNKETLLDDNRTLAR 881

                    rlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkade
                     l LR +Y+  Ln +q   LK +R+     t       E    +    +e
  gi|2574553   882 SLALRLPYLNALNWLQVALLKQLRE----ATADEATTDERSTTE--TTNE 925

                    LvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        n    +   L   + Lt+ GiA G+ ntG
  gi|2574553   926 ATSDN-ETSYTAAL-NLVHLTINGIAQGLRNTG    956

gi|19745716|ref|NP_606852.1|: domain 1 of 1, from 1 to 920: score 270.6, E = 3.7e-78
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLD.iLqDLHGedLkEa
                           L+ L     s+++ +i  +  Ll   L++i   + G+d   +
  gi|1974571     1    ---MPLKKL---ESSNNQAIIAEEVALLKEMLEnITRRMIGDDAFTV 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +     ls     K+D   Le    ++  +   +  ++ + ++ +  L n
  gi|1974571    42 IESIMVLSE----KQDYIELEK---VVANISNQEMEVISRYFSILPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v+lAy    +     D+           +  t+K L  k
  gi|1974571    85 ISEDVDLAYEINYQNNTDTDYLGK--------LALTIKDLAGKD-----N 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      + L    v  vltAHPtq  R+ +L   + i   L +       v
  gi|1974571   122 GKDILEQVNVVPVLTAHPTQVQRKTILELTTHIHKLLRKYRDAKAGVISL 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +     L R +     tD iR  +   + E++  m Y+   + + v K
  gi|1974571   172 EKWRQELYRYVEMIMQTDIIREKKLQVKNEIKNVMQYYDGSLIQAVTK-- 219

                    RRvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRDvC
                        t  Kn+     l  d P +i    W+GGDRDG nP vt E
  gi|1974571   220 --LTTEYKNLAQKHGLELDNPKpITMGMWIGGDRDG-NPFVTAETLCLSA 266

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     +   +  n Yi+++  L   +s+    + L     E+ r a   +
  gi|1974571   267 TVQSEVILNYYIDKLAALYRTFSL---SSTLVQPNSEVERLASLSQDQSI 313

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRER......aRHLLAtGi..se
                    Y         +EPYR     +   L  t    ++++ aR     G+++s
  gi|1974571   314 Y-------RGNEPYRRAFHYIQSCLKQTQIQltnqpaARMSSSVGLntSA 356

                    isEeA.......vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                     +  A+ +++   y    +F   L    +sL + G  ++ +G L +++
  gi|1974571   357 CPSPAslenpilAYDSPVDFKADLKAIEQSLLDNGNSALIEGDLREVMQA 406

                    vstFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLl
                    v  FG  L  +D+Rq+s  q   +  + +  +i   Y + sE  + + L+
  gi|1974571   407 VDIFGFFLASIDMRQDSSVQEACVAELLKGANIvDDYSSLSETEKCDVLV 456

                    aELkGK.RPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiism
                      L   +R L  + + k + ++  l  +    EL ++ + +     iis
  gi|1974571   457 QQLMEEpRTLSSAAVAKSDLLEKELAIYTTARELKdklgEEVIKQHIISH 506

                    ataPsDvLAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLF
```

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                    + + sD+    ++ +E g+ ++++  +++vPLFE + DL+ A   ++
  gi|1974571   507 TESVSDMFELAIMLKEVGLvdqqRARVQIVPLFETIEDLDNACDIMAAYL 556

                    siDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                    s D  +  i   ++ qe+m+GYsDs KD G l+  W LYkAq E+  +
  gi|1974571   557 SHDIVKSWIATNrnyQEIMLGYSDSNKDGGYLASGWTLYKAQNELTAIGE 606

                    kyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf
                    ++GvK++ FHGRGGtvGRGGGP   Ai sqP   i+  +R t qGE+iE
  gi|1974571   607 EHGVKITFFHGRGGTVGRGGGPSYDAITSQPFGSIKDRIRLTEQGEIIEN 656

                    sFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtE
                     +G  ++ +  L     A +   +   +    E +++R++m+ +
  gi|1974571   657 KYGNKDVAYYHLEMLISASINRMVTQMITDSNEidsFREIMDSIVADSNM 706

                    EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                     YR +v+  P F +YF  A P  E   +niGsRPa Rk    i+ LRAiP
  gi|1974571   707 IYRKLVFDNPHFYDYFFEASPIKEVSSLNIGSRPAARKTITEITGLRAIP 756

                    WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                    W+F+W q R   P W GvG AFK  id+   nl +L+ mY++WPFF   l
  gi|1974571   757 WVFSWSQNRIMFPGWYGVGSAFKRYIDRAQGNLERLQHMYQTWPFFHSLL 806

                    DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                      ++mv  K    iA  y +L  + +++    ++ d+++ tk+ +L i
  gi|1974571   807 SNVDMVLSKSNMNIAFQYAQLAESQDVRDVFYEILDEWQLTKNVILAIQD 856

                    HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                    H DlLE  P LK  l+ R +Y   Ln +q   +KR R  +
  gi|1974571   857 HDDLLEDNPSLKHSLKSRLPYFNVLNYIQIELIKRWRNNQL--------- 897

                    KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        dEn    + L++                 + GiA G+ n G
  gi|1974571   898 ----DEN---DEKLIHTT----------------INGIATGLRNSG    920

gi|71910318|ref|YP_281868.1|: domain 1 of 1, from 15 to 937: score 269.7, E = 6.7e-78
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         D  L l       +++ + e  ALL +    i   + G+d   ++
  gi|7191031    15    --DGHLPLKKLESSNNQDIIAEEVALLKEMLENITRRMIGDDAFTVI 59

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls     K+D   Le    ++  +   +  ++ + ++ +  L n+
  gi|7191031    60 ESIMVLSE----KQDYIELEK---VVANISNQEMEVISRYFSILPLLINI 102

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     E+v+lAy    +     D+           +  t+K L  k
  gi|7191031   103 SEDVDLAYEINYQNNTDTDYLGK--------LALTIKDLAGKD-----NG 139

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     + L    v  vltAHPtq  R+ +L   + i   L +       v   +
  gi|7191031   140 KDILEQVNVVPVLTAHPTQVQRKTILELTTHIHKLLRKYRDAKAGVINLE 189

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                         L R i     tD iR  +   + E++  m Y+   + + v K
  gi|7191031   190 KWRQELYRYIEMIMQTDIIREKKLQVKNEIKNVMQYYDGSLIQAVTK--- 236

                    RvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRDvCL
                       t  Kn+     l  d P +i    W+GGDRDG nP vt E
  gi|7191031   237 -LTTEYKNLAQKHGLELDNPKpITMGMWIGGDRDG-NPFVTAETLCLSAT 284

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    +   +  n Yi+ +  L   +s+    + L     E+ r a   +    Y
  gi|7191031   285 VQSEVILNYYIDELAALYRTFSL---SSTLVQPNSEVERLASLSQDQSIY 331

                    iEFWKqvPPtEPYRviLGdvRDKLYntRER......aRHLLAtGi..sei
                             +EPYR     +  +L  t    ++++ aR     G+++s
  gi|7191031   332 -------RGNEPYRRAFHYIQSRLKQTQIQltnqpaARMSSSVGLntSAW 374

                    sEeA.......vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqv
                    s  A+ +++   y    +F   L    +sL + G  ++ +G L +++  v
  gi|7191031   375 SSPAslenpilAYDSPVDFKADLKAIEQSLLDNGNSALIEGDLREVMQAV 424
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                    stFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLla
                      FG  L  +D+Rq+s  q   +  + +  +i   Y + sE  + + Ll
  gi|7191031   425 DIFGFFLASIDMRQDSSVQEACVAELLKGANIvDDYSSLSETEKCDVLLQ 474

                    ELkGK.RPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiisma
                     L   +R L  + + k + ++  l  +    EL ++ + +     iis +
  gi|7191031   475 QLMEEpRTLSSAAVAKSDLLEKELAIYTTARELKdklgEEVIKQHIISHT 524

                    taPsDvLAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLFs
                     + sD+    ++ +E g+ ++++  +++vPLFE + DL+ A   ++   s
  gi|7191031   525 ESVSDMFELAIMLKEVGLvdqqRARVQIVPLFETIEDLDNARDIMAAYLS 574

                    iDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKk
                     D  +  i   ++ qe+m+GYsDs KD G l+  W LYkAq E+  +  +
  gi|7191031   575 HDIVKSWIATNrnyQEIMLGYSDSNKDGGYLASGWTLYKAQNELTAIGEE 624

                    yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                    +GvK++ FHGRGGtvGRGGGP   Ai sqP   i+  +R t qGE+iE
  gi|7191031   625 HGVKITFFHGRGGTVGRGGGPSYDAITSQPFGSIKDRIRLTEQGEIIENK 674

                    FGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEE
                    +G  ++ +  L     A +   +   +    E +++R++m+ +
  gi|7191031   675 YGNKDVAYYHLEMLISASINRMVTQMITDPNEidsFREIMDSIVADSNII 724

                    YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPW
                    YR +v+  P F +YF  A P  E   +niGsRPa Rk    i+ LRAiPW
  gi|7191031   725 YRKLVFDNPHFYDYFFEASPIKEVSSLNIGSRPAARKTITEITGLRAIPW 774

                    iFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlD
                    +F+W q R   P W GvG AFK  id+   nl +L+ mY++WPFF   l
  gi|7191031   775 VFSWSQNRIMFPGWYGVGSAFKRYIDRAQGNLERLQHMYQTWPFFHSLLS 824

                    LlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGH
                     ++mv  K    iA  y +L    +++    ++ d+++ tk+ +L i  H
  gi|7191031   825 NVDMVLSKSNMNIAFQYAQLAERQDVRDVFYEILDEWQLTKNVILAIQDH 874

                    kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                      lLE  P LK  l+ R +Y   Ln +q   +KR R  +
  gi|7191031   875 DALLEDNPSLKHSLKSRLPYFNVLNYIQIELIKRWRNNQL---------- 914

                    EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       dEn    + L++                  + GiA G+ n G
  gi|7191031   915 ---DEN---DEKLIHTT----------------INGIATGLRNSG    937

gi|241663753|ref|YP_002982113.1|: domain 1 of 1, from 56 to 1002: score 269.5, E = 7.8e-78
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       s+    R    G  +  ++ ++ D   l + L+D+L +  G    E
  gi|2416637    56    SLGPTSRR-SSGSAAAKDQPLKEDIRFLGRLLgDVLREQEGGAAFET 101

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      +  +    D +  +EL   L +L    +  v +a++    LAn
  gi|2416637   102 VETIRQTAVRFRRDGDRQAEQELDRLLKALSREQTNSVVRAFSYFSHLAN 151

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+ +   RRR++ +        +s      +   l  +   +  s e
  gi|2416637   152 IAEDQHHNRRRRVHALA-------GSPPQPGSMMRALLSVADEG-VSGET 193

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                              +  vltAHPt   R+s+L  +  i   La      +t  ++
  gi|2416637   194 LRRFFDAALIVPVLTAHPTEVQRKSILDAQREIARLLAE-RDTPLTTRER 242

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +     L   +   + t  +R ++    DE+   +sY+  t  + +P
  gi|2416637   243 ERNTTLLRAHVTKLWQTRMLRTTRLMVADEIENALSYYQTTFLREIPALY 292

                    RRvDtALKni....GinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                    R  +  +  + +++G        +P  +  sW+GGDRDG nP vt E  R
  gi|2416637   293 RELEEDVAAVfprrGARGEPTPLAPFFQMGSWIGGDRDG-NPFVTAETLR 341

                    DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
```

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                          +    Y++ +  L  Elsm    + + v AE l    ++
  gi|2416637   342 YAARKQASVILAWYLEEIHALGAELSM--STSQVDVSAELLALAEQSPDR 389

                   vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLA..tGiseisE
                     +           EPYR  L  v  +L  t    R L  ++ G   +
  gi|2416637   390 SEH--------RSDEPYRRALIGVYARLAAT---CRELTGedAGRHAVGP 428

                   eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                      y + Ee    + +   sL      v+AD  L  l R +  FG  L
  gi|2416637   429 APAYSNAEELRADIQIVIDSLAAHHGEVLADARLASLARAIDVFGFHLSS 478

                   LDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaELkGKRPLl
                   +D+Rq s+ +   +  + +  +++G+Y   sE  ++  Ll EL+  R L
  gi|2416637   479 IDLRQVSDVHEATVAELLKVAGVeGAYAALSEADKRTLLLRELQQPRVLT 528

                   gsDLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAvE
                    +     E     +d fr  ++v A          Yiis + + sD L v
  gi|2416637   529 LPFHAYSEQTTSEIDIFRaareVRARYGNRIVRNYIISHTETLSDLLEVM 578

                   LLqRECgvkqt...........LrvvPLFEkLADLeAAPAavekLFsi..
                   LLq+E g+ +t+ +++++   ++ v+PLFE + DL+ AP  +  L  +++
  gi|2416637   579 LLQKEAGMFRTgangsgsaaldVMVIPLFETIEDLRNAPEIMGDLLDLpg 628

                   .DWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGv
                    D         qevm+GYsDs KD G l   W LYkA   ++   ++ Gv
  gi|2416637   629 fDAVLAAQGNEQEVMLGYSDSNKDGGFLTSNWELYKAELALVELFQRKGV 678

                   KLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGE
                   +L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGE+i   F
  gi|2416637   679 RLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEIISSKFAN 728

                   EnLCFrsLqRFtAAtLEHGmnPPvs.Pk..PEWRkLmeemAvvAtEEYRs
                    ++  r L    AAtLE  + P   +Pk+  E+   m+ +   A   YR
  gi|2416637   729 PEIGRRNLETIVAATLEATLLPTRNrPKglEEFEAAMQALSDNAFAAYRN 778

                   vvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....GiesLRAiP
                   +v+  P F +YF   tP +E   +n+GsRPa Rk   ++++ ie LRAiP
  gi|2416637   779 LVYETPGFKDYFFATTPITEIADLNLGSRPASRKLMDkkhrRIEDLRAIP 828

                   WiFaWtqtRFHLPvWLGvGAAFKhAidKD......iKnlqkLkEmYkeWP
                   W F+W q R  LP W G+G A +  +d  ++ + +   l  Lk m k+WP
  gi|2416637   829 WGFSWGQCRLLLPGWFGFGSAVQRWLDDAgnakarAARLTTLKRMHKQWP 878

                   FFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk.PFGksLRdkYvEtkd
                   FF   l  ++mv  K D  +A+ y +L     L++    ++ +++  t++
  gi|2416637   879 FFANLLSNMDMVLSKADLNVASRYAQLCDDRKLRnAVFSRISAEFTLTEQ 928

                   lLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykv
                   +L  i G  + L   P L   ++ R +Y+  Ln +q   LKR R
  gi|2416637   929 MLAAITGQSERLADNPLLARSIKNRFPYLDPLNHLQVELLKRFRS----- 973

                   tlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmq
                          K   d+   +    ++L                + GiAAG+
  gi|2416637   974 ------GKAGSDDA--RVRRGIHLS----------------INGIAAGLR 999

                   ntG<-*
                   n G
  gi|2416637  1000 NSG    1002

gi|15674689|ref|NP_268863.1|: domain 1 of 1, from 1 to 920: score 269.4, E = 8.2e-78
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           L+ L        + + e  ALL +    i   + G+d   ++
  gi|1567468     1    ---MPLKKLESSNNQ--DIIAEEVALLKEMLENITRRMIGDDAFTVI 42

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        ls     K+D   Le    ++  +   +  ++ + ++ +  L n+
  gi|1567468    43 ESIMVLSE----KQDYIELEK---VVANISNQEMEVISRYFSILPLLINI 85

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    E+v+lAy    +     D+           +  t+K L  k
  gi|1567468    86 SEDVDLAYEINYQNNTDTDYLGK--------LALTIKDLAGKD-----NG 122
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                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     + L    v  vltAHPtq  R+ +L   + i   L +       v   +
  gi|1567468   123 KDILEQVNVVPVLTAHPTQVQRKTILELTTHIHKLLRKYRDAKAGVINLE 172

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                         L R i     tD iR  +   + E++  m Y+   + + v K
  gi|1567468   173 KWRQELYRYIEMIMQTDIIREKKLQVKNEIKNVMQYYDGSLIQAVTK--- 219

                    RvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRDvCL
                       t  Kn+     l  d P +i    W+GGDRDG nP vt E
  gi|1567468   220 -LTTEYKNLAQKHGLELDNPKpITMGMWIGGDRDG-NPFVTAETLCLSAT 267

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    +   +  n Yi+ +  L   +s+    + L     E+ r a   +    Y
  gi|1567468   268 VQSEVILNYYIDELAALYRTFSL---SSTLVQPNSEVERLASLSQDQSIY 314

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGise...isEeA.
                             +EPYR     +  +L  t        A  +s + ++   A
  gi|1567468   315 -------RGNEPYRRAFHYIQSRLKQTQIQLTNQPAASMSSsvgLNTSAw 357

                    ...........vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqv
                    +++ + +++   y    +F   L    +sL + G  ++ +G L +++  v
  gi|1567468   358 sspaslenpilAYDSPVDFKADLKAIEQSLLDNGNSALIEGDLREVMQAV 407

                    stFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLla
                      FG  L  +D+Rq+s  q   +  + +  +i   Y + sE  + + Ll
  gi|1567468   408 DIFGFFLASIDMRQDSSVQEACVAELLKGANIvDDYSSLSETEKCDVLLQ 457

                    ELkGK.RPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiisma
                     L   +R L  + + k + ++  l  +    EL ++ + +     iis +
  gi|1567468   458 QLMEEpRTLSSAAVAKSDLLEKELAIYTTARELKdklgEEVIKQHIISHT 507

                    taPsDvLAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLFs
                     + sD+    ++ +E g+ ++++  +++vPLFE + DL+ A   ++   s
  gi|1567468   508 ESVSDMFELAIMLKEVGLvdqqRARVQIVPLFETIEDLDNARDIMAAYLS 557

                    iDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKk
                     D  +  i   ++ qe+m+GYsDs KD G l+  W LYkAq E+  +  +
  gi|1567468   558 HDIVKSWIATNrnyQEIMLGYSDSNKDGGYLASGWTLYKAQNELTAIGEE 607

                    yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                    +GvK++ FHGRGGtvGRGGGP   Ai sqP   i+  +R t qGE+iE
  gi|1567468   608 HGVKITFFHGRGGTVGRGGGPSYDAITSQPFGSIKDRIRLTEQGEIIENK 657

                    FGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEE
                    +G  ++ +  L     A +   +   +    E +++R++m+ +
  gi|1567468   658 YGNKDVAYYHLEMLISASINRMVTQMITDPNEidsFREIMDSIVADSNII 707

                    YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPW
                    YR +v+  P F +YF  A P  E   +niGsRPa Rk    i+ LRAiPW
  gi|1567468   708 YRKLVFDNPHFYDYFFEASPIKEVSSLNIGSRPAARKTITEITGLRAIPW 757

                    iFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlD
                    +F+W q R   P W GvG AFK  id+   nl +L+ mY++WPFF   l
  gi|1567468   758 VFSWSQNRIMFPGWYGVGSAFKRYIDRAQGNLERLQHMYQTWPFFHSLLS 807

                    LlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGH
                     ++mv  K    iA  y +L    +++    ++ d+++ tk+ +L i  H
  gi|1567468   808 NVDMVLSKSNMNIAFQYAQLAERQDVRDVFYEILDEWQLTKNVILAIQDH 857

                    kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                     DlLE  P LK  l+ R +Y   Ln +q   +KR R  +
  gi|1567468   858 DDLLEDNPSLKHSLKSRLPYFNVLNYIQIELIKRWRNNQL---------- 897

                    EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       dEn    + L++                  + GiA G+ n G
  gi|1567468   898 ---DEN---DEKLIHTT----------------INGIATGLRNSG    920

gi|225024256|ref|ZP_03713448.1|: domain 1 of 1, from 1 to 902: score 269.4, E = 8.3e-78
                    *->siDAqLRlLvPGKvsedekLieYDALLlD..kFLD.iLqDLHGedLk
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                      + P       +    DA L D+  FL + Lq +   +
gi|2250242     1    --------MMPEPSG---QHPYKDAPLFDdvAFLTgALQTVLAAQTD 36

                   EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                     vqE   ++A   G      +     +L   +  D i   + +  +Ln+
gi|2250242    37 CPVQEA--VAALLGGEAPQDVVTRSLPQLNDQQLEDLIRACSLFAQILNI 84

                   AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                   A  A       RRR    +     D a  t       tl  L  ++  s
gi|2250242    85 AEDAHH----QRRRLAHSQ---TRDNAKST----FGHTLDLLQQQG-VSA 122

                   eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                   e   + L    v  vltAHPt   R   L  +  iRn L q   +    +
gi|2250242   123 EALQQQLNHTEVAAVLTAHPTEVQRQTTLTLHRQIRNLLDQRANQ--AGQ 170

                   DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     + L   +   +   + t E R  + t  DE+  G+ Y+    +  vP
gi|2250242   171 NEERLQQQVQTMLWTLWQTNENRHFKITVADEISNGIMYFPLSFFSAVPG 220

                   FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     R+ + AL+      RlP    +++   W+GGDRDG nP v  +  R
gi|2250242   221 VYRKLEAALQVAFPHTRLP---NVLHIGGWIGGDRDG-NPFVSADTLRTA 266

                   CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                             +Y sq+  L  E ++s+ R n    v A   ++
gi|2250242   267 FAQQASAVFRFYRSQLYKLYEElpMSIRRVNVSPEVLALSAKSPDTER-- 314

                   vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                                +EPYR  L  +  +   t  R    L   +  +
gi|2250242   315 ----------AHEEEPYRRALAYILARTVATAHRFGSGLGSQFGLLEP-- 352

                   vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                    y  vEeFL  L +   sLC  G + +ADG L Dl+R  s F   L+ LD
gi|2250242   353 -YDTVEEFLADLHIVHTSLCANGSRLLADGRLADLIRAASVFRFYLMPLD 401

                   iRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
                   +Rq ++++ Dv+  +    ++  +    E  R   Ll EL+  RPL  +
gi|2250242   402 LRQHAQKHIDVVAELFAAAGLEDFAALNEAERERVLLRELSSPRPLHSPF 451

                   LPktEEvkDvldafrvLAELPi....DsFGaYiismataPsDvLAvELLq
                       E+ +  l  fr  AE+  + ++++    iis a   s++LA  L+
gi|2250242   452 ARYSEDTEHELAIFRAAAEIKAgfgeEAIRQSIISNAENVSEMLALALIM 501

                   RECgvkq.........tLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                   +E g+ + ++++ +++ L +vPLFE +  L+     +++LFs+ WY+  +
gi|2250242   502 KETGLLRlnteglpesRLNIVPLFETIEALQDCIGVMDHLFSLPWYRHLL 551

                   dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                     +++ qe+m+GYsDs KD G +   W LY+A   ++K   k+ v+L lF
gi|2250242   552 ADRsniQEIMLGYSDSNKDGGYVTSQWVLYQAEQALVKLFAKHQVRLRLF 601

                   HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                   HGRGG vGRGGGP   A+L+qP   + G +R+t qGEvi   + + +
gi|2250242   602 HGRGGSVGRGGGPSYEAVLAQPAGSVAGQIRITEQGEVITAKYADADNAE 651

                   rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                   r L    AA LE  + P     P+   Lm+ +   A   YR ++   P F
gi|2250242   652 RNLETLVAAALEASLLPHRTEEPD-AALMQSLSDAAFAYYRELITH-PDF 699

                   vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                   v YF    P  E   +niGsRPa Rk    i+ LRAiPW+F+Wtq R  L
gi|2250242   700 VGYFLQTSPINEIASLNIGSRPASRKTLARIQDLRAIPWVFSWTQNRLML 749

                   PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                   P W G+G A    +     nl  L+ m +   FF   l  +E v AK D
gi|2250242   750 PAWYGFGSAVEQLLRDNPANLEHLRHMVQHSAFFQAMLSNMEQVMAKADL 799

                   GiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                    iA  y  L   +   +   + +  +++  +  LL++     lL     L
gi|2250242   800 DIARAYVGLADQpQAAQAMFELIAGEFERSRRALLQLIEQDHLLTDNRSL 849
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                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                       l LR +Y+  Ln +q   L R+R               +   +
  gi|2250242   850 ARSLALRIPYLNALNWLQVALLARLR--------------QHPGNP---- 881

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     +L++L               Lt+ G+A G+ ntG
  gi|2250242   882 -QLIHLI-------------HLTINGVAQGLRNTG    902

gi|121608028|ref|YP_995835.1|: domain 1 of 1, from 1 to 930: score 269.2, E = 9.4e-78
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                               + P   ++ +  +  D  Ll + L+D++ +  G+ +
  gi|1216080     1    --------MQP---ADKDLPLMDDIRLLGRILgDVIREQEGPRVYAL 36

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls  +    D +    L   L sL  + ++ v +a+     LAn
  gi|1216080    37 VEQVRKLSVSFRRDADQEADRALKKLLESLSTGQTVGVIRAFTYFSHLAN 86

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAE+ +   RRR    + GD       t E  iE  l +L   +  +P+
  gi|1216080    87 LAED-RHRIRRRAVHERAGD-------TQEGSIELALARLRAAG-IAPQT 127

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL.........aqLs
                    + + L    v  vltAHPt   R+s+L  +  i   L ++++ + +a L+
  gi|1216080   128 IAQTLAGSHVAPVLTAHPTEVQRKSILDAERSIAQLLaerddiqarARLY 177

                    ..AKDvtveDKkELDEALHRE.iqAAFRtDEiRRaqPtPqDEmRaGmsYi
                    ++A D          EAL R ++   + t  +R ++ t  DE+   +sY+
  gi|1216080   178 dgANDALTPRALAANEALLRArVTQLWQTRLLRYSKLTVADEIENALSYY 227

                    HEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknP
                      t  + +P      + AL    +          ++   W+GGDRDG nP
  gi|1216080   228 EATFLREIPEIYAALENALGQHPVHS-------FLRMGQWIGGDRDG-NP 269

                    RvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRv..RAEE
                      t             +A   Y+  v  L  Els+      + ++  A
  gi|1216080   270 NATAQTLQYALGRQAEVALRHYLTEVHYLGGELSLSTRLVQVSApmQALA 319

                    lyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntR......ER
                    l +  + +          +q    EPYR  L  +  +L  t +  +++E
  gi|1216080   320 LRSPDRNE---------HRQ---DEPYRLALTGIYARLAATLkaltggEA 357

                    aRHLLAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLD
                    aRH +A      + +A y    eFL  L +   sL      ++A G L
  gi|1216080   358 ARHAVA------PQNA-YASAQEFLADLRVIEDSLTAHHGAALAAGRLHP 400

                    lLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRq
                    l+R v  FG  L  +D+Rq s+++  v+  +     +  +Y + +E  ++
  gi|1216080   401 LIRAVQVFGFHLATVDLRQSSDKHELVVAELLATARVQErYADLPEAGKR 450

                    EWLlaELkGKRPLlgsDLPktEEvk...DvldafrvLAE.LPiDsFGaYi
                      L+  L   RPL           +++  + ++ r L E+   ++   Yi
  gi|1216080   451 ALLIRLLNDARPLRVVGARYSAHAQgelAIFETARALRErFGAEAIRHYI 500

                    ismataPsDvLAvELLqRECgv.........kqtLrvvPLFEkLADLeA
                    is + + sD L v LL +E g+ +++ ++   ++ L vvPLFE +ADL+
  gi|1216080   501 ISHTETMSDLLEVLLLHKEVGLmsgtlddaaaRNQLIVVPLFETIADLRN 550

                    APAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkA
                    A   +   ++ +++   + r  G q++m+GYsDs KD G +   W LY+A
  gi|1216080   551 AAPIMREFYAlpgVAALVQRSGGEQDIMLGYSDSNKDGGIFTSNWELYRA 600

                    qEEiiK....vAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinG
                       +++  ++ A  +G++L +FHGRGGtvGRGGGP   AiL+qPP t+ G
  gi|1216080   601 EIALVQlfdeLAASHGIQLRMFHGRGGTVGRGGGPSYQAILAQPPGTVRG 650

                    slRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE.WRk
                     +R t qGEvi   +   ++  r L    AAtLE  +  P  P P ++
  gi|1216080   651 QIRLTEQGEVIASKYANPEIGRRNLEILVAATLEATLLQPTKPAPKtFLA 700

                    LmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkP
                       ++       YR++v+  P F EYF  AtP  E   +niGsRPa Rk
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  gi|1216080   701 AAGQLSQASMAAYRALVYETPGFTEYFFNATPIREIAELNIGSRPAARKA 750

                   sGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK....nlqk
                   s  ie LRAiPW F+W q R  LP W G+GAA    ++   K+++  l
  gi|1216080   751 SQKIEDLRAIPWGFSWGQCRLTLPGWYGFGAAVAAFVNLQGKtpgaQLAL 800

                   LkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksL
                   L+ mY++WPFFR  l  ++mv AK D  +A+ y +L+    L+k     +
  gi|1216080   801 LQRMYRQWPFFRTLLSNMDMVLAKSDLALAGRYSELVSDARLrKKVFAAI 850

                   RdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLK
                    +++  t d L +i G +  L     L   ++ R +Yi  L  +q   ++
  gi|1216080   851 EAEWHSTADALSRITGDQQRLAHNSALARSIKHRFAYIDPLHHLQVELVR 900

                   RiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLt
                   R R               A  +  + +  +++
  gi|1216080   901 RWR----------------AGQDDERVQTGIHIS---------------- 918

                   mKGiAAGmqntG<-*
                   + GiAAG+ ntG
  gi|1216080   919 INGIAAGLRNTG    930

gi|171057452|ref|YP_001789801.1|: domain 1 of 1, from 15 to 950: score 269.1, E = 9.9e-78
                   *->siDAqLRlLvPGKvsed....ekLieYDALLlDkFL.DiLqDLHGed
                         A      P + s+d  ++++ +  D  Ll + L+D++ +  G+d
  gi|1710574    15    KSAARRSPETPQRRSDDaaekNRPLMDDIRLLGRILgDVIREQEGQD 61

                   LkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmL
                     + +     ls  Y  K+D+         L  L    ++ v +a++
  gi|1710574    62 AFDLIERVRQLSVAYRFKQDANAGKTFDRLLKNLTVDQTVSVIRAFSYFS 111

                   nLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnK
                    LAn+AE+ +   RRR    +       a    E  +  t+ +L
  gi|1710574   112 HLANIAED-RHHVRRRQVHER-------AGNLQEGSLAMTFDRLAEAD-I 152

                   sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt
                     +++   L    +  vltAHPt   R+s+L  +  +   +      D+
  gi|1710574   153 RAADIAKSLAHAYISPVLTAHPTEVQRKSILDAERAVAELIGE--RDDLH 200

                   veDKkELDEALHRE.iqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                      ++   EAL R ++   + t  +R ++ t  DE+   +sY+  t  +
  gi|1710574   201 TAGQRADNEALLRArVTQLWQTRMLRYTKLTVADEIENALSYYRSTFLRQ 250

                   vPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                   +P+  R v+ AL    i           +   W+GGDRDG nP vt +
  gi|1710574   251 IPRMYRAVEQALPGHDIGN-------FFRMGNWIGGDRDG-NPFVTADTL 292

                   RDvCLLaRmmAanl..YisqvEDLmFElsmWRCndELRvRAEElyrtaar
                   +    L+R   + l++Y+  v  L  Elsm    + L     E++  aa
  gi|1710574   293 K--LALSRQSETVLrhYLTEVHALGAELSM---SQMLAPVTPEMQALAAA 337

                   dkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseis
                           E        EPYR +L  +  +L  t      L A    e
  gi|1710574   338 SPDQSSHRE-------DEPYRRVLIGMYARLAAT------LHAFTGTEAL 374

                   EeAv.....ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstF
                     Av+++++yt+  + L  L +   sL     +++    L  l+R v  F
  gi|1710574   375 RHAVppqnpYTDAGQLLADLQVIETSLKFHHAQALIAPRLAPLMRAVQVF 424

                   GLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELk
                   G  L  +D+Rq s+++  v+  +     + ++Y    E  R+E L+  L
  gi|1710574   425 GFHLATVDLRQSSDKHEAVVAELLACARVEAdYSALDEGARRELLMRLLN 474

                   GKRPLlgsDLPktE....EvkDvldafrvLAELPiDsFGaYiismataPs
                     RPL        E++ +E++    a  +LA     +   Yiis +   s
  gi|1710574   475 ETRPLRVIGAEYSEhtvgELAIFETARTMLAQYGRAAIRHYIISHTEDVS 524

                   DvLAvELLqRECgv.........kqtLrvvPLFEkLADLeAAPAavekLF
                   D L v LLq+E g+  +  + +  ++L vvPLFE + DL+ A   +   +
  gi|1710574   525 DLLEVLLLQKEAGLlvgaldadaTNALIVVPLFETIGDLRNAAPIMRAFY 574
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                    s...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                    + ++i   i r  G q++m+GYsDs KD G +   W LY A   ++
  gi|1710574   575 AlpgIKQMIVRSGGEQDIMLGYSDSNKDGGFFTSNWELYDAELALVELFE 624

                    ky....GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGE
                      ++++G+ L lFHGRGGtvGRGGGP   AiL+qPP t+nG +R t qGE
  gi|1710574   625 ALgrsdGITLRLFHGRGGTVGRGGGPSYQAILAQPPGTVNGQIRLTEQGE 674

                    viEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE.WRkLmeemAvvA
                    vi   +   ++  r L    AAtLE  +  P    P ++     e+
  gi|1710574   675 VIASKYSHPEIGLRNLETLVAATLEATLLHPTQSAPKgFLAAAAEISDAS 724

                    tEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRA
                       YR +v+    F +YF + tP  E   +niGsRPa Rk    ie LRA
  gi|1710574   725 MAAYRKLVYETDGFTDYFFSTTPIREIAELNIGSRPASRKATRAIEDLRA 774

                    iPWiFaWtqtRFHLPvWLGvGAAFKhAi.....dKDiKnlqkLkEmYkeW
                    iPW F+W q R  LP W G+G A    ++ +++dK    l  L+ m+k+W
  gi|1710574   775 IPWGFSWGQCRVALPGWCGFGSAIEAFLsaqgeDKRKSRLTLLQRMFKQW 824

                    PFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtk
                    PFFR  +  l+mv AK D  iAa y +L     L+k     + +++  t
  gi|1710574   825 PFFRTLMSNLDMVLAKTDLRIAARYVDLSEDKKLgKKIFAAIEAEWALTD 874

                    dlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsyk
                    + L +i G k  L   P L   +  R +Y+  Ln +q   ++R R
  gi|1710574   875 QALTQITGEKNRLASNPSLARSIEHRLPYLDPLNHLQVELMRRYRQ---- 920

                    vtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGm
                            KE    n  + +  +++                 + G+AAG+
  gi|1710574   921 -------RKEGDPAN-ERLQRGIHIS----------------INGVAAGL 946

                    qntG<-*
                     ntG
  gi|1710574   947 RNTG    950

gi|113868876|ref|YP_727365.1|: domain 1 of 1, from 65 to 1012: score 268.7, E = 1.3e-77
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        i    R  +   v      ++ D   l + L++ L +  G+   E+
  gi|1138688    65    TIAPTARRTADKDVP-----LREDIRFLGRLLgECLREQEGDAAFEV 106

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      +  +    D     EL   L  L    +  v +a++    LAn
  gi|1138688   107 VETIRQTAVRFRRENDRAAGAELDRLLKRLSRDQTNQVVRAFSYFSHLAN 156

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+ +   RRR++ +        +s      +   l  +   +  + +
  gi|1138688   157 IAEDQHHNRRRRVHALA-------GSPPQAGSLAHALEAIDAAG-VTGKQ 198

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                        L    +  vltAHPt   R+s+L  +  i   La      +t  ++
  gi|1138688   199 LRKFLDEALIVPVLTAHPTEVQRKSILDAEREIARLLAE-RDLPMTARER 247

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                          L   +   + t  +R ++ t  DE+   +sY+     +G+P+ +
  gi|1138688   248 DHNTAQLRAKVTTLWQTRMLRDSRLTVADEIENALSYYRTCFLRGIPQLM 297

                    RRvD........tALKniGinERlPYd.vPLikFssWmGGDRDGknPRvt
                       +++     +t  K  G     P   +P ++  sW+GGDRDG nP vt
  gi|1138688   298 SELEediaavfpTTRKRKGTPGAQPAPlAPFLQMGSWIGGDRDG-NPNVT 346

                    PEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE.Elyrt
                     E           m    Y++ v  L  Elsm    + L v A +El
  gi|1138688   347 AETLEHAASQQGQMIIDWYLDEVHALGAELSM----STLMVDASpELLAL 392

                    aardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGis
                    a r                EPYR  L  +  +L  t   ++ L  + +
  gi|1138688   393 AERS-------PDHSEHRADEPYRRALIGIYARLAAT---SKALTGHAVP 432

                    e..isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstF
                     ++++    y   E F   + +   sL     +++A G +  l R +  F
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  gi|1138688   433 RrpVAPAEPYDSAEAFAADVQVVVDSLRANHGQALANGRIEALARAIGVF 482

                   GLsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELk
                   G  L  +D+Rq s+ +  v+  +    +i + Y   +E ++ E LlaEL+
  gi|1138688   483 GFHLASVDMRQVSDVHEAVIAELFAAAGIApDYAALPEARKLELLLAELR 532

                   GKRPLlgsDLPktEEvkDvldafrvLAELPi....DsFGaYiismataPs
                     R L  +     E  +  l  f    EL  + ++     Yiis + + s
  gi|1138688   533 QPRLLTLPWHEYSEQTRKELAIFAAARELRArygkRIARNYIISHTETLS 582

                   DvLAvELLqRECgv.............kqtLrvvPLFEkLADLeAAPAave
                   D + v LLq+E g+ +++ ++++++ +  L v+PLFE + DL+ A   ++
  gi|1138688   583 DLVEVMLLQKESGMlqgtlgsktdpaRMELMVIPLFETIEDLRNAAGIMQ 632

                   kLFsi...DWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiK
                    L  +++ D  i +    qevm+GYsDs KD G l   W LYkA  E+++
  gi|1138688   633 SLLDLpgfDSVIAHHGVEQEVMLGYSDSNKDGGFLTSTWELYKAELELVQ 682

                   vAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEv
                      +  vKL lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGE+
  gi|1138688   683 LFEQRQVKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEI 732

                   iEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEWRkLmeemAvv
                   i   F   ++  r L    AAtLE  + P  ++Pk+   +  +m+++
  gi|1138688   733 INSKFANAEIGRRNLETVVAATLEASLLPQQnAPKdlDMFEAVMQQLSDR 782

                   AtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....Gi
                   A   YR +v+  P F +YF   tP +E   +n+GsRPa Rk   ++++ i
  gi|1138688   783 AFTAYRDLVYETPGFKDYFFATTPITEIADLNLGSRPASRKLMDkknrRI 832

                   esLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAi.....dKDiK.nlqkLk
                   e LRAiPW F+W q R  LP W G+G A K  +++ ++dK  K  +  L+
  gi|1138688   833 EDLRAIPWGFSWGQCRLLLPGWYGFGSAVKSLLdtapdDKARKlAVTTLR 882

                   EmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRd
                    m k+WPFF   l  ++mv AK D  +A+ y +L     L++   +++
  gi|1138688   883 RMVKTWPFFSTLLSNMDMVLAKTDLAVASRYAQLCDDAALrRTVFNRISK 932

                   kYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRi
                   ++  t ++L  + GH++ L   P L   ++ R +Y+  Ln +q   LKR
  gi|1138688   933 EWHLTCEMLTLVTGHQERLADNPLLARSIKNRFAYLDPLNHLQVELLKRY 982

                   RDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmK
                   R                    s k  + +++            + Lt+
  gi|1138688   983 R--------------------SGKDGDDIRVR----------RGIHLTIN 1002

                   GiAAGmqntG<-*
                   G+AAG+ ntG
  gi|1138688  1003 GVAAGLRNTG    1012

gi|283821743|ref|ZP_06348554.1|: domain 1 of 1, from 1 to 919: score 267.9, E = 2.3e-77
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       iD     L  G   + e  ++ D  Ll   L+D + +  G++   +
  gi|2838217     1    MIDTLSPTL--GGLPDLESRLQDDIRLLGALLgDTIREQEGDEAFRI 45

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +     ls  +E   Dt     +   +  + P  a+++A+a++    LAn
  gi|2838217    46 IETIRRLSVAFEREADTDAARAMDEIMARVTPEQAVIIARAFSYFSHLAN 95

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE+ +     R+ + +     DE     E  ++ t+ +L   +  + e
  gi|2838217    96 IAEDRHRIRAARVALER---RPDEQ----EGSLDLTFDRLAKAG-IATET 137

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   vF+ L    v  vltAHPt   RRs+L   + i   L     +D
  gi|2838217   138 VFDMLGTSLVSPVLTAHPTEVQRRSILDATSSIERLLEE---RDRLTGLE 184

                   kELDEALHR.EiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                       EAL R+ +   + t  +R +  t  DE+   + ++   +   +P
  gi|2838217   185 LKRNEALLRgRVLQLWQTRLLRSSHLTVADEIENALRFYKSSLLTEIP-- 232
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                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                     R  +t  + iG     P      +  sW+GGDRDG nP v  +  R
  gi|2838217   233 -RLYETLEQRIG----KPHAGSFFQMGSWIGGDRDG-NPNVNTDTLRLAL 276

                    LLaRmmAanlYisqvEDLmFEl....smWRCndELRvRAEElyrtaardk
                         +A   Y+  v +L  E++ ++ +  C  EL + AE
  gi|2838217   277 RRQSEIALRNYLTEVNELGIEMplstRLTQCTPELQALAERSNDNDPHR- 325

                    vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                                  EPYR  L  +  +L  t  +     A      s e
  gi|2838217   326 ------------ADEPYRRALTGIYARLAMTLRKLADKSALRPPLTSAE 362

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      ytk E+FL  L +   sL      ++ +  L  l R v  FG  L  +
  gi|2838217   363 P-YTKAEDFLADLVVIEESLLANKGGALIETRLGPLRRAVEVFGFHLATV 411

                    DiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPL..
                    D+Rq s+++ +v+  +     + ++Y++ sEe +q  Ll+ L   R L+
  gi|2838217   412 DLRQNSDKHEEVVAELLATARVSAdYKSLSEEEKQAVLLSVLGDPRQLri 461

                    ...lgsDLPktE.EvkDvldafrvLAELPiDsFGaYiismataPsDvLAv
                    ++   sDL   E  + D   a+r        +   Yiis + + sD L v
  gi|2838217   462 ptaAYSDLASSElGILDTARAMR--GTYGERAIRQYIISHTETVSDLLEV 509

                    ELLqRECgv.........kqtLrvvPLFEkLADLeAAPAavekLFs...
                     +Lq+E g+ ++  ++++ + +L vvPLFE + DL+ A   +   F+ ++
  gi|2838217   510 IVLQKEAGLmkgalgdpeaRVALIVVPLFETIPDLRRAEHIMRDFFAlpg 559

                    iDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGv
                    i       dG qevm+GYsDs KD G +   W + +A   +     + G
  gi|2838217   560 IHRLAAAGDGIQEVMLGYSDSNKDGGFFTSNWEVCRASVALEGLCSEEGL 609

                    KLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGE
                    +L lFHGRGGtvGRGGGPt  A+L+qP  t+nG +R+t qGEvi   +
  gi|2838217   610 RLRLFHGRGGTVGRGGGPTYQAVLAQPAGTVNGQIRITEQGEVIASKYAH 659

                    EnLCFrsLqRFtAAtLEHGmnPPvsPk.PEWRkLmeemAvvAtEEYRsvv
                     ++  r L   +AA +E  +  P  P +PE+ +  e++       YR++v
  gi|2838217   660 AEIARRNLESLAAASIEATLLSPRQPVpPEFLEAAEQLSALSMKSYRALV 709

                    vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWt
                    +    F  +F  AtP  E   +niGsRPa Rk    ie LRAiPW F+W
  gi|2838217   710 YDMEGFDAFFFAATPIAEIAELNIGSRPASRKANQRIEDLRAIPWSFSWG 759

                    qtRFHLPvWLGvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEm
                    q R  LP W G+G A +++A +        L+ m +eWPFFR  l  ++m
  gi|2838217   760 QARAALPGWYGFGTAVRsYAKEAPFERTALLRRMRREWPFFRTLLSNMDM 809

                    vFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtkdlLLkiAGHkDl
                    v AK D  iA  y +L+   +L +     L  ++  t + L  i G
  gi|2838217   810 VLAKADMRIARRYADLVPDRQLaRRVTGALLVEWNATVEALNIITGSPHR 859

                    LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                    L   P L   +  R +Yi  Ln +q   L+R R  ++
  gi|2838217   860 LADNPPLARVISRRIPYIAPLNHLQIELLRRWRRGDH------------- 896

                    dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +E        ++L             + + + G+AAG+ ntG
  gi|2838217   897 AEK-------IRLA------------IQISINGVAAGIRNTG    919

gi|228476844|ref|ZP_04061489.1|: domain 1 of 1, from 1 to 940: score 267.8, E = 2.5e-77
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                              +      s+++++i  +  +l   L+D    + Ge+
  gi|2284768     1    ------MAFNKLESSNNQEIISEEVGILKELLdDATRGMAGEQGLTT 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmL.nLA
                    +q   El  e     D   L    + +t     D ++vA+ +  +L+ L
  gi|2284768    42 IQHLVELYDE----GDYVALTQAISEMTN----DDMVVASRYFSLLpLLI 83

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+ E+v+lAy    k        DE+     s   Et+  +v       +
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gi|2284768    84 NISEDVDLAYEVNHKNNI-----DESYLGKLS---ETFD-VVAES----D 120

                 EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    + L    v  vltAHPtq  R+ +L     i   L +
gi|2284768   121 NARDILEHVNVVPVLTAHPTQVQRKTMLELTNHIHELLRKHRDVKAGLIN 170

                 KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                 K      L R +     tD iR  +   + E+   m Y+   + k +
gi|2284768   171 KDKWYADLRRYVEIMMQTDIIREKKLKVKNEITNVMEYYNSSLIKAITN- 219

                 LRRvDtALKniGinERlPYdvPL.ikFssWmGGDRDGknPRvtPEvtRDv
                         K + +   +  d P +i    W+GGDRDG nP vt E  +
gi|2284768   220 ---LSHEFKRLAVEKGIELDNPTpITMGMWIGGDRDG-NPFVTAETLKLS 265

                 CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                   L   +  n Yi++v+ L   +s+    + L    + +   a+    +
gi|2284768   266 ATLQSEVILNYYIEKVDNLYRSFSL---SSRLTEVSDTVAEMAKHSPDTS 312

                 yYiEFWKqvPPtEPYRviLGdvRDKLYn..........tRERaRHLLAtG
                  Y E       +EPYR     +  KL  +    ++++ t+ER    L
gi|2284768   313 VYRE-------NEPYRRAFSYIQSKLIQtllffkegnfTKERVAKRLSEN 355

                 i.......seisEeAv.................ytkvEeFLEPLELCYk
                 ++ ++ ++ e+  + v+++ +++ +  ++++++ y   ++F + L
gi|2284768   356 VrlgsastGEVVADYVqqrlsqslqavsqqttefYETADDFHDDLLAIKN 405

                 sLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAitt
                 sL e  D v+  G   +lL  v  FG  L  +D+Rq+s  +   +  + +
gi|2284768   406 SLLENDDAVLISGDFEELLQAVEVFGFYLATIDMRQDSSVHEACVAELLK 455

                 HLei.GsYReWsEeKRqEWLlaELkGK.RPLlgsDLPktEEvkDvldafr
                   +i   Y e  E  +   Ll EL+  +R L    +Pk E ++  l  fr
gi|2284768   456 SANIvDNYSELTEVEKVAVLLKELQEDpRTLSSTNVPKSETLEKELAIFR 505

                 vLAELPiDsFG.....aYiismataPsDvLAvELLqRECgv....kqtLr
                   A L  D  G++  +  iis + + sD+    +L +E g+ ++++  ++
gi|2284768   506 T-ARLLKDYIGedvikQHIISHTESVSDMFELAILLKEVGLvdteRARVQ 554

                 vvPLFEkLADLeAAPAavekLFsiDWYinri...dGKqevmvGYsDsGKD
                 +vPLFE + DLe     +++    D  +  i++++  qe+m+GYsDs KD
gi|2284768   555 IVPLFETIEDLENSNDIMKQYLGYDIVKRWIknsNNYQEIMLGYSDSNKD 604

                 AGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiL
                  G ls  W LYkAq E+ K+  + G+K++ FHGRGGtvGRGGGP   Ai
gi|2284768   605 GGYLSSGWTLYKAQNELTKIGEERGIKITFFHGRGGTVGRGGGPSYDAIT 654

                 sqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv
                 sqP  ti+  +R t qGEvi   +G  +  +  L     A L+  +   +
gi|2284768   655 SQPFGTIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLVSAALDRMVTRQI 704

                 sPkPE...WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkm
                 +   E  ++R++m+ +       YR +v+    F +YF  A P  E   +
gi|2284768   705 ADPDElvdFREIMDGIVNDSNVIYRDLVFGNEHFYDYFFEASPIKEVSSL 754

                 niGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidK
                 niGsRPa Rk    i  LRAiPW+F+W q R   P W GvG AF   i+
gi|2284768   755 NIGSRPAARKTITEISGLRAIPWVFSWSQNRIMFPGWYGVGSAFNRFIQA 804

                 DiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk
                 +  nl kL+ m+++WPFFR  l  ++mv  K D  iA  y +L  +Ee++
gi|2284768   805 EEGNLEKLQHMFETWPFFRSLLSNVDMVLSKSDMNIAFHYAQLAESEEVR 854

                 PFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvf
                    + + d+++ tkd +L i  H   L+  P LK  l  R +Y   Ln +
gi|2284768   855 SVFNIILDEWQLTKDVILAIEKHDGFLDESPSLKASLDFRLPYFNVLNYI 904

                 qAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLE
                 q   +KR+R              +  d++      L+++
gi|2284768   905 QIELIKRLRN------------NDLTDDE----ISLIHIT---------- 928

                 DtLiLtmKGiAAGmqntG<-*
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                      + GiA G+ n G
  gi|2284768   929 ------INGIATGLRNSG    940

gi|227890073|ref|ZP_04007878.1|: domain 1 of 1, from 2 to 912: score 267.3, E = 3.7e-77
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      si            s d  ++  +  +l   L++    L G+ +
  gi|2278900     2    SIKKL-------ENSSDHAMVAEEVKILTNLLnESTRQLSGDVIFNK 41

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +q+   +sA+    kD   Le    ++ sL   + i+vA+ +  +  L n
  gi|2278900    42 IQDLIKISAQ----KDYDALEK---QIASLTNQEMIVVARYFATLPLLIN 84

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   + E+velA           D+           +E+t+  Lv++     e
  gi|2278900    85 ISEDVELASEVNLLNNTDQDYLGK--------LEDTID-LVSQK----EN 121

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     e LK   v  vltAHPtq  R+ +L     i   L            +
  gi|2278900   122 ASEILKHVNVVPVLTAHPTQVQRKTVLELTDQIHGLLRSYREVKNGTINQ 171

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    E  E L   i     tD iR  +     E+   ++Y+   +   + KF
  gi|2278900   172 AEWTEKLRAYIEILMQTDIIRSHKLQVSNEITNVLAYYPKALIPAITKFT 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R     K   +n  l    P i    W+GGDRDG nP vt E  +
  gi|2278900   222 ARYQELAKKHNLN--LVGATP-ITMGMWIGGDRDG-NPYVTAETLKLSAT 267

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   L   +    Yi q+  L   +sm           E l   +  d
  gi|2278900   268 LQSQVIFEYYIKQLNNLYRTISMSTSYMKPSSAVEKLSELSNDD------ 311

                   iEFWKqvPPtEPYRviLGdvRDKLYntR.......ERaRHLLAtGiseis
                            +EPYR     +  +L  t  +  ++ ++   +    + ++
  gi|2278900   312 ----SPFRTNEPYRRAFYYIESRLLHTEytllgtaDKNSFVKKRDLENLD 357

                   EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                      vy +  +F   L     sL e  D+++     ++lL  +  FG  L
  gi|2278900   358 KIPVYKNPQDFKADLITIKESLEEDYDQAVVRSFFIELLEAIDIFGFHLA 407

                   KLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK.RP
                    +D+Rq+s  +   +  + + +i + Y   +E  +   Ll EL   +R
  gi|2278900   408 TIDMRQDSSVNETCVAELLKGAGICdDYSALPEKDKVKVLLNELNNDpRN 457

                   LlgsDLPktEEvkDvldafrvLAELPiDsFG.....aYiismataPsDvL
                   L     Pk E ++  l  ++    L  D+ G++  +  iis + + sD L
  gi|2278900   458 LHANNKPKSELLQKELKIYKTARQL-KDCIGedvikQHIISHTESVSDLL 506

                   AvELLqRECgvkqt....LrvvPLFEkLADLeAAPAavekLFsiDWYinr
                      ++ +E  + + ++ +++vvPLFE + DLe     ++    +D  +
  gi|2278900   507 EQAIMLKEYDLLNNqgarIQVVPLFETVEDLENSREIMKEFLNLDIVKRW 556

                   i...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                   + +++  qe+m+GYsDs KD G l+  W LYkAq ++  + Kk Gv ++
  gi|2278900   557 LasqNNYQEIMLGYSDSNKDGGYLASCWNLYKAQKDLTAMGKKLGVNITF 606

                   FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                    HGRGGtvGRGGGP   Ai +qP   in  +R+t qGE+i   +G  +
  gi|2278900   607 MHGRGGTVGRGGGPSYEAITAQPFGSINDRIRMTEQGEIIQNKYGNQDTA 656

                   FrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEEYRsvvvK
                   +  L   + At++  +   +    + +++R  m+e+       YR +v+
  gi|2278900   657 YYNLEMLASATIDRIVSKQIVSEDDiggFRSSMDEIVLDSNKIYRKLVFE 706

                   EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                    P F +YF  AtP      +niGsRPa Rk       LRAiPW+F+W q
  gi|2278900   707 TPAFLDYFLQATPIKQISNLNIGSRPAARKKITDFSGLRAIPWVFSWSQS 756

                   RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                   R   P W GvG AFKh id    nl  L+ mY+ WPFF   l  ++mv
  gi|2278900   757 RIMFPGWYGVGSAFKHFIDANPNNLHTLQKMYQGWPFFHSLLSNVDMVLS 806
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                    KGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                    K    iA  y +L   E+ k   + + ++++ tk+ +L+i G k+lL
  gi|2278900   807 KSNMDIAKQYADLCEDEDTKKVFDTICQEWKLTKEVILQIEGNKELLADN 856

                    PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                    P LK  l  R +Y   Ln +q   +KR R
  gi|2278900   857 PSLKMSLNYRMPYFNILNYIQIEMIKRDR---------------------- 885

                    kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                +++a   E  L +t+ G+  G+ n G
  gi|2278900   886 -----------VDEIAGVYESILPITINGVTSGLRNSG    912

gi|227832350|ref|YP_002834057.1|: domain 1 of 1, from 1 to 884: score 266.8, E = 4.9e-77
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            +   +P +v ed   i++   +l +   ++    Ged+ E v
  gi|2278323     1    -----MSTPAPEQVRED---IRFLGRVLGR---VIAQQEGEDVFELV 36

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ++ +    +   K e+L a    Ld +   lvA+a++    +AnL
  gi|2278323    37 ESTRRMAFDIA--HGDAKPEDLVAIFRDLDITKVNLVARAFSYFALIANL 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE                D  DE+     s +  t+ kL   +  +P++
  gi|2278323    85 AE----------------DLDDESVEAPVS-LRKTFAKLKEEG-VAPADA 116

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       ++   v  vltAHPt   RR +   ++Ri+  L           D
  gi|2278323   117 ASVIRGAHVAPVLTAHPTETRRRTVFDTQTRIKTLLKESH----RGGDMA 162

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     ++  +   +   + t  iR a+Pt  DE+  G+ Y+   + + vP   R
  gi|2278323   163 AIEKEMYLRMTLLWQTALIRIARPTLEDEIDVGLRYYKLSLLDQVPALNR 212

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     +  A++       lP d P+++  sW+GGD DG nP v
  gi|2278323   213 AIRHAMRET-FGQQLP-DSPVVRPGSWIGGDHDG-NPFVNEHTLTYATRK 259

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    a       Y + + +L  Els+    d       El   a       +
  gi|2278323   260 AAATVLQYYADELGELERELSL---SDRYSSSSKELGALADAS----HND 302

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    E  +     EPYR  +  +R K          +LA    e s  A y
  gi|2278323   303 EKSRV---DEPYRRAIFGIRKK----------VLARLEGEASPSA-YASP 338

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    Ee    L++  +sL +  D +iAD  L  l   v tFG  L  LD+Rq s
  gi|2278323   339 EELKRDLDVIDRSLRQFNDDIIADDRLARLRSAVTTFGFHLSTLDMRQNS 388

                    eRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLl..gsDLP
                    e    vl  i     i + YR   Ee +   L+ EL+  RPLl +g +
  gi|2278323   389 ESFENVLTEIFAAARITpDYRALGEEEKVALLVRELQTNRPLLfpGTEKE 438

                    ktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvELLqR
                     tE+ +  l+ fr  A    D FG+++ ++ iism+ + sD+L   +L +
  gi|2278323   439 FTEDTAKELGIFRAAARAVRD-FGPksvshCIISMTGTVSDILEPMVLLK 487

                    ECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...qevm
                    E g+ q + vvPLFE + DL+A    +ekL+ +  Y+ ++  +++ qevm
  gi|2278323   488 EVGLGQ-VDVVPLFETIEDLKAGASILEKLWQMPVYREHLRSRgdvQEVM 536

                    vGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRG
                    +GYsDs KD G l A W LY A   ++    ++Gv L l HGRGG vGRG
  gi|2278323   537 LGYSDSNKDGGYLQANWALYDAELALVELCVRHGVELRLAHGRGGAVGRG 586

                    GGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAt
                    GGPt  AiL+qP   + Gs+R+t qGEvi   +G  +   r L  F
  gi|2278323   587 GGPTYDAILAQPKGAVSGSVRITEQGEVISAKYGAPETARRHLEAFISGA 636

                    LEHGm..nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAt
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                    LE  + +  P++      ++m e+A      YR +v  +P F+ YF   t
  gi|2278323   637 LEASLldTEPIADPERAYEIMRELADLSGTAYRQLV-DDPGFIAYFTQST 685

                    PElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGA
                    P  E G +n+GsRP+ Rk    i+ LRAiPW+ +W q R  +P W GvG
  gi|2278323   686 PLHEIGELNLGSRPTSRKQTTAITDLRAIPWVLSWSQSRTNIPGWFGVGS 735

                    AFKhAidK....DiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    A    +++ ++++ K    L+E+Y++WPFFR     +  v AK +  +A
  gi|2278323   736 AVTAWVQQaggdEEKRWEELRELYRTWPFFRSVFANMAQVMAKAEMQLAR 785

                    LyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                    Ly +L+   e  ++ FG  +  +++ t++  Lk+ G  Dl+
  gi|2278323   786 LYANLVDDKETadRIFG-LISVEFERTREVYLKVTGNADLVSENQRQARS 834

                    lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                    l+ R +Y+  Ln +q   L+R R                      + d+
  gi|2278323   835 LKRRYPYLLPLNAIQLELLRRYR----------------------RGDDQ 862

                    vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      +            t+ +tm G+A  + n G
  gi|2278323   863 FLVS----------KTIQVTMNGLATALRNAG    884

gi|261855598|ref|YP_003262881.1|: domain 1 of 1, from 3 to 938: score 266.4, E = 6.7e-77
                    *->siDAqLRlLvPGKvsed.ekLieYDALLlDkFL.DiLqDLHGedLkE
                                K s+d++k ++    L    L+++L++  G+ + +
  gi|2618555     3    ------------KNSKDnDKALRARVRLFGNLLgEVLKEQTGDHVFD 37

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                     v            K+ +k    L   L  LdP     v +a+     L
  gi|2618555    38 TVETLRRGFIKLRLKHNPKLHAKLMVLLRTLDPDTLNFVVRAYNLYFSLV 87

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AEE +  +  R k+ +       +         +t++    ++  sP+
  gi|2618555    88 NIAEE-DFMHQHRRKQVR------LGLRLWRGSFYDTMREFSKQG-MSPD 129

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    +    L       v+tAHPt + RR ++  + +i    a L   +    +
  gi|2618555   130 DLQTLLNRLIYMPVFTAHPTEAKRRTVMDLQRKIFLLCAELDHPEAKGIE 179

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    +  L   +   i    +t E+R ++P   DE+R G+ Y+   +++ vP
  gi|2618555   180 RDRLHQQVKSVILSLLKTNEVRTTRPEVHDEIRLGLYYFSTSIFDAVPLA 229

                    LRRvDtALKniGinERlPYdvP.....LikFssWmGGDRDGknPRvtPEv
                     R  + A+  +  nE+ P d+P + ++L +F sW+GGDRDG nP vt Ev
  gi|2618555   230 YRYLERAV-DVNFNEKFP-DAPvtvpsLFRFGSWIGGDRDG-NPYVTHEV 276

                    tRDvCLLaRmmAanlYisqvE..DLmFElsmWRCndE......LRvRAEE
                    t      a       Y++ + + D +   s   C + + ++ +L   A E
  gi|2618555   277 TTFAVCSATQTILQEYLDRLAgmDRVLTHSCRLCPEIdleglgLHQDAVE 326

                    lyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLA
                    l   +  +    ++ E        EPYR  L  +  +L    +    LL
  gi|2618555   327 LGLASPENSGDSFFTE--------EPYRLKLRIIGQRLKHNLDYVTALLD 368

                    tGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvs
                    +   ++s  A y + ++FL  L      L   GD+ +ADG + Dl+R
  gi|2618555   369 KKPINLSAHA-YAHKDQFLSDLYRIRDTLISTGDQLLADGEIKDLIRLAE 417

                    tFGLsLvKLDiRqEseRqtDvlDAittHLe.iGsYReWsEeKRqEWLlaE
                    tFG  L KLDiRqEs R+t  +  i + L++   Y    E  R+  Ll+
  gi|2618555   418 TFGWHLFKLDIRQESTRHTQTVADILKQLQpKTDYMALDEAGRMT-LLTQ 466

                    LkGKRPLlgsDL.PktEEvkDvldafrvLAEL....PiDsFGaYiismat
                    L  K      D+     E ++ l+ f+v  EL ++   ++FG Y+ism+
  gi|2618555   467 LINKSRHKAIDMaALSAESAETLEVFKVKRELidtiSRECFGTYVISMTH 516

                    aPsDvLAvELL........qRECgvkqtLrvvPLFEkLADLeAAPAavek
                    a s v+ v  L    +  ++R  +    +++ PLFE + DL+     +
  gi|2618555   517 AASHVMEVMFLavlaglagKRKSQWFCDIQISPLFETIEDLHQIENVLSV 566
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                    LFsiDWYin..ridGK.qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKv
                    LF    Y+   r+ G  qe m+GYsDs KD G l+  W LY Aq  +  +
  gi|2618555   567 LFENPVYREliRVSGDlQEAMLGYSDSCKDGGSLASVWSLYNAQKRVLSI 616

                    AKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEvi
                     +k G+   lFHGRGGtv RGGGPtH  iLs P  t++G ++ t qGEv+
  gi|2618555   617 TQKNGIECRLFHGRGGTVARGGGPTHESILSLPAGTVEGQIKFTEQGEVL 666

                    EfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkP...EWRkLmeemAvvA
                       +   +     +   +   +    +  +   P + E  +++ e+A
  gi|2618555   667 SSKYSNTETAIYEITMGATGLMKASAHLVMENNPapaEHEQVVAELATYG 716

                    tEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLR
                       YR +    P F  YF  AtP  E G +niGsRPa Rk +     s+R
  gi|2618555   717 EKAYRELTDETPFFFNYFFEATPVRELGLLNIGSRPASRKVGDlSKASVR 766

                    AiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFR
                    AiPW+F W q R  LP W G+G A +   +        L+ +++eWPFF
  gi|2618555   767 AIPWVFGWSQSRHTLPAWYGIGSALRAWRQSHKDQPELLHTLFNEWPFFH 816

                    vtlDLlEmvFAKGDPGiAaLyDkLLvaE.eLkPFGksLRdkYvEtkdlLL
                      l    +   KG+  iA  y  L+    +  P  +++  +Y  t d LL
  gi|2618555   817 SMLRNTQLSLTKGEMTIAREYASLVADQaQALPVYDKISTEYYRTLDELL 866

                    kiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlr
                    ++A    l+E D Y+   +  R++Y+  Ln +q   L+R RD s
  gi|2618555   867 RVARVDSLVEIDEYIGTSMMRRNPYLDVLNHIQIVLLRRYRDDS------ 910

                    PhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG
                             E+  +a+    L             L+  +  iA Gm ntG
  gi|2618555   911 ---------EP--EAERQKWLL-----------PLLRSINAIASGMRNTG 938

                    <-*

  gi|2618555     -     -

gi|194290491|ref|YP_002006398.1|: domain 1 of 1, from 55 to 1009: score 265.6, E = 1.1e-76
                    *->siDAqLRlLvPGKvsedekL.ieYDALLlDkFL.DiLqDLHGedLkE
                       s      +  P +   d +++++ D   l + L+D L +  G+   E
  gi|1942904    55    SSNGTTIAPTPARRTTDKDVpLREDIRFLGRLLgDCLREQEGDAAFE 101

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    +v      +  +    D     EL   L  L    +  v +a++    LA
  gi|1942904   102 VVETIRQTAVRFRRENDRAAGAELDRLLKRLSRDQTNQVVRAFSYFSHLA 151

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE+ +   RRR++ +        +s      +   l k+   +  + +
  gi|1942904   152 NIAEDQHHNRRRRVHALA-------GSPPQAGSLQHALEKIDAAG-VTGK 193

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                         L    +  vltAHPt   R+s+L  +  i   La      +t  +
  gi|1942904   194 QLRKFLDEALIVPVLTAHPTEVQRKSILDAEREIARLLAE-RDLPMTARE 242

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    +      L   +   + t  +R a+ t  DE+   +sY+  t  +G+P+
  gi|1942904   243 RDHNTAQLRAKVTTLWQTRMLRDARLTVADEIENALSYYRTTFLRGIPQL 292

                    LRRvDtALKniGinER....lPYdv......PLikFssWmGGDRDGknPR
                    +   +  +  +    R++++ P d+++ + +P ++  sW+GGDRDG nP
  gi|1942904   293 MSELEEDIAAVFPATRrrkgAPGDAktaplsPFLQMGSWIGGDRDG-NPN 341

                    vtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE.Ely
                    vt E           +    Y++ v  L  Elsm    + L v A +El
  gi|1942904   342 VTAETLEHAAGQQAQLILDWYLEEVHALGAELSM----SMLMVDASpELL 387

                    rtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtG
                      a r                 EPYR  L  +  +L  t        At
  gi|1942904   388 ALAERS-------PDHSEHRADEPYRRALIGIYARLAATCKALSGHAATR 430

                    iseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstF
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                     + e  y   E F   + +   sL     +++A   +  l R +  F
  gi|1942904   431 RPVAPAEP-YDSAEAFGADIQVVIDSLRAHHGQALASHRIDALARAIAVF 479

                   GLsLvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELk
                   G  L  +D+Rq s+ +  v+  +    +i + Y   +E+++ E LlaEL+
  gi|1942904   480 GFHLASVDMRQVSDVHEAVIAELFAAAGIApDYAALPEQRKLELLLAELR 529

                   GKRPLlgsDLPktEEvkDvldafrvLAELPi....DsFGaYiismataPs
                     R L  +     E  +  l  f    EL  + ++     Yiis + + s
  gi|1942904   530 QPRLLTLPWHEYSEQTRKELAIFAAARELRArygkRVARNYIISHTETLS 579

                   DvLAvELLqRECgv............kqtLrvvPLFEkLADLeAAPAave
                   D + v LLq+E g+ +++ ++++++ +  L v+PLFE + DL+ A   ++
  gi|1942904   580 DLVEVMLLQKESGMlrgtlgsktdpaRMELMVIPLFETIEDLRNAAGIMQ 629

                   kLFsi...DWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiK
                    L  +++ D    +    qevm+GYsDs KD G l   W LYkA   +++
  gi|1942904   630 SLLDLpgfDAVLAHHGVEQEVMLGYSDSNKDGGFLTSNWELYKAELALVQ 679

                   vAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEv
                      +  vKL lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGE+
  gi|1942904   680 LFEQRNVKLRLFHGRGGTVGRGGGPTYDAILSQPPGTVNGQIRLTEQGEI 729

                   iEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEWRkLmeemAvv
                   i   F   ++  r L    AAtLE  + P  ++Pk+   +  +m+++
  gi|1942904   730 INSKFANAEIGRRNLETVVAATLEASLLPQQnAPKdlDTFEAVMQQLSDR 779

                   AtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....Gi
                   A   YR +v+  P F +YF   tP +E   +n+GsRPa Rk   ++++ i
  gi|1942904   780 AFTAYRDLVYETPGFKDYFFATTPITEIADLNLGSRPASRKLMDkknrRI 829

                   esLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAi.....dKDiKn.lqkLk
                   e LRAiPW F+W q R  LP W G+G A +  +++ ++dK  K  +  L+
  gi|1942904   830 EDLRAIPWGFSWGQCRLLLPGWYGFGSAVRSLLdsapdDKARKQaVTTLR 879

                   EmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRd
                    m k+WPFF   l  ++mv AK D  +A+ y +L     L++   +++
  gi|1942904   880 RMVKTWPFFSTLLSNMDMVLAKTDLAVASRYAQLCDDAALrRNVFNRISK 929

                   kYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRi
                   ++  t d+L  i GH++ L   P L   ++ R +Y+  Ln +q   LKR
  gi|1942904   930 EWHLTCDMLALITGHQERLADNPLLARSIKNRFAYLDPLNHLQVELLKRY 979

                   RDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmK
                   R               A  +     + +++             + Lt+
  gi|1942904   980 R----------------AGKD----GDDIRVR----------RGIHLTIN 999

                   GiAAGmqntG<-*
                   G+AAG+ ntG
  gi|1942904  1000 GVAAGLRNTG    1009

gi|255021660|ref|ZP_05293702.1|: domain 1 of 1, from 1 to 930: score 265.4, E = 1.3e-76
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                             +   Kv +d  L      L     ++L++  G+ +  av
  gi|2550216     1    --------MENKKVPNDRALRARVKRLGNLLGEVLKEQAGDRVFNAV 39

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                              ++D+k    L   + +L   D +lv +a+     L n+
  gi|2550216    40 EQLRQGYIRLHRREDPKLRKRLARFIDALPQDDLVLVIRAFNTYFSLVNI 89

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEE e  +  R ++++       ++A      EEt++ L  ++
  gi|2550216    90 AEE-EFQHLQRRRLLQ------RSEALWVGSFEETFRALQQQG--IHSGQ 130

                   FeALKnqsvDL.vltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + L  q   L+v+tAHPt s RR +L    Ri      L    +  e+
  gi|2550216   131 LQYLLGQIRYLpVFTAHPTESKRRTVLHGLRRIFLTSKMLDDPSLSQEEE 180

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    ++   L   iq  + t+E+R  +P  qDE+  G+ Y+ + +++ vP
  gi|2550216   181 NDVLRQLKAQIQILWETEEVRSNRPQVQDEVENGLFYFRDSLFNAVPMCY 230
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                    RRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDvC
                         A++ +  n  +  d+P  i+F sW+GGDRDG nP vt  +t
  gi|2550216   231 HAARRAVRRVYGNPNV--DIPaFIRFGSWIGGDRDG-NPNVTAAITGWAL 277

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                        m     Y   + DL   l          v    l +  +
  gi|2550216   278 RTQSMEVLREYQRRLADLYQLLG--HSSRFCAVSPVLLASLERDADDFPE 325

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                      E+  q  P EPYR  L  +  +L     R R L    i + +    y
  gi|2550216   326 LAEWVNQRFPSEPYRRKLRYMMTRL---DLRLRQLENGQILNEAAGPGYS 372

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                       eFLE L L   sL    D+ iA+  +  l+    tFG  L  LDiRq
  gi|2550216   373 SASEFLEDLLLVRDSLRGHRDHYIAEHDVQNLVWLLETFGFHLAALDIRQ 422

                    EseRqtDvlDAittHL.eiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    Es  +   +  + + + +   Y e +Ee+R   L   L+    L+
  gi|2550216   423 ESTVHGQTIAELFRDVaGFANYLEQPEEQRLLTLAEALRRPGCLVTETPE 472

                    ktEEvkDvldafrvLAELPi....DsFGaYiismataPsDvLAvELLqRE
                         ++    fr +A L  + ++++FG+Y+ism+   s +L v LL +E
  gi|2550216   473 LSPLAAETCAMFRCIAQLRRevspEAFGSYVISMTHEASHILEVLLLAKE 522

                    Cgvk........qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK
                     g+ + ++++    + v PLFE + DLe   A + +L     Y   +  +
  gi|2550216   523 FGLAgwsreglySEIAVTPLFETIHDLERMEAVMSRLLDDPVYAEILRSQ 572

                    ...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    ++ qevm+GYsDs KD G ls  W LY+Aq  ++  A +  +++ +FHGR
  gi|2550216   573 gnlQEVMLGYSDSCKDGGILSSSWSLYQAQIRLAELADRRRIQIRVFHGR 622

                    GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                    GG vGRGGGPt  Ai++qPPDt+ G +++t qGEv+ f +   +     L
  gi|2550216   623 GGSVGRGGGPTYEAIMAQPPDTVRGQIKITEQGEVLSFKYANLETAVYEL 672

                    qRFtAAtLEH..GmnPPvs.PkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                        A  +  + G+   v   +P++ ++m e+  +    YR +    P F
  gi|2550216   673 TVGVAGLIRAsvGLVRRVElDRPDYLQVMSELVEIGEAVYRDLTEHTPGF 722

                    vEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqtRFH
                    ++YF  AtP  E  +mniGsRP+ R+ + + + s+RAiPW+FaW q R
  gi|2550216   723 MDYFYEATPLNEIAHMNIGSRPSHRHRGDrSMASIRAIPWVFAWAQSRHV 772

                    LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                    LP W G+G A       D   l  L++m k WPFFR  l  + m  AK
  gi|2550216   773 LPAWYGLGSALARWRGDDPDRLNTLRDMAKHWPFFRALLGNISMAMAKTH 822

                    PGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDP
                      +A  y  L    e  +k F k +R++Y+     LL        L   P
  gi|2550216   823 LDLAREYAGLPQDQECaqKIFAK-IRAEYELSLAELLTALDLPAPLADNP 871

                    YLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnsk
                     L   l  R+ Y+  Ln +q   L+R R  +   t++     E+ +
  gi|2550216   872 TLAFSLQRRNVYMEPLNHIQLALLRRYRNED---TPQ-----EFRETW-- 911

                    kadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                           L            L+ t+  iAAG  ntG
  gi|2550216   912 -------LD-----------PLLRTINAIAAGQRNTG    930

gi|125718332|ref|YP_001035465.1|: domain 1 of 1, from 1 to 948: score 265.4, E = 1.3e-76
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           +        s+ e + e  A+L D   Di   L  +
  gi|1257183     1    -----MSFNKLESYSNKEVIREEVAILTDLLADITRNLLSP------ 36

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E +E     E     +K  EL a +  L   + + + + ++ +  L n+
  gi|1257183    37 -ETFEKISLMEDLAVNSKYHELKAIVEELTTDEMVYISRYFSILPLLINI 85

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
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                E+v+lAy    +     D+    s t +         L++      e
gi|1257183    86 SEDVDLAYEINHQNNINQDYLGKLSTTID---------LISTR----ENA 122

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLs.AKDvtveDK
                 e L n  v  vltAHPtq  R+ +L     i   L q  + K   v++K
gi|1257183   123 QEILENLNVVPVLTAHPTQVQRKTILDLTNHIHSLLRQHRdVKAGLVNEK 172

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                k L   L R i     tD iR  +     E+   m Y+     + +  F+
gi|1257183   173 KWLGN-LRRYIELMMQTDMIREKKLKVTNEITNVMEYYNSSFLQAITNFM 221

                RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                          Gi    P     i    W+GGDRDG nP vt E  +
gi|1257183   222 VEYRRLAEERGIKLDNPKP---ITMGMWIGGDRDG-NPFVTAETLKLSAT 267

                LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                L   +  n Yi++v  L   +s+    +E      E+   +  +     Y
gi|1257183   268 LQSEVILNYYIDKVYTLYRTFSLSTNLSETSQAVAEMAALSTDK---SVY 314

                iEFWKqvPPtEPYRviLGdvRDKLYnt.............RERa...
                 E       +EPYR     +  KL  t    ++++ ++++++  +Ra+++
gi|1257183   315 RE-------NEPYRRAFHYIQSKLIQTllylkegnfsndgqrlTDRAeek 357

                .............RHLLAtGi.seisEeAv.........ytkvEeFLEPL
                 + + + + ++++R ++   i+s isE   + +++++++y    eF E L
gi|1257183   358 lsakanlsvsnkgREIIPNYIqSRISETLTelkkeetpsYKTAQEFKEDL 407

                ELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvl
                 + Y sL e    ++  G L +lL  v  FG  L  +D+Rq+s  +   +
gi|1257183   408 QVIYDSLIEHHGEALVSGDLTELLQAVDVFGFFLASIDMRQDSSVHEACV 457

                DAittHLeiGs.YReWsEeKRqEWLlaE.LkGKRPLlgsDLPktEEvkDv
                  +    +i  +Y + sEe +   Ll   L+  R L     Pk E ++
gi|1257183   458 AELLASANIVQdYSSLSEEEKCQVLLKQlLEDPRILSATHEPKSELLQKE 507

                ldafrvLAELPiDsFG.....aYiismataPsDvLAvELLqRECgvkqt.
                l+ f+    L  D+ G++  +  iis +t+ sD L   ++ +E g+   +
gi|1257183   508 LEIFKTARQL-KDAIGeevikQNIISHSTSVSDLLELAIMLKEVGLIDEn 556

                ...LrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...qevmvGYs
                + ++++vPLFE + DL+    ++ek  s+      i  K++ qe+m+GYs
gi|1257183   557 garVQIVPLFETIEDLDNSCNTMEKYLSLPIAQKWIASKdnyQEIMLGYS 606

                DsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPt
                Ds KD G ls  W LYkAq  +  +  k+GvK++ FHGRGGtvGRGGGPt
gi|1257183   607 DSNKDGGYLSSCWTLYKAQQQLTAIGDKFGVKITFFHGRGGTVGRGGGPT 656

                HLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHG
                  Ai sqP   in  +R t qGEvi   +G  +  +  L     A +
gi|1257183   657 YEAITSQPLRSINDRIRLTEQGEVIGNKYGNKDAAYYNLEMLVSAAINRM 706

                mnPPvs...PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPEl
                +    s+++    + ++m+++       YR +v+ + RF +YF    P
gi|1257183   707 VTHKKSdshTSDKYERIMDQVVNRSYQIYRDLVFGDERFYDYFFESSPIK 756

                EYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFK
                     niGsRPa Rk    i  LRAiPW+F+W q R   P W GvG  FK
gi|1257183   757 AISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWYGVGSSFK 806

                hAidKD.iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL
                  id D+  nl  L+ mYk WPFF+  l  ++mv  K    iA  y +L
gi|1257183   807 EFIDEDpENNLAFLQFMYKRWPFFKSLLSNVDMVLSKSNMNIAFEYAQLC 856

                vaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYi
                   +++   + + d+++ tkd +L+i GH +lL    YL+  l  R +Y
gi|1257183   857 EDQNVRDIFNIILDEWQLTKDVILEIEGHDELLAENTYLRDSLHYRMPYF 906

                ttLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpter
                  Ln +q   +KR R  + + t+         +E       L+++
gi|1257183   907 NVLNYIQLELIKRQR--NGQLTPD--------QEK------LIHIT---- 936
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                    vaPGLEDtLiLtmKGiAAGmqntG<-*
                                + GiA G+ n G
  gi|1257183   937 ------------INGIATGLRNSG    948

gi|227904011|ref|ZP_04021816.1|: domain 1 of 1, from 1 to 912: score 265.3, E = 1.4e-76
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                     s d+ ++  +  +l k L++    L G+d
  gi|2279040     1    ------MTFTKLENSSDQAVVAEEVKILTKLLnESTRQLIGDDAFAK 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +q+  + sA     kD k+Le   +k+ sL+  + i+vA+ +  +  L n
  gi|2279040    42 IQDLIDTSAS----KDQKQLE---SKISSLNNREMIVVARYFATLPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+velA +  +      D+    s t +         Lv +     ++
  gi|2279040    85 ISEDVELASKVNVFNNTDQDYLGKLSDTID---------LVAQK----DD 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                        L n  v  vltAHPtq  R+ +L    +i   L            +
  gi|2279040   122 AKRILENVNVVPVLTAHPTQIQRKTVLELTDKIHHLLRSYRDVKNGTINQ 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +E  E L   i     tD iR  +     E+   ++Y+   +   + KF
  gi|2279040   172 REWTEQLRACIEILMQTDIIRGHKLKVSNEITNVLAYYPKALIPAITKFT 221

                    RRvDtALK..niGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     R     K++n+ +    P     i    W+GGDRDG nP vt +
  gi|2279040   222 TRYKELAKehNLTLDQATP-----ITMGMWIGGDRDG-NPYVTADTLELS 265

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      L   +    Y+  +  L   +s+        +  E l + +  d
  gi|2279040   266 ATLQSQVIFEYYMKELKKLYRAISLSTSYMQPSAAVEKLSKLSNDD---- 311

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntR.......ERaRHLLAtGise
                                EPYR     +  +L  t ++  +  ++   +  + + +
  gi|2279040   312 ------SPFRTDEPYRRAFYYIESRLVHTEkellgiiDKNIFIKPHDLEN 355

                    isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                    +    vy +  eF   LE    sL e  D+++       +L  +  FG
  gi|2279040   356 LDNIPVYNNPQEFKSDLETIKASLDEDHDQAVTHSFFTQILEAIDVFGFH 405

                    LvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK.
                    L  +D+Rq+s  +   +  + +  +i + Y + sE  + E Ll+EL+  +
  gi|2279040   406 LATIDMRQDSSVNESCVAELLKSAGICdNYSDLSEKEKVELLLSELENDp 455

                    RPLlgsDLPktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDv
                    R L     Pk E ++++  +  + r L ++L  D     iis + + sD+
  gi|2279040   456 RNLHANNKPKSELLQkelKIYKTARQLKDrLGEDVIKQHIISHTESVSDM 505

                    LAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLFsi....D
                    L   ++ +E  + +++k  ++vvPLFE + DL  A   + +  s +  +
  gi|2279040   506 LEQAIMLKEYNLvdseKARIQVVPLFETVEDLLNAREIITQYLSFpivkK 555

                    WYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                    W + + +  qe+m+GYsDs KD G l+  W LYkAq ++  +  k GvK+
  gi|2279040   556 WLVSQ-NNYQEIMLGYSDSNKDGGYLASCWNLYKAQKDLTAIGEKLGVKI 604

                    vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                    +  HGRGGtvGRGGGP   Ai +qP   in  +R+t qGE+i   +G  +
  gi|2279040   605 TYMHGRGGTVGRGGGPSYEAITAQPFKSINDRIRMTEQGEIIQNKYGNKD 654

                    LCFrsLqRFtAAtLEHGm.nPPvsPk..PEWRkLmeemAvvAtEEYRsvv
                      +  L   + A ++  +++  vs  +  ++R  m+++       YR +v
  gi|2279040   655 TAYYNLEMLASAAIDRMVsKQAVSEEriTDFRSSMDKIVEESNKIYRKLV 704

                    vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWt
                    +  P F +YF  AtP  E   +niGsRPa Rk       LRAiPW+F+W
  gi|2279040   705 FENPAFLDYFFQATPIKEISNLNIGSRPASRKKLTDFSGLRAIPWVFSWS 754

                    qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                    q R   P W GvG AF   i+ D   l+ L+EmYk WPFF   l  ++mv
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  gi|2279040   755 QSRIMFPGWYGVGSAFANFINADPTHLKELQEMYKGWPFFHSLLSNVDMV 804

                   FAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE
                     K    iA  y  L   Ee k   + + ++++ tk+ +L+i  H DlL
  gi|2279040   805 LSKSNMEIAREYASLCDDEETKKVFDIIYQEWKLTKKVILQIEDHDDLLA 854

                   GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                     P LKq l  R +Y   Ln +q   +KR R+ + +   +  +
  gi|2279040   855 EAPILKQSLDYRMPYFNILNYIQIEMIKRGREDEIQGVYQSII------- 897

                   nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   +       + +n                  G+A G+ n G
  gi|2279040   898 P-------ITIN-----------------GVASGLRNSG    912

gi|20196778|emb|CAC86361.1|: domain 1 of 1, from 1 to 383: score 265.0, E = 1.8e-76
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2019677     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2019677     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2019677     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                                +tAHPtqs+RRsLLqKnaRiRnCL+qLsAKD t+eDKk
  gi|2019677     1 -----------FTAHPTQSARRSLLQKNARIRNCLTQLSAKDTTPEDKK 38

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL REiqAAFRtDEiRRaqPtPqDEmR+GmsYiHEtvWkGvPKFLR
  gi|2019677    39 ELDEALQREIQAAFRTDEIRRAQPTPQDEMRYGMSYIHETVWKGVPKFLR 88

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALKniG+nERlPY+vPLikF+sWmGGDRDG nPRvtPEvtRDvCLL
  gi|2019677    89 RVDTALKNIGVNERLPYNVPLIKFCSWMGGDRDG-NPRVTPEVTRDVCLL 137

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   +RmmAanlYi+qvEDLmFElsmWR n ELR++A+El +t+a++kv+KyYi
  gi|2019677   138 SRMMAANLYIDQVEDLMFELSMWRSNAELRAKADELLSTPASKKVTKYYI 187

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWKq+P +EPYRviLG+vRDKLYntRERaRHLLAtG+s+isE+ v+t +
  gi|2019677   188 EFWKQIPENEPYRVILGAVRDKLYNTRERARHLLATGFSDISEDSVFTSI 237

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   E+ LEPLELCYksL +CGDk+iADGsLLDlLRqv+ FGLsLvKLDiRqEs
  gi|2019677   238 EQLLEPLELCYKSLIDCGDKAIADGSLLDLLRQVFIFGLSLVKLDIRQES 287

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   eR+tDv+DAittHL+iGsYR+W+E+KR E+L++ELkGKRPLl++DLP+tE
  gi|2019677   288 ERHTDVIDAITTHLGIGSYRSWPEDKRVEFLVSELKGKRPLLPPDLPMTE 337

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E++Dv++a++v+AELP+DsFG+Yiism+taPsDvLAvELLqRECg+
  gi|2019677   338 EIADVIGAMKVIAELPSDSFGPYIISMCTAPSDVLAVELLQRECGI---- 383

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG

  gi|2019677     - ---------------------------------------------- -

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|2019677     - ---------------------------------------------- -

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

  gi|2019677     - ---------------------------------------------- -
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                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|2019677     - ------------------------------------------------- -

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|2019677     - ------------------------------------------------- -

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|2019677     - ------------------------------------------------- -

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|2019677     - ------------------------------------------------- -

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|2019677     - ------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|2019677     - -------------    -

gi|187929645|ref|YP_001900132.1|: domain 1 of 1, from 56 to 1001: score 263.6, E = 4.6e-76
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                     s+    R    G  +  ++ ++ D   l + L+D+L +  G    E
  gi|1879296    56    SLGPTSRR-SSGSAAAKDQPLKEDIRFLGRLLgDVLREQEGGAAFET 101

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v      +  +    D +  +EL   L +L    +  v +a++    LAn
  gi|1879296   102 VETIRQTAVRFRRDGDRQAEQELDRLLKALSREQTNSVVRAFSYFSHLAN 151

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  +AE+ +   RRR++ +        +s      +   l  +   +  s e
  gi|1879296   152 IAEDQHHNRRRRVHALA-------GSPPQPGSMMRALLSVADEG-VSGET 193

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                           +  vltAHPt   R+s+L  +  i   La      +t  ++
  gi|1879296   194 LRRFFDAALIVPVLTAHPTEVQRKSILDAQREIARLLAE-RDTPLTTRER 242

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  +     L   +   + t  +R ++    DE+   +sY+  t  + +P
  gi|1879296   243 ERNTTLLRAHVTKLWQTRMLRTTRLMVADEIENALSYYQTTFLREIPALY 292

                  RRvDtALKni....GinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                  R  +  +  + +++G        +P  +  sW+GGDRDG nP vt E  R
  gi|1879296   293 RELEEDVAAVfprrGARGEPTPLAPFFQMGSWIGGDRDG-NPFVTAETLR 341

                  DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                          +    Y++ +  L  Elsm    + + v AE l    ++
  gi|1879296   342 YAARKQASVILAWYLEEIHALGAELSM--STSQVDVSAELLALAEQSPDR 389

                  vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLA..tGiseisE
                    +           EPYR  L  v  +L  t    R L  ++ G   +
  gi|1879296   390 SEH--------RSDEPYRRALIGVYARLAAT---CRELTGedAGRHAVGP 428

                  eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                     yt  Ee    + +   sL      ++AD  L  l R +  FG  L
  gi|1879296   429 APAYTSAEELRADIQIVTDSLAAHHGEALADARLASLARAIDVFGFHLSS 478

                  LDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaELkGKRPLl
                  +D+Rq s+ +   +  + +  +++G+Y   sE  ++  Ll EL+  R L
  gi|1879296   479 IDLRQVSDVHEATVAELLKVAGVeGAYAALSEADKRTLLLRELQQPRLLT 528

                  gsDLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAvE
                   +     E     +d fr  ++v A         Yiis + + sD L v
  gi|1879296   529 LPFHAYSEQTTQEIDIFRaareVRARYGNRIVRNYIISHTETLSDLLEVM 578

                  LLqRECgvkqt..........LrvvPLFEkLADLeAAPAavekLFsi...
                  LLq+E g+ +++ ++ + + ++ v+PLFE + DL+ A   +  L ++++
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  gi|1879296   579 LLQKEAGMFRAnangagvgldVMVIPLFETIEDLRNASQIMGDLLALpgf 628

                    DWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvK
                    D         qevm+GYsDs KD G l   W LYkA   ++    + Gv+
  gi|1879296   629 DAVLAAQGNEQEVMLGYSDSNKDGGFLTSNWELYKAELALVELFERKGVR 678

                    LvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEE
                    L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGE+i   F
  gi|1879296   679 LRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEIISSKFANP 728

                    nLCFrsLqRFtAAtLEHGmnPPvs.Pk..PEWRkLmeemAvvAtEEYRsv
                    ++  r L    AAtLE  + P   +Pk+  E+   m+ +   A   YR +
  gi|1879296   729 EIGRRNLETIVAATLEATLLPTRNrPKglEEFEAAMQALSDNAFAAYRNL 778

                    vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....GiesLRAiPW
                    v+  P F +YF   tP +E   +n+GsRPa Rk   ++++ ie LRAiPW
  gi|1879296   779 VYETPGFKDYFFATTPITEIADLNLGSRPASRKLMDkkhrRIEDLRAIPW 828

                    iFaWtqtRFHLPvWLGvGAAFKhAidKD......iKnlqkLkEmYkeWPF
                     F+W q R  LP W G+G A +  +d  ++ + +   l  Lk m k+WPF
  gi|1879296   829 GFSWGQCRLLLPGWFGFGSAVQRWLDDAgnakarAARLTTLKRMHKQWPF 878

                    FRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk.PFGksLRdkYvEtkdl
                    F   l  ++mv  K D  +A+ y +L     L++    ++ +++  t+++
  gi|1879296   879 FANLLSNMDMVLSKADLNVASRYAQLCDDRKLRnAVFSRISAEFALTEQM 928

                    LLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvt
                    L  i G  + L   P L   ++ R +Y+  Ln +q   LKR R
  gi|1879296   929 LAAITGQSERLADNPLLARSIKNRFPYLDPLNHLQVELLKRFRS------ 972

                    lrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqn
                          K   d+   +    ++L                + GiAAG+ n
  gi|1879296   973 -----GKAGSDDA--RVRRGIHLS----------------INGIAAGLRN 999

                    tG<-*
                     G
  gi|1879296  1000 SG    1001

gi|83749206|ref|ZP_00946208.1|: domain 1 of 1, from 67 to 1020: score 263.2, E = 5.9e-76
                    *->siDAqLRlLvP......GKvsedekLieYDALLlDkFL.DiLqDLHG
                       +  A    L P++++++G  +  ++ ++ D   l + L+D+L +  G
  gi|8374920    67    ARGAAGTTLGPtsrrssGSAAAKDQPLKEDIRFLGRLLgDVLREQEG 113

                    edLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailH
                        E v      +  +    D +  +EL   L  L    +  v +a++
  gi|8374920   114 AAAFETVETIRQTAVRFRRDGDRQAEQELDRLLKTLSRDQTTSVVRAFSY 163

                    mLnLAnLAEEvelAyRRRikkkkhGDFaDEasA..ttEsDiEEtlKkLvl
                       LAn+AE+ +   RRR++ +  G     +s  +   s  +E l    l
  gi|8374920   164 FSHLANIAEDQHHNRRRRVHALA-GSPPQPGSLlrALLSAADEGLSGEAL 212

                    klnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsA
                    +        F+A     +   vltAHPt   R+s+L  +  i   La   A
  gi|8374920   213 RR------FFDA---ALIVPVLTAHPTEVQRKSILDAQREIARLLAERDA 253

                    KDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtv
                      +t  +++     L   +   + t  +R ++    DE+   +sY+  t
  gi|8374920   254 -PLTARERERNTTLLRAHVTKLWQTRMLRTTRLMVADEIENALSYYQTTF 302

                    WkGvPKFLRR....vDtALKniGinERlPYdvPLikFssWmGGDRDGknP
                     + +P   R  +++v t     G            +  sW+GGDRDG nP
  gi|8374920   303 LREIPALYREleedVATVFPRRGARGEPATLPAFFQMGSWIGGDRDG-NP 351

                    RvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEly
                     vt    R        +    Y++ +  L  Elsm    + + v AE l
  gi|8374920   352 FVTAQTLRHAARRQASVILTWYLDEIHALGAELSM--STSLVDVSAELLA 399

                    rtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLA..
                       ++     +  +        EPYR  L  v  +L  t    R L  ++
  gi|8374920   400 LAERSPDHSEHRAD--------EPYRRALIGVYARLAAT---CRELTGed 438
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                    tGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvs
                     G   +     yt  E+    + +   sL      ++AD  L  l R +
  gi|8374920   439 AGRHAVGPAPAYTSPEDLRADIRIVIDSLAAHHGEALADARLTSLARAID 488

                    tFGLsLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaE
                     FG  L  +D+Rq s+ +   +  + +  +++G+Y   sE  ++  Ll E
  gi|8374920   489 VFGFHLASIDLRQVSDVHEATVAELLKVAGVeGAYAALSEADKRTLLLRE 538

                    LkGKRPLlgsDLPktEEvkDvldafr....vLAELPiDsFGaYiismata
                    L+  R L  +     E  +  l+ fr  ++v A   +     Yiis + +
  gi|8374920   539 LQQPRLLTLPFHTYGETTASELEIFRaareVRARYGSRIVRNYIISHTET 588

                    PsDvLAvELLqRECgv.kq.........tLrvvPLFEkLADLeAAPAav
                     sD L v LLq+E g+ +++++++++ +  + v+PLFE + DL+ AP  +
  gi|8374920   589 LSDLLEVMLLQKESGMfRHgtnggggaglDVMVIPLFETIEDLRNAPQIM 638

                    ekLFsi...DWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEii
                      L ++++ D      d  qevm+GYsDs KD G l   W LYkA   ++
  gi|8374920   639 GDLLALpgfDAVLAAQDNEQEVMLGYSDSNKDGGFLTSNWELYKAELALV 688

                    KvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGE
                        ++Gv+L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGE
  gi|8374920   689 DLFERHGVRLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGE 738

                    viEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs.Pk..PEWRkLmeemAv
                    +i   F   ++  r L    AAtLE  + P   +Pk+  E+   m+ +
  gi|8374920   739 IISSKFANPEIGRRNLETIVAATLEATLLPTRNrPKglEEFEAAMQALSD 788

                    vAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....G
                     A   YR +v+  P F +YF   tP +E   +n+GsRPa Rk   ++++
  gi|8374920   789 HAFSAYRNLVYETPGFKDYFFATTPITEIADLNLGSRPASRKLMDkkqrR 838

                    iesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD......iKnlqkL
                    ie LRAiPW F+W q R  LP W G+G A +  +d  ++ + +   l  L
  gi|8374920   839 IEDLRAIPWGFSWGQCRLLLPGWFGFGSAVQRWLDEAgsakakAARLATL 888

                    kEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk.PFGksLR
                    k m k+WPFF   l  ++mv  K D  +A+ y +L     L++    ++
  gi|8374920   889 KRMHKQWPFFANLLSNMDMVLSKADLNVASRYAQLCDDRKLRnAVFSRIS 938

                    dkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKR
                    +++  t ++L  i G  + L   P L   ++ R +Y+  Ln +q   LKR
  gi|8374920   939 AEFTLTGQMLAAITGQSERLADNPLLARSIKNRFPYLDPLNHLQVELLKR 988

                    iRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtm
                     R                A  n  +    ++L                 +
  gi|8374920   989 FRSGK-------------AGSNDARVRRGIHLS----------------I 1009

                    KGiAAGmqntG<-*
                     GiAAG+ n G
  gi|8374920  1010 NGIAAGLRNSG    1020

gi|256759173|ref|ZP_05499837.1|: domain 1 of 1, from 1 to 936: score 262.7, E = 8.5e-76
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                             R  +    s+ +  +  D  Ll + L+D++ +  G+++ ++
  gi|2567591     1    ---MSTRPSAARNASDPDAPLFDDIRLLGRLLgDLIREQEGQEMFDI 44

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ls  +    D+k    L   L sL    a+ v +a++    LAn
  gi|2567591    45 VETVRQLSVKFHRDGDAKDRRALDKLLSSLSRDQAVSVIRAFSYFSILAN 94

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+ ++  R      +       +       +   l  L   +    +
  gi|2567591    95 IAEDHHVLRRAEQDAER-------GAPPQRDSVRAALETLKDSG-VDRQQ 136

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      +      +  vltAHPt   R+s+L  +  +   L    A  + ++ +
  gi|2567591   137 LLQFFDQALISPVLTAHPTEVQRKSVLDAERALARLLVERDATRL-PQKR 185

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     ++++A+   +   + t  +R  +    DE++  +s++  t +   P+
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  gi|2567591   186 ADIEDAMRARVVQLWQTRLLRYVKLKVSDEIKNALSFYGATFFSQFPRLY 235

                   RRvD...tALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtR
                   R  +++  AL   G  +    d P   +   W+GGDRDG nP vt +
  gi|2567591   236 RNLErdiEALFPAGGQDLAKTDLPaFFRMGHWIGGDRDG-NPFVTADTLS 284

                   DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE.Elyrtaardk
                       +    A  +Y+  v  +  Els+    + L + A +El   a +
  gi|2567591   285 YALRMQSRTAIEFYMAEVHAIGGELSI----SALLASASpELMALAEQS- 329

                   vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                                  EPYR  L  +  +L     +   + A  + e+
  gi|2567591   330 ------PDLSEHRSDEPYRRALIGMYARLAANLRKLAGVQAL-LPEVGSA 372

                   AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                     y + +eF+  L +   sL       +A   L  l+R    FG  L  +
  gi|2567591   373 EPYANADEFIADLRIIHDSLHRHHAGPLAQTRLDPLIRAAGVFGFRLATI 422

                   DiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlg
                   D+Rq s+ +  vl  +    ++ + Y    E  +q  L+  L   RPL
  gi|2567591   423 DLRQSSDQHEAVLRELLAAAGLCpDYSHQDEAAKQALLIRCLNDPRPLRL 472

                   sDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvE
                   +     +  +  l  f        D FG++  ++Yiis + + sD L
  gi|2567591   473 PHHVYSDWARSELAVFDRAYSARRD-FGPrairqYIISHSETVSDLLELL 521

                   LLqRECgvkq.........tLrvvPLFEkLADLeAAPAavekLFs...i
                   LLq+E g+ +++ +++++   L v PLFE + DL+ APA +   ++ ++i
  gi|2567591   522 LLQKEAGLFHgtlgshdsyaELLVAPLFETIEDLRNAPAIMRDFYAlpgI 571

                   DWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAq....EEiiKvAKk
                      + r  G qe+m+GYsDs KD G +   W LY A     E   +   +
  gi|2567591   572 AGLVQRSGGEQEIMLGYSDSNKDGGFFTSNWELYCAEvalaEQFEQLKAE 621

                   yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                   +G+ L lFHGRGGtvGRGGGP   AiL+qPP t+nG +R t qGEvi
  gi|2567591   622 HGITLRLFHGRGGTVGRGGGPSFDAILAQPPGTVNGQIRLTEQGEVITSK 671

                   FGEEnLCFrsLqRFtAAtLEHGmnPP..vsPkPEWRkLmeemAv..vAtE
                   +G  ++  r L    AAtL   + P ++ + kP  R L    A ++
  gi|2567591   672 YGNPEIGLRNLETLVAATLQATLLPQtkTASKPPARFLDAAAALseASMA 721

                   EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                    YR +v+  P F +YF +AtP  E   +niGsRP+ Rk    i  LRAiP
  gi|2567591   722 AYRKLVYETPEFTDYFYSATPISEIAELNIGSRPSSRKATRAIADLRAIP 771

                   WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                   W F+W q R  LP W G+G   +  +d     l+ L+ m k+WPFF   l
  gi|2567591   772 WGFSWGQCRVALPGWYGFGSGVQAFLDANPDGLKLLQRMAKQWPFFATLL 821

                   DLlEmvFAKGDPGiAaLyDkLLv.aEeLkPFGksLRdkYvEtkdlLLkiA
                     ++mv AK D  +A  y +L+ ++   +   k L  +++ t d+L  i
  gi|2567591   822 SNIDMVLAKTDLRVAQRYAELVAdSKTRQKVLKALQREWQLTTDMLTAIT 871

                   GHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhl
                   G  + L   P LK  +R R +Yi  Ln +q   L R R+ +
  gi|2567591   872 GNTERLADNPTLKRSIRARFPYIDPLNHLQIELLHRFREGQ--------- 912

                   sKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        dE        ++L                + GiAAG+ ntG
  gi|2567591   913 ----TDER---TKRGIHLS----------------INGIAAGLRNTG    936

gi|116629723|ref|YP_814895.1|: domain 1 of 1, from 14 to 929: score 262.4, E = 1.1e-75
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           L  +     s d  ++  +  +l   L++    L G+ +
  gi|1166297    14    --GNFLMSIKKLENSSDHAMVAEEVKILTNLLnESTRQLSGDVVFNK 58

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +q+   +sA+    kD   Le    ++ sL   + ++vA+ +  +  L n
  gi|1166297    59 IQDLIKISAQ----KDYDALEK---QIASLTNQEMMVVARYFATLPLLVN 101
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                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                + E+velA           D+           +E+t+  Lv +     e
gi|1166297   102 ISEDVELASEVNLLNNTDQDYLGK--------LEDTID-LVAQK----EN 138

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  e LK   v  vltAHPtq  R+ +L     i n L            +
gi|1166297   139 ANEILKHVNVVPVLTAHPTQVQRKTVLELTDQIHNLLRNYREVKNGTINQ 188

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                 E  E L   i     tD iR  +     E+   ++Y+   +   + KF
gi|1166297   189 AEWTEKLRAYIEILMQTDIIRSHKLQVSNEITNVLAYYPKALIPAITKFT 238

                RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                 R     K    n  l    P i    W+GGDRDG nP vt +  +
gi|1166297   239 ARYQELAKK--YNLDLKGATP-ITMGMWIGGDRDG-NPYVTADTLKLSAS 284

                LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                L   +    Yi ++  L   +sm           E l   +  d
gi|1166297   285 LQSQVIFEYYIKKLNKLYRTISMSTSYMKTSTAVEKLSALSNDD------ 328

                iEFWKqvPPtEPYRviLGdvRDKLYntR.......ERaRHLLAtGiseis
                        +EPYR     +  +L  t  +  ++ ++   +    + ++
gi|1166297   329 ----SPFRTNEPYRRAFYYIESRLLHTEyqllgtvDKNSFVKRRDLENLD 374

                EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                   vy +   F   L     sL +  D+++      +lL  +  FG  L
gi|1166297   375 KIPVYNNPQAFKADLITIKESLEQDHDQAVIRSFFTELLEAINIFGFHLA 424

                KLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK.RP
                 +D+Rq+s  +   +  + +  +i + Y e +E  +   Ll EL   +R
gi|1166297   425 TIDMRQDSSVNEACVAELLKSAGICdNYSELPEKEKVQVLLKELNDDpRN 474

                LlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLA
                L     Pk + ++  l  ++   EL ++ + D     iis + + sD L
gi|1166297   475 LHANNKPKSDLLQKELKIYKTARELKdrigEDVIKQHIISHTESVSDLLE 524

                vELLqRECgvkqt....LrvvPLFEkLADLeAAPAavekLFsiDWYinri
                  ++ +E  +   ++ +++vvPLFE + DLe     ++    +D  +  +
gi|1166297   525 QAIMLKEYDLLDNqgarIQVVPLFETVEDLENSREIMKEFLNLDIVKKWL 574

                ...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                 +++  qe+m+GYsDs KD G l+  W LYkAq ++  + Kk Gv ++
gi|1166297   575 asqNDYQEIMLGYSDSNKDGGYLASCWNLYKAQKDLTAMGKKLGVNITFM 624

                HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                HGRGGtvGRGGGP   Ai +qP   in  +R+t qGE+i   +G  +  +
gi|1166297   625 HGRGGTVGRGGGPSYEAITAQPFGSINDRIRMTEQGEIIQNKYGNQDTAY 674

                rsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEEYRsvvvKE
                  L   + At++  +   +    + +++R+ m+++       YR +v+
gi|1166297   675 YNLEMLASATIDRIVSKQIVSEDDiggFRDSMDKIVLDSNKVYRKLVFET 724

                PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
                P F +YF  AtP      +niGsRPa Rk       LRAiPW+F+W q R
gi|1166297   725 PAFLDYFLQATPIKQISNLNIGSRPAARKKITDFSGLRAIPWVFSWSQSR 774

                FHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAK
                   P W GvG AFKh id D+ nl  L+ mY+ WPFF   l  ++mv  K
gi|1166297   775 IMFPGWYGVGSAFKHFIDADSHNLETLQKMYQGWPFFHSLLSNVDMVLSK 824

                GDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDP
                    iA  y +L   E+ k   + + ++++ tk+ +L+i G k+lL   P
gi|1166297   825 SNMDIAKQYADLCEDEDTKQVFDTIYQEWKLTKEVILQIEGNKELLADNP 874

                YLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnsk
                 L+  l  R +Y   Ln +q   +KR R
gi|1166297   875 SLQMSLNYRMPYFNILNYIQIEMIKRDR---------------------- 902

                kadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                            +a   E  L +t+ G+  G+ n G
gi|1166297   903 ----------VADIAGVYESILPITINGVTSGLRNSG    929
```

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gi|268319407|ref|YP_003293063.1|: domain 1 of 1, from 2 to 912: score 262.0, E = 1.4e-75
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                     si            s d  ++  +  +l   L++    L G+ +
  gi|2683194     2    SIKKL-------ENSSDHAMVAEEVKILTNLLnESTRQLSGDVIFNK 41

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  +q+   +sA+    kD   Le   a Lt     + i+vA+ +  +  L n
  gi|2683194    42 IQDLIKISAQ----KDYDTLEKRVANLTN---QEMIVVARYFATLPLLVN 84

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  + E+velA           D+           +E+t+  Lv +     e
  gi|2683194    85 ISEDVELASEVNLLNNTDQDYLGK--------LEDTID-LVAQK----EN 121

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    e LK   v  vltAHPtq  R+ +L     i n L            +
  gi|2683194   122 ANEILKHVNVVPVLTAHPTQVQRKTVLELTDQIHNLLRSYREVKNGTINQ 171

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   E  E L   i     tD iR  +     E+   ++Y+   +   + KF
  gi|2683194   172 AEWTEKLRAYIEILMQTDIIRSHKLQVSNEITNVLAYYPKALIPAITKFT 221

                  RRv.DtALK.niGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                   R ++ A K+n+ +    P     i    W+GGDRDG nP vt +  +
  gi|2683194   222 ARYqELAEKhNLDLKGATP-----ITMGMWIGGDRDG-NPYVTADTLKLS 265

                  CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                    L   +    Yi ++  L   +sm           E l   +  d
  gi|2683194   266 ASLQSQVIFEYYIKKLNKLYRTISMSTSYMKTSPAVERLSELSNDD---- 311

                  yYiEFWKqvPPtEPYRviLGdvRDKLYntR.......ERaRHLLAtGise
                              +EPYR     +  +L  t  +  ++ ++   +    + +
  gi|2683194   312 ------SPFRTNEPYRRAFYYIESRLLHTEyqllgtaDKNSFVKKRDLEN 355

                  isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                  +    vy +  +F   L     sL +  D+++      +lL  +  FG
  gi|2683194   356 LDKIPVYNDPQDFKADLVTIKESLEQDHDQAVIISFFTELLEAIDIFGFH 405

                  LvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK.
                  L  +D+Rq+s  +   +  + +  +i + Y e +E  +   Ll EL   +
  gi|2683194   406 LATIDMRQDSSVNEACVAELLKSAGICdNYSELPEKDKIKVLLNELNNDp 455

                  RPLlgsDLPktEEvkDvldafrvLAELPiDsFG.....aYiismataPsD
                  R L     Pk E ++  l  ++    L  D+ G++  +  iis + + sD
  gi|2683194   456 RNLHANNKPKSELLQKELKIYKTARQL-KDCIGedvikQHIISHTESVSD 504

                  vLAvELLqRECgvkqt....LrvvPLFEkLADLeAAPAavekLFsiDWYi
                   L   ++ +E  +   ++ +++vvPLFE + DLe     ++    +D  +
  gi|2683194   505 LLEQAIMLKEYDLLDNqgarIQVVPLFETVEDLENSREIMKEFLNLDIVK 554

                  nri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                    + +++  qe+m+GYsDs KD G l+  W LYkAq ++  + Kk Gv +
  gi|2683194   555 KWLasqNDYQEIMLGYSDSNKDGGYLASCWNLYKAQKDLTAMGKKLGVNI 604

                  vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                  +  HGRGGtvGRGGGP   Ai +qP   in  +R+t qGE+i   +G  +
  gi|2683194   605 TFMHGRGGTVGRGGGPSYEAITAQPFGSINDRIRMTEQGEIIQNKYGNRD 654

                  LCFrsLqRFtAAtLEHGmnPPvsPkP...EWRkLmeemAvvAtEEYRsvv
                    +  L   + At++  +   +    + +E+R  m+++       YR +v
  gi|2683194   655 TAYYNLEMLASATIDRIVSKQIVSEDdigEFRASMDKIVLDSNKVYRKLV 704

                  vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWt
                  +  P F +YF  AtP      +niGsRPa Rk       LRAiPW+F+W
  gi|2683194   705 FETPAFLDYFLQATPIKQISNLNIGSRPAARKKITDFSGLRAIPWVFSWS 754

                  qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                  q R   P W GvG AFKh id D+ nl  L+ mY+ WPFF   l  ++mv
  gi|2683194   755 QSRIMFPGWYGVGSAFKHFIDADSHNLDTLQKMYQGWPFFHSLLSNVDMV 804

                  FAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE
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                    K    iA  y +L   E+ k   + + ++++ tk+ +L+i G k+lL
  gi|2683194   805 LSKSNMDIAKQYADLCEDEDTKKVFDTIYQEWKLTKEVILQIEGNKELLA 854

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                      P LK  l  R +Y   Ln +q   +KR R
  gi|2683194   855 DNPSLKMSLNYRMPYFNILNYIQVEMIKRDR------------------- 885

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                 + +a   E  L +t+ G+  G+ n G
  gi|2683194   886 -------------VDDIAGVYESILPITINGVTSGLRNSG    912

gi|227505333|ref|ZP_03935382.1|: domain 1 of 1, from 1 to 892: score 261.7, E = 1.7e-75
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                               +    +      ++ D  Ll + L+ +L    Ged+ E
  gi|2275053     1    --------MTNPHID----QVREDIRLLGRVLgRVLAQQEGEDVFEL 35

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     ++  +   +   K e+L a+   Ld   a lvA+a++    LAn
  gi|2275053    36 VESTRKMA--FNVAHGNAKPEDLVAVFRDLDINKANLVARAFSYFALLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAE               D aDEa     s +  t+ kL   +  +P++
  gi|2275053    84 LAE----------------DLADEAVEAPVS-LRKTFAKLKEEG-VAPAD 115

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                        ++   v  vltAHPt   RR +   ++Ri+    qL        D
  gi|2275053   116 AAAVIRDAQVAPVLTAHPTETRRRTVFDTQTRIK----QLLIDAHRGGDM 161

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      ++  +   +   + t  iR a+Pt  DE+  G+ Y+   + + vP
  gi|2275053   162 DAIEREMYLRMTLLWQTALIRIARPTLEDEVDVGLRYYKLSLLEQVPALN 211

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R +   ++       lP d+P+++  sW+GGD DG nP v
  gi|2275053   212 RAIRHSMRET-FGLQLP-DAPVVRPGSWIGGDHDG-NPYVNERTLTYATR 258

                    LaRmmAanlYisqvEDLmFElsm....WRCndELRvRAEElyrtaardkv
                     a       Y s +++L  Els++++   C  EL   AE       +
  gi|2275053   259 KAAKTILRYYESELDELERELSLsdrySSCSTELLSLAEIANNDWESR-- 306

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRH.LLAtGiseisEe
                                  EPY       R  +Y  R R R +L A G    +
  gi|2275053   307 ------------VDEPY-------RRAIYGIRNRVRAnLHALGEKKAPKG 337

                    Av..ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                      ++y   Ee    L++  +sL +  D +iAD  L  +   v tFG  L
  gi|2275053   338 DFtpYASPEELQRDLDVIDRSLRQFNDDIIADDRLARIRSAVTTFGFHLY 387

                    KLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPL
                     LD+Rq s     vl  +     + + Y   sE  + E L+ EL+  RPL
  gi|2275053   388 SLDMRQNSKSFEQVLTEVFAAASLCdDYAALSEAEKVELLVRELQTARPL 437

                    l..gsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDv
                    l +g+D    E  +  l+ fr  A   +  FG+++ ++ iism+ + sD+
  gi|2275053   438 LfpGADQDFSEVTAKELGIFRA-ASQAVRKFGPqsvshCIISMTGSVSDI 486

                    LAvELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                    L   +L +E g+ + + vvPLFE + DL+A    +e+L+++ +Y+ ++
  gi|2275053   487 LEPMVLLKEVGLSE-VDVVPLFETIDDLKAGARILERLWAVPFYREHLRA 535

                    K...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                    +++ qevm+GYsDs KD G l A W LY A   ++    ++G+ L l HG
  gi|2275053   536 RgdiQEVMLGYSDSNKDGGYLQANWALYDAELSLVELCTQHGIELRLAHG 585

                    RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                    RGG vGRGGGPt  AiL+qP   + Gs+R+t qGEvi   +G  +   r
  gi|2275053   586 RGGAVGRGGGPTYDAILAQPKGAVSGSVRITEQGEVISAKYGAPETARRH 635

                    LqRFtAAtLEHGm..nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                    L  F    LE  + +  P++       +m e+A    E Y  ++  +P F
  gi|2275053   636 LEAFVSGALEASLldTEPIADTERAYAIMRELAALSGERYDDLI-GDPGF 684
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                    vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                    +EYF   tP  E G +n+GsRPa R     i  LRAiPW+ +W q R  +
  gi|2275053   685 IEYFTQSTPLHEIGDLNLGSRPAARNQTTAISDLRAIPWVLSWSQSRTNI 734

                    PvWLGvGAAFKhAidK.....DiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                    P W GvG A    +++ + ++       L+E+Y++WPFFR  l  +  v
  gi|2275053   735 PGWFGVGSAVTQWVEQapaseQAARWEELRELYRTWPFFRSVLSNMAQVM 784

                    AKGDPGiAaLyDkLL....vaEeLkPFGksLRdkYvEtkdlLLkiAGHkD
                    AK +  +A Ly +L++++ va+ +      + d++  t++  L+i G  D
  gi|2275053   785 AKAELSLARLYADLVddkaVADRIYAL---IADEFALTREVYLHITGNAD 831

                    lLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEy
                    l          l+ R +Y+  Ln +q   L+R R
  gi|2275053   832 LTAENQRQARSLKRRYPYLLPLNAVQLELLRRYR---------------- 865

                    AdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    A ++        +          +  t+ +tm G+A  + n G
  gi|2275053   866 AGDD--------QFL--------VSKTIQVTMNGLATALRNAG    892

gi|269123480|ref|YP_003306057.1|: domain 1 of 1, from 1 to 884: score 261.5, E = 1.9e-75
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +D  +  L P      ++ i+     + k + i++ +    L E+v
  gi|2691234     1    -MDSVI--LKP------DDEIKLNKEWISKEINIVKNI----LSEIV 34

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     +  ++    +  k  k +e +              v + +  +  L n+
  gi|2691234    35 PDI-DIDSILDNEKHFKDIEKINPD-----------VVRVLTILPLLINI 72

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     E+v        k +k   +   +   tE  ++  l kL l      e
  gi|2691234    73 VEDVY-----QSKILK---YNTITKNYTEGMLDNLLYKLDLNN-MNKENL 113

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     e   n  v  vltAHPtq  R+s+L     i   L +    +    D
  gi|2691234   114 TEIFSNIRVVPVLTAHPTQVQRKSILDLTQNIYEILEKRELVEHNLLDEN 163

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    E    L + i   +RtD +R ++     E+   +sY+  t  k +PK
  gi|2691234   164 EWMNELRKNINLLWRTDILRSSKLRVGNEITNSLSYYDSTFLKAIPKINI 213

                    RvDtALKniGi..nERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    +     K +Gi +n   P     i    W+GGDRDG nP vt E
  gi|2691234   214 KFKEIAKKLGIfsNSYTP-----ILMGTWIGGDRDG-NPFVTEETLLNAA 257

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                          A   Yis +  L  E+s+    +E      El + ++ +   +
  gi|2691234   258 YSQFETAIEYYISELKKLYREFSISSLKNEYSDELKELEKLSKDNLEHRT 307

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                    Y          EPYR ++  + D L   + +   LL   + e++ +  y
  gi|2691234   308 Y----------EPYRLVISYIIDNLQDVKVK---LLKEKL-ELPYDSYY- 342

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  + L  L    ks+    D +iA G L +l+  v  FG  L  +D+Rq
  gi|2691234   343 NSKKLLNDLLAIRKSIKLYSDEIIAYGRLDELIESVKVFGYHLSSIDLRQ 392

                    EseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK.RPLlgsDL
                    +s      +  +     i + Y    Ee + E L+  ++  +R L
  gi|2691234   393 DSSVYEFCVNELLNIAKITdNYSALTEEEKCEILINQIENEpRKLSSVNC 442

                    PktEEvkDvldafrvLAELPiDsFG.....aYiismataPsDvLAvELLq
                     k E ++  l  f  +  L i  FG++  +  iis +   sD+L   LL
  gi|2691234   443 KKSEILEKELSIFSTMKKL-INIFGkniieQNIISHTVEISDMLELALLL 491

                    RECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri..dGK.qev
                    +E  +   + + PLFE + DL+     ++  F +D  +  ++++G  qe+
  gi|2691234   492 KEFDLDGKVNISPLFESIEDLKNSEKIMKTWFELDILKKWMsnNGSlQEI 541

                    mvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGR
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                    m+GYsDs KD G +   W LYkAq E++  A+kyGvKL  FHGRGGtvGR
  gi|2691234   542 MLGYSDSNKDGGYITSSWHLYKAQKELVSLAQKYGVKLNFFHGRGGTVGR 591

                    GGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAA
                    GGGP   AiLsqP + i G +R t qGEvi   +G  +L    L     A
  gi|2691234   592 GGGPSYEAILSQPSESILGKIRLTEQGEVIGAKYGNLDLGKFNLEALLSA 641

                    tLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtP
                    tLE  ++       E+ ++me++  +  E YR +v+    F EYF   tP
  gi|2691234   642 TLEKSLKDDTKDIKEYENIMEQISNISYEKYRNLVYETEGFSEYFFESTP 691

                    ElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAA
                      E   +niGsRP+ Rk    ie LRAiPW+F+W q R  LP W GvG
  gi|2691234   692 INEVSSLNIGSRPSSRKKVLDIEGLRAIPWVFSWSQIRVMLPGWYGVGTS 741

                    FKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkL
                    F   i K+   l  Lk mY++WPFF+  l  lEmv  K D  iA  y kL
  gi|2691234   742 FNKWI-KENNGLETLKLMYRNWPFFKALLSNLEMVLSKTDMNIAKEYAKL 790

                    LvaEeL.kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRds
                    +  E+L+    + + d++  t +lL +i G   lLE    L   l+ R +
  gi|2691234   791 VKNENLsTKIFNMINDEWILTFNLLKEITGINYLLEDNEMLTLSLKNRLP 840

                    YittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpt
                    Y   Ln +q   +K  R                + n          n t
  gi|2691234   841 YFNALNYLQIELIKQQR-----------------AGN----------N-T 862

                    ervaPGLEDtLiLtmKGiAAGmqntG<-*
                    e+    +   +  t+ GiA G+ n G
  gi|2691234   863 EE----INKAIHTTINGIATGLRNSG    884

gi|58337382|ref|YP_193967.1|: domain 1 of 1, from 1 to 912: score 261.5, E = 2e-75
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                     s d+ ++  +  +l k L++    L G+d
  gi|5833738     1    ------MTFTKLENSSDQAVVAEEVKILTKLLnESTRQLIGDDAFAK 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +q+  + sA     kD k+Le   +k+ sL+  + i+vA+ +  +  L n
  gi|5833738    42 IQDLIDTSAS----KDQKQLE---SKISSLNNREMIVVARYFATLPLLIN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+velA +  +      D+    s t +         Lv +     ++
  gi|5833738    85 ISEDVELASKVNVFNNTDQDYLGKLSDTID---------LVAQK----DD 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                        L n  v  vltAHPtq  R+ +L    +i   L            +
  gi|5833738   122 AKRILENVNVVPVLTAHPTQIQRKTVLELTDKIHHLLRSYRDVKNGTINQ 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +E  E L   i     tD iR  +     E+   ++Y+   +   + KF
  gi|5833738   172 REWTEQLRACIEILMQTDIIRGHKLKVSNEITNVLAYYPKALIPAITKFT 221

                    RRvDtALK..niGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     R     K++n+ +    P     i    W+GGDRDG nP vt +
  gi|5833738   222 TRYKELAKehNLTLDQATP-----ITMGMWIGGDRDG-NPYVTADTLELS 265

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      L   +    Y+  +  L   +s+        +  E l + +  d
  gi|5833738   266 ATLQSQVIFEYYMKELKKLYRAISLSTSYMQPSAAVEKLSKLSNDD---- 311

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntR.......ERaRHLLAtGise
                                EPYR     +  +L  t ++  +  ++   +  + + +
  gi|5833738   312 ------SPFRTDEPYRRAFYYIESRLVHTEkellgiiDKNIFIKPHDLEN 355

                    isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                    +    vy +  eF   LE    sL e  D+++       +L  +  FG
  gi|5833738   356 LDNIPVYNNPQEFKSDLETIKASLDEDHDQAVTHSFFTQILEAIDVFGFH 405

                    LvKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK.
                    L  +D+Rq+s  +   +  + +  +i + Y + sE  + E Ll+EL+  +
  gi|5833738   406 LATIDMRQDSSVNESCVAELLKSAGICdNYSDLSEKEKVELLLSELENDp 455
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                    RPLlgsDLPktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDv
                    R L     Pk E ++++  +  + r L ++L  D     iis + + sD+
  gi|5833738   456 RNLHANNKPKSELLQkelKIYKTARQLKDrLGEDVIKQHIISHTESVSDM 505

                    LAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLFsi....D
                    L   ++ +E  + +++k  ++vvPLFE + DL  A   + +  s +  +
  gi|5833738   506 LEQAIMLKEYNLvdseKARIQVVPLFETVEDLLNAREIITQYLSFpivkK 555

                    WYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                    W + + +  qe+m+GYsDs KD G l+  W LYkAq ++  +  k GvK+
  gi|5833738   556 WLVSQ-NNYQEIMLGYSDSNKDGGYLASCWNLYKAQKDLTAIGEKLGVKI 604

                    vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                    +  HGRGGtvGRGGGP   Ai +qP   in  +R+t qGE+i   +G  +
  gi|5833738   605 TYMHGRGGTVGRGGGPSYEAITAQPFKSINDRIRMTEQGEIIQNKYGNKD 654

                    LCFrsLqRFtAAtLEHGm.nPPvsPk..PEWRkLmeemAvvAtEEYRsvv
                      +  L   + A ++  +++  vs  +  ++R  m+++       YR +v
  gi|5833738   655 TAYYNLEMLASAAIDRMVsKQAVSEEriTDFRSSMDKIVEESNKIYRKLV 704

                    vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWt
                    +  P F +YF  AtP  E   +niGsRPa Rk       LRAiPW+F+W
  gi|5833738   705 FENPAFLDYFFQATPIKEISNLNIGSRPASRKKLTDFSGLRAIPWVFSWS 754

                    qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                    q R   P W GvG AF   i+ D   l+ L+EmYk WPFF   l  ++m
  gi|5833738   755 QSRIMFPGWYGVGSAFANFINADPTHLKELQEMYKGWPFFHSLLSNVDMF 804

                    FAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE
                      K    iA  y  L   Ee k   + + ++++ tk+ +L+i  H DlL
  gi|5833738   805 LSKSNMEIAREYASLCDDEETKKVFDIIYQEWKLTKKVILQIEDHDDLLA 854

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                      P LKq l  R +Y   Ln +q   +KR R+ + +   +  +
  gi|5833738   855 EAPILKQSLDYRMPYFNILNYIQIEMIKRGREDEIQGVYQSII------- 897

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +       + +n                  G+A G+ n G
  gi|5833738   898 P-------ITIN------------------GVASGLRNSG    912

gi|78221527|ref|YP_383274.1|: domain 1 of 1, from 10 to 931: score 261.2, E = 2.4e-75
                    *->siDAqLRl..LvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLk
                       + D  +Rl++L     +  +  ++ D   l + L++++++  G+
  gi|7822152    10    ADDQAVRLneLMTLDPALKDIPLRRDVRSLGRLLgEVIKEQAGPAAY 56

                    EavqECYElsAeYEGKkDt..........kKLeELGakLts.LdPaDail
                    +a  E   l+       D ++   +++ ++ L+E   ++ +++  a++
  gi|7822152    57 DAEEELRRLAISHRALADQeeavldspaeQELQERAVRIVGtMTVAETYQ 106

                    vAkailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtl
                    + ka+     L nLAE  +   RRR  ++        a       +  tl
  gi|7822152   107 IVKAFGTFFELTNLAETNHRMRRRRATQLS------PAAPVKPGSLLGTL 150

                    KkLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL
                     ++   +  + e   + L+   +  v+tAHPt  +RR +L K  Ri   L
  gi|7822152   151 MRMRDGG-ITAEKALDLLRQVEIMPVFTAHPTEVARRVVLFKRRRIAREL 199

                    aqLsAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsY
                    a L    +  ++     EA+  Ei A + tDE+RR +    DE+R+G+
  gi|7822152   200 AELDLLPLAGDEADRRQEAIFAEITALWQTDEVRRRPQGVTDEIRMGLDH 249

                    iHEtvWkGvPKFLRRvDtALKniGinERlPYdvP.LikFssWmGGDRDGk
                    +   +          +    + +   +      P++i+F sW+GGDRDG
  gi|7822152   250 YPGSLMAPLAGLYEEMAEDFRQVYGADLPDAAFPtVIRFGSWIGGDRDG- 298

                    nPRvtPEvtRDvCLLaRmmAanlYisqvEDL..mFElsmWRCndELRvR.
                    nP vt   tR     aR m    Y++ vE+L+++   s  R       R+
  gi|7822152   299 NPNVTVGTTRHALESARQMILARYLDGVEELkeLLTPSTNRVTVSPQLRe 348

                    AEElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRH
```

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                    A E y  a         i      P  EPYR  L  v  +L  tR+   H
  gi|7822152   349 ALERYVAALAGAAAETGI-----YPECEPYRKFLRCVHHRLMQTRDGEDH 393

                    LLAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLR
                      A           y +   F   L L   sL +     +A   +  lLR
  gi|7822152   394 PDA-----------YPDAGAFAADLMLVRTSLAQGEGERLARRYVDPLLR 432

                    qvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLl
                    qv tFG  L  LDiRq +  +   +  +    + Gs  e
  gi|7822152   433 QVETFGFHLHALDIRQHARIHARAVAELAA--GAGSCEE----------- 469

                    aELkGKRPLlgsDLPktEEvkDvldafrvLAELPi.DsFGaYiismataP
                        G  P+ ++    t E+ D l a+  L    ++ +  +Y+is a +
  gi|7822152   470 ----GVHPVPPPPSAETTELLDTLRAVAKLKQRYSpKAIRSYVISGASSA 515

                    sDvLAvELLqRECgvkqt.........LrvvPLFEkLADLeAAPAavekL
                     D L    L   Cg++ + +++++++++  vPLFE + DL+ AP     L
  gi|7822152   516 RDTLSLIWLMELCGIRVAaspdgkdpgVMPVPLFESIEDLRNAPGICRAL 565

                    FsiDWYinridG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvA
                    +    Y   +d  +++qevm+GYsDs KD G +   W + kA  ++ +vA
  gi|7822152   566 WCSPEYGPFLDSwgrRQEVMLGYSDSNKDGGMFTSTWEIHKAHRDLQRVA 615

                    KkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviE
                    ++ Gv+L lFHGRGGtvGRGGGPtH Ai++qP D   G+l++t qGEvi
  gi|7822152   616 QECGVRLRLFHGRGGTVGRGGGPTHRAIIAQPADGFSGALKITEQGEVIN 665

                    fsFGEEnLCFrsLqRFtAAtLEHGmnPPvs...PkPEWRkLmeemAvvAt
                      + +  L  r L    AA LE      + +++P P W + +eem   A
  gi|7822152   666 WKYSDPSLAKRNLELMVAASLETLARAGLVetrPEPAWEEALEEMSGSAF 715

                    EEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAi
                      YR  +   P    YF  AtP lE+    iGsRPa+R  s  i  LRAi
  gi|7822152   716 TFYRERITGNPDILPYFEQATPVLEFELAKIGSRPARRSRSRDIAELRAI 765

                    PWiFaWtqtRFHLPvWLGvGAAF.KhAidKDiKnlqkLkEmYkeWPFFRv
                    PW F W q R  +P W GvG A +++A+  + + l  L+ m   +PFF
  gi|7822152   766 PWGFGWIQSRHVIPGWFGVGFALdRFAVGGEGR-LEFLRSMMGRFPFFFD 814

                    tlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLk
                     +  +E+   K D  +A Ly  L+    ++ +    + ++Y+ t+ ++L
  gi|7822152   815 LIRNVELALTKVDLPLARLYASLVTDAGIRErVFAMIVEEYQRTRRMVLA 864

                    iAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrP
                    + G   lLE  P L   lRLR++Yi  L ++q   L+R R
  gi|7822152   865 VTGQARLLEKNPALTASLRLRNPYIDPLSMIQIELLRRKR---------- 904

                    hlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<
                          A E+   +de   Ln            L  t+ GiAAG+ ntG
  gi|7822152   905 ------AGEE---SDE---LN----------YVLAATINGIAAGLRNTG  931

                    -*

  gi|7822152     -    -

gi|238020526|ref|ZP_04600952.1|: domain 1 of 1, from 1 to 900: score 261.1, E = 2.6e-75
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           qL lL   K +   +L+  DA  +   L  + D H +   E+v
  gi|2380205     1    ---MQLSLLNNPKDA---ELLA-DAEFMTASLYAVLDNHAD---EIV 37

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         + A+    +D++K+  +   L sL    +  +  a+     + n+
  gi|2380205    38 VNALKILAN---AQDSSKI--ITELLPSLSDEQTENLITAVGIFAQILNI 82

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+v+   RR ++ ++       +sA  +  i Et++kL      + e v
  gi|2380205    83 AEDVHHERRRLVHEQQ-------GSAAQDGSIAETVRKLQAEQ-IAQEVV 124

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     + L    v  vltAHPt   R ++L  + +iR  L          ++
  gi|2380205   125 QDVLNHTLVSPVLTAHPTEVQRQAVLVSHRKIRELLPRRELCR-SADEMS 173
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                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    EL   +   +   + t E R  +   q E+  G+  +    +   P+  R
  gi|2380205   174 ELQREMNIVLLTLWQTSETRHFKLSVQSEIQNGVNIFPRSFFSALPRVYR 223

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     ++   +      R+P    ++k   W+GGDRDG nP v     RD
  gi|2380205   224 DMEKHFQAAYPQIRIP---DVLKIGGWIGGDRDG-NPFVSAQTLRDAFRH 269

                    aRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkvvKy
                        A   Y   ++ L  E +ls+ R n    v    + +    d
  gi|2380205   270 HANTAFHYYRRELDALYQElpLSIRRVNVSDGVL---VLSAKTPD----- 311

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                      E  +q   +EPYR  +  v  ++     +a  L A           y
  gi|2380205   312 -TEVARQ---EEPYRRAVAYVMARMVG---KAHELGAPLGCRFGVGEPYA 354

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    +  eFL  L     sL +    ++A G + D++R  s  G  L+ LD+Rq
  gi|2380205   355 DAAEFLRDLRTLQNSLRDNRSEALANGRIADIIRTASVCGFHLMPLDLRQ 404

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                     +e++  v+  + +  ++  Y   +E+ +q  Ll EL+ +RPL+ + +
  gi|2380205   405 HAEKHANVVAELFQAADLEDYLRLPENEKQAVLLRELQHQRPLYTPFIAY 454

                    tEEvkDvldaf....rvLAELPiDsFGaYiismataPsDvLAvELLqREC
                     EE +  l  f++ +++      D+    iis +  PsD LA  L+ +E
  gi|2380205   455 SEETQRELAIFhearKIKDAFGEDAITQSIISNCEQPSDLLALALILKET 504

                    gv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri...d
                    g+   +++++   + +vPLFE +  L  A   ++ LFs DWY+  + ++d
  gi|2380205   505 GLlalrdgqpESRINIVPLFETIEALANAVPVMQTLFSNDWYRALVasrD 554

                    GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRG
                      qe+m+GYsDs KD G +s  W LY+A   +++  +++ +++ lFHGRG
  gi|2380205   555 NIQEIMLGYSDSNKDGGYISSTWGLYQAEIGLVRLFRQHNIRIRLFHGRG 604

                    GtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLq
                    G vGRGGGP   AiL+qP   + G +R+t qGEv+   +G++    + L
  gi|2380205   605 GSVGRGGGPSYQAILAQPAGSVGGQIRITEQGEVLTAKYGDDSNAQHNLA 654

                    RFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                       AAtLE  +  P +P P+  kLm+ +       YR+++ +   F++YF
  gi|2380205   655 ALVAATLEATLL-PAAPDPDV-KLMNALSESSFAHYRALITRQG-FIDYF 701

                    RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                        P      +n+GsRPa Rk    i+ LRAiPW+F+Wtq R  LP W
  gi|2380205   702 LQTSPIEQIASLNLGSRPASRKTLARIQDLRAIPWVFSWTQNRLMLPAWY 751

                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    G+G A +   ++D+  l++L+   +e  FFR  l  +E v AK D  +A
  gi|2380205   752 GFGSAVQELCEQDSGSLKMLQQHAQENRFFRAMLSNMEQVMAKTDLTLAE 801

                    LyDkLLv.aEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrl
                     y  L  + E        ++++Y+   + LL i     lL     L   l
  gi|2380205   802 HYAALSQdNEHGADIFATIKAEYQRSLKALLDILQTETLLADNRPLARSL 851

                    RLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLv
                     LR +Y+  L  +q   L+++R                 +E+
  gi|2380205   852 ALRIPYLNALGGLQVALLRKLR-----------------QEP-------- 876

                    kLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      n  erv   +  t+     G+A G+ ntG
  gi|2380205   877 --N-NERVLQMVHQTI----NGVAQGLRNTG    900

gi|148652373|ref|YP_001279466.1|: domain 1 of 1, from 3 to 932: score 260.8, E = 3.3e-75
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkE.a
                       s    LR  v    s        DA+      D Lq +  e L+ ++
  gi|1486523     3    SNNEVLRSRVRLLGS-----FLGDAIARQSGEDTLQTI--ETLRKgF 42

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
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                +qE  +          +   + L   + sLd      v + ++    LAn
gi|1486523    43 IQERRD--------PNPANKQKLIDLIASLDNKTLKNVIRGFSIYFFLAN 84

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                L EE  l   RR  k++   F + +   t   + E  ++ +       +E
gi|1486523    85 LTEENFLREERRTLKQQSQNFWEGSFRHT---LLECQQRHIAAD--QIKE 129

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD.
                  + LK      v+tAHPt + RR  +       n L  L+A     +D
gi|1486523   130 LIDQLKFIP---VFTAHPTEARRRTTM-------NILQTLYAHSTALNDl 169

                ......KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvW
                ++++   +E        i   +  DE+R  +P   DE+  G+ Y+   ++
gi|1486523   170 pegslaYQEAKQKTAETIDLLWSSDEVRTRKPLVYDEINNGLHYFNASLF 219

                kGvPKFLRRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtP
                  +P+  R +  A+  +   E   Y  P  + F sW+GGDRDG nP vt
gi|1486523   220 TAIPQVYRNIKNAIVDV-YPELSDYALPaFLSFGSWIGGDRDG-NPFVTH 267

                EvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrt.a
                E t    LL        Y   v  L  El          +  + + + ++
gi|1486523   268 ETTEMAVLLHANTVLRHYQVMVRKLRREL----------IHSDTIASIsP 307

                ardkvvKyYiEFWKqv.......PPtEPYRviLGdvRDKLYntRERaRHL
                +  + +K+Y E    +   ++++  +EPYR +L  +  K+  t E   H+
gi|1486523   308 KIYQRIKHYSELDERIfyynpddYNNEPYRRLLSIILAKIAATNE---HI 354

                LAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                  +G    +    y +    L+ L L   sL    Dk+ A+G LLD++R
gi|1486523   355 QSQGNKPEAAADAYSNPQALLDDLRLIRESL-STHDKAHAEGLLLDMIRL 403

                vstFGLsLvKLDiRqEseRqtDvl.DAittHLeiGsYReWsEeKRqEWL.
                v t G  L  LDiRq+s  + +v+ D      ++  YR+ sE  Rq WL+
gi|1486523   404 VKTCGFHLAALDIRQDSGYHGEVIaDIFDNASNLPDYRQLSETERQQWLt 453

                .laELkGKRPLlgsDLPk.tEEvkDvldafrvLAELP.iDsFGaYiisma
                +l E  G   ++   L k+t E    ++++  L  L + D+FG+Yiism+
gi|1486523   454 rLLEQPGTPLIYVDNLSKqTQEQLALINSIAKLRKLVgEDTFGSYIISMT 503

                taPsDvLAvELLqRECg.........vkqtLrvvPLFEkLADLeAAPAav
                   s  L v LL R  g ++ ++++++  +L+v PLFE + DL+     +
gi|1486523   504 NNASQLLEVLLLMRFSGlsgindsgeLYAALPVAPLFETIEDLKNIDHIL 553

                ekLFsiDWYinrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEii
                  +     Y+  +++++  qe+m+GYsDs KD G +  AWqLY Aq  i
gi|1486523   554 PAVLDNPLYRKLLEqsgNTQEIMLGYSDSSKDGGIITSAWQLYSAQQTIT 603

                KvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGE
                 +AKkyG+   lFHGRGG v RGGG tH Ai +qP  t+nG ++ t qGE
gi|1486523   604 EIAKKYGINTRLFHGRGGSVSRGGGSTHQAIAAQPAGTLNGQIKFTEQGE 653

                viEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPkP..EWRkLmeemAv
                v+   +   +     L       L       v+ Pk  + +  L  ++A
gi|1486523   654 VLYAKYANPDTAVFELTMGITGALKATSSRFVeQPKQlnSYEALFARLAE 703

                vAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs.GGies
                     YR++      F E++  AtP  E   +niGsRPa Rk +     +
gi|1486523   704 AGEQQYRALTDNTEGFYEFYSQATPVQEISLLNIGSRPAHRKKGlPSKST 753

                LRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPF
                +RAiPW+F W   RF LP W GvG A    +++D      ++Em ++WPF
gi|1486523   754 IRAIPWVFGWSLARFTLPAWYGVGSALN-SVKQDE---ALMQEMNDNWPF 799

                FRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdl
                F   +  +Em F K +  iA  y +L   E L+ +  + + d+   t++
gi|1486523   800 FNAFISNIEMAFTKSEMSIAQAYSQLCEDETLRArIMQAVIDEHDLTQQG 849

                LLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvt
                L  +     lL     L   l  R++Y+  +n +q   LKR+R  +
gi|1486523   850 LNSLLNQDTLLSNQQELASSLEWRNAYLDPINYIQIELLKRLRQNN---E 896
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                    lrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqn
                      P  s  + + +         +         +ED Li  +  +AAG+ n
  gi|1486523   897 QAPDTSSGHTQND--------DIS--------VEDPLIRSINALAAGLRN 930

                    tG<-*
                    tG
  gi|1486523   931 TG    932

gi|226819197|ref|ZP_03808316.1|: domain 1 of 1, from 2 to 912: score 259.5, E = 7.9e-75
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       si            s d  ++  +  +l   L++    L G+ +
  gi|2268191     2    SIKKL-------ENSSDHAMVAEEVKILTNLLnESTRQLSGDVVFNK 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +q+   +sA+    kD   Le    ++ sL   + ++vA+ +  +  L n
  gi|2268191    42 IQDLIKISAQ----KDYDALEK---QIASLTNQEMMVVARYFATLPLLVN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+velA           D+           +E+t+  Lv +     e
  gi|2268191    85 ISEDVELASEVNLLNNTDQDYLGK--------LEDTID-LVAQK----EN 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      e LK   v  vltAHPtq  R+ +L     i n L            +
  gi|2268191   122 ANEILKHVNVVPVLTAHPTQVQRKTVLELTDQIHNLLRNYREVKNGTINQ 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     E  E L   i     tD iR  +     E+   ++Y+   +   + KF
  gi|2268191   172 AEWTEKLRAYIEILMQTDIIRSHKLQVSNEITNVLAYYPKALIPAITKFT 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                     R     K    n  l    P i    W+GGDRDG nP vt +  +
  gi|2268191   222 ARYQELAKK--YNLDLKGATP-ITMGMWIGGDRDG-NPYVTADTLKLSAS 267

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L   +    Yi ++  L   +sm           E l   +  d
  gi|2268191   268 LQSQVIFEYYIKKLNKLYRTISMSTSYMKTSTAVEKLSALSNDD------ 311

                    iEFWKqvPPtEPYRviLGdvRDKLYntR.......ERaRHLLAtGiseis
                             +EPYR     +  +L  t  +  ++ ++   +    + ++
  gi|2268191   312 ----SPFRTNEPYRRAFYYIESRLLHTEyqllgtvDKNSFVKRRDLENLD 357

                    EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                       vy +   F   L     sL +  D+++      +lL  +  FG  L
  gi|2268191   358 KIPVYNNPQAFKADLITIKESLEQDHDQAVIRSFFTELLEAINIFGFHLA 407

                    KLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaElkGK.RP
                     +D+Rq+s  +   +  + + +i + Y e +E  +   Ll EL   +R
  gi|2268191   408 TIDMRQDSSVNEACVAELLKSAGICdNYSELPEKEKVQVLLKELNDDpRN 457

                    LlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLA
                    L     Pk + ++  l  ++   EL ++ + D     iis + + sD L
  gi|2268191   458 LHANNKPKSDLLQKELKIYKTARELKdrigEDVIKQHIISHTESVSDLLE 507

                    vELLqRECgvkqt....LrvvPLFEkLADLeAAPAavekLFsiDWYinri
                      ++ +E  +   ++ +++vvPLFE + DLe     ++    +D  +  +
  gi|2268191   508 QAIMLKEYDLLDNqgarIQVVPLFETVEDLENSREIMKEFLNLDIVKKWL 557

                    ...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                     +++  qe+m+GYsDs KD G l+  W LYkAq ++  + Kk Gv ++
  gi|2268191   558 asqNDYQEIMLGYSDSNKDGGYLASCWNLYKAQKDLTAMGKKLGVNITFM 607

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGGtvGRGGGP   Ai +qP   in  +R+t qGE+i   +G  +  +
  gi|2268191   608 HGRGGTVGRGGGPSYEAITAQPFGSINDRIRMTEQGEIIQNKYGNQDTAY 657

                    rsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEEYRsvvvKE
                      L   + At++  +   +    + +++R+ m+++       YR +v+
  gi|2268191   658 YNLEMLASATIDRIVSKQIVSEDDiggFRDSMDKIVLDSNKVYRKLVFET 707

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
                    P F +YF  AtP      +niGsRPa Rk       LRAiPW+F+W q R
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  gi|2268191   708 PAFLDYFLQATPIKQISNLNIGSRPAARKKITDFSGLRAIPWVFSWSQSR 757

                   FHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAK
                      P W GvG AFKh id D+ nl  L+ mY+ WPFF   l  ++mv  K
  gi|2268191   758 IMFPGWYGVGSAFKHFIDADSHNLETLQKMYQGWPFFHSLLSNVDMVLSK 807

                   GDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDP
                       iA  y +L   E+ k   + + ++++ tk+ +L+i G k+lL   P
  gi|2268191   808 SNMDIAKQYADLCEDEDTKQVFDTIYQEWKLTKEVILQIEGNKELLADNP 857

                   YLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnsk
                    L+  l  R +Y   Ln +q   +KR R
  gi|2268191   858 SLQMSLNYRMPYFNILNYIQIEMIKRDR---------------------- 885

                   kadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                +a   E  L +t+ G+  G+ n G
  gi|2268191   886 ----------VADIAGVYESILPITINGVTSGLRNSG    912

gi|222055605|ref|YP_002537967.1|: domain 1 of 1, from 35 to 931: score 258.8, E = 1.3e-74
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        D     +  G v    +     A + +  L  L   H +
  gi|2220556    35    --DVRSLGMLLGMVI--REQAGEQAFIAEEELRHLAIQHRQLHDNQA 77

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     C +l  e E ++ ++      + +  +  a+a  + ka++    L nL
  gi|2220556    78 TACLDLPGERELQEKAE------SIIGRMTVAEAYQIVKAFSTYFELTNL 121

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AE  +   R R +++        +       +  tl ++   +  s e
  gi|2220556   122 AETNHRKRRQRASRLI------STAPDKPGSLRGTLLRMRQSG-ISVEQA 164

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    + L+   v  v+tAHPt  +RR +  K  Ri   L  L    +t
  gi|2220556   165 LQWLRMVDVVPVFTAHPTDVARRVVHFKRRRIAQDLEALDTLPLTYAKAL 214

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                       A+  E+ A + tDE+RR +Pt  DE+++G+  + + +    P
  gi|2220556   215 QGQNAMLAEVSALWQTDEVRRRKPTVLDEIKMGLDHYPDSLITPLPALYE 264

                   RvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDvCL
                    +  A++ i        + P++++F sW+GGDRDG nP vt + tR
  gi|2220556   265 DMAAAIQEIYGLSISQSELPtVVHFGSWIGGDRDG-NPYVTADSTRAALQ 313

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                     R      Y   +E+L   l    C   +      l       + +  +
  gi|2220556   314 KGREAILGEYTTTLEELRRLLTSSTCRVPV---SPQLAAAVTNYHATLNF 360

                   iEFWK.qvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vy
                    E  K+ +P  E YR     +   LY  R   R          +E A+ y
  gi|2220556   361 AELQKsAIPECEQYRRFADCI---LYRLRRTLRE---------PEHAdAY 398

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLD.lLRqvstFGLsLvKLDi
                       eF   L L   sL   G   +A  sL+D+lLR + tFG  L  LDi
  gi|2220556   399 VAAVEFSTDLHLIRASLAAGGGERLAR-SLVDpLLRRIDTFGFHLHSLDI 447

                   RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                   Rq +  +   +  +      G   + +                 L ++
  gi|2220556   448 RQHAKVHATAVKELAAGATTGTVTSAA-----------------LPPAPS 480

                   PktEEvkDvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLqRECg
                     t E+ D l a+  L  + P  +   Y+is a    D LA   L   Cg
  gi|2220556   481 AATTELLDTLRAIAGLKRsYPPQAIQRYVISGASCVQDSLALVWLLELCG 530

                   vkqt........LrvvPLFEkLADLeAAPAavekLFsiDWYinridG...
                   v+ + +++++++L  vPLFE + DL+ AP     L+s D Y+  +d  ++
  gi|2220556   531 VRVAadnsgdpgLMPVPLFESIEDLRQAPHICRILWSSDDYKPYLDSwgr 580

                   KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                   +qevm+GYsDs KD G l  AW + k   E+ +vA + Gv+LvlFHGRGG
  gi|2220556   581 RQEVMLGYSDSNKDGGMLTSAWEIHKTHRELHRVAAECGVRLVLFHGRGG 630
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                    tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                    tvGRGGGPtH Ai++qP     Gsl++t qGEvi   + +  L  r L
  gi|2220556   631 TVGRGGGPTHRAIVAQPAGAFTGSLKITEQGEVINWKYSDASLAQRNLEV 680

                    FtAAtLEH....GmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFv
                      AA LE    +Gm+      P W + me +   A   YR  +   P
  gi|2220556   681 MVAASLEAlaltGMQEE-QASPKWAQTMETLSSDAFAFYRKHIAENPDIF 729

                    EYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLP
                     YF  AtP lE+    iGsRPa+R     +  LRAiPW F W q R  +P
  gi|2220556   730 PYFEQATPVLEFELAKIGSRPARRGVTRDLSDLRAIPWGFGWMQSRHVIP 779

                    vWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPG
                     W GvG A      +    + +L+ m   +PFF   l  +E+   K D
  gi|2220556   780 GWFGVGYALERFAARQPGAMGQLQAMMGRFPFFIDLLRNVELALTKVDLP 829

                    iAaLyDkLLvaEeLkPFGksL.RdkYvEtkdlLLkiAGHkDlLEGDPYLK
                    +A  y  L+   eL+    +L  ++Y+ t+ +LL i G   lLE    L
  gi|2220556   830 LARCYSTLVTDMELRQRVFDLvVEEYQRTRRMLLAITGQSHLLENNAPLA 879

                    qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                      +RLR++Y+  L  +q   L+R R                A E+s
  gi|2220556   880 RSIRLRNPYVDPLSLIQIELLRRKR----------------AGEESE--- 910

                    eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       +Ln            L  t+ Gi AG+ ntG
  gi|2220556   911 ---ELN----------YVLAATISGISAGLRNTG    931

gi|17547077|ref|NP_520479.1|: domain 1 of 1, from 39 to 985: score 258.3, E = 1.8e-74
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       ++    R    G  +  ++ ++ D   l + L+D+L +  G    E
  gi|1754707    39    ALGPTSRR-SSGSAAAKDQPLKEDIRFLGRLLgDVLREQEGAAAFET 84

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      +  +    D +  +EL   L  L    +  v +a++    LAn
  gi|1754707    85 VETIRQTAVRFRRDGDRQAEQELDRLLKTLSRDQTTSVVRAFSYFSHLAN 134

                    LAEEvelAyRRRikkkkhGDFaDEasA..ttEsDiEEtlKkLvlklnKsP
                    +AE+ +   RRR++ +  G     +s  +   s  +E l    l+
  gi|1754707   135 IAEDQHHNRRRRVHALA-GSSPQPGSLlrALLSAADEGLSGDALRR---- 179

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                       F+A     +  vltAHPt   R+s+L  +  i   La   A  +tv
  gi|1754707   180 --FFDA---ALIVPVLTAHPTEVQRKSILDAQREIARLLAERDA-PLTVR 223

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    +++     L   +   + t  +R ++    DE+   +sY+  t  + +P
  gi|1754707   224 ERERNVTLLRAHVTKLWQTRMLRTTRLMVADEIENALSYYQTTFLREIPA 273

                    FLRR....vDtALKniGin.ERlPYdvPLikFssWmGGDRDGknPRvtPE
                      R  +++v t     G  +E  P  +   +  sW+GGDRDG nP vt
  gi|1754707   274 LYREleedVATVFPRRGARgEPAPLPA-FFQMGSWIGGDRDG-NPFVTAQ 321

                    vtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaar
                      R        +    Y++ +  L  Elsm      + v A+ l    ++
  gi|1754707   322 TLRHAAQRQASVILTWYLDEIHALGAELSM--STLLVDVSADLLALAERS 369

                    dkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLA..tGise
                         +  +        EPYR  L  v  +L  t     R L  ++ G
  gi|1754707   370 PDHSEHRAD--------EPYRRALIGVYARLAAT---CRELTGedAGRHA 408

                    isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                    +     yt+ Ee    L +   sL      ++AD  L  l R +  FG
  gi|1754707   409 VGPAPAYTRAEELRADLQIVIDSLAAHHGEALADARLASLARAIDVFGFH 458

                    LvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaELkGKR
                    L  +D+Rq s+ +   +  + +  +++G+Y   sE  ++  Ll EL+  R
  gi|1754707   459 LASIDLRQVSDVHEATVAELLRVAGVeGAYAALSEADKRTLLLRELQQPR 508

                    PLlgsDLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvL
                     L  +     E  +  ld fr  ++v A   +     Yiis + + sD L
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  gi|1754707   509 LLTLPFHTYSETTASELDIFRaareVRARYGSRIVRNYIISHTETLSDLL 558

                   AvELLqRECgv.kq.........tLrvvPLFEkLADLeAAPAavekLFs
                    v LLq+E g+ +++++++++ +  + v+PLFE + DL+ AP  +  L +
  gi|1754707   559 EVMLLQKEAGMfRHgtngsggaglDVMVIPLFETIEDLRNAPQIMGELLA 608

                   i...DWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKk
                   +++ D         qevm+GYsDs KD G l   W LYk    ++    +
  gi|1754707   609 LpgfDAVLAAQGNEQEVMLGYSDSNKDGGFLTSNWELYKTELALVELFER 658

                   yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                    Gv+L lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGE+i
  gi|1754707   659 KGVRLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEIISSK 708

                   FGEEnLCFrsLqRFtAAtLEHGmnPPvs.Pk..PEWRkLmeemAvvAtEE
                   F   ++  r L    AAtLE  + P   +Pk+  E+   m+ +   A
  gi|1754707   709 FANPEIGRRNLETIVAATLEATLLPTRNrPKglEEFEAAMQALSDHAFSA 758

                   YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....GiesLR
                   YR +v+  P F +YF   tP +E   +n+GsRPa Rk   ++++ ie LR
  gi|1754707   759 YRHLVYETPGFKDYFFATTPITEIADLNLGSRPASRKLMDrkqrRIEDLR 808

                   AiPWiFaWtqtRFHLPvWLGvGAAFKhAidKD......iKnlqkLkEmYk
                   AiPW F+W q R  LP W G+G A +  +d  ++ + +   l  Lk m k
  gi|1754707   809 AIPWGFSWGQCRLLLPGWFGFGSAVQRWLDEAgsakakAARLATLKRMHK 858

                   eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLk.PFGksLRdkYvE
                   +WPFF   l  ++mv  K D  +A+ y +L     L++    ++ +++
  gi|1754707   859 QWPFFANLLSNMDMVLSKADLNVASRYAQLCEDRKLRnAVFSRISAEFTL 908

                   tkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPs
                   t++ L  i G  + L   P L   ++ R +Y+  Ln +q   LKR R
  gi|1754707   909 TEQVLGAITGQSERLADNPLLARSIKNRFPYLDPLNHLQVELLKRFRSGK 958

                   ykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAA
                               A  n  +    ++L                 + GiAA
  gi|1754707   959 ------------AGSNDARVRRGIHLS----------------INGIAA 979

                   GmqntG<-*
                   G+ n G
  gi|1754707   980 GLRNSG    985

gi|157149951|ref|YP_001450059.1|: domain 1 of 1, from 4 to 948: score 257.5, E = 3.3e-74
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          +L       v  +e  i  D LL D    iL
  gi|1571499     4    ---NKLESFSNKEVIREEVSILTD-LLTDVTRKILSP---------- 36

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    E +E  A  E     +K +EL   +  L   + + + + ++ +  L n+
  gi|1571499    37 -ETFEKIAMMEDLAVHSKYQELKEIVEELTTEEMVYISRYFSILPLLINI 85

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    E+v+lAy    +     D+    s t +         L++      e
  gi|1571499    86 SEDVDLAYEINHQNNIDQDYLGKLSTTID---------LISTR----ENA 122

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLs.AKDvtveDK
                    e L n  v  vltAHPtq  R+ +L     i   L q  + K   v++K
  gi|1571499   123 KEILENLNVVPVLTAHPTQVQRKTMLDLTNHIHTLLRQHRdVKAGLVNEK 172

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   k L   L R i     tD iR  +     E+   m Y+     + +  F+
  gi|1571499   173 KWLGN-LRRYIELMMQTDMIRDKKLKVTNEITNVMEYYNSSFLQAITNFM 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                             Gi    P     i    W+GGDRDG nP vt E  +
  gi|1571499   222 VEYKRLAEERGIKLDNPKP---ITMGMWIGGDRDG-NPFVTAETLKLSAT 267

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   L   +  n Yi++v  L   +s+    +E      E+   +  +     Y
  gi|1571499   268 LQSEVILNYYIDKVYTLYRTFSLSTNLSETSQAVAEMAALSTDK---SVY 314
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                    iEFWKqvPPtEPYRviLGdvRDKLYnt..............RERa...
                     E       +EPYR     +  KL  t    ++++ ++++++  +Ra+++
  gi|1571499   315 RE-------NEPYRRAFHYIQSKLIQTllylkegnfsnegqrlTDRAekt 357

                    .............RHLLAtGi.seisEeAv.........ytkvEeFLEPL
                     + +++++ ++++R ++   i+s isE   + +++++++y    eF E L
  gi|1571499   358 lsakttpslsnkgREIIPNYIqSRISETLTelkkeetpsYKTAKEFKEDL 407

                    ELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvl
                     + Y sL e    ++  G L +lL  v  FG  L  +D+Rq+s  +   +
  gi|1571499   408 QVIYDSLIEHHGEALVTGDLTELLQAVDVFGFFLASIDMRQDSSVHEACV 457

                    DAittHLeiG.sYReWsEeKRqEWLlaE.LkGKRPLlgsDLPktEEvkDv
                      +    +i + Y + sEe +   Ll   L+  R L     Pk E ++
  gi|1571499   458 AELLASANIVkDYSSLSEEEKCQVLLKQlLEDPRILSATHEPKSELLQKE 507

                    ldafrvLAELPiDsFG.....aYiismataPsDvLAvELLqRECgvkqt.
                    l+ f+    L  D+ G++  +  iis +t+ sD L   ++ +E g+   +
  gi|1571499   508 LEIFKTARQL-KDALGeevikQNIISHSTSVSDLLELAIMLKEVGLIDEn 556

                    ...LrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...qevmvGYs
                    ++++++vPLFE + DL+    ++ek  s+      i  K++ qe+m+GYs
  gi|1571499   557 gtrVQIVPLFETIEDLDNSCETMEKYLSLPIAQKWIASKnnyQEIMLGYS 606

                    DsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPt
                    Ds KD G ls  W LYkAq  +  +  k+GvK++ FHGRGGtvGRGGGPt
  gi|1571499   607 DSNKDGGYLSSCWTLYKAQQQLTAIGDKFGVKITFFHGRGGTVGRGGGPT 656

                    HLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHG
                      Ai sqP   in  +R t qGEvi   +G  +  +  L     A +
  gi|1571499   657 YEAITSQPLRSINDRIRLTEQGEVIGNKYGNKDAAYYNLEMLVSAAINRM 706

                    mnPPvsPkP...EWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPEl
                    +    s   +++ + ++m+++       YR +v+ + RF +YF    P
  gi|1571499   707 VTHKKSDAHtsnKYERIMDQVVERSYQIYRDLVFGDERFYDYFFESSPIK 756

                    EYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFK
                         niGsRPa Rk    i  LRAiPW+F+W q R   P W GvG  FK
  gi|1571499   757 AISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWYGVGSSFK 806

                    hAidKD.iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL
                      id+D+  nl  L+ mYk WPFF+  l  ++mv  K    iA  y +L
  gi|1571499   807 EFIDQDpENNLAFLQLMYKRWPFFKSLLSNVDMVLSKSNMNIAFEYAQLC 856

                    vaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYi
                       +++   + + d+++ tk+ +L+i GH +lL    YL+  l  R +Y
  gi|1571499   857 EDQNVRDIFNIILDEWQLTKNVILEIEGHDELLAENTYLRDSLDYRMPYF 906

                    ttLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpter
                      Ln +q   +KR R  + + t+         +E       L+++
  gi|1571499   907 NVLNYIQLELIKRQR--NGQLTPD--------QEK------LIHIT---- 936

                    vaPGLEDtLiLtmKGiAAGmqntG<-*
                                + GiA G+ n G
  gi|1571499   937 ------------INGIATGLRNSG    948

gi|94311682|ref|YP_584892.1|: domain 1 of 1, from 60 to 1009: score 256.3, E = 7.4e-74
                    *->siDAqLRlLvPGKvsedekL.ieYDALLlDkFL.DiLqDLHGedLkE
                       +        +P +   d +L+++ D   l + L+D + +  G+   +
  gi|9431168    60    AAPTAAATTIPARRTADKDLpLREDIRFLGRLLgDCVREQEGDAAFD 106

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                     v      +  +    D     EL   L  L    +  v +a++    LA
  gi|9431168   107 LVETIRQTAVRFRRENDRAAGTELDRLLKRLSRDQTNSVVRAFSYFSHLA 156

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    n+AE+ +   RRR++ +        +s      +   l+ +   +  + +
  gi|9431168   157 NIAEDQHHNRRRRVHALA-------GSPPQPGSLSRALQAIDAAG-VTGK 198

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                       e L    +  vltAHPt   R+s+L  +  i   La      +t  +
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  gi|9431168   199 QLREFLDDALIMPVLTAHPTEVQRKSILDAEREIARLLAE-RDLPMTTRE 247

                   KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                   +      L   +   + t  +R ++    DE+   +sY+  t  +G+P+
  gi|9431168   248 RDHNTAQLRARVTTLWQTRMLRNTRLMVVDEIENALSYYRTTFLQGIPRL 297

                   LRRvDtALKni....GinERlPYd.vPLikFssWmGGDRDGknPRvtPEv
                   +   +  +  + +++      P   +P ++  sW+GGDRDG nP vt E
  gi|9431168   298 MAELEEDIAEVfprrSKTGATPAPlAPFLQMGSWIGGDRDG-NPNVTAET 346

                   tRDvCLLaRmmAanlYisqvEDLmFEl....smWRCndELRvRAEElyrt
                             +    Y++ +  L  El+ ++ m     EL + AE
  gi|9431168   347 LEHAARQQATLLFDWYLDELHALGAELplssLMVDASPELLALAEASPDH 396

                   aardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGis
                   +                  EPYR  L  +  +L  t       +A+
  gi|9431168   397 SEHR--------------ADEPYRRALIGMYARLAATSQLLTGHVAQR-H 431

                   eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                    +++ A y + E F   + +   sL      ++A G +  l+R +  FG
  gi|9431168   432 PVADVAPYENAEAFAADVQIVVDSLRTHHGEALARGRVDALVRAIAVFGF 481

                   sLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK
                    L  +D+Rq s+ +  v+  +    +i s+Y   +E ++ E LlaEL+
  gi|9431168   482 HLASIDMRQVSDVHEAVIAELFATAGIESdYAALPEARKLELLLAELRQP 531

                   RPLlgsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsD
                   R L  +     E  +  l  f +  +L    +Ga+  ++Yiis + + sD
  gi|9431168   532 RLLTLPWHDYSEQTRSELAIFAMARDLRA-RYGAriarnYIISHTETLSD 580

                   vLAvELLqRECgv............kqtLrvvPLFEkLADLeAAPAavek
                    + v LLq+E g+ +++ ++++++ +  L v+PLFE + DL+ A   +e
  gi|9431168   581 LIEVMLLQKEAGMlrgtlgsktdpaRMELMVIPLFETIEDLRNAAGIMES 630

                   LFsi...DWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKv
                   L  +++ D  i +    qevm+GYsDs KD G l   W LYkA   ++K
  gi|9431168   631 LLDLpgfDSVIAHHGVEQEVMLGYSDSNKDGGFLTSNWELYKAELALVKL 680

                   AKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEvi
                     +  vKL lFHGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGE+i
  gi|9431168   681 FEERRVKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEII 730

                   EfsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEWRkLmeemAvvA
                      F   ++  r L    AAtLE  + P  ++Pk+   +  +m+++   A
  gi|9431168   731 NSKFANAEIGRRNLETVIAATLEASLLPTQnAPKdlATFEGVMQQLSDHA 780

                   tEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....Gie
                      YR +v+  P F +YF   tP +E   +n+GsRPa Rk   ++++ ie
  gi|9431168   781 FSAYRDLVYETPGFKDYFFATTPITEIADLNLGSRPASRKLMDkkhrRIE 830

                   sLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidK..DiK....nlqkLkE
                    LRAiPW F+W q R  LP W G+G A +  +d  +D K+++  +  Lk
  gi|9431168   831 DLRAIPWGFSWGQCRLLLPGWFGFGSAVQALLDAapDEKsrkaTVATLKR 880

                   mYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdk
                   m k WPFF   l  ++mv AK D  +A+ y  L     L+k    ++ ++
  gi|9431168   881 MVKSWPFFSTLLSNMDMVLAKTDLAVASRYAGLCEDTALrKAVFSRISAE 930

                   YvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiR
                   +  t d+L  i G ++ L   P L   ++ R +Y+  Ln +q   LKR R
  gi|9431168   931 WHLTSDMLGLITGRQERLADNPLLARSIKNRFAYLDPLNHLQVELLKRYR 980

                   DPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKG
                                  A  +    d  v+             + Lt+ G
  gi|9431168   981 ----------------AGKD--GDDVRVRRG-----------IHLTING 1000

                   iAAGmqntG<-*
                   +AAG+ n G
  gi|9431168  1001 VAAGLRNSG    1009
```

gi|93006646|ref|YP_581083.1|: domain 1 of 1, from 2 to 926: score 256.2, E = 7.9e-74

```
                *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                    iD     +   ++s           Ll  FL+D +    Ge+
gi|9300664     2    IIDND---ILRERIS-----------LLGSFLgDAISRQTGEQTLHT 34

                vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                +        +          + L   + sLd      v ++++    LAn
gi|9300664    35 IETLRKGFIQQRREPNEAHKQKLIDFIASLDNQSLKNVIRSFSIYFFLAN 84

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkl...nKs
                L EE  l   R   + +           E   E  +++  l  +++n
gi|9300664    85 LSEENYLREERHALRMQ----------SEQSWEGSFRRTLLECrerNIE 123

                PeEvFeALKnqsvDLvltAHPtqsvRRs...LLqKnaRiRnCLaqLsAKD
                P+ + e +       v+tAHPt + RR + +LLq        L  +
gi|9300664   124 PAQMQELIEQLKFIPVFTAHPTEARRRTtmnLLQGLFTHSDALNNVAQNS 173

                vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWk
                   e  +   E     i   +  DE+R  +P   DE+  G+ Y+   +++
gi|9300664   174 FAYEQAR---EKTAQTIDLLWSSDEVRTRKPLVYDEINNGLHYFNASLFN 220

                GvPKFLRRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPE
                 +PK  R +  A+  i   E   Y  P +i F sW+GGDRDG      P
gi|9300664   221 AIPKVYRNIKNAIIDI-YPELTDYPLPaIISFGSWIGGDRDG-----NPF 264

                vtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE.Elyrtaa
                vt D   +a +m a   +     L+  l      ++  v  E+++y
gi|9300664   265 VTHDTTEMAVLMHADTVLRHYQVLLKKLRRQLIHSDTIVTIEpDVYAKIE 314

                rd.kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGise
                + + + +   ++      +EPYR  L  +  K+  t      +  +G
gi|9300664   315 SYsELDRRVFDYNLDDYGNEPYRRFLSLILNKVKAT---NLLIQSKGSDT 361

                isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                 +    y +  e LE L +  +s+ +  D +  +G LLD++R v t G
gi|9300664   362 EAKKDAYANPQELLEDLRIIRQSV-NTHDTAHGEGLLLDIIRLVKTCGFH 410

                LvKLDiRqEseRqtDvl.DAittHLeiGsYReWsEeKRqEWLlaEL.kGK
                L  LDiRqEs  + +v+ D      ++  Y +  E  RqEWL   L+k
gi|9300664   411 LAALDIRQESSYHSEVIaDIFANASNLPDYQSLNETERQEWLTRLLeKPG 460

                RPLlgsD..LPktEEvkDvldafrvLAELP.iDsFGaYiismataPsDvL
                 PL+  D+   kt E    + ++  L  L + D+FG+Y+ism+   s  L
gi|9300664   461 TPLIYTDnlTDKTREQLALMHSVATLRKLVgQDTFGSYVISMTNNASQLL 510

                AvELLqR.........ECgvkqtLrvvPLFEkLADLeAAPAavekLFsiD
                 v LL R  +  + ++E  +   L+v PLFE + DL+     +  +
gi|9300664   511 EVLLLMRfaglcrvddEGRLSADLPVAPLFETIEDLKNIDQILPAVLDNP 560

                WYi...nridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyG
                 Y++   + d  qe+m+GYsDs KD G +  AWqLY Aq  i  +A kyG
gi|9300664   561 LYRgllRHSDNTQEIMLGYSDSSKDGGIITSAWQLYSAQQTINSIAEKYG 610

                vKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFG
                +K  lFHGRGG v RGGG tH Ai +qP  t++G ++vt qGEv+   +
gi|9300664   611 IKTRLFHGRGGSVSRGGGSTHKAIAAQPAGTLHGQIKVTEQGEVLYAKYA 660

                EEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEEYR
                  +     L      tL       v   PE +++  L  ++A      YR
gi|9300664   661 NTDTAVFELTMGITGTLKACSSRFVVQPPElphYEALFARLADAGEQRYR 710

                svvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWi
                 +      F  ++  AtP  E   +niGsRPa R  +    ++LRAiPW+
gi|9300664   711 KLTDHTEGFYQFYSQATPVAEISLLNIGSRPAHRNKGlPSKTTLRAIPWV 760

                FaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDL
                F W   RF LP W GvG A    id +      +kEm + WPFF v +
gi|9300664   761 FGWSLARFTLPAWYGVGSALHSVIDDEA----LMKEMIDCWPFFNVFISN 806

                lEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGH
                +Em F K D  iA  y +L   E L+ +    + d+ + t+  L  +
gi|9300664   807 IEMAFTKSDMSIAHAYSQLCDDERLREqIMTAVTDEHELTHSGLNSLLNQ 856
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                  kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                    lLE    L   l  R++Y+   n +q   LKR R             K
  gi|9300664   857 ESLLEHQQNLAASLEWRNAYLDPTNYIQIELLKRARQ------------K 894

                  EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                  +   +      +   L         +ED Li  +  +AAG+ ntG
  gi|9300664   895 DATSDT-----NHGDLD--------VEDPLIRSINALAAGLRNTG    926

gi|227521038|ref|ZP_03951087.1|: domain 1 of 1, from 9 to 924: score 255.6, E = 1.1e-73
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                          L  +     s d  ++  +  +l   L++    L G+ +
  gi|2275210     9    --GNFLMSIKKLENSSDHAMVAEEVKILTNLLnESTRQLSGDVVFNK 53

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  +q+   +sA+    kD   Le    ++ +L   + ++vA+ +  +  L n
  gi|2275210    54 IQDLIKISAQ----KDYDALEK---QIAGLTNQEMMVVARYFATLPLLVN 96

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  + E+velA       ++       a+      +E+t+  Lv +     e
  gi|2275210    97 ISEDVELA---SEVNLR-----NNADQDYLGKLEDTID-LVAQK----EN 133

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    e LK   v  vltAHPtq  R+ +L     i   L             +
  gi|2275210   134 AREILKHVNVVPVLTAHPTQVQRKTVLELTDQIHGLLRSYREVKNGTINQ 183

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   E  E L   i     tD iR  +     E+   ++Y+   +   + KF
  gi|2275210   184 AEWTEKLRAYIEILMQTDIIRSHKLQVSNEITNVLAYYPKALIPAITKFT 233

                  RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   R     K    n  l    P i    W+GGDRDG nP vt +  +
  gi|2275210   234 ARYQELAKK--HNLDLKCATP-ITMGMWIGGDRDG-NPYVTADTLKLSAG 279

                  LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                  L   +    Yi ++  L   +sm           E l   +  d
  gi|2275210   280 LQSQVIFEYYIKKLNKLYRTISMSTSYMKTSSAVEKLSELSNDD------ 323

                  iEFWKqvPPtEPYRviLGdvRDKLYntR.......ERaRHLLAtGiseis
                           +EPYR     +  +L  t  +  ++ ++   +    + ++
  gi|2275210   324 ----SPFRTNEPYRRAFYYIESRLLHTEyqllgtaDKNSFVKKRDLENLD 369

                  EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                     vy +  +F   L     sL +  D+++      +lL  +  FG  L
  gi|2275210   370 KIPVYKNPQDFKADLITIKASLEQDHDQAVIKSFFTELLEAIDIFGFHLA 419

                  KLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK.RP
                   +D+Rq+s  +   +  + + +i + Y + +E  +   Ll EL   +R
  gi|2275210   420 TIDMRQDSSVNEACVAELLKSAGICdNYSDLPEKEKVQVLLKELNEDpRN 469

                  LlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLA
                  L     Pk + ++  l  ++    L ++ + D     iis + + sD L
  gi|2275210   470 LHANNKPKSDLLQKELKIYKTARQLKdrigEDVIKQHIISHTESVSDLLE 519

                  vELLqRECgvkqt....LrvvPLFEkLADLeAAPAavekLFsiDWYinri
                    ++ +E  +   ++ +++vvPLFE + DLe     ++    +D  +  +
  gi|2275210   520 QAIMLKEYDLLDNqsarIQVVPLFETVEDLENSREIMKEFLNLDIVKKWL 569

                  ...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                   +++  qe+m+GYsDs KD G l+  W LYkAq ++  + Kk Gv ++
  gi|2275210   570 asqNNYQEIMLGYSDSNKDGGYLASCWNLYKAQKDLTAMGKKLGVNITFM 619

                  HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                  HGRGGtvGRGGGP   Ai +qP   in  +R+t qGE+i   +G  +  +
  gi|2275210   620 HGRGGTVGRGGGPSYEAITAQPFGSINDRIRMTEQGEIIQNKYGNQDTAY 669

                  rsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEEYRsvvvKE
                    L   + At++  +   +    + +++R+ m+++       YR +v+
  gi|2275210   670 YNLEMLASATIDRIVSKQIVSEDDiggFRDSMDKIVLDSNKVYRKLVFET 719

                  PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
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                    P F +YF  AtP      +niGsRPa Rk       LRAiPW+F+W q R
  gi|2275210   720 PAFLDYFLQATPIKQISNLNIGSRPAARKKITDFSGLRAIPWVFSWSQSR 769

                    FHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAK
                       P W GvG AFKh id D+ nl  L+ mY+ WPFF   l  ++mv  K
  gi|2275210   770 IMFPGWYGVGSAFKHFIDADSHNLETLQKMYQGWPFFHSLLSNVDMVLSK 819

                    GDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDP
                        iA  y +L   E+ k   + + ++++ tk+ +L+i G k+lL   P
  gi|2275210   820 SNMDIAKQYADLCEDEDTKQVFDTIYQEWKLTKEVILQIEGNKELLADNP 869

                    YLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnsk
                     L+  l  R +Y   Ln +q   +KR R
  gi|2275210   870 SLQMSLNYRMPYFNILNYIQIEMIKRDR---------------------- 897

                    kadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                              + +a   E  L +t+ G+  G+ n G
  gi|2275210   898 ----------VDDIAGVYESILPITINGVTSGLRNSG    924

gi|238853373|ref|ZP_04643752.1|: domain 1 of 1, from 2 to 912: score 255.6, E = 1.2e-73
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       si            s d  ++  +  +l   L++    L G+ +
  gi|2388533     2    SIKKL-------ENSSDHAMVAEEVKILTNLLnESTRQLSGDVVFNK 41

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +q+   +sA+    kD   Le    ++ sL   + ++vA+ +  +  L n
  gi|2388533    42 IQDLIKISAQ----KDYDALEK---QIASLTNQEMMVVARYFATLPLLVN 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+velA           D+           +E+t+  Lv +     e
  gi|2388533    85 ISEDVELASEVNLLNNTDQDYLGK--------LEDTID-LVAQK----EN 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      e LK   v  vltAHPtq  R+ +L     i n L            +
  gi|2388533   122 ANEILKHVNVVPVLTAHPTQVQRKTVLELTDQIHNLLRNYREVKNGTINQ 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     E  E L   i     tD iR  +     E+   ++Y+   +   + KF
  gi|2388533   172 AEWTEKLRAYIEILMQTDIIRSHKLQVSNEITNVLAYYPKALIPAITKFT 221

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                     R     K    n  l    P i    W+GGDRDG nP vt +  +
  gi|2388533   222 ARYQELAKK--YNLDLKGATP-ITMGMWIGGDRDG-NPYVTADTLKLSAS 267

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L   +    Yi ++  L   +sm           E l   +  d
  gi|2388533   268 LQSQVIFEYYIKKLNKLYRTISMSTSYMKTSTAVEKLSALSNDD------ 311

                    iEFWKqvPPtEPYRviLGdvRDKLYntR.......ERaRHLLAtGiseis
                             +EPYR     +  +L  t  +  ++ ++   +    + ++
  gi|2388533   312 ----SPFRTNEPYRRAFYYIESRLLHTEyqllgtvDKNSFVKRRDLENLD 357

                    EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                       vy +   F   L     sL +  D+++      +lL  +  FG  L
  gi|2388533   358 KIPVYNNPQAFKADLITIKESLEQDHDQAVIRSFFTELLEAINIFGFHLA 407

                    KLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK.RP
                     +D+Rq+s  +   +  + + +  +i + Y e +E  +   Ll EL   +R
  gi|2388533   408 TIDMRQDSSVNEACVAELLKSAGICdNYSELPEKEKVQVLLKELNDDpRN 457

                    LlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLA
                    L     Pk + ++  l  ++   EL ++ + D     iis + + sD L
  gi|2388533   458 LHANNKPKSDLLQKELKIYKTARELKdrigEDVIKQHIISHTESVSDLLE 507

                    vELLqRECgvkqt....LrvvPLFEkLADLeAAPAavekLFsiDWYinri
                      ++ +E  +   ++ +++vvPLFE + DLe     ++    +D  +  +
  gi|2388533   508 QAIMLKEYDLLDNqgarIQVVPLFETVEDLENSREIMKEFLNLDIVKKWL 557

                    ...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                     +++  qe+m+GYsDs KD G l+  W LYkAq ++  + Kk Gv ++
  gi|2388533   558 asqNDYQEIMLGYSDSNKDGGYLASCWNLYKAQKDLTAMGKKLGVNITFM 607
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                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGGtvGRGGGP   Ai +qP   in  +R+t qGE+i   +G  +  +
  gi|2388533   608 HGRGGTVGRGGGPSYEAITAQPFGSINDRIRMTEQGEIIQNKYGNQDTAY 657

                    rsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEEYRsvvvKE
                      L   + At++  +   +    + +++R+ m+++       YR +v+
  gi|2388533   658 YNLEMLASATIDRIVSKQIVSEDDiggFRDSMDKIVLDSNKVYRKLVFET 707

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
                    P F +YF  AtP      +niGsRPa Rk       LRAiPW+F+W q R
  gi|2388533   708 PAFLDYFLQATPIKQISNLNIGSRPAARKKITDFSGLRAIPWVFSWSQSR 757

                    FHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAK
                       P W GvG AFKh id D+ nl  L+ mY+ WPFF   l  ++mv  K
  gi|2388533   758 IMFPGWYGVGSAFKHFIDADSHNLETLQKMYQGWPFFHSLLSNVDMVLSK 807

                    GDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDP
                        iA  y +L   E+ k   + + ++++ tk+ +L+i G k+lL   P
  gi|2388533   808 SNMDIAKQYADLCEDEDTKQVFDTIYQEWKLTKEVILQIEGNKELLADNP 857

                    YLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnsk
                     L+  l  R +Y   Ln +q   +KR R
  gi|2388533   858 SLQMSLNYRMPYFNILNYIQIEMIKRDR---------------------- 885

                    kadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                +a   E  L + + G+  G+ n G
  gi|2388533   886 ----------VADIAGVYESILPIIINGVTSGLRNSG    912

gi|292656740|ref|YP_003536637.1|: domain 1 of 1, from 1 to 897: score 255.0, E = 1.7e-73
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           +R L    v   +++ e  ALL     D+L         E v
  gi|2926567     1    -----MR-LHTRDVR--QDVRELGALL----GDVLEAQTSTASFETV 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E    +  Y  K ++   e L  ++  L+P    +vA+a+     L nL
  gi|2926567    36 EELRQAAISYR-KGESGSRERLYDVVGDLEPERESVVARAFTTYFELINL 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEE     R R++  +  + + E+  t E  i +tl  L        eE
  gi|2926567    85 AEE-----RERVRVIR--EASQEG--TLEDGILDTLDALDDEE--VDEEL 123

                    F.eALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     +  L    ++  +tAHPt + R+ +  K   i n L  L  + +t  +
  gi|2926567   124 LgRVLEDVLIEPTFTAHPTEARRKTVKSKLRSIANRLETLDERRLTDLEH 173

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                          +  E+   + t  +R  +P P DE R    Y+  t+++ v
  gi|2926567   174 DQEWRHVVAEVTSLWQTSQVRDRRPEPTDEARNVQWYLENTLFDVVGEVY 223

                    RRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDvC
                       +  L+     E    dvP+L +F sW G DRDG nP vtPEvt D
  gi|2926567   224 EELEEELR----AEYPGLDVPkLFEFRSWAGSDRDG-NPFVTPEVTEDTL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                       R +A   Y + +  L   ls      +     E   +  + +
  gi|2926567   269 ERQRSVALEKYSDSLKRLSGVLSQDATRIDPGHELERSLKADREH--LPV 316

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                      E      P+EPYR  L  +R++L     Ra  +   G+++ sE
  gi|2926567   317 VAEEADERYPNEPYRQKLKLMRERL----RRAEDVRPNGYADASE----- 357

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                         +  LE+   sL   G   +AD  +  l+Rqv tFG  L  LD+R
  gi|2926567   358 ----LMADLEVVDASLRRTGAEQVADVYVEPLMRQVDTFGFTLASLDLRD 403

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP.
                      e +t+ +     H ++  Y + sE+ R E L   +    P++  + P+
  gi|2926567   404 HQENHTEAVHEALAHEGLDYYGS-SEQERVELLTDAILQEEPVVDLEDPg 452

                    .ktEEvkDvldafrvLA....ELPiDsFGaYiismataPsDvLAvELLqR
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                    +  E  + vl  fr L + ++E  + +   Y ism+  Ps vL v  L
  gi|2926567   453 dVSETAERVLRRFRKLGewqrEYGVGAIDTYCISMTEEPSHVLEVLFLAD 502

                    ECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK..
                      gv + +++  + vvPL E    L+ A   +  LF  + Y   +  +++
  gi|2926567   503 QAGVvslpdHCGIDVVPLLETESALNGARRIMGTLFENEAYGTALAARnd 552

                    .qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                     qe+m+GYsDs K+ G l+A W LYk q  ++ +  ++ v + lFHGRGG
  gi|2926567   553 vQEIMLGYSDSNKENGFLAANWDLYKNQRRLADICDDFDVTMRLFHGRGG 602

                    tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                     + RGGGP   A+L+ P +t+ G ++ t qGE i   +    +  r L
  gi|2926567   603 SISRGGGPMNEAMLALPNETVTGQIKFTEQGEAIAEKYANPRIAERNLEQ 652

                    FtAAtLEHGmnPPvsPkPE....WRkLmeemAvvAtEEYRsvvvKEPRFv
                       A +   ++    P  E +++W + m+ mA  A  EYR + +    Fv
  gi|2926567   653 MLNAQIRARLQAIRTPEEEvpdrWVDAMDTMAAAARAEYRDL-LESDGFV 701

                    EYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLP
                     YF  AtP +    +n+GsRPa R     +e LRAiPW+F+Wtq R  LP
  gi|2926567   702 SYFEQATPITVIEELNLGSRPASRSDERSVEDLRAIPWVFSWTQSRCILP 751

                    vWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPG
                     W  + AA   A   D   +  L+EmY+eW FFR t D   m  A+ D
  gi|2926567   752 GWYSL-AAGVNAFLEDGGDMDDLREMYDEWAFFRSTFDNAAMALARTDLE 800

                    iAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                    iA+ y +L   E    F  +L ++Y++  dl+L i     lL  + +L
  gi|2926567   801 IATEYANLADEELREEFFTRLTEEYEDAADLMLDISERSSLLKRE-WLEE 849

                    rlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkade
                     lR R++Y+  Ln +q   L          t r        dE+
  gi|2926567   850 SLRRRNPYVDPLNLLQTHLLSQ--------THR-------TDEE------ 878

                    LvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                 E tL Lt+KGiAAGm+ntG
  gi|2926567   879 --------------ERTLRLTVKGIAAGMKNTG    897

gi|227893638|ref|ZP_04011443.1|: domain 1 of 1, from 1 to 906: score 254.8, E = 2e-73
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           + +      s+ + + +   +L     +    L Ged    +
  gi|2278936     1    -----MTVKKLENNSDVNAMADEVKILTNLLNESTEQLVGEDAFAKI 42

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    q    +sA       ++  e L  ++ +L+  + i+vA+ +  +  L n+
  gi|2278936     43 QNLVKISA-------AQGQEKLKKQIAGLNNQEMIVVARYFATLPLLINI 85

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     E+ve A +       h D+      t +         +v k  K  eE+
  gi|2278936     86 SEDVEFASKVNLLNNTHQDYLGKLKDTID---------IVAKK-KNAEEI 125

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     e +    v  vltAHPtq  R+ +L     i   L           D+
  gi|2278936    126 LEHV---NVVPVLTAHPTQVQRKTVLELTDNIHQLLRSYREVNNGTIDRD 172

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    E  E L   i     tD iR  +     E+   + Y+   +   + KF
  gi|2278936    173 EWTEQLRACIEILMQTDIIRGHKLKVANEITNVLTYYTKALIPAITKFTT 222

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R     +  G+n  +    P i    W+GGDRDG nP vt +       L
  gi|2278936    223 RYKELAQEHGLN--VSKATP-ITMGMWIGGDRDG-NPYVTADTLELSATL 268

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                       +    Yi ++ +L   +s+        +    l   +  d
  gi|2278936    269 QSRVIFEYYIKKINELYRTISLSTSYMKPSAAVSNLSELSNDD------- 311

                    EFWKqvPPtEPYRvi.......LGdvRDKLYntRERaRHLLAtGiseisE
                           +EPYR      +++L     KL n       L    + ++
  gi|2278936    312 ---SPFRVNEPYRRAfyyiqsrLVHTEQKLLNITNINTFLKERDLENLNK 358
```

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                    eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                       y +  eF   LE+   sL e  D+++       +L  +  FG  L
  gi|2278936   359 IPAYQNAQEFKADLEVIKTSLEENHDQAVVKTGFTQILEAIDIFGFYLAT 408

                    LDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGK.RPL
                    +D+Rq+s  +   +  + +  +i + Y +  E  +   Ll EL   +R L
  gi|2278936   409 IDMRQDSSINEACVAELLKSAGICdHYSDLNEKEKVSLLLKELNDDpRNL 458

                    lgsDLPktEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDvLAv
                         Pk E ++++  +  + r L ++L  D     iis + + sD+L
  gi|2278936   459 HANNQPKSELLQkelKIYKTARQLKDrLGEDVIKQHIISHTESVSDMLEQ 508

                    ELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri.
                     ++ +E  + +++k  ++vvPLFE + DL+ A   ++     D  +  ++
  gi|2278936   509 AVMLKEYDLldnqKARIQVVPLFETVEDLNNARDIIKEYLNFDIVKKWLk 558

                    ..dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                    +++  qe+m+GYsDs KD G l+  W LYkAq ++  +  + G+K++  H
  gi|2278936   559 sqNNYQEIMLGYSDSNKDGGYLASCWNLYKAQKDLTAIGEDLGIKITFMH 608

                    GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                          GRGGGP   Ai +qP   in  +R+t qGE+i   +G  +  +
  gi|2278936   609 ------GRGGGPSYEAITAQPFKSINDRIRMTEQGEIIQNKYGNKDTAYY 652

                    sLqRFtAAtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEP
                     L   + At++      +   ++  E+R  m+++     E YR +v+  P
  gi|2278936   653 NLEMLASATIDRMASKQIVSEdhiDEFRSSMDKIVTESNEVYRKLVFDNP 702

                    RFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRF
                     F+ YF  AtP  E  k+n+GsRPa Rk       LRAiPW+F+W q R
  gi|2278936   703 NFIKYFFQATPIKEVSKLNVGSRPASRKKLTDFSGLRAIPWVFSWSQSRV 752

                    HLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                      P W GvG AFK  id D  nl+ L++mYk WPFF   l  ++mv  K
  gi|2278936   753 MFPGWYGVGSAFKDFIDSDPDNLKELQDMYKGWPFFHSLLSNVDMVLSKS 802

                    DPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                       iA  y +L   E++k   + +  +++ tk+ +L+i GH +lLE  P
  gi|2278936   803 NMEIAKQYADLCEGENVKSVFDIIYKEWQLTKQVILQIEGHNELLEDNPA 852

                    LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                    LK+ l  R +Y   Ln +q   +KR R
  gi|2278936   853 LKKSLDYRMPYFNILNYIQLEMIKRDR---------------------- 879

                    adeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                             te+v    E  + +t+ G+A G+ n G
  gi|2278936   880 ---------TEEVQGVYESIIPITINGVASGLRNSG    906

gi|292492516|ref|YP_003527955.1|: domain 1 of 1, from 8 to 932: score 254.7, E = 2.3e-73
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        i A    L     s  e L +   LL       + D  G+ +   +
  gi|2924925     8    DIKAEESGL-----S--EPLAKQLTLLGTLLEQAIRDQAGPKMLNLM 47

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         l  + + +  +   e   +++  L     + + +a+     LAn
  gi|2924925    48 GKLHQLCGQVDTQDNATLCEGADTQIQKLSRDQIVWLLHAYTSFFHLANQ 97

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE  e+      + ++    +       Es i+E + +L  ++  + e v
  gi|2924925    98 AEQQEIIRINWERVRQ----SRIDKPRPES-IDEAIHHLQKQG-YAREQV 141

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL..sAKDvtveD
                     + L    +   ltAHPt + RRs+L K+ Ri   La L+++     +e
  gi|2924925   142 LQLLGQLDIQPTLTAHPTEARRRSILFKQQRISGLLAGLnqYSSTTPPET 191

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                     + LD+ L   i     tDE+R  +Pt + E+  G+ ++   +W+   +
  gi|2924925   192 ERILDD-LYNQIALLLATDEVRAERPTVKQEIHQGLYFMRIAIWEVAVQI 240

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
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                     R    AL+        P   P +++ sW+GGDRDG nP vtPE+tR
  gi|2924925   241 YRDTQRALQQ--YYGEAPDFPPFLHYRSWIGGDRDG-NPHVTPEITRWTI 287

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    +  R  A   Y   + +L  Els+      +           ar+  +
  gi|2924925   288 ITHRETALRRYCTELQELYHELSLSERQVGIPPALYRSLEQDARE--TTL 335

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                       F  q+   EPYR        K+     R   LL         e  y
  gi|2924925   336 GHKFSEQL-QREPYRL-------KISYMMARLGKLLKPPNQTETGENTY- 376

                    kvEeFLEPLELCYksLCeCG.DkviADGsLLDlLRqvstFGLsLvKLDiR
                    +  +F+E L L  + L e G  k+   G L  lL    tFG  L  LD+R
  gi|2924925   377 NSKRFIEDLQLLKRCLEESGfGKISRHGRLGRLLILTQTFGFHLAALDVR 426

                    qEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgsDL
                    q s  +   + A+ +  +i + Y   sE  R   L a L+   PL  +
  gi|2924925   427 QHSHIHEKAVAALLQIAGITrDYLALSEKERLAVLSAQLQKPHPLRVPNS 476

                    PktEEvkDvldafrvLAELPi...DsFGaYiismataPsDvLAvELLqRE
                       E  + vl++f v+ +   +++++ G+Y+ism+ + sD L v LL +E
  gi|2924925   477 VLPESTQQVLETFAVIRDAIAqepEAIGSYVISMTHTISDLLEVMLLAKE 526

                    Cgvkq........tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK
                     ++ q ++++   +L  vPLFE +  LeAA   +  L     Y+ +i  +
  gi|2924925   527 AQLWQlqdgkvicPLDFVPLFETIEALEAADKRMLALIKHPIYRQQIAAR 576

                    ...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    ++ qe+m+GYsDs KD G   A W L kAq  + K   +  +   lFHGR
  gi|2924925   577 ghfQEIMLGYSDSSKDGGYWMANWALHKAQKRLGKLCHQQKIDFRLFHGR 626

                    GGtvGRGGGPt.HLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                    GGtvGRGGG t+  AiL+ PP   nG +R t qGEvi f +    +  r
  gi|2924925   627 GGTVGRGGGRTsQTAILAMPPAVHNGRIRFTEQGEVISFRYALPAMARRH 676

                    LqRFtAAtLEHGmnPPvs.PkPE....WRkLmeemAvvAtEEYRsvvvKE
                          A +        s+ kP +++   +Lme++A  A   YR ++ ++
  gi|2924925   677 TEQIVNAMIQATAVAAQSgDKPSddsyHEDLMERIAQQAMGAYRTLIEQD 726

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGie..sLRAiPWiFaWtq
                      F  ++   tP     ++ i sRP  R  +  ++ + LRAiPW+FaWtq
  gi|2924925   727 G-FWSWYTQVTPIEHISHLPIASRPISRTSATEVDfkNLRAIPWVFAWTQ 775

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                    tR+ +P W G+G A +  i  D      L+ mY++WPFF   +D
  gi|2924925   776 TRYLVPGWFGLGQALQK-IMGDETLQETLQKMYQQWPFFNTVIDDAQREM 824

                    AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                    A+     A+ y +L    e + F + + ++++  ++++L++ G ++lL+
  gi|2924925   825 ARARLKTASHYARLANQNETR-FHDIIVADFEKARKIILEMSGQQELLDN 873

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                     P +++ +  R++Y   Ln +q   +KR R               A En
  gi|2924925   874 TPTIQKTIIFRNPYTDVLNLLQIELMKRYRQ--------------APEN 908

                    skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                         +L++             L L + GiAA mq tG
  gi|2924925   909 ---EKGLLRQA-----------LFLSLNGIAAAMQSTG    932

gi|182677139|ref|YP_001831285.1|: domain 1 of 1, from 3 to 932: score 254.5, E = 2.6e-73
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          A   ++       d++L e   LL     + + +  G++  + +
  gi|1826771     3    TKGARTDIMTNLARQADDRLNEEIRLLGQILGETIREQEGDESFDRI 49

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         ls  +E   D+   e L + L +L    a+ v ++++    LAn+
  gi|1826771    50 ETIRRLSVAFERGADAAAGETLDTLLRGLSAEQAVSVIRSFSYFSHLANI 99

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+ e   RR i      + a       + D +  + +L   +    + +
  gi|1826771   100 AEDHE-TIRRSIAETGTEEPAGQETDSADDDFDGGMARLTAAG-VDKARI 147
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                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   eAL+      vltAHPt   R+s L  +  i   L            ++
  gi|1826771   148 IEALRQSFLSPVLTAHPTEVQRKSQLDAEHAIFSLLVEREHLGPGAARRR 197

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    D  L   i  A+ t  +R a+ t  DE+   +sY+  t  +  P
  gi|1826771   198 N-DALLAACITQAWQTRLLRNAKLTVRDEIENALSYYQTTFLRQLPALYA 246

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    +  L   G+ + lP     ++  sW+GGDRDG nP v  E t D+ L
  gi|1826771   247 ELEEWL---GVRD-LP---CFLRMGSWIGGDRDG-NPNVNAE-TLDIALR 287

                  aRm.mAanlYisqvEDLmFElsmWR....CndELRvRAEElyrtaardkv
                     ++A   Y+s v  L  Els+ R   +C ++L   AE     +
  gi|1826771   288 RQAeVALRHYLSEVRALGNELSLSRllvgCSQDLLRLAETSGDDSPHR-- 335

                  vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                               EPYR  L +++ +L  t            + +  +A
  gi|1826771   336 ------------ADEPYRRALIAIKGRLAATLKELTGQEDSKPAPLGTQA 373

                  vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                   y +    L  L +  ksL e   +++    L  + R v  FG  L  +D
  gi|1826771   374 -YPDASALLADLAIIEKSLAENHGRALIGPRLAPFQRAVKVFGFHLATVD 422

                  iRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgs
                  +Rq s+R+ + +  + +   +  +Y    E  Rq+ L+  L+  R L  +
  gi|1826771   423 LRQSSDRHAETIGELLRVAKVVEdYDALDEKARQDLLMRLLQDPRLLHVP 472

                  DL...PktEEvkDvldafrvL..AELPiDsFGaYiismataPsDvLAvEL
                   L+ + +tEE   v ++ r L++   P  +   Yiis + + sD L v L
  gi|1826771   473 YLrysARTEEELAVFETARRLrrSHGPL-AIRQYIISHTETVSDLLEVLL 521

                  LqRECgv............kqtLrvvPLFEkLADLeAAPAavekLFsiDW
                  Lq+ECg+ ++  ++++++++  L vvPLFE + DL+ A   ++  F++
  gi|1826771   522 LQKECGLiegligdpeqkpRAELMVVPLFETIEDLRNAQGIMADFFALPG 571

                  Yinrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEii.KvAKkyG
                      +  ++G qe+m+GYsDs KD G +   W LY+    +++  A + G
  gi|1826771   572 MADLVRasgGVQEIMLGYSDSNKDGGFFTSNWELYRVSIALAgFFAAQEG 621

                  vKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFG
                  + L lFHGRGGt+GRGGGP H AiL+qPP t nG +R t qGEvi   +
  gi|1826771   622 IVLRLFHGRGGTIGRGGGPSHQAILAQPPGTANGLIRLTEQGEVISSKYA 671

                  EEnLCFrsLqRFtAAtLEHGmnPPvsPkPE.WRkLmeemAvvAtEEYRsv
                    ++  r L    AA +E  +       PE + +    +    t  YR +
  gi|1826771   672 QPEIGRRNLETLVAANIEATLLGGDEAPPEaFLEAAHFLSEASTKAYRGL 721

                  vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaW
                  v+  P Fv+YF  AtP  E   +niGsRPa Rk s  ie LRAiPW F+W
  gi|1826771   722 VYDLPGFVDYFYAATPIAEIADLNIGSRPASRKSSRKIEDLRAIPWSFSW 771

                  tqtRFHLPvWLGvGAAFKhAi.dKDiKnlqkLkEmYkeWPFFRvtlDLlE
                   q R  LP W G+G A    ++d     l  L+ m +eWPFF   l  ++
  gi|1826771   772 GQARVSLPGWFGFGTAVEAFLnDAPEEKLALLQRMAREWPFFHALLSNMD 821

                  mvFAKGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHk
                  mv AK D  +A  y  L+    L ++ FG  +  ++  t    L +i G +
  gi|1826771   822 MVLAKADRKLARRYAALVPDQALaeRIFG-IIDTEWTRTLHALDEITGVH 870

                  DlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKE
                  + L   P L   +  R +Yi  Ln +q   L+R R           l K
  gi|1826771   871 ERLADNPALAHSISRRFPYIAPLNHLQVELLRRWR----------LGKT 909

                  yAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   A         L+ +n                  GiAAG+ n G
  gi|1826771   910 DARTY---NGILISIN-----------------GIAAGLRNSG    932

gi|262282657|ref|ZP_06060425.1|: domain 1 of 1, from 1 to 948: score 254.4, E = 2.8e-73
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
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                      +        s+ + + e   +L D   D+   +  ++  E +
gi|2622826     1    -----MSFNKLESFSNKDVIREEVSILTDLLTDVTRKILSPETFEKI 42

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       +l+         +K +EL   +  L   + + + + ++ +  L n+
gi|2622826    43 EMMQDLAVH-------SKYQELKEIVEELTTEEMVYISRYFSILPLLINI 85

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    E+v+lAy    +     D+    s t +         L++      e
gi|2622826    86 SEDVDLAYEINHQNNIDQDYLGKLSTTID---------LISTR----ENA 122

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLs.AKDvtveDK
                    e L n  v  vltAHPtq  R+ +L     i   L q  + K   v++K
gi|2622826   123 KEILENLNVVPVLTAHPTQVQRKTMLDLTNHIHTLLRQHRdVKAGLVNEK 172

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   k L   L R i     tD iR  +     E+   m Y+     + +  F+
gi|2622826   173 KWLGN-LRRYIELMMQTDMIRDKKLKVTNEITNVMEYYNSSFLQAITNFM 221

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                             Gi    P     i    W+GGDRDG nP vt E  +
gi|2622826   222 VEYKRLAEERGIKLDNPKP---ITMGMWIGGDRDG-NPFVTAETLKLSAT 267

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   L   +  n Yi++v  L   +s+    +E      E+   +  +     Y
gi|2622826   268 LQSEVILNYYIDKVYTLYRTFSLSTNLSETSQAVAEMAALSTDK---SVY 314

                   iEFWKqvPPtEPYRviLGdvRDKLYnt.....................
                    E       +EPYR     +  KL  t    ++++ ++++++ +++ +++
gi|2622826   315 RE-------NEPYRRAFHYIQSKLIQTllylkegnfsnegqrltdqaekt 357

                   .............RERaRHLLAtGisei......sEeAvytkvEeFLEPL
                    + +++++ ++++RE     +   ise  ++ ++ E   y    eF E L
gi|2622826   358 lsakttpsvsnkgREIIPNYIQSRISETltelkkEETPSYKTAKEFKEDL 407

                   ELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvl
                    + Y sL e    ++  G L +lL  v  FG  L  +D+Rq+s  +   +
gi|2622826   408 QVIYDSLIEHHGEALVTGDLTELLQAVDVFGFFLASIDMRQDSSVHEACV 457

                   DAittHLeiG.sYReWsEeKRqEWLlaE.LkGKRPLlgsDLPktEEvkDv
                     +    +i + Y + sEe +   Ll   L+  R L     Pk E ++
gi|2622826   458 AELLASANIVkDYSSLSEEEKCQVLLKQlLEDPRILSATHEPKSELLQKE 507

                   ldafrvLAELPiDsFG.....aYiismataPsDvLAvELLqRECgvkqt.
                   l+ f+    L  D+ G++  +  iis +t+ sD L   ++ +E g+   +
gi|2622826   508 LEIFKTARQL-KDALGeevikQNIISHSTSVSDLLELAIMLKEVGLIDEn 556

                   ...LrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...qevmvGYs
                   ++++++vPLFE + DL+    ++ek  s+      i  K++ qe+m+GYs
gi|2622826   557 gtrVQIVPLFETIEDLDNSCDTMEKYLSLPIVQKWIASKnnyQEIMLGYS 606

                   DsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPt
                   Ds KD G ls  W LYkAq  +  +  k+GvK++ FHGRGGtvGRGGGPt
gi|2622826   607 DSNKDGGYLSSCWTLYKAQQQLTAIGDKFGVKITFFHGRGGTVGRGGGPT 656

                   HLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHG
                     Ai sqP   in  +R t qGEvi   +G  +  +  L     A +
gi|2622826   657 YEAITSQPLRSINDRIRLTEQGEVIGNKYGNKDAAYYNLEMLVSAAINRM 706

                   mnPPvsPkP...EWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPEl
                   +    s   +++ + ++m+++       YR +v+ + RF +YF    P
gi|2622826   707 VTHKKSDAHtsnKYERIMDQVVERSYQIYRDLVFGDERFYDYFFESSPIK 756

                   EYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFK
                        niGsRPa Rk    i  LRAiPW+F+W q R   P W GvG  FK
gi|2622826   757 AISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWYGVGSSFK 806

                   hAidKD.iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLL
                     id+D+  nl  L+ mYk WPFF+  l  ++mv  K    iA  y +L
gi|2622826   807 EFIDQDpENNLAFLQLMYKRWPFFKSLLSNVDMVLSKSNMNIAFEYAQLC 856
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                    vaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYi
                       +++   + + d+++ tk+ +L+i GH +lL    YL+  l  R +Y
  gi|2622826   857 EDQNVRDIFNIILDEWQLTKNVILEIEGHDELLAENTYLRDSLDYRMPYF 906

                    ttLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpter
                      Ln +q   +KR R  + + t+         +E       L+++
  gi|2622826   907 NVLNYIQLELIKRQR--NGQLTPD--------QEK------LIHIT---- 936

                    vaPGLEDtLiLtmKGiAAGmqntG<-*
                                + GiA G+ n G
  gi|2622826   937 ------------INGIATGLRNSG    948

gi|229538486|ref|ZP_04427622.1|: domain 1 of 1, from 3 to 931: score 253.9, E = 3.7e-73
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       s          G       ++  D   l   L+  + +  G dL
  gi|2295384     3    SNQVTRSDPETGNDMSAKPILSSDVETLTSLLgGAIVEQAGSDLAAL 49

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                          ls e      +   e L   L +L+     l+ k+++    LAn
  gi|2295384    50 LMRIRQLSRERRVGL-PGAAERLVELLAGLNEDQLDLLTKSLSIYFDLAN 98

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+ +   R R+ +++  +   E+s   Es + + + +L  ++  + e
  gi|2295384    99 VAEDLQ---RIRVIRQR--ERQSEGSVRKES-LGDAIAQLKKQG-ATAEA 141

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v   L    + Lv+tAHPt + RR        +R  L+     D+ + +
  gi|2295384   142 VQHLLDKLHIGLVFTAHPTEAKRRTTRRILRQLRSDLTTAHQGDLLPRES 191

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L E +   +   +  D +R  +Pt   E+  G+ ++ + +W+ vP
  gi|2295384   192 GVLQERIRGSLTLLWQIDPMRPQPPTVMQEVERGL-FFFDGLWDIVPLIF 240

                    RRvDtALKni..GinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                         AL    +G    +P   P +kF sW+GGDRDG nP vt  vt D
  gi|2295384   241 QDLRSALAEHypGFKFHVP---PFLKFGSWIGGDRDG-NPFVTAQVTSDT 286

                    CLLaRmmAanlYisqvEDL..mFElsmWRCndELRvRAEElyrtaardkv
                      L    A    +    +L ++  +s      +  v A  l++t   +
  gi|2295384   287 LRLLETTAIERHLKTTRELadLLVVSDRGMQPDDPVYA-ALQKTFGAH-- 333

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                               P  EPYR  +  +  KL   R R    LA  +      A
  gi|2295384   334 -PELDQLVGDAPEAEPYRRWIKVIELKL---RKRIEPALASPLKAYQTAA 379

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                          + +E   L  k     GD++ A   L   L q+ tFGL +  LD
  gi|2295384   380 ELEADARLIEESLLRRK-----GDRIHA-SFLAAWLDQIRTFGLQVSALD 423

                    iRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaELkGKRPLlgs
                    +Rq+s  + Dvl  +    +i   Y +  E  Rq  L +       +l
  gi|2295384   424 VRQDSRVHVDVLQEVFARAGIyAEYAKADEKTRQKILTTPHDLGMNVLEG 473

                    DLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvELL
                    +L   +  ++    ++ +AE  + ++i+ FG  i+sm+   sD+L +
  gi|2295384   474 EL--SDMARETFSLYKLMAETVraggIERFGGHIVSMTHYASDILVILWF 521

                    qR........ECgvkqt.LrvvPLFEkLADLeAAPAavekLFsi.DW..Y
                     +   + + +E +   ++L+ +PL E + DL+  PA +  L s++D+  Y
  gi|2295384   522 WKwawkvtagESKAELPhLPLMPLLETIDDLRQGPAILTDLLSVpDYlaY 571

                    inridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvK
                      + +G ++ q+vmvGYsDs KD G l+A W LY+AqE +  v    Gv+
  gi|2295384   572 LKKDQGAqplQNVMVGYSDSTKDGGYLAASWGLYRAQEQLSDVLASQGVR 621

                    LvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEE
                    L +FHGRGG  GRGGGP   AiLs PP  ++GslRvt qGEv+   + E
  gi|2295384   622 LRVFHGRGGALGRGGGPAARAILSLPPKSVDGSLRVTEQGEVLAERYDEP 671

                    nLCFrsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvK
                    ++ Fr L   t AtL            +W   ++e+A      YR +v
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  gi|2295384   672 QIAFRHLEQVTWATLLVSSTQEGHWPEDWFTHLDELAQQSYLHYRKLV-D 720

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                    +P F  YF  AtP  E  ++ iGsRPa+R+    +  LRAiPW FaWtq
  gi|2295384   721 DPGFLMYFDRATPISEIERLPIGSRPARRRERKSLSDLRAIPWTFAWTQS 770

                    RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                    R  +P W G+G A   A+ +      + +EmY++WP F   +D   +
  gi|2295384   771 RHMIPAWFGLGKALHDAVARNNEDWSRYQEMYRTWPIFQAIIDNATLALM 820

                    KGDPGiAaLyDkLL....vaEeLkPFGksLRdkYvEtkdlLLkiAGHkDl
                    K D  iA  y +L+++++va  L+     + ++Y   +  +L i G   l
  gi|2295384   821 KADLQIANRYADLVedreVAKRLW---SMIHEEYDRSRASVLMITGESSL 867

                    LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                    L   P+L+  +  R++Y+  Ln +q   LKR R
  gi|2295384   868 LSNTPWLQTSIQERNPYVDPLNLIQVELLKRAR----------------- 900

                    dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     E s +ad   +L             + Lt++G+AAG+  tG
  gi|2295384   901 -EGSIEADRAARLQ----------HSVRLTIQGVAAGLRTTG    931

gi|226355772|ref|YP_002785512.1|: domain 1 of 1, from 2 to 828: score 253.3, E = 5.9e-73
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                 G  s        D  Ll + L+ +L++  Ge   E
  gi|2263557     2    -----------GIRS--------DVNLLGRTLgQVLKEQEGEAFFEL 29

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     l  e     D     EL a L  L  a+a  +A+a+     L n
  gi|2263557    30 VERTRALVREVRAGGDDT---ELSAMLAELSGAEAGRLARAFTWYFQLVN 76

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAEE e     R++ +     + E+       +E  l  L  ++  s +E
  gi|2263557    77 LAEEYE-----RVRVLS----SVEG--VRPQSLEQALMDLKAQG-MSAQE 114

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v   L      L +tAHPt   RR +      +   +  Ls   +  +
  gi|2263557   115 VEALLSRLDLGLTFTAHPTEMRRRTVRGHLVEVARAIPELSQPTLAEDAT 164

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + +  A H E  A + t E+RR +Pt  DE++ G+sY+   + +  P
  gi|2263557   165 ERI--AAHVE--AMWSTPELRRLKPTVLDEVKGGLSYMPN-IARALPMLQ 209

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R    A   +        + PL  F+sWmGGDRDG nP vtP  t D
  gi|2263557   210 RDLSRAFERV-YGHSSEAQLPL-SFTSWMGGDRDG-NPFVTPQATHDALA 256

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L R  A  + is +     +ls             E +   +++
  gi|2263557   257 LHRERAREVLISSIAQAYADLS----------QEKEGQEPYRQE------ 290

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                                R +  +vRD                    e v
  gi|2263557   291 ------------LRALHNAVRD--------------------GEPV--- 304

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      e L  LE   + LC  G +  AD  L  lL     FG  Lv LDiR
  gi|2263557   305 --ELLPRLEALHRRLCAEGQRRSADQLLTPLLTVARVFGQHLVSLDIREH 352

                    seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    s      + A+ +  ++  +Y   +E  RqE L  EL+ +RPL ++  P
  gi|2263557   353 SAQTGAAVAALLKAAGVENdYEALAEHARQEVLTRELRSRRPLWPAGEPF 402

                    tEEvkDvldafr.vLA...ELPiDsFGaYiismataPsDvLAvELLqREC
                     E ++  ++ +r+v A ++ +   +FG Yi+sma + sDvL   +L RE
  gi|2263557   403 PETLETAIGPIRqVQAatrQVGPRAFGRYIVSMAESVSDVLEPLILAREV 452

                    gvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri.dGKqevmvGYs
                    g + +L+ vPLFE L DL+ AP  v  L si  Y+  ++   qe+m+GYs
  gi|2263557   453 GFR-ALP-VPLFETLDDLQRAPQVVWELLSIPEYRAALgSDVQEIMLGYS 500
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                    DsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPt
                    Ds KDAG l+A W L  Aq  i  v ++ Gv+   FHGRG  +GRGGGP
  gi|2263557   501 DSNKDAGFLAANWALHEAQRAISEVCRRAGVRWRFFHGRGTSIGRGGGPA 550

                    HLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHG
                      AiL qP  ti+  lR+t qGE +   +    L  r L       L
  gi|2263557   551 SRAILGQPAGTIDAGLRITEQGEALADKYSHPVLARRNLEQALYGVLLAA 600

                    mnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYG
                      P v+P   W + m+  A      YR++v  +P F  +F   tP  E
  gi|2263557   601 ARPAVAPPEAWTRGMDTAARASAAAYRALV-DDPGFLPFFEAVTPIHEIA 649

                    kmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAi
                    ++ni sRP +R  +  +  LRAiPW+  Wtq R  LP W G+
  gi|2263557   650 RLNIASRPVRRPGAPTLGNLRAIPWVMCWTQNRANLPGWYGLHEGL---- 695

                    dKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEe
                          +   +EmY++WPFFR  lD   m  AK DP i   +D+ L
  gi|2263557   696 --STLGVDLAREMYRDWPFFRTVLDNAQMSLAKSDPLI---FDEYLRLMG 740

                    LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLn
                     +P   +L++ Y+ t  l+  + G   l+ G+P LK  + LR++Yi  +
  gi|2263557   741 EHPLATQLKAAYQATVALVQDVVG-APLMAGEPRLKESIALRNPYIDPIH 789

                    vfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPG
                     +q   L+R R            sKE   ++
  gi|2263557   790 RIQVELLRRSR------------SKEGGLDE------------------- 808

                    LEDtLiLtmKGiAAGmqntG<-*
                     E  L+L ++GiAAG+ ntG
  gi|2263557   809 FEVPLLLSIQGIAAGVRNTG    828

gi|271962867|ref|YP_003337063.1|: domain 1 of 1, from 2 to 879: score 252.6, E = 9.4e-73
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       s  A   +     v e  + ++ D  Ll   L+ ++ +  G+dL
  gi|2719628     2    SAIAHHQAERSSAVTEMPDELRADVRLLGELLgQVIAEYGGDDLLAD 48

                    vqECYE.lsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    v      + A   GK     ++E+ a +       a+ +A+a+     LA
  gi|2719628    49 VERLRKaVIAARRGK---VSVDEITAMVAEWPVERAVQIARAFTCYFHLA 95

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    nLAEE    +R R  + +          t E  + E l + v  l    e
  gi|2719628    96 NLAEE---HFRIRTLRVR---------DTGEEPLPESLAQAVQEL--GGE 131

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                     v e +       vltAHPt + RR+++    Ri   La     +    +
  gi|2719628   132 RVTELVEGLRLHPVLTAHPTEARRRAVVTAIQRISGQLAAYNSPERGAAE 181

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    + E    L  Ei   +Rt  +R ++  P DE+R  m+ + Et+++ vP
  gi|2719628   182 RAETRRRLLEEIDLLWRTSQLRSTKLDPLDEVRTAMAAFDETLFRVVPLV 231

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                     R  D AL   G   R P   P i++ sW+GGDRDG nP vt  vtRD
  gi|2719628   232 YRSLDAALGE-GTGTREPLARPFIRYGSWIGGDRDG-NPNVTAKVTRDAV 279

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    L+          +    +   l +         R       a  d
  gi|2719628   280 LIQAEHVLIALENATHRIARTLTLTAGYTPASPRLRAALTAAEND--HPE 327

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                     +       P+EP R  L  v  ++  tR R   L             y
  gi|2719628   328 LVSEMATRSPQEPHRQWLLFVAARIVATRQRGLDL------------AYR 365

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                      Ee L  L     sL   G    A G L  l+ qv tFG  L  L++Rq
  gi|2719628   366 SPEELLGDLRTAQESLVAAGAERQAYGELQHLIWQVETFGFHLAELEVRQ 415

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                     s+ +   l                         aEL   R    s+  +
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  gi|2719628   416 HSQVHAAAL------------------------AELAAGR---TSE--R 435

                   tEEvkDvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLq.RECgv
                   t+Ev   + ++  + E+  + +   Y++s + +  D+ Av  L +   g
  gi|2719628   436 TDEVLATIRTIGWIQErYGVTACSRYVVSFTRSADDIAAVYALAgHALGD 485

                   kqt.LrvvPLFEkLADLeAAPAavekLFsiDWYinri..dGKq.evmvGY
                   k ++L vvPLFE  ADL  AP  +  +  i     r+  +G+  evm+GY
  gi|2719628   486 KAPqLDVVPLFESGADLANAPGVLSGMLEIPGIQQRLaaNGRRlEVMLGY 535

                   sDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGP
                   sDs K+ G  +A  +LY AqE ++  A ++ v+L+lFHGRGG  GRGGGP
  gi|2719628   536 SDSAKELGPAAATLKLYEAQEALAAWAAEHDVRLTLFHGRGGALGRGGGP 585

                   tHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEH
                      A+L+q P  + G  +vt qGEvi   +G   +  r +   t A L
  gi|2719628   586 ANRAVLAQAPGSVGGRFKVTEQGEVIFARYGHAAIARRHMEQVTSAVL-L 634

                   GmnPPvsPkPE.....WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAt
                      P +  +  +  +++R + e++A      YRs+    P F E+F l
  gi|2719628   635 ASTPSIEARTAeaagrFRGMAEQVASASEKAYRSL-TEAPGFPEWFSLVS 683

                   PElEYGkmniGsRPaKRkPsG..GiesLRAiPWiFaWtqtRFHLPvWLGv
                   P  E G + +GsRPa+R  + ++ ++ LRAiPW+FaW qtR  LP W G+
  gi|2719628   684 PLEEIGSLRLGSRPARRGLGAprSLDDLRAIPWVFAWAQTRVNLPGWYGL 733

                   GAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLy
                   G   +  i      l  L+  Y+eWP F   lD +Em  AK D  iAa y
  gi|2719628   734 GSGLQAVISES--GLDELRAAYREWPLFASLLDNVEMSLAKTDRDIAARY 781

                   DkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLR
                     L   ++   F +++  +Y  t+ l+L+i GH  lLE    L   + LR
  gi|2719628   782 LALGGRDD---FVEQVLREYDLTRRLVLEITGHSRLLENRRVLSRAVQLR 828

                   dsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLn
                   d+Y+  L  +q   L R+R               Ad+          L
  gi|2719628   829 DPYVDALSHLQLRALSRLR----------------ADDG---------LS 853

                   ptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     e+    L   L+L + G+AAG+qntG
  gi|2719628   854 --EEERERLSTLLLLSVNGVAAGLQNTG    879

gi|291295381|ref|YP_003506779.1|: domain 1 of 1, from 13 to 892: score 252.0, E = 1.4e-72
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       +D   R+L  GK                        L G+ + E
  gi|2912953    13    EVDVLGRAL--GKAI--------------------RTLSGPRIFELE 37

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       El          +  + L   + +L  ++a  + +a++    L nL
  gi|2912953    38 EQVRELTKSLRQGYSLEARQQLLEIVRGLSLSEAENMVRAFSTYFHLVNL 87

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnK....s
                   AEE    +R R+ + +      E + t  +   E +  Lv  l K+++ s
  gi|2912953    88 AEE---RHRVRVNRER------EKNSTPGAPRGESFLALVGAL-KqqglS 127

                   PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                    +   + L      L +tAHPt   RR        i   L  L+  D+t
  gi|2912953   128 YDQTVDLLSRLRLHLTFTAHPTETRRRTQRHHINEIEKLLDSLYLDDLTA 177

                   eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                        +   L   +   + t E+R+++P   DE++ G+ Yi  t+Wk vP
  gi|2912953   178 AADSSV---LDARVALLWGTSELRKSRPSVEDEVKGGLFYITYTLWKAVP 224

                   KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                   + +   + A+       R P   P + F sW+GGDRDG nP v PEvt
  gi|2912953   225 RLVDGLERAVEA--HYGRRPNLSPPLVFRSWIGGDRDG-NPNVLPEVTGW 271

                   vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                       aR  A   +++ v+ L+ +ls+    ++ Rv      r a  d+
  gi|2912953   272 AQAYARETALRRFVEDVDSLIRDLSL----SDERVTITHELRLALEDHAK 317
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                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                    +  +    q    EPYR      R KL       R LL
  gi|2912953   318 RLALPERFQ---GEPYRQFGMGLRYKL-------RALLGE-----QPGPG 352

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y +  eF+  L    +sL + G  +iA   L  +      FGL Lv LD+
  gi|2912953   353 YNNTAEFVSDLGKAERSLEQLGLGAIARACLKPIRLNAEAFGLDLVSLDL 402

                    RqEseRqtDvlDAittHLeiG....sYReWsEeKRqEWLlaELkGKRPLl
                    R Es   t   +A  + L iG+ ++ Y   + ++R   L  EL   RPL
  gi|2912953   403 REESRALT---EAAAELLKIGgvheQYAALPPQQREALLTRELATARPLA 449

                    gsDL.PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLq
                    +   +P+   ++  l+a+r        + Ga ++sm+  PsD L v LL
  gi|2912953   450 PVGYrPQSKSLQTALEALR-----QWKARGAHVVSMTHYPSDLLEVMLLA 494

                    RECgvkq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK.
                    RE g+ ++++  +  vvPLFE L DL+ AP  v++L     ++ +++G++
  gi|2912953   495 REVGLYRpgralPFDVVPLFETLGDLQNAPEVVARLLDNPVFRAHVQGRg 544

                    .qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                    + evm+GYsDs KDAG l+A W LY+AqE i KvA++ Gv +  FHGRG
  gi|2912953   545 gLEVMIGYSDSNKDAGFLAANWALYQAQEAITKVARERGVPVYYFHGRGT 594

                    tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                       RGGG    Ai s PP t+   +R t qGE +   +   +L +r L
  gi|2912953   595 STARGGGTAGRAIASLPPGTVGSRMRLTEQGEALADRYAHPELAYRNLEQ 644

                    F......tAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPR
                       +   + A    G   P  PkPEW + me+ A   t  YR + ++ P
  gi|2912953   645 MlyhmalASARDLYGQAEP--PKPEWLEAMERAAERSTQVYRELLLR-PG 691

                    FvEYFRlAtPElEYGkmniGsRPaKRk.PsGGiesLRAiPWiFaWtqtRF
                    F E++   tP  E G +ni sRP  R +    i+ LRAiPW+ +Wtq R
  gi|2912953   692 FFEFYEQLTPIREIGALNIASRPVYRSgRVREIKDLRAIPWVMSWTQVRL 741

                    HLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                     LP W G+    +         l   +Em+++WPFF  tlD   +  AK
  gi|2912953   742 LLPGWYGLAEGLQEI------PLALRQEMFQQWPFFATTLDSAAIALAKA 785

                    DPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                    D GiA  y +L+  E    F  ++   ++ tk  +L+      lL   P
  gi|2912953   786 DLGIAREYLRLVKPELAERFFPDIARSFEQTKT-ILEETFQSTLLFKHPV 834

                    LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                    L  +  LR++Y+  +  +q   L R     y+ t+ P+     A E
  gi|2912953   835 LARQTELRNPYVDPISLVQVELLER-----YRRTP-PE-----APER--- 870

                    adeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                  GLE  L+L + GiAAG+ n G
  gi|2912953   871 --------------TGLERALMLSLLGIAAGLRNAG    892

gi|227506616|ref|ZP_03936665.1|: domain 1 of 1, from 37 to 918: score 251.4, E = 2.2e-72
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +D  L +L        + L e+D  Ll  F ++       +   +
  gi|2275066    37    DMDLCLHILR-------DVLGEFDEKLLTVFDEVRLNAVNASTAHFA 76

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    q       +  G +D   L+    k+ ++d  D  l+A+a+     LAnL
  gi|2275066    77 Q-----MVDAQGTED-DGLNKAVEKINGMDLPDMQLLARAFATYFHLANL 120

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     EE    yR  +  ++  +  +        ++   + kL      sP+
  gi|2275066   121 CEE---NYRVSVLHQRECEVEESNPVDPVNELTCAYHKLLTEM--SPAQA 165

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     e L       v+tAHPt + R+++  K  Ri   L++     +   DK+
  gi|2275066   166 KELLNKLEFHPVFTAHPTEARRKAVAGKIRRISKLLSK--HNRLGGSDKR 213

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    E    L  Ei A  Rt  i   +PtP +E    +  +  t+++ +P   R
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  gi|2275066   214 ENYRRLYNEIDALLRTSPIALKKPTPVEEADTILDIFDATLFNTIPLVYR 263

                    RvDtAL..KniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDv
                    R D  L +K  G+   +P   P   +  sW+G DRDG nP vt  v R v
  gi|2275066   264 RFDDWLlgKKAGL---VPPRCPaFFHPGSWIGSDRDG-NPNVTAKVSRQV 309

                    CLLaRmmAanlYisqvEDLmFElsmWRC.ndELRvR...AEElyrtaard
                       ++   +n  +  +E+   E+   +C   E R  +++ E l    ++
  gi|2275066   310 A--SKF--SNHVLKALEERTREVG--KClTMETRTTppsVELLELWNRQR 353

                    kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                     +     E    v   EP R ++  + D+L  t  R   L+
  gi|2275066   354 EMSEQLTENASDVSNSEPHRAVMLVMADRLHHTISRNTDLM--------- 394

                    eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                       y   EeF+E L +  +sL e GD   A G L Dl+ q  tFG  +v
  gi|2275066   395 ---YHSCEEFIEDLRIVQRSLAEAGDARAAYGPLQDLIWQAQTFGFHMVE 441

                    LDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlg
                    ++ Rq s  +   l+ i +H                    L+G R   g
  gi|2275066   442 MEFRQHSLVHSRALEDIREH--------------------GLHGER---G 468

                    sDLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvEL
                    +  P+t E   vld+fr L  + +++++ +   Yiis a +   v  v
  gi|2275066   469 PLQPMTRE---VLDTFRALGAIQkrngMRAARRYIISFAKSAQHVRDVFE 515

                    LqRECgvk....qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG.
                    L R    ++++  t+ v+PLFE+L DL+     +e +  i     r+  +
  gi|2275066   516 LNRLAFAHpqdaPTIDVIPLFEQLEDLQNSVNVLEEIIKIPEVQARLKAt 565

                    ..KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    ++K evm+GYsDs KDAG  sA   L  AqE i++ AK++ + L+lFHGR
  gi|2275066   566 grKMEVMLGYSDSSKDAGPTSATLALHSAQERIAQWAKDHDIDLTLFHGR 615

                    GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                    GG vGRGGGP   A+L+qP   +n   + t qGEvi   +G   L  r L
  gi|2275066   616 GGAVGRGGGPANRAVLAQPVGSVNCRFKLTEQGEVIFARYGNPILAIRHL 665

                    qRFtAAtLEHGmnPPvsPkPEWRkLmeemAv...vAtEEYRsvvvKEPRF
                       +AAtL            E  +   +mA + +vA        ++   F
  gi|2275066   666 ESVAAATLLQSAPSVEKTNTEMTHKYADMAQkldVAAHNRFIDLLQTDDF 715

                    vEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqtRFH
                      +F   tP  E G + iGsRPaKR  + + ++ LR iPW+F+W q R
  gi|2275066   716 TPWFSTVTPLSEIGLLPIGSRPAKRGLGAkSLDDLRTIPWVFSWAQARIN 765

                    LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                    L  W G+G A           l  L+  Y+eWP F   +D +Em  AK D
  gi|2275066   766 LAAWYGLGTACEK-----FGDLETLRRAYEEWPLFSTFIDNIEMSLAKTD 810

                    PGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                      iA +y  L   E+L    +++  + + t++++L+i G k  L     L
  gi|2275066   811 ERIARMYLSLGDREDLS---DKVLSEMQLTRKWVLQIVGDKWPLQHRHVL 857

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                     q +R+R +Y+  L v+q   L ++R          ++ KE   E   +
  gi|2275066   858 GQAIRVRSPYVDALSVIQSLALHKLRN---------KVDKEELSES--QQ 896

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +e + L             + t+ G+AAG+qntG
  gi|2275066   897 AEFIYLI-------------LCTVSGVAAGLQNTG    918

gi|71065696|ref|YP_264423.1|: domain 1 of 1, from 2 to 926: score 249.6, E = 7.6e-72
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                        i      +   ++s           Ll  FL+D +    Ge+
  gi|7106569     2    TINNH---ILRERIS-----------LLGSFLgDAISRQTGEQTLHT 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +        +          + L   + sLd      v ++++    LAn
  gi|7106569    35 IEILRKGFIQQRREPNEAHKQQLIDFIASLDNQALKNVIRSFSIYFFLAN 84
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                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                L EE  l   R   + +  + + E+s         tl     +    P+
gi|7106569    85 LSEENYLREQRHTLRMQ-SEHSWEGS------FRRTLLECRERN-IEPAQ 126

                vFeALKnqsvDLvltAHPtqsvRRs...LLqKnaRiRnCLaqLsAKDvtv
                + e +       v+tAHPt + RR + +LLq        L
gi|7106569   127 MQELIEQLKFIPVFTAHPTEARRRTtmnLLQSLFTHSDALNNFAKNSFAY 176

                eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                e  k   E     i   +  DE+R  +P   DE+  G+ Y+   +++ +P
gi|7106569   177 EQAK---EQTAQTIDLLWSSDEVRTRKPLVYDEINNGLHYFNASLFNAIP 223

                KFLRRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtR
                K  R +  A+  i   E + Y  P  + F sW+GGDRDG      P vt
gi|7106569   224 KVYRNIKDAIVEI-YPELIDYPLPaFMSFGSWIGGDRDG-----NPFVTH 267

                DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE.Elyrtaardk
                D   +a +m a   +     L+  l      ++  v  E+++y     +
gi|7106569   268 DTTEMAVLMHADAVLRHYQVLLKKLRRQLIHSDTIVTIEpDVY----AK- 312

                vvKyYiEFWKqvPP.......tEPYRviLGdvRDKLYntRERaRHLLAtG
                 +  YiE  + v   + ++ ++EPYR +L  +  K+  t      +  +G
gi|7106569   313 -IESYIELDRRVFDynlddygNEPYRRLLSLILSKVKAT---NYLIQSKG 358

                iseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstF
                    +    y +  e LE L +  +s+ +  D +  +G LLD++R v t
gi|7106569   359 SDSEAKKDAYANPQELLEDLRIIRQSV-NTHDTAHGEGLLLDVIRLVKTC 407

                GLsLvKLDiRqEseRqtDvl.DAittHLeiGsYReWsEeKRqEWLlaEL.
                G  L  LDiRqEs  +  v+ D      ++  Y    E  Rq WL   L+
gi|7106569   408 GFHLAALDIRQESSYHSGVIaDIFANAANLPDYQTLNETERQQWLTRLLe 457

                kGKRPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismataP
                k   PL+  D   t+  ++ l  ++ +A L +  + D+FG+Y+ism+
gi|7106569   458 KPGTPLIYTD-NLTDKTREQLALMNSVATLRklvgQDTFGSYVISMTNNA 506

                sDvLAvELLqR...ECgvkqt......LrvvPLFEkLADLeAAPAavekL
                s  L v LL R  + C v   ++ + +L+v PLFE + DL+     +  +
gi|7106569   507 SQLLEVLLLMRfagLCRVDDKgqlsadLPVAPLFETIEDLKNIDKILPAV 556

                FsiDWYi...nridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvA
                     Y++   + d  qe+m+GYsDs KD G +  AWqLY Aq  i ++A
gi|7106569   557 LDNPLYRgllQHSDNTQEIMLGYSDSSKDGGIITSAWQLYSAQQTINRIA 606

                KkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviE
                 +yG+K  lFHGRGG v RGGG tH Ai +qP  t++G ++vt qGEv+
gi|7106569   607 EEYGIKTRLFHGRGGSVSRGGGSTHKAIAAQPAGTLHGQIKVTEQGEVLY 656

                fsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAt
                  +   +     L      tL       v   PE +++  L  ++A v
gi|7106569   657 AKYANTDTAVFELTMGITGTLKACSSRFVVQPPElpqYEALFARLADVGE 706

                EEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPs.GGiesLRA
                  YR +      F E++  AtP  E   +niGsRPa R  +    ++LRA
gi|7106569   707 QRYRKLTDHTEGFYEFYSQATPVAEISLLNIGSRPAHRNKGlPSKTTLRA 756

                iPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRv
                iPW+F W   RF LP W GvG A    ++ D      +kEm + WPFF v
gi|7106569   757 IPWVFGWSLARFTLPAWYGVGSALD-SVKEDE---ALMKEMNDCWPFFNV 802

                tlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLk
                 +  +Em F K D  iA  y +L   E L+ +    + d+ + t   L
gi|7106569   803 FISNIEMAFTKSDMSIAHAYSQLCDDEMLREqIMTAVTDEHELTYSGLNS 852

                iAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrP
                +   + lL     L   l  R++Y+   n +q   LKR R
gi|7106569   853 LLNQQSLLSSQQNLSASLEWRNAYLDPTNYIQIELLKRARQ--------- 893

                hlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<
                   KE   +      +   L         +ED Li  +  +AAG+ ntG
gi|7106569   894 ---KEASGDA-----NHGDLD--------VEDPLIRSINALAAGLRNTG  926
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                  -*

  gi|7106569     -    -

gi|258545813|ref|ZP_05706047.1|: domain 1 of 1, from 11 to 924: score 249.5, E = 8.2e-72
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkE.a
                      +   +RlL+ G      k+ie  A       + Lq +  e L+ ++
  gi|2585458    11    -LRTRIRLLA-GLLG---KVIERQA-----GAETLQTI--EYLRQgF 45

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  + E            D+++   L   + +Ld      v + ++    LAn
  gi|2585458    46 IEE--------RNNPDPERRAALMRTIAALDNDRLKHVIRGFSLYFALAN 87

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  LAEE  l  +R   + +       +    E     tl++       sPe
  gi|2585458    88 LAEEDLLRQKRADLRAR-------GGELWEGSFRHTLQQCRDND-LSPEQ 129

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRi.RnCLaqLsAKDvtveD
                    e +       v+tAHPt + RR  +     i R C +   A +  +
  gi|2585458   130 LAELIGQLRFIPVFTAHPTEARRRTTMSVLQEIyRHCATLDHAPENSPAW 179

                  KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                   + + E     i   +  DE+R  +    DE+  G+ Y+   +++ +P+
  gi|2585458   180 NHAVAETADL-IDLLWSSDEVRSRKTLVYDEINNGLHYFNVSLFQAIPQV 228

                  LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                   R    AL  i          PL++F sW+GGDRDG nP vt   t
  gi|2585458   229 YRNLRSALNDIYPELEKMVLPPLLRFGSWIGGDRDG-NPFVTHQTTEQAV 277

                  LLaRmmAanlYisqvED....LmFElsmWRCndELRvRAEElyrtaardk
                  L+        Y  q+   +++L+   s+      + +R E   r
  gi|2585458   278 LMHADNVLRYYSKQLKHlrkrLLHCASIIAIDPAIDARNEHYARLGVTV- 326

                  vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                     y  E +     +EPYR +L  +R K+  t    R +   G  + + e
  gi|2585458   327 -FDYNPEDYN----NEPYRRLLALMRAKIQHT---NRYIQSMGEDQAAAE 368

                  AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                    y + E FL+ L L   +L +  D   A G + Dl+R v   G  +  L
  gi|2585458   369 HAYPNAEAFLDDLILIRNALKQ-HDPEQARGDIQDLIRLVRSCGFHMASL 417

                  DiRqEseRqtDvlDAittHL.eiGsYReWsEeKRqEWL..laELkGKRPL
                  DiRqEs  +t v+  +  H +++  Y    E  Rq  L++l    G   L
  gi|2585458   418 DIRQESTWHTNVVADLFAHApNLPDYHALDEAGRQQALsqLIAAPGTPLL 467

                  lgsDL.PktEEvkDvldafrvLAELP.iDsFGaYiismataPsDvLAvEL
                  +   L+P t E    + ++  L EL +  +FG+Yiism+   s +L v
  gi|2585458   468 FEQNLsPETQEQLALMRTVARLRELVgARTFGSYIISMTNRTSHILEVLF 517

                  LqRECgv.........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYin
                  L R  g++++++++++  +L++ PLFE + DL+     + +L     Y+
  gi|2585458   518 LMRFAGLsgqdeqgrpYAALPIAPLFETIEDLKNIDTILPQLLDNPTYRA 567

                  ridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                   +  ++++qe+m+GYsDs KD G l  AWqLY+Aq  i  +A++y +K
  gi|2585458   568 LLTNQhdtQEIMLGYSDSSKDGGILTSAWQLYRAQQTILDIARRYHIKTR 617

                  lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGE.En
                  lFHGRGG v RGGG tH Ai +qPP t++G ++ t qGEv+   +  +E
  gi|2585458   618 LFHGRGGSVSRGGGSTHHAIAAQPPGTLQGEIKFTEQGEVLYAKYANpET 667

                  LCFrsLqRFtAAtLEHGmnPPvsPk..PEWRkLmeemAvvAtEEYRsvvv
                    +      t A           P +   + +L+e++A      YR +
  gi|2585458   668 AVYELTMGITGALKASSTRFAKTPAklAQYEQLVERLADACENRYRDLTD 717

                  KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi.esLRAiPWiFaWt
                  +      +F  AtP  E   +niGsRPa R+ +   ++++RAiPW+F W
  gi|2585458   718 RTEGLYQFFADATPVREISLLNIGSRPAHRRKGTPTkQTIRAIPWVFGWS 767

                  qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
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                     RF LP W GvG A   Ai  + + l  + +m ++WPFF   +  +Em
  gi|2585458   768 LARFTLPAWYGVGSALA-AIRPEDQPL--IDDMREQWPFFDAFISNIEMA 814

                    FAKGDPGiAaLyDkLLvaEeLk.PFGksLRdkYvEtkdlLLkiAGHkDlL
                    FAK +P  A  y +L   E L++   + +Rd+Y+ t   L  i     lL
  gi|2585458   815 FAKTEPATAEAYSHLCADEPLRqTVMRAIRDEYQKTLAGLNTILKQNHLL 864

                    EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                    E  P L   lR Rd+Y+  +n +q   L+R R                 +
  gi|2585458   865 EHQPRLAESLRWRDPYLDPINHIQIELLRRSR-----------------A 897

                    EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     ns  a+    +n          D Li  +  +AAG+ ntG
  gi|2585458   898 KNSEDAE----IN----------DPLIRSINALAAGLRNTG    924

gi|20196788|emb|CAC86366.1|: domain 1 of 1, from 1 to 396: score 249.0, E = 1.1e-71
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2019678     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2019678     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2019678     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                           +vDLvltAHPtqs RRsLL+K++RiRnCL+qL+AKD+t +DKk
  gi|2019678     1 -------TVDLVLTAHPTQSLRRSLLKKHTRIRNCLTQLYAKDITEDDKK 43

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    EL+EAL REiqAAFRtDEiRRaqP PqDEmR+Gm YiHEt+WkGvPKFLR
  gi|2019678    44 ELEEALQREIQAAFRTDEIRRAQPAPQDEMRYGMNYIHETIWKGVPKFLR 93

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKniGi ERlPYd+PLikFssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2019678    94 RVDTALKNIGIDERLPYDAPLIKFSSWMGGDRDG-NPRVTPEVTRDVCLL 142

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlYisq+E+LmFElsmWRCndELR+RA+El    a+ kvvK+Y
  gi|2019678   143 ARMMAANLYISQIEELMFELSMWRCNDELRARADELD--GASRKVVKHYT 190

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFW+q+P +EPYRv+L dvRDKLYntRER RHLLAtG+sei+E+A  t+v
  gi|2019678   191 EFWRQIPTNEPYRVVLADVRDKLYNTRERMRHLLATGFSEIPEDATVTDV 240

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                     +FLEPLELCYksLC+ GDk iADGsLLDl+RqvstFGLsL KLDiRqEs
  gi|2019678   241 AKFLEPLELCYKSLCDSGDKTIADGSLLDLMRQVSTFGLSLTKLDIRQES 290

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+t+v+D ittHL+iGsYR+W+EeKRqEWLl+EL+GKRPLl +DLP+ E
  gi|2019678   291 DRHTEVIDTITTHLGIGSYRSWPEEKRQEWLLSELQGKRPLLSPDLPQSE 340

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+D l++frvLAELP DsFG+YiismataPsDvLAvELLqREC+v  +L
  gi|2019678   341 EVADALGTFRVLAELPRDSFGPYIISMATAPSDVLAVELLQRECKVADPL 390

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLF
  gi|2019678   391 PVVPLF---------------------------------------- 396

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|2019678     - ---------------------------------------------- -

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

  gi|2019678     - ---------------------------------------------- -
```

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                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|2019678     - ------------------------------------------------ -

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|2019678     - ------------------------------------------------ -

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|2019678     - ------------------------------------------------ -

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|2019678     - ------------------------------------------------ -

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|2019678     - ------------------------------------------------ -

                  tmKGiAAGmqntG<-*

  gi|2019678     - -------------    -

gi|283782535|ref|YP_003373289.1|: domain 1 of 1, from 37 to 918: score 248.0, E = 2.4e-71
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      +D  L +L        + L e+D  Ll  F D+       +   +
  gi|2837825    37    DMDLCLHILR-------DVLGEFDEKLLAVFDDVRLNAVEASAAHFA 76

                  qEC.YElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  q  +  + A+         L    +kL +++  D+ l+A+a+     LAn
  gi|2837825    77 QMVdAKVTAD-------DGLSKAVSKLNGMNLHDTQLLARAFATYFHLAN 119

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  L EE    yR  +  ++  +  D        ++   + kL      sP+E
  gi|2837825   120 LCEE---NYRVSVLHQRECEVEDSLPVDPVNELTCAYHKLLTEM--SPAE 164

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    e L       v+tAHPt + R+++  K  Ri   L+      +   DK
  gi|2837825   165 AKELLAKLEFHPVFTAHPTEARRKAVAGKIRRISQLLSE--HHRLGGSDK 212

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  +E    L  Ei A  Rt  i   +PtP +E    +  +  t+++ +P
  gi|2837825   213 RENYRRLYNEIDALLRTSPIALKKPTPVEESDTILDIFDATLFDTIPVVY 262

                  RRvDtAL..KniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRD
                  RR D  L +K  G+   +P   P   +  sW+G DRDG nP vt  v R
  gi|2837825   263 RRFDDWLlgKKAGL---VPPRCPaFFHPGSWIGSDRDG-NPNVTAKVSRQ 308

                  vCLLaRmmAanlYisqvEDLmFElsmWRC.ndELRvR...AEElyrtaar
                  v   aR   +   +  +E    E+   +C   E R  +++ E l    ++
  gi|2837825   309 V---ARKF-SDHVLAALENRTREVG--KClTMETRTTppsVELLELWNRQ 352

                  dkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseis
                    +     E    v   EP R ++  + D+L  t  R   L+
  gi|2837825   353 REMSEQLTENASDVSNSEPHRAVMLVMADRLHRTISRDTDLM-------- 394

                  EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                      y   E+F+E L +  +sL e GD   A G L Dl+ q  tFG  +v
  gi|2837825   395 ----YHSCEDFIEDLQIVQRSLAEGGDPRAAYGPLQDLIWQAQTFGFHMV 440

                  KLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLl
                   ++ Rq s  +   l+ i +H                    L+G R
  gi|2837825   441 EMEFRQHSLVHSRALEDIREH--------------------GLHGER--- 467

                  gsDLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvE
                  g+  P+t E   vld+fr L  + +++++ +   Yiis a +   v  v
  gi|2837825   468 GPLQPMTRE---VLDTFRALGAIQkrngMRAARRYIISFAKSAQHVRDVF 514

                  LLqRECgvk....qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
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                     L R    ++++  t+ v+PLFE+L DL+     +e +  i     r+
  gi|2837825   515 ELNRLAFAHpqdaPTIDVIPLFEQLEDLQNSVNVLEEIIKIPEVQARLKA 564

                     ...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                     +++K evm+GYsDs KDAG  sA   L  AqE i+K AKk+ + L+lFHG
  gi|2837825   565 tgrKMEVMLGYSDSSKDAGPTSATLALHSAQERIAKWAKKHDIDLTLFHG 614

                     RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                     RGG vGRGGGP   A+L+qP   +n   + t qGEvi   +G   L  r
  gi|2837825   615 RGGAVGRGGGPANRAVLAQPVGSVNCRFKLTEQGEVIFARYGNPILAIRH 664

                     LqRFtAAtLEHGmnPPvsPkPEWRkLmeemAv...vAtEEYRsvvvKEPR
                     +   + AtL            +  k   +mA + +vA  E     ++
  gi|2837825   665 VESVASATLLQSSPSVEKTNTDMTKKYADMAAkldVAAHERFLDLLQTDD 714

                     FvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqtRF
                     F  +F   tP  E G + iGsRPaKR  + + ++ LR iPW+F+W q R
  gi|2837825   715 FTPWFSTVTPLSEIGLLPIGSRPAKRGLGAkSLDDLRTIPWVFSWAQARI 764

                     HLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                      L  W G+G A           l  L+  Y+eWP F   +D +Em  AK
  gi|2837825   765 NLAAWYGLGTACEK-----FGDLETLRRAYEEWPLFSTFIDNIEMSLAKT 809

                     DPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                     D  iA +y  L   E+L    +++  + + t++++L+i   k  L
  gi|2837825   810 DERIARMYLSLGDREDLS---DKVLSEMQLTRKWVLQIVDDKWPLQHRHV 856

                     LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                     L q +R+R +Y+  L v+q   L ++R          ++ KE   E   +
  gi|2837825   857 LGQAIRVRSPYVDALSVIQSLALHKLRN---------KVDKEELSES--Q 895

                     adeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      +e + L              + t+ G+AAG+qntG
  gi|2837825   896 QAEFIYLI-------------LCTVSGVAAGLQNTG    918

gi|38233712|ref|NP_939479.1|: domain 1 of 1, from 1 to 902: score 247.7, E = 2.9e-71
                     *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                               +s   + ++ D  Ll + L+ ++    Ge++ E
  gi|3823371     1    ---------MTAAIS---DRVREDIRLLGRVLgRVIAQQEGEEVYEL 35

                     vqECYElsAeY.EGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                     v     ++ + + G  D+   e+L      Ld + + lvA+a++    LA
  gi|3823371    36 VEATRRMAFDVsHGDADP---EDLMVIFRDLDITKTNLVARAFSYFALLA 82

                     nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                     nL E+                 D+ s   +  +  t+ kL   +  s +
  gi|3823371    83 NLVEDL-----------------DDESVEADVSLRKTFAKLKREG-VSAA 114

                     EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                     +    ++   v  vltAHPt   RR +   ++Ri+    qL        D
  gi|3823371   115 DAASVIRSAEVAPVLTAHPTETRRRTVFDTQTRIK----QLLKDAHHGGD 160

                     KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                      + ++  +   +   + t  iR a+Pt  DE+  G+ Y+   + + vP
  gi|3823371   161 MQVIEQEMYLRMTLLWQTALIRIARPTLEDEIDVGLRYYKKSLLEQVPAL 210

                     LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                      R +   ++       lP d+ +++  sW+GGD DG nP v
  gi|3823371   211 NRSIRHSMRET-FGLQLP-DIAVMRPGSWIGGDHDG-NPYVNARTLTYAT 257

                     LLaRmmAanlYisqvEDLmFElsm....WRCndELRvRAEElyrtaardk
                       a    a  Y++q+ +L  Els++++   C  EL + AE       +
  gi|3823371   258 RQAAKTVARYYVEQLGELERELSLsdrySSCSKELLALAEASGNNWESR- 306

                     vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                                   EPYR  +  +R ++    +       t     s
  gi|3823371   307 -------------VDEPYRRAVYGMRARMKSNVDALERPEKTAGKKSSKR 343

                     AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                       y   EeFL  L++  +sL    D viAD  L  +   v tFG  L  L
  gi|3823371   344 TPYATPEEFLRDLDVIDRSLRAHNDDVIADDRLARIRSAVTTFGFHLYTL 393
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                    DiRqEseRqtDvlD...AittHLeiGs.YReWsEeKRqEWLlaELkGKRP
                    DiRq se    v+++  A  + +  G +Y e +E  + E L+ EL+  RP
  gi|3823371   394 DIRQNSESFEAVIEevfAAARRVPGGKrYSELAEAEKVELLIQELQTPRP 443

                    .LlgsDLPk........tEEvkDvldafrvLAELPiDsFGaYiismataP
                     L++  L  ++  + ++t E+   l a + + +  + s    iism+ +
  gi|3823371   444 lLFPGALEVedafsadtTKELGIFLAAAQAVRDFGSRSIAHCIISMTATV 493

                    sDvLAvELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                    sD+L   +L +E g++  + vvPLFE + DL+   A +  L+s  +Y+ +
  gi|3823371   494 SDILEPMVLLKEVGLRD-VDVVPLFETIDDLRCGAAILRELWSHPFYREH 542

                    idGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                    +  +++ qevm+GYsDs KD G l A W LY A   ++   +++ + L l
  gi|3823371   543 LRARgdiQEVMLGYSDSNKDGGYLQANWALYDAELGLVELCREHNIELRL 592

                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                     HGRGG vGRGGGPt  AiL+qP   + Gs+R+t qGEvi   +G  +
  gi|3823371   593 AHGRGGAVGRGGGPTYDAILAQPKGAVSGSVRITEQGEVISAKYGAPETA 642

                    FrsLqRFtAAtLEHGm..nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKE
                     r L  F    LE  + +  P++       +m ++A      Y  +v  +
  gi|3823371   643 RRHLEAFVSGALEASLldTEPIADPDRAYAIMRDLAGFSGQRYQELV-GD 691

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
                    P F+EYF   tP  E G +n+GsRPa Rk    i  LRAiPW+ +W q R
  gi|3823371   692 PGFIEYFTQSTPLHEIGELNLGSRPAARKQTTAISDLRAIPWVLSWSQSR 741

                    FHLPvWLGvGAA...FKhAi.dKDiK.nlqkLkEmYkeWPFFRvtlDLlE
                      +P W GvG A ++F  A+++KD  +  q L+++Y +WPFFR  +  +
  gi|3823371   742 TNIPGWFGVGSAvsrFVSAVpEKDREsRWQELRDLYATWPFFRSVMSNMA 791

                    mvFAKGDPGiAaLyDkLLvaEeLkPFGksLRd.kYvEtkdlLLkiAGHkD
                     v AK +  +A Ly +L+   e+      L +++++ t+   L i G
  gi|3823371   792 QVMAKAEISLARLYADLVDDPEVADRIYALIAeEFELTRRAYLAITGNEA 841

                    lLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiR..DPsykvtlrPhlsK
                    l+         l+ R +Y+  Ln +q   L+R R++D ++ v      sK
  gi|3823371   842 LVSENQRQARSLKRRYPYLLPLNAIQLELLRRYRggDDQFLV------SK 885

                    EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                                t+ +tm G+A  + n G
  gi|3823371   886 ----------------------------TIQVTMNGLATALRNAG    902

gi|269921664|ref|ZP_06170573.1|: domain 1 of 1, from 1 to 902: score 246.8, E = 5.3e-71
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                              + v    + d++L e   LL     +++ D  G+dL + +
  gi|2699216     1    -------MPVSAEPAADDRLREEVRLLGGLLGEVIRDEGGQDLYDRI 40

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          s  Y     ++   EL   L  L   Da+ +A+ +     LAn+
  gi|2699216    41 EAVRVASVGYHRHSGARGSAELERLLSDLSLDDAVGLAHGFAVFSLLANV 90

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+   A +RR + +     a+ a   t    E  l +L   + +s e+
  gi|2699216    91 AEDR--AGKRRARSQT----AEGARPDTP---EGSLARLAQAG-RSVEDA 130

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L    +  vltAHP    R+s++ + a +   L      D+     +
  gi|2699216   131 RTLLSEALISPVLTAHPSEVRRKSVIDRIAAVSDLLDACDRDDLACAP-E 179

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +   L R     + t  +R +    qDE+   +s++     k  P  L
  gi|2699216   180 VMVNGLRRQTVILWATRLVRTTGLVVQDEIDTVVSFLERVFLKVAPEQL- 228

                    RvDtALKniGinERl..PYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                            i    Rl+ P   P i+  +W+GGDRDG nP v     R
  gi|2699216   229 --------IDWRRRLnaPDLKPFIRIGAWVGGDRDG-NPNVDAAALRAAF 269

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
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                          Y++ v  L  Els+      L +    l+  aa+
  gi|2699216   270 ATPAKAVLRHYLEAVNTLGAELSL---SGSLAAVSPALQALAASS----- 311

                      YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                                 EPYR  L ++  +L  t     H L tG    +  A +
  gi|2699216   312 --GDGSPHRADEPYRRALSQIYARLSAT-----HPLLTG-ETAPRPAPFA 353

                      k.....vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                       ++ ++ + F + L +   sL      v AD  L  l+  v  FG  +
  gi|2699216   354 AppydgPDAFRDDLAVLQDSLVASHGAVFADDGLSRLIATVDVFGFHMAT 403

                      LDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLl
                      LD+Rq s+ +  v+  + +  ++ + Y    Ee R   L aEL   R L+
  gi|2699216   404 LDLRQNSDVHARVVGHLLRVAGVCpDYAALDEEARIALLSAELAAPRLLF 453

                      gsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAv
                       +      Ev      ++  AE    +FG++  ++ i+s + a sD L v
  gi|2699216   454 SPYEDYDPEVLKERAILQAAAE-ALRTFGPqairtHIVSKTDAASDLLEV 502

                      ELLqRECgvkq.......tLrvvPLFEkLADLeAAPAavekLFs..iDWY
                       LL +E g+ +++++ + +++  PLFE + DL+AA  ++ +L  ++
  gi|2699216   503 YLLLKEVGLYRhddpatcPIQAAPLFETIDDLRAAKPTLSRLLQepSALA 552

                      inridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                      + r  G qevm+GYsDs KD   l   W L  A   +  v    Gv+L l
  gi|2699216   553 VARARGVQEVMIGYSDSNKDGSYLTSTWELHEASRALLSVTEAVGVRLQL 602

                      FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                      FHGRGG vGRGGG     ++sqP  t+ G +R+t qGEvi   +GE ++
  gi|2699216   603 FHGRGGAVGRGGGSSFAGVISQPTGTVAGRIRITEQGEVIANKYGEPDVA 652

                      FrsLqRFtAAtLEHGmnPP..vsPkPEWRkLmeemAvvAtEEYRsvvvKE
                       r L   tA tL   + PP++ +           + v     YR++v+
  gi|2699216   653 RRNLDALTAGTLIASLAPPpdEAMTAKHGATASALSVASMAAYRALVYET 702

                      PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
                      P Fv+YFR AtP  E   + iGsRP+ R  s  ie LRAiPW+ +W q R
  gi|2699216   703 PGFVDYFRAATPINEIAELKIGSRPTSRTASSAIEDLRAIPWVLSWSQSR 752

                      FHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAK
                        LP W G+G A +       + +  L+ m  +WPFFR  l  +Em+ AK
  gi|2699216   753 VMLPGWFGFGSAVR------GRDMEELRAMAADWPFFRTLLQNMEMIMAK 796

                      GDPGiAaLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLkiAGHkDlLEG
                       D  iA  y  L+    L  + FG  LR+++  t+d +L i G  DlL G
  gi|2699216   797 SDMTIARRYAGLVPDQALAAsiFG-ALRAEWDRTRDAVLAITGQSDLLGG 845

                      DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                       P L   +RLR +Y+  Ln +q   ++R R                d++
  gi|2699216   846 QPELDRLIRLRMPYVEPLNHVQIELIRRRRS--------------GDDD 880

                      skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                     P + + ++Lt+ G+AAG+ n G
  gi|2699216   881 -----------------PRVREGILLTINGVAAGLRNSG    902

gi|226942050|ref|YP_002797124.1|: domain 1 of 1, from 4 to 907: score 244.6, E = 2.4e-70
                      *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           D  L l              D + l + L +++ +  G+ +
  gi|2269420     4    DFDKDLPL-------------TRDRMRLTRLLaEVVREQVGDAVWQE 37

                      vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                      v     l+        t+ L  L + L  L P     + ++   +  L n
  gi|2269420    38 VEQIPQLACH------TEDLSPLRTHLQQLSPVVLDTLLRSSGLLAQLEN 81

                      LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                      LAE+ +   RR+ ++k        +s      +   l  L   +  + +
  gi|2269420    82 LAEDLHHNRRRKAHRKA-------GSPPQPGSLARALTILREHG-ITADT 123

                      vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                          L    +  vltAHPt   R   L  +  iR  L  L   Dv  +
  gi|2269420   124 LAGLLEYAQIVPVLTAHPTEVQRQTTLDCQRAIRKFLQLLDHPDVDADAE 173
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                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L   L R +   + t +iR  + t +DE+  G++Y   t  +  P
  gi|2269420   174 AALTAKLKRVLLTLWQTADIRPFKLTVKDEIENGIAYHPLTFLDALPALY 223

                    RRv.DtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                     R +D      G    +P      +  sW+GGDRDG nP v  +  R
  gi|2269420   224 GRLeDDIAATFGTRIEIP---NFYRIGSWIGGDRDG-NPFVNADLLRYAL 269

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE.Elyrtaardkvv K
                         +A   Y   +E L  Els+    ++ Rv   + ++  +     +
  gi|2269420   270 SRQAEIAFAHYDYELEGLYRELSL----SDRRVQVSpAVQALSDCSPDTA 315

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                       E       +EPYR  +     +L  t  R R +  +     +E A y
  gi|2269420   316 ISRE-------EEPYRRAIATLLARLAAT-ARERDIPFHSRFGHAEAAPY 357

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     +  e    L    +sL   G   +A G L +l R vs FG  L+ LD R
  gi|2269420   358 RDRHELGADLTAIARSLDTHGSTLLAGGRLRELRRAVSVFGFFLMPLDQR 407

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    q ++     +  +    +   Y    E  ++ WLlaEL   RPL  + +
  gi|2269420   408 QHADLYGAAVAELFARAGQPGYDALDEAGKRAWLLAELAHARPLASPFIE 457

                    ktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvELLqR
                        v+  ld f     L  D +G +  ++ iis +   sD L v LL +
  gi|2269420   458 YSPGVQRELDLFAATRAL-QDRYGEgalpnLIISNCAEASDLLEVALLMK 506

                    ECgv.........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                    E g+ + + +++++    ++PLFE + DLe A   +  LF+i  Y+  +
  gi|2269420   507 ESGLlpleadgrhRARANIIPLFETIEDLEHADTVMRELFAIPLYRDLLA 556

                    GK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                     +++ qevm+GYsDs KD G l   W LY A   ++ v   +Gv++ lFH
  gi|2269420   557 SRqdvQEVMLGYSDSNKDGGYLMSQWALYAAEKRLVAVFDLFGVRIRLFH 606

                    GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                    GRGG vGRGGGP   AiL+qP  t+ G +R+t qGEvi   + +  +  r
  gi|2269420   607 GRGGSVGRGGGPSFDAILAQPAGTVAGQIRITEQGEVIASKYADRTIGQR 656

                    sLqRFtAAtLEHGmnP.PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                     L    AAtLE  + P+P  P  E   +  e+A      YR ++  +  F
  gi|2269420   657 NLEALLAATLEASLVPrPSCPTDE--SVFGELAADSYQAYRQLIETDG-F 703

                    vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                    ++YF  AtP  E  k+niGsRPa Rk    i  LRAiPW+F+W q R  L
  gi|2269420   704 IDYFLAATPINEIAKLNIGSRPASRKTLASISDLRAIPWVFSWMQSRVML 753

                    PvWLGvGAAFKhAidKD.iKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                    P W GvG A    + + +     +L  +++e  FFRv lD +Emv AK D
  gi|2269420   754 PGWYGVGSAMSAFLARHgTTGRDRLAALWQESAFFRVALDNMEMVLAKAD 803

                    PGiAaLyDkLL....vaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                      iAa y  L++++ v E +      +R +++ t+d    i G   lL G
  gi|2269420   804 MQIAAEYASLVpdpaVRERVYGL---IRGEFERTRDAFCAITGQTRLLAG 850

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiR.DPsykvtlrPhlsKEyAdE
                     P L   l  R +Y ttLn +q   L R+R+DP+      P+l   yA
  gi|2269420   851 NPTLARSLAARMPYFTTLNLLQIDGLARLRqDPD-----NPELL--YAIH 893

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +                          t+ G+A G+ n G
  gi|2269420   894 Q-------------------------TINGLATGLRNSG    907

gi|1213341|dbj|BAA05398.1|: domain 1 of 1, from 1 to 384: score 244.2, E = 3.1e-70
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1213341     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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gi|1213341     - ------------------------------------------------ -

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1213341     - ------------------------------------------------ -

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1213341     - ------------------------------------------------ -

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1213341     - ------------------------------------------------ -

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1213341     - ------------------------------------------------ -

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1213341     - ------------------------------------------------ -

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                  FWK +PPtEPYRviLGdvRDKLY tRER+R LL  Gis+i+ eA +t+v
gi|1213341     1 -FWKTIPPTEPYRVILGDVRDKLYHTRERSRQLLSNGISDIPAEATFTNV 49

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                 EeFLEPLELCY+sLC CGD+ iADGsLLD+LRqvstFGLsLvKLDiRqEs
gi|1213341    50 EEFLEPLELCYRSLCACGDRPIADGSLLDFLRQVSTFGLSLVKLDIRQES 99

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                 eR+tDvlDAit+HL+  sYR+WsEe+RqEWLlaEL+GKRPL+g+DLPktE
gi|1213341   100 ERHTDVLDAITKHLDGSSYRDWSEERRQEWLLAELSGKRPLFGPDLPKTE 149

                 EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                 E++Dvld+++v+ ELP+D+FGaYiismat+PsDvLAvELLqREC+vk++L
gi|1213341   150 EIADVLDTLKVISELPSDCFGAYIISMATSPSDVLAVELLQRECHVKKPL 199

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                 rvvPLFEkLADLeAAPAav +LFs+DWY+nri+GKqevm+GYsDsGKDAG
gi|1213341   200 RVVPLFEKLADLEAAPAAVSRLFSLDWYKNRINGKQEVMIGYSDSGKDAG 249

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 RlsAAW LYkAqEE++KvAKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1213341   250 RLSAAWELYKAQEELVKVAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 299

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                 PPDt+nGslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGmnPPvsP
gi|1213341   300 PPDTVNGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMNPPVSP 349

                 kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                 kPEWR L++ mAvvAtEEYRsvv++EPRFvEYFRl
gi|1213341   350 KPEWRALLDAMAVVATEEYRSVVFQEPRFVEYFRL--------------- 384

                 PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

gi|1213341     - ------------------------------------------------ -

                 qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

gi|1213341     - ------------------------------------------------ -

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

gi|1213341     - ------------------------------------------------ -

                 KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

gi|1213341     - ------------------------------------------------ -
```

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                  tmKGiAAGmqntG<-*

  gi|1213341     - -------------    -

gi|1213343|dbj|BAA05396.1|: domain 1 of 1, from 1 to 384: score 243.7, E = 4.6e-70
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1213343     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1213343     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1213343     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1213343     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1213343     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1213343     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1213343     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    FWK +PPtEPYRviLGdvRDKLY tRER+R LL  Gis+i+EeA +t+v
  gi|1213343     1 -FWKTIPPTEPYRVILGDVRDKLYHTRERSRQLLSNGISDIPEEATFTNV 49

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                  E+FLEPLELCY+sLC CGD+ iADG LLD+LRqvstFGLsLv+LDiRqEs
  gi|1213343    50 EQFLEPLELCYRSLCSCGDRPIADGTLLDFLRQVSTFGLSLVRLDIRQES 99

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  eR+tDvlDAit+HL+  sYR+WsEe+RqEWLl+EL+GKRPL+g+DLPktE
  gi|1213343   100 ERHTDVLDAITKHLDGSSYRDWSEERRQEWLLSELSGKRPLFGPDLPKTE 149

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++Dvld+f+v+ ELP+D+FGaYiismat+PsDvLAvELLqREC+vk +L
  gi|1213343   150 EIADVLDTFKVISELPSDCFGAYIISMATSPSDVLAVELLQRECHVKTPL 199

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLeAAPAav +LFs+DWY+nri+GKqevm+GYsDsGKDAG
  gi|1213343   200 RVVPLFEKLADLEAAPAAVSRLFSLDWYKNRINGKQEVMIGYSDSGKDAG 249

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAW LYkAqEE++KvAKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1213343   250 RLSAAWELYKAQEELVKVAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 299

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDt+nGslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGmnPPvsP
  gi|1213343   300 PPDTVNGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMNPPVSP 349

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++ mAvvAtEEYRsvv++EPRFvEYFRl
  gi|1213343   350 KPEWRALLDAMAVVATEEYRSVVFQEPRFVEYFRL--------------- 384

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|1213343     - ---------------------------------------------- -

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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  gi|1213343     - ------------------------------------------------ -

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|1213343     - ------------------------------------------------ -

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1213343     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|1213343     - -------------    -

gi|253999144|ref|YP_003051207.1|: domain 1 of 1, from 20 to 952: score 242.6, E = 9.5e-70
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +      +     s +ekL++     l + L+++++   Ge+  +
  gi|2539991    20    -MVIGEHGMTSRIYSHNEKLLRENIRYLGRVLgEVIKSKEGEETFDR 65

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +      + ++     tk    L   L  L    ai v +a++    L n
  gi|2539991    66 IEAIRTAAVNFHRHGNTKAAKSLEKLLKTLTVEQAIPVIRAFSYFKHLVN 115

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +AE+ +     R    +    a  +  t        l+kL        +E
  gi|2539991   116 IAEDLHAHQQSRLVEDQ----AAPGMLT------HSLQKLAASD-LDAAE 154

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   + +   n  +  vltAHPt   R+s+L  + R    L       v + +
  gi|2539991   155 IGDFFANALISPVLTAHPTEVQRKSILDTE-RALSLLLVEKSNVVSIREA 203

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   +  +  +   i   + t  +R ++ t   E+   +sY+  t  + +P  +
  gi|2539991   204 ERNERMIVGAITTLWQTRILRFSKLTVANEIENALSYYRMTFLQVIPELM 253

                   RRvDtALKniGinERlP.YdvP.LikFssWmGGDRDGknPRvtPEvtRDv
                      +  L+ +      P+Y  P+ ++  sW+GGDRDG nP v
  gi|2539991   254 QDFENDLRHVFADKLSPeYKLPsFLQMGSWIGGDRDG-NPFVNGATLEQA 302

                   CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                    +     A   Y++qvE L  Els       L  R   +  t+a  k+ +
  gi|2539991   303 IIQQSATAFAYYLEQVEALRSELS-------LSTRL--VGVTPALVKLAQ 343

                   yYiE..FWKqvPPtEPYRviLGdvRDKLYntRE...RaRHLLAtGiseis
                      E++  +q    E YR  L  +  +L  t       R  +   is i+
  gi|2539991   344 ASGEqsLHRQ---DETYRLALNGIHARLAQTAKllvNERGDVRREISAIP 390

                   EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                       yt  E  L  + +   sL      ++    L  l++ + tFG  L
  gi|2539991   391 ----YTSAEALLADMNVIAESLQSQQGEALIYPRLGKLIKAIETFGFHLA 436

                   KLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPL
                    +D+Rq s+ +  v+  +    +    Y    E+ + E Ll ELk  R L
  gi|2539991   437 TVDLRQSSDVHELVIKELFLKAGQDfNYATLDEDEKVEVLLEELKQPRLL 486

                   lgsDLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAv
                   + +     E v+  ++ +++ +++ A     +   Yiis + + sD L v
  gi|2539991   487 FSPFQQYSELVQSEMEVLQkargIRAGYGKRAIRQYIISHTETLSDLLEV 536

                   ELLqRECg..........vkqtLrvvPLFEkLADLeAAPAavekLFsiDW
                    LLq+E g  ++  ++ +v+  L +vPLFE +ADL+ AP  + +  s+
  gi|2539991   537 ALLQKETGmlrgvwgsakVQMDLNIVPLFETIADLRHAPMIMGQWLSLLG 586

                   Yin..ridG.KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGv
                    +   r +G+ qe+m+GYsDs KD G +   W LYkA   ++   ++  +
  gi|2539991   587 IRHllRYQGnEQEIMLGYSDSNKDGGFITSNWELYKAEISLVELFRQANI 636

                   KLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGE
                   +L lFHGRGGtvGRGGGPt  Ai++qP  t++G +R t qGE+i   + E
  gi|2539991   637 RLRLFHGRGGTVGRGGGPTYQAIMAQPQGTVDGQIRLTEQGEIIANKYSE 686
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                    EnLCFrsLqRFtAAtLEHGmnPP....vsPkPEWRkLmeemAvvAtEEYR
                      +  + L    AAt++  + PP++     +  +  +mee+   A   YR
  gi|2539991   687 PRVGRQHLETLVAATIDGSLFPPdpllAKKRRSFEIIMEELSATAMTAYR 736

                    svvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiF
                     +v+    F EYF  AtP  E   +niGsRPa Rk    ie LRAiPW F
  gi|2539991   737 TLVYETAGFAEYFFNATPISEIAELNIGSRPASRKATQRIEDLRAIPWGF 786

                    aWtqtRFHLPvWLGvGAAFKhAidKDiK....nlqkLkEmYkeWPFFRvt
                    +W q R  LP W GvG A    +  + K ++  l+ L++m ++WP FR
  gi|2539991   787 SWGQCRLLLPGWFGVGSAIHEYLFIEDKlqpaRLKTLHDMLEQWPLFRSL 836

                    lDLlEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLki
                    +  ++mv AK D  +A  y  L+    L+ +    +  +Y+ t + L  +
  gi|2539991   837 ISNVDMVLAKTDLAVAQRYSMLVPDKKLREgIFAAIEHEYQLTTEALNLL 886

                    AGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPh
                        + L   P L   +  R +Y+  Ln +q                 +
  gi|2539991   887 LNSTERLSSNPALANSIQNRLPYLDPLNHLQV-----------------E 919

                    lsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-
                    l + y +      ++ vkL             + Lt+ GiAAG+ ntG
  gi|2539991   920 LIRQYRQGA---TNDRVKLA------------IHLTINGIAAGLRNTG   952

                    *

  gi|2539991     -   -

gi|110669081|ref|YP_658892.1|: domain 1 of 1, from 1 to 897: score 242.5, E = 1e-69
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +D   R      v   +++ e  ALL     D+L D   +   E v
  gi|1106690     1    -MDLHSRG-----VK--QDIQELGALL----GDVLADQTSDAAFETV 35

                    qECYElsAeY.EGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                     +    + +Y+ GK  t+  + L   L  Ld      vA+a+     L n
  gi|1106690    36 EDIRTAAIDYrNGKLATR--NQLDQLLDELDSERESTVARAFTTYFELVN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAEE e A   R   +   D  D   At Es i+          +   e
  gi|1106690    84 LAEERERARVVREGAQT-EDLDDGLIATVESLID---------ADADSET 123

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v   L    ++  +tAHPt + R+ +  K   i n L  L  + +t  +
  gi|1106690   124 VQRVLDEVLIEPTFTAHPTEARRKTVKAKLRSIANKLEELDEQRITNREH 173

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   +  Ei   + t  +R  +P PqDE R    Y+   +++ v
  gi|1106690   174 DQIWRKVDAEITSLWQTSQVRGRRPEPQDEARNVQWYLESILFDVVGE-- 221

                    RRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDvC
                      v      i   E     vP+L +F sW G DRDG nP vtPEvt D
  gi|1106690   222 --VYAEFEDIIGSEYPDVSVPkLFEFRSWAGSDRDG-NPFVTPEVTTDTL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                       R +    Y + +  L   ls           A+ +    + ++  K
  gi|1106690   269 ERQRGVVLEKYSQALKRLSGVLS---------QDADRVDISTQLKRSLKT 309

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                      E    v  +   R      R KL   RE  R      i ++  +  y
  gi|1106690   310 DYERLPGVTAETEERYPGEPYRQKLKLMREQLRR-----IDDVRPDG-YS 353

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                    + E FL  LE+  +sL   G  v+AD  +  l+Rqv tFG  L  LD+R
  gi|1106690   354 DPEAFLSDLEVIDQSLRKNGGEVVADEYVEPLMRQVDTFGFTLASLDLRD 403

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP.
                        +t+ +  +    +i  Y ++ E  R E L   +    P++  + P+
  gi|1106690   404 HQKNHTEAVHEVFINSGI-EYDSYDEADRIEILTEAILQTEPVVDLEDPg 452

                    .ktEEvkDvldafrvLA....ELPiDsFGaYiismataPsDvLAvELLqR
                    +  +  + vl  f +L + ++E  + +   Y ism+  Ps vL v  L
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  gi|1106690   453 dVSDTARRVLRRFSMLGewqrEFGVGAIDTYCISMTENPSHVLEVLFLAD 502

                   ECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri...dG
                     gv + +++  L +vPL E    L+ A   +  LF  D Y   ++ +d
  gi|1106690   503 QAGVvslpdHCGLDIVPLLETESALNGAREIMGTLFENDAYAAALsarDN 552

                   KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                    qe+m+GYsDs K+ G l+A W LYk q  ++++  ++ v + lFHGRGG
  gi|1106690   553 VQEIMLGYSDSNKENGFLAANWDLYKNQRRLAQICDDFDVTMRLFHGRGG 602

                   tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                    + RGGGP   A+L+ P +t+ G ++ t qGE i   +    +  r L
  gi|1106690   603 SISRGGGPMNEAMLALPNETVTGQIKFTEQGEAIAEKYANPLIAERNLEQ 652

                   FtAAtL...EHGmnPPvsPkP.EWRkLmeemAvvAtEEYRsvvvKEPRFv
                      A ++ +   +  P    P+ W + meemA  A   Y  +   +  F+
  gi|1106690   653 MLNAQVrarHNAIREPTEDVPsAWIDAMEEMASAARKQYYDLLNTDG-FI 701

                   EYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLP
                    YF  AtP      +n+GsRPa R     +e LRAiPW+F+Wtq R  +
  gi|1106690   702 TYFGQATPIGVIEDLNLGSRPASRSGERTVEDLRAIPWVFSWTQSRCIIT 751

                   vWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPG
                    W  +G   +  +d     +  Lk mY +WPFFR tlD   +  A+ D
  gi|1106690   752 GWYALGGGIQSYLD-NGGDITTLKSMYTDWPFFRTTLDNAALALARTDLD 800

                   iAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                   iA  y  L   E    F   LR +    ++l+ ++ G   lLE + +L q
  gi|1106690   801 IAEHYASLADPELREDFFPHLRTECNRSRELVCEVSGRDSLLERE-WLDQ 849

                   rlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkade
                    lR R++Y+  Ln +q   L          t r        dE+
  gi|1106690   850 SLRRRNPYVDPLNLLQTHLLEQ--------THR-------TDEE------ 878

                   LvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                               E tL Lt+KGiAAGm+ntG
  gi|1106690   879 --------------ERTLRLTVKGIAAGMKNTG    897

gi|269128325|ref|YP_003301695.1|: domain 1 of 1, from 8 to 892: score 241.4, E = 2.2e-69
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       +    R      +    + ++ D  Ll   L++iL +  G+dL E
  gi|2691283     8    QVPSEQRKALREEMP---EPLRRDVRLLGAMLgEILVEYGGPDLLED 51

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v       A  + ++    ++E  a + + d   a lvA+a+     L n
  gi|2691283    52 VERLRH--AVIDARQGRVSIDEAAALVAGWDLERAELVARAFTVYFHLTN 99

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   LAEE    +R R  + +    +D a     s +   + ++   ++   +
  gi|2691283   100 LAEE---HHRIRALRER---DTDPAHPVSGS-LAAAVAQIRGTGEHRLAQ 142

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   v + L       v+tAHPt + RR+++    Ri   L           ++
  gi|2691283   143 VLDGLEFRP---VFTAHPTEARRRAVVTAIMRISALLQDFNDPRKGAAER 189

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    E+   L  Ei   +Rt   R +q  P DE+R  m+ + Et+++ vP+
  gi|2691283   190 DEIRRQLREEIDLLWRTALRRHTQMDPLDEVRTAMAAFDETIFRVVPQLY 239

                   RRvDtALKniGin.....ERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                   R  D AL  +G  ++ ++ R P     ++F sW+GGDRDG nP vt  +t
  gi|2691283   240 RALDSAL-DVGASgpasgARPPRAHAYLRFGSWIGGDRDG-NPYVTAQIT 287

                   RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk
                   R+  L+         +    +   l +        +        a+
  gi|2691283   288 REAVLIQSDHVLRALENACTRIGRRLTVSSATTPPSAALRNALDAARTA- 336

                   vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                        i    +  P+EP R  L  v +++  t  RaRH           +
  gi|2691283   337 -YPLLIAELAKRSPEEPHRQYLLYVAERIAAT--RARH----------AD 373
```

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                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y   Ee L  L L   sL   G    A G L  l+ q  tFG  L  L
  gi|2691283   374 MAYRSPEELLADLRLVQESLAGAGAVRQAYGELQHLIWQTETFGFHLAEL 423

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                    +iRq s+ +   l                e R    l+E
  gi|2691283   424 EIRQHSQVHEKAL----------------AEVRAGGALSE---------- 447

                    DLPktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLqRE
                       +tEEv D l  +  +     + +   Y++s + +  D+ Av  L
  gi|2691283   448 ---MTEEVLDTLRVVSwIQRRFGVRACHRYVVSFTRSADDIAAVYELAES 494

                    Cgvkqt.LrvvPLFEkLADLeAAPAave...kLFsiDWYinridGKqevm
                     g + + L vvPLFE   DL+ AP  +e+  kL ++         + evm
  gi|2691283   495 LGDHAPvLDVVPLFETGEDLDRAPSVLEgmlKLPAVQRRLAETGRRLEVM 544

                    vGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRG
                    +GYsDs K  G  sA   LY Aq  ++  A + G+ L+lFHGRGG  GRG
  gi|2691283   545 LGYSDSAKQLGPTSATLRLYDAQAALAAWAARNGITLTLFHGRGGSLGRG 594

                    GGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAt
                    GGP   AiL+q P  +nG  +vt qGEvi   +G  ++  r +   t A
  gi|2691283   595 GGPANRAILAQAPGSVNGRFKVTEQGEVIFARYGQREIAKRHIEQVTNAI 644

                    LEHGmnPPvsPkPE.....WRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                    +     P v  +  +   ++R L +++   A   +R+++  E  F E+F
  gi|2691283   645 M-LASTPAVEARAHeaavrFRPLADRISAAAQAAFRALIETEG-FAEWFA 692

                    lAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG
                       P  E  ++ iGsRPa+R     +e LRAiPW+FaWtqtR  LP W G
  gi|2691283   693 RVSPLEEISRLRIGSRPARRTATRSLEDLRAIPWVFAWTQTRVNLPGWYG 742

                    vGAAFKhAi..dKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiA
                    +G      +++  D   l  L+E Y+ WP F v lD  Em  AK D  iA
  gi|2691283   743 LGSGLEAVLggGDDEAGLAELQEAYRSWPLFAVMLDNAEMSLAKADRAIA 792

                    aLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrl
                      y  L    eL    +++ ++Y  t+ l+L + GH+ lLE    L   +
  gi|2691283   793 ERYLALGGRPELT---ERVLAEYDRTRSLVLAVTGHRRLLENRRVLSRAV 839

                    RLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLv
                     LR++Y+  L  +q   L  +R                  E    ad+
  gi|2691283   840 ELRNPYVDALSLLQLRALTALR-----------------EG--VADDAE 869

                    kLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +          LE+ L+L + G+AAG+qntG
  gi|2691283   870 RAR--------LEELLLLSVNGVAAGLQNTG    892

gi|284167583|ref|YP_003405861.1|: domain 1 of 1, from 1 to 896: score 238.3, E = 1.9e-68
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                              L    +s  +++ +  ALL      iL +    +  E v
  gi|2841675     1    ------MELHDRSIS--QDIHDLGALL----GNILEEQTSLEAFETV 35

                    qECYElsAeYE.GKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    + C   + +Y +G  Dt+  + L a L +L P    +vA+a+     L n
  gi|2841675    36 KSCRRAAIDYRsGDLDTR--DPLIAELEGLSPHNQRIVARAFTTYFELIN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAEE     R Ri+  +    +   + t +  +E+    L        e
  gi|2841675    84 LAEE-----RERIRTIR----TGSHERTLDDGLEDAAAELGEAD---DET 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v   L    ++  +tAHPt + R+ +  K   i   L  L  + +t  +
  gi|2841675   122 VQRILDDILIEPTFTAHPTEARRKTVKSKLRDISTSLETLDERLLTEKEE 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + +   +  E+   + t  +R  qP P DE R    Y+  t+++ v
  gi|2841675   172 EQVWRDIDAEVTSLWQTPQVRNRQPEPEDEARNVQWYLENTLFDVVGEVY 221

                    RRvDtALKniGinERlP..YdvP.LikFssWmGGDRDGknPRvtPEvtRD
                       D A     i   lP++ dvP+L +F sW G DRDG nP vtPEvt
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  gi|2841675   222 DELDDA-----IDSELPrdIDVPkLFEFRSWAGSDRDG-NPYVTPEVTAN 265

                   vCLLaRmmAanlYisqvEDLmFElsm........WRCndELRvRAEElyr
                   v    R +    Y + +  L   ls ++++ + +      L v  E l +
  gi|2841675   266 VLERQREVVLEKYRDELKRLSGVLSQdggridagGEFEASLEVDRERLPS 315

                   taardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi
                    a+       Y        P EPY       R KL   RER R      +
  gi|2841675   316 VARTA--EERY--------PGEPY-------RQKLKLMRERLRR-----V 343

                   seisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFG
                    ++     y +v+e LE L++   sL + G   + +  +  + R v tFG
  gi|2841675   344 GDVRPGG-YDDVDELLEDLDVIATSLRNNGGETVVEAHVDPIRRRVDTFG 392

                   LsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGK
                    sL  LD+R   +++tD +    +  +i  YR  sE  R E+L   +
  gi|2841675   393 FSLASLDLRDHQQKHTDAIAEALEREGI-DYRGLSEAERVEFLTDAVLQD 441

                   RPLlgsDLPktEEvkD....vldafrvLA....ELPiDsFGaYiismata
                    P+l  DL  t+ + D++++vl+ f  LA+ ++E  +++   Y ism+
  gi|2841675   442 EPVL--DLGETDGLTDdstrVLELFDSLAdwqtEYGVEAIDTYCISMTDE 489

                   PsDvLAvELLqRECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsi
                   Ps vL v  L    gv + +++  + +vPL E    L  A   +  LF
  gi|2841675   490 PSHVLEVLFLADQAGVvslpeHSGIDIVPLLETEYALSGARRIMGTLFEN 539

                   DWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKky
                   + Y   ++ ++++qe+m+GYsDs K+ G l+A W L k q  +  +  ++
  gi|2841675   540 EAYSQALEARgrtQEIMLGYSDSNKENGFLAANWSLHKNQRRLGEICDDH 589

                   GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF
                    v + lFHGRGG + RGGGP   A+L+ P  ti G ++ t qGE i   +
  gi|2841675   590 DVTMRLFHGRGGSISRGGGPMNEALLALPNNTITGQVKFTEQGEAIAEKY 639

                   GEEnLCFrsLqRFtAAtLEHGmnPPvsP....kPEWRkLmeemAvvAtEE
                   G   +  r +     A L    +    P+++ + EW + me mA  A  E
  gi|2841675   640 GNPRIAERNIEQMLNAQLRARKQAIDQPeedvHAEWIDAMETMADAARQE 689

                   YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPW
                   YR + +    Fv YF  AtP +    +n+GsRPa R     +e LRAiPW
  gi|2841675   690 YRDL-LESDGFVRYFEQATPITVIEDLNLGSRPASRSGERTVEDLRAIPW 738

                   iFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlD
                   +F+Wtq R  LP W  +       +d     +  L+EmY+eWPFFR tlD
  gi|2841675   739 VFSWTQSRCILPGWYALATGIEAYLD-NGGSMDTLQEMYDEWPFFRTTLD 787

                   LlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGH
                      +   + +  iA  y  +  a     F  ++ d+Y+   +l+ +i G
  gi|2841675   788 NAALSLSRTELEIAEQYAGMADAALRDRFFPRVTDEYERATELITEI-GQ 836

                   kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                   +D L    +L   l  R++Y+  Ln++q   L R
  gi|2841675   837 RDRLHTRDWLGENLEQRNPYVDPLNMLQVHLLDR---------------- 870

                   EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        n         +          E tL Lt+KGiAAGm+ntG
  gi|2841675   871 -----N-----HRTNIE---------ERTLRLTVKGIAAGMKNTG    896

gi|46198568|ref|YP_004235.1|: domain 1 of 1, from 2 to 858: score 238.0, E = 2.3e-68
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      s D    +L    v            Ll + L++ +  L Ge
  gi|4619856     2   SQDPF--ALLKAEVD----------LLGRLLgEAIRTLSGERFFAL 35

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   v E   l A    + D    e L a++ +L   +a  + +a+ H   L n
  gi|4619856    36 VEEVRAL-AKARRQGDEAAGEALLARVEGLSTEEAEALVRAFTHYFHLVN 84

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnK....
                   LAEE    +R R+ +++          t Es   E +  L   l K+++
  gi|4619856    85 LAEE---RHRVRVNRLR------AQAETLESPRPEGFLALAKAL-Kergl 124
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                    sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt
                    s eE    L      L +tAHPt   RR L       R  L  L  +++
  gi|4619856   125 SLEEAEAHLNRLELLLTFTAHPTETRRRTL-------RHHLEALQ-RELE 166

                    veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGv
                      D+    E L   +   + t+E+R+a+Pt  DE++ G+ Y+  t+W+ v
  gi|4619856   167 AGDR----ERLAARVALLYGTEEVRKARPTVEDEIKGGLYYLPTTLWEAV 212

                    PKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                    P+ +   + AL    +  R P     ++F sW+GGDRDG nP vtPEvt
  gi|4619856   213 PRVVAGLEAALER--VYGRRPRLKSPVRFRSWIGGDRDG-NPFVTPEVTA 259

                    DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                         aR +A   +++ +EDL+ +ls+     E Rv      r
  gi|4619856   260 FAGRYAREVARRRFLEALEDLVRDLSL----AEARVPVPREVRERGEG-- 303

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                    v  ++         EPYR    +    LY   ER             EeA
  gi|4619856   304 VERFM--------GEPYRRYFAA----LYRALER-------------EEA 328

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                         E  L  L    + L e G   +A+  L  l    s FGL L  LD
  gi|4619856   329 ---TTEGLLAALKAAERGLREVGLGRVAEAFLDPLEARLSAFGLELAPLD 375

                    iRqEseRqtDvlDAittHLeiGs....YReWsEeKRqEWLlaELkGKRPL
                    +R Es R    l+A  + L +G  ++++   + e R   L  ELk  RPL
  gi|4619856   376 LREESGR---LLEAAAELLRVGGvhpdFLALPQEERERLLTEELKTARPL 422

                    lgs.DLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                    l+ ++ P  E ++  l+a++   +      Ga ++sm+  P D LAv LL
  gi|4619856   423 LPVgEAPEGEALRVALGALKAWRDK-----GAHVVSMTHHPEDLLAVFLL 467

                    qRECgvkq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK
                     RE g+ +++++ +  vvPLFE L DL+ AP  + +L     +  +  G+
  gi|4619856   468 AREVGLYRpgrplPFDVVPLFETLEDLRRAPGVLRRLLENPVFLAHARGR 517

                    ..qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRG
                    ++ evm+GYsDs KDAG l A   LY AqE + +v  + G  +  FHGRG
  gi|4619856   518 ggVEVMIGYSDSNKDAGFLMANLALYEAQEALSRVGEEVGLPVYFFHGRG 567

                    GtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLq
                        RGGGP   Ai s PP  +   +R t qGE +   +   +L  r L
  gi|4619856   568 TSTARGGGPAGRAIASLPPRSVGRRIRLTEQGEALADRYSHPDLAVRHLE 617

                    RFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                              + P   P   WR+ + + A   t  YR++ ++E  F ++F
  gi|4619856   618 QMLYHFALAALGPGQEPEARWREALAQAAEESTRRYRAL-LQEEGFFDFF 666

                    RlAtPElEYGkmniGsRPaKRk.PsGGiesLRAiPWiFaWtqtRFHLPvW
                       tP  E G + i sRP  R++    i  LRAiPW+ aWtq R  LP W
  gi|4619856   667 EAFTPIREIGELPIASRPVYRRgRVRDIRDLRAIPWVMAWTQVRVLLPGW 716

                    LGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiA
                     G+ A        +   l  L+EmY+ WPFF  tl+   m  AK D G+A
  gi|4619856   717 YGLSAL-------EELPLDLLREMYRGWPFFASTLEAAAMALAKADMGVA 759

                    aLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrl
                     Ly + Lv E L+ F ++L ++   t   LL+      lL     L  ++
  gi|4619856   760 RLYLR-LVPEPLRFFYRRLAEEHARTVA-LLEAVFQAPLLHNQRTLERQI 807

                    RLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLv
                    RLR++Y+  +n++q   L+R R P           KE  dE
  gi|4619856   808 RLRNPYVDPINIVQVELLRRYRAPG---------GKE--DEA-------- 838

                    kLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                              L   L+L + G+AAG+ n G
  gi|4619856   839 -----------LRRALLLSILGVAAGLRNAG    858

gi|20196774|emb|CAC86359.1|: domain 1 of 1, from 1 to 375: score 237.0, E = 4.8e-68
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
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gi|2019677     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|2019677     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|2019677     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                                       RRsLLqKnaRiRnCL+qLsAKD+t +DKk
gi|2019677     1 --------------------RRSLLQKNARIRNCLTQLSAKDITADDKK 29

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                  ELDEAL   iqAAFRtDEiRRaqPtPqDEmR+GmsYiHEtvWkGvPKFLR
gi|2019677    30 ELDEALQIGIQAAFRTDEIRRAQPTPQDEMRYGMSYIHETVWKGVPKFLR 79

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                  RvDtALKniGinERlPY+vPLikF+sWmGGDRDG nPRvtPEvtRDvCLL
gi|2019677    80 RVDTALKNIGINERLPYNVPLIKFCSWMGGDRDG-NPRVTPEVTRDVCLL 128

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                  aRmmAanlYi+qvE+LmFElsmWRCn+ELR RAEEl++t+a++kv+KyYi
gi|2019677   129 ARMMAANLYIDQVEELMFELSMWRCNEELRCRAEELQSTPASKKVTKYYI 178

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                  EFWKq+PP+EPYRviLG+vRDKLYntRERaRHL+AtG+sei Ee v+t+v
gi|2019677   179 EFWKQIPPNEPYRVILGAVRDKLYNTRERARHLVATGYSEIGEESVFTNV 228

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                  +eFLEPLELCYksLC CGDk+iADGsLLDlLRqv+tFGLsLvKLDiRqEs
gi|2019677   229 DEFLEPLELCYKSLCACGDKAIADGSLLDLLRQVFTFGLSLVKLDIRQES 278

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  eR+tDv+DAitt L+iGsYR+W+Ee+R+EWL++EL+GKRPLl++DLP+tE
gi|2019677   279 ERHTDVIDAITTYLGIGSYRDWPEEQRMEWLVSELQGKRPLLPPDLPQTE 328

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  E++Dv++a+rvLAELP+DsFG+Yiism+taPsDvLAvELLqRECg++
gi|2019677   329 EIADVIGAMRVLAELPSDSFGPYIISMCTAPSDVLAVELLQRECGIR--- 375

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG

gi|2019677     - ---------------------------------------------- -

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

gi|2019677     - ---------------------------------------------- -

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

gi|2019677     - ---------------------------------------------- -

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

gi|2019677     - ---------------------------------------------- -

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

gi|2019677     - ---------------------------------------------- -

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

gi|2019677     - ---------------------------------------------- -

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

gi|2019677     - ---------------------------------------------- -

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
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  gi|2019677     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|2019677     - -------------    -

gi|222480720|ref|YP_002566957.1|: domain 1 of 1, from 1 to 900: score 235.5, E = 1.4e-67
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                             +L    v    ++ e  AL+     D+L      +  E v
  gi|2224807     1    ------MVLHNRDVR--TDVRELGALV----GDVLSAQTSTEAYETV 35

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    +    + +Y  + D+   + L   +  L  +   +vA+a+     L nL
  gi|2224807    36 EDLRHAAIDYR-RGDAASRDILRESVEELSTTREEIVARAFTTYFELINL 84

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEE     R R++  +    aDE     +s  + t+          P+E
  gi|2224807    85 AEE-----RERVRAIR---NADENGSLHDS-FDATIAEFAEAD-VGPDEL 124

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    e L    ++  +tAHPt +    +  K   i n L  L  + +t  ++
  gi|2224807   125 RELLADVLIEPTFTAHPTEARQATVKAKLRSIANHLEALDERNLTERERN 174

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    +   +  E+   + t  +R   P P DE R    Y+  t+++ v
  gi|2224807   175 AIWRDITAEVTSLWSTRQVRQRSPEPEDEARNVQWYLENTLFDVVGDAYE 224

                   RvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDvCL
                     +  +      E    d P+L +F sW G DRDG nP vtPEvt +
  gi|2224807   225 EFEETIS----KEYDDVDCPkLFEFRSWAGSDRDG-NPFVTPEVTDETLA 269

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy.
                     R +A   Y +    L   ls      E  +  + l    a d v +++
  gi|2224807   270 RQREVAVEKYRDRCKRLSAVLSQ---DGERYAVDDRLAESLAAD-VERFp 315

                   .YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                   + +E  +   P EPY       R KL   RER   +      +      y
  gi|2224807   316 tVVEEARERYPDEPY-------RQKLRLMRERLDRV------DDVRPGEY 352

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                    + + FL  L++   sL   G  ++ +  +  l Rqv tFGL L  LD+R
  gi|2224807   353 PDGDAFLADLDVIADSLATDGQDAVRESFVEPLRRQVDTFGLTLASLDLR 402

                   qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                      e++t+ + A t  +e   YRe  E+ RqE+L   +    P++ +D P
  gi|2224807   403 DHREKHTETV-AETVAVEGVDYREMDEDARQEFLTEAILQDDPVVDADEP 451

                   ..ktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvELL
                   ++  E  + vl  f+  AE   D +G++  ++Y ism+  Ps vL v  L
  gi|2224807   452 gdVSETTERVLRRFQEFAEW-QDEYGPqaidtYCISMTEEPSHVLEVLFL 500

                   qRECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK
                       gv + +++  L vvPL E    L+ A   +  LF  + Y   ++ +
  gi|2224807   501 ADQVGVvslpdHCGLDVVPLLETESALNGAERILGELFDNEAYATALEVR 550

                   ...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                   ++ qevm+GYsDs K+ G l+A W LY  q  i++  ++  v L lFHGR
  gi|2224807   551 geiQEVMLGYSDSNKENGFLAANWDLYENQRQIARFCREEDVTLRLFHGR 600

                   GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                   GG + RGGGP   A+L+ P +t+ G ++ t qGE i   +    +  r L
  gi|2224807   601 GGSISRGGGPMNEALLALPNETVTGQVKFTEQGEAIAEKYANRRIAERFL 650

                   qRFtAAtL...EHGmnPPvsPkPE.WRkLmeemAvvAtEEYRsvvvKEPR
                        A ++ +    + P    P++W + me mA  A E YR +   +
  gi|2224807   651 EQMLDAQIrarQEATEEPTEDVPDsWVDAMETMAPAARETYRDLLNTDG- 699

                   FvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFH
                   Fv YF  AtP      +n+GsRPa R     +e LRAiPW+F+WtqtR
  gi|2224807   700 FVSYFGQATPISVVENLNLGSRPASRSGERTVEDLRAIPWVFSWTQTRLI 749
```

```
                    LPvWLGvGAAFKhAidK..DiKnlqkLkEmYkeWPFFRvtlDLlEmvFAK
                    LP W  +       +d  ++   +  L+EmY eWPFFR tl    +  A+
  gi|2224807   750 LPGWYSLASGIDAYLDEvgEEEGFETLQEMYAEWPFFRTTLNNAALALAR 799

                    GDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDP
                     +P iAa y +L   +    F  +L  +Y+  ++l+L+i G +D L
  gi|2224807   800 TEPEIAAEYADLADDDLRERFFPELIGEYERGRELVLEISG-RDELIRRE 848

                    YLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnsk
                    +L   l  R++Y+  Ln +qA  L R        t r        +E+
  gi|2224807   849 WLAESLDRRNPYVDPLNLLQANLLGR--------THR-------TEEE-- 881

                    kadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                     E tL Lt+ GiAAGm+ntG
  gi|2224807   882 ------------------ERTLRLTVNGIAAGMKNTG    900

gi|284165765|ref|YP_003404044.1|: domain 1 of 1, from 1 to 897: score 234.3, E = 3e-67
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            +R L    +   +++ e  ALL     D+L D    +  E v
  gi|2841657     1    -----MR-LHNREIR--QDVRELGALL----GDVLEDQTSRQGFETV 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                      C   + +Y    D +  e L ++L +L P    +vA+a+     L nL
  gi|2841657    36 ESCRRAAIDYRS-GDLESREPLISRLEGLSPHNQRIVARAFTTYFELINL 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEE     R R++  +    ++  + t E  +E     L  ++    + v
  gi|2841657    85 AEE-----RERVRTIR----TESNEGTLEDSLEMAAEELGERG---VDTV 122

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     + L    ++  +tAHPt + R+ +  K   i   L  L  + +t  ++
  gi|2841657   123 EDVLDDVLIEPTFTAHPTEARRKTVKSKLRTISTHLETLDERLLTEKEQS 172

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +   +  E+   + t  +R  qP P DE R    Y+  t+++ v
  gi|2841657   173 QVWRDIDAEVTSLWQTPQVRNRQPEPEDEARNVQWYLENTLFDVVGEVYD 222

                    RvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDvCL
                        A   i        ++P+L +F sW G DRDG nP vtPEvt  v
  gi|2841657   223 ELADA---IDAETAGDLEIPkLFEFRSWAGSDRDG-NPYVTPEVTANVLE 268

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                      R +    Y + +  L   ls      +     E      +
  gi|2841657   269 RQREVVLEKYRDELKRLSGVLSQDGSRIDTGGEFEASLEDDRER--LPGS 316

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                            P EPY       R KL   RER    LA  + ++     y +
  gi|2841657   317 ARTAEDRYPGEPY-------RQKLKLMRER----LAR-VGDVRPGG-YDD 353

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    v+e L+ L +  +sL +     + +  +  + Rqv tFG sL  LD+R
  gi|2841657   354 VDELLDDLAVIAQSLRNNSGESVVEAHVDPIRRQVATFGFSLASLDLREH 403

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                     +++t  +    +  +i  YR+ sE+ R E L   +    PL+  DL  t
  gi|2841657   404 QQKHTGAIAEALEREGI-DYRSLSEDERVELLTDAVLQDDPLV--DLSET 450

                    ....EEvkDvldafrvL....AELPiDsFGaYiismataPsDvLAvELLq
                    ++ +E+ + vl+ f  L++ + E  +++   Y ism+  Ps vL v  L
  gi|2841657   451 sdlsEDSARVLELFDSLgdwqTEYGVEAIDTYAISMTDEPSHVLEVLFLA 500

                    RECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK.
                       gv + +++  + +vPL E    L  A   +  LF  + Y   ++ ++
  gi|2841657   501 DQAGVvslpeHAGIDIVPLLETEYALSGARRIMGTLFENEAYSQALEARg 550

                    ..qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRG
                    ++qe+m+GYsDs K+ G l+A W L+k q  +  +  +y v++ lFHGRG
  gi|2841657   551 rtQEIMLGYSDSNKENGFLAANWSLFKNQRRLGEICDDYDVQMRLFHGRG 600

                    GtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLq
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                    G + RGGGP   A+L+ P  ti G ++ t qGE i   +    +  r +
  gi|2841657   601 GSISRGGGPMNEALLALPNNTITGQVKFTEQGEAIAEKYANPRIAERNIE 650

                    RFtAAtLEHGmnPPvsPk.....PEWRkLmeemAvvAtEEYRsvvvKEPR
                        A L   +     P +++ + EW + me mA  A  EYR + +
  gi|2841657   651 QMLNAQLRARLYAKEEPDeeelpEEWFDAMETMADAARQEYRDL-LESDG 699

                    FvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFH
                    Fv YF  AtP      + +GsRPa R     +e LRAiPW+F+Wtq R
  gi|2841657   700 FVQYFEQATPISVIEDLDLGSRPASRSGERTVEDLRAIPWVFSWTQSRCI 749

                    LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                    LP W  v A    A   D   +  ++EmY++WPFFR tlD   +   + +
  gi|2841657   750 LPGWYAVAAGID-AYLEDGGSMETMQEMYDQWPFFRTTLDNAALSLSRTE 798

                    PGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                      iA  y +L  +E    F  ++ d+Y+   +l+ +i    Dl   D +L
  gi|2841657   799 LEIADQYADLADSELRERFFPRITDEYQRATELITEIGQREDLHTRD-WL 847

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                       l  R++Y+  Lnv+q Y L R                     n
  gi|2841657   848 GENLARRNPYVDPLNVLQVYLLDR---------------------N---- 872

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                         +          E tL Lt+KGiAAGm+ntG
  gi|2841657   873 -HRTDVE---------ERTLRLTVKGIAAGMKNTG    897

gi|89900503|ref|YP_522974.1|: domain 1 of 1, from 1 to 957: score 232.4, E = 1.2e-66
                    *->siDAqLRlLvPG.KvsedekLieYDALLlDkFL.DiLqDLHGedLkE
                        i  q   ++P +++ ++e+ +  D  Ll + L+D++ +  G    E
  gi|8990050     1    MIKPQ--KVAPTqRIQDNERPLVDDIRLLGRILgDVIREQEGVAAYE 45

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                     + E   ls  +    D      L   L +L    a+ v +a+     LA
  gi|8990050    46 LIEEIRQLSVAFRRDADHDADKALKKLLKGLSSDQAVSVTRAFTYFSHLA 95

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    nLAE+ +   RR i+ +  GD       t E  iE  + +L   +  +Pe
  gi|8990050    96 NLAEDRHHIRRRAIHERA-GD-------TQEGSIEVAMARLHAAG-ITPE 136

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL......sAK
                     +   L       vltAHPt   R+s+L  +  i   L+  ++ + + A
  gi|8990050   137 SIASSLASSYLSPVLTAHPTEVQRKSILDAERDIAQLLTARdeikvnAAA 186

                    DvtveDKkEL...DEALHREiqAAFR......tDEiRRaqPtPqDEmRaG
                       v+ Kk+  ++ E L  E q   R  +  +t  +R ++ t  DE+
  gi|8990050   187 HRSVNTKKDAltpRELLLNEQQMKARvlqlwqTRLLRSSKLTVADEVENA 236

                    msYiHEtvWkGvPKFLRRvDtAL.KniGinERlPYdvPLikFssWmGGDR
                    +sY+  t    +P    R  t L++ +G n   P    L +   W+GGDR
  gi|8990050   237 LSYYETTFLSEIP----RLYTELeRELGPN---PVHSFL-RMGQWIGGDR 278

                    DGknPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFEls....mWRCndE
                    DG nP v              +A   Y+  v  L  Els +  +  C
  gi|8990050   279 DG-NPHVNAQTLAHALRRQADVALRHYLTEVHYLGGELSlsamLVNCLAP 327

                    LRvRAEElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntR.
                    + + AE    r + ++       E  K     EPYR  L  v  +L    +
  gi|8990050   328 MQALAE---RSPDSN-------EHRK----DEPYRRALIGVYARLAAVLk 363

                    .....ERaRHLLAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkvi
                    + +++E aRH +A      + +A y + EeFL  L +   sL      ++
  gi|8990050   364 dltggEAARHAVA------PQNA-YANAEEFLADLRIIEASLLAHHGEAL 406

                    ADGsLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YRe
                        L  l+R v  FG  L  +D+Rq s+ +  v+  +     + s Y +
  gi|8990050   407 VAQRLHPLIRAVEVFGFHLATVDLRQSSDQHEAVMAELLAVARLESaYPQ 456

                    WsEeKRqEWLlaELkGKRPL..lgsDL.PktEEvkDvldafrvLAEL.Pi
                      E  ++  L+  L   RPL+ +g+  +  t     v ++ +v+  L
  gi|8990050   457 LDEMAKRRLLMGLLNDARPLrvMGATYsALTQSELAVFETAKVMRSLfGA 506
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                    DsFGaYiismataPsDvLAvELLqRECgv.........kqtLrvvPLFEk
                     +   Yiis + + sD L v LLq+E g+ +++ +++ +  L vvPLFE
  gi|8990050   507 QAIRHYIISHTETVSDLLEVLLLQKEVGLlegtldeqaRCDLIVVPLFET 556

                    LADLeAAPAavekLFsiDWYinrid.......GKqevmvGYsDsGKDAGR
                    + DL+ A   +   +++      + ++++++   q++m+GYsDs KD G
  gi|8990050   557 IEDLRHAASIMREYYALPGIHALVSrgrpdqyHEQDIMLGYSDSNKDGGI 606

                    lsAAWqLYkAqEEiiKvAKky..................GvKLvlFHGRGG
                    +   W LY+A   ++ v  +   +++ +++ ++ ++ + ++L lFHGRGG
  gi|8990050   607 FTSNWELYQAEIALVDVFDEMaasqnipsdagsvtevrAIQLRLFHGRGG 656

                    tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                    tvGRGGGP   AiL+qPP t+ G +R t qGEvi   +   ++  r L
  gi|8990050   657 TVGRGGGPSYQAILAQPPGTVRGQIRLTEQGEVIGSKYANPEIGRRNLET 706

                    FtAAtLEHG.mnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                      AAtLE   ++P  s    + k   e+       YR +v+  P F +YF
  gi|8990050   707 LVAATLEATlLQPTKSASAPFLKAAAELSLSSMAAYRQLVYETPGFTDYF 756

                    RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                      AtP  E   +n+GsRPa RkPs  ie LRAiPW F+W q R  LP W
  gi|8990050   757 FAATPIREIAELNLGSRPASRKPSHKIEDLRAIPWGFSWGQCRLTLPGWY 806

                    GvGAAFKhAidKDiKn..lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                    G+G A    + +D + ++l  L+ m ++WPFF+  l  ++mv AK D  +
  gi|8990050   807 GFGSAVESFLAQDGQKdpLALLQKMHRQWPFFKTLLSNMDMVMAKSDLAL 856

                    AaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLK
                     + y +L+    L++k FG  + +++  t d L  i G    L     L+
  gi|8990050   857 GSRYAELVTDARLrkKIFG-AIEAEWHRTADALSLITGDPHRLAHNTALQ 905

                    qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                      +R R +Yi               DP ++  l+ +l + y + +    d
  gi|8990050   906 RSMRHRFPYI---------------DPLHH--LQVELVRRYRAGQ---TD 935

                    eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    e +k              + + + GiAAG+ ntG
  gi|8990050   936 ERLKRG------------IHISINGIAAGLRNTG    957

gi|108759396|ref|YP_632739.1|: domain 1 of 1, from 2 to 889: score 232.0, E = 1.5e-66
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                          A LR++        ++ ++ D  Ll + L+++L +  G+ L +
  gi|1087593     2    ---ARLRAV--------DQPLRRDVRLLGRLLgEVLVEQEGQALFDL 37

                    vqECYElsAe.....YEGKkDtkKLeELGakLtsLdPaDailvAkailHm
                      E   l+ ++++++  G++      EL  +L  L    a  v +a++
  gi|1087593    38 EEEVRRLAIQrrrgpVAGRRAVA--AELAEVLQRLPLERAEPVLRAFSVY 85

                    LnLAnLAEEvelAyRRRikkkkhGDFaDEasAt.tEsDiEEtlKkLvlkl
                      L nLAE     +R R  + +    a+ asA +    +E tl+ L   +
  gi|1087593    86 FQLVNLAEQ---HHRIRRARTH----AEVASAKpQRGSLEATLQVLKEAG 128

                    nKsPeE.vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK
                       P+E+v eA++   v L ltAHPtq+vRR LL K  R+   L
  gi|1087593   129 --IPAErVREAMRTMRVTLTLTAHPTQAVRRTLLEKLYRMAGLLEERDRC 176

                    DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvW
                    ++t+ +       L  Ei   + tDE+RR +Pt  DE++  + Y+ E +
  gi|1087593   177 ELTPRESSVNLALLREEITLLWQTDELRRERPTVGDEVKNVLWYVEEVLA 226

                    kGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPE
                    +         D A          P d P ++  sW+GGD DG nP vtP+
  gi|1087593   227 DELSLLPELLDWAFERAYGEPLGPVDTP-VRIHSWVGGDMDG-NPLVTPD 274

                    vtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvR.AEElyrtaa
                    v  D     R       +  +E L   ls     +   +++ EEl +  a
  gi|1087593   275 VFADTLRAHRARGLRRLLLDLERLGGRLS----QSARHAKpSEELLSSVA 320

                    rdkvvKyYiEFWKqvPPt...EPYRviLGdvRDKLYntRERaRHLLAt..
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                    +d       +  +   P +++EP R  L  + ++L     Ra H + +++
  gi|1087593   321 KD--AEELPDTERRYGPRtpgEPLRHKLRFMEERLH----RALHYVTQqr 364

                    .GiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvs
                     G s    +  y   E  L  L++  ++L            +  +   v
  gi|1087593   365 aGTSVPMPQGAYRTPEALLADLDVLGRALEASKGTHAGLRDVRQVRERVL 414

                    tFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaEL
                      GLsL  L++R  +e      DA+      Gs+
  gi|1087593   415 ALGLSLAELEVRAPAE------DAVSA---AGSFNG-------------- 441

                    kGKRPLlgsDLPktEEvkDvldafrvLAELPiDs....FGaYiismataP
                     G  P        tE  +  l+ +  L E  ++s+++     i+sma +
  gi|1087593   442 -GPAP--------TEGGARLLEVLARLKEAQSESgesaCRTLILSMASTA 482

                    sDvLAvELLqRECgvkq......tLrvvPLFEkLADLeAAPAavekLFsi
                     DvLA     +  g+  ++++  t  vvPLFE+L  L+  P  +  LF+
  gi|1087593   483 EDVLAAFRCLKHAGLWDekrgcaTANVVPLFEQLGALDSGPDVLRTLFAD 532

                    DWYinrid..GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyG
                      Y+ ++d +G qevmvGYsDsGK+ G l+A   LY+Aq  +  v ++ G
  gi|1087593   533 AEYRKHLDvrGGQEVMVGYSDSGKEVGLLAASAALYRAQVALTEVSREAG 582

                    vKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFG
                    v L lFHGRG  v RGGGP   AiL+ PP  + G  + t qGE ++  +
  gi|1087593   583 VPLRLFHGRGESVARGGGPAQEAILALPPGAVAGGYKATEQGEALDHKYA 632

                    EEnLCFrsLqRFtAAtLEHGmnPPvsPkPE....WRkLmeemAvvAtEEY
                      +L  r++       L H ++    P PE ++++R + + +A      Y
  gi|1087593   633 RPELARRTVELILGGVLLHTLDAQPRPEPEaertFRTVFDTLAETGRKAY 682

                    RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWi
                    R++v  +PRF E+F  AtP  E   + iGsRP+KR+ +GG+++LRAiPW+
  gi|1087593   683 RALVWEDPRFLEFFTAATPVEEIASLPIGSRPSKRR-AGGLDTLRAIPWV 731

                    FaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDL
                    FaWtq R  LP W GvG A   A  K+     +Lk mY+eWPFFR  +D
  gi|1087593   732 FAWTQNRAILPGWYGVGSALE-AFSKEEGGAAQLKRMYQEWPFFRAVIDN 780

                    lEmvFAKGDPGiAaLyDkLL..vaEeLkPFGksLRdkYvEtkdlLLkiAG
                    + mv AK D  iA+ y  L ++ +  L+   +++ ++   t+  + ++ G
  gi|1087593   781 VTMVLAKSDMAIAGRYASLAppATRSLW---RRIQQEHRRTRRQVKRLTG 827

                    HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                       lL+  P L+  + LR++Y+  +  +q   LKR R+ + +v
  gi|1087593   828 ESKLLDNNPQLQRSISLRNPYVDPMSFLQVELLKRKREGQAEV------- 870

                    KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        d +                       L+Lt+ GiAAGm ntG
  gi|1087593   871 ----DRP----------------------LLLTLNGIAAGMRNTG    889

gi|269958054|ref|YP_003327843.1|: domain 1 of 1, from 20 to 913: score 231.3, E = 2.4e-66
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          A  R+++   +   + L +   LL      iL++  G+dL + v
  gi|2699580    20    --QATERVVARYEMP--DPLRDDIRLLGGLLGTILKEAGGQDLLDDV 62

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        El     G  D+  L    a + sL    a  +A+a+     LAnL
  gi|2699580    63 EHLRELTIRAYG-DDAAALAAAAAHVNSLSLDRADQIARAFTCYFHLANL 111

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEE    +R R+ + +  D a E s   E  i   + +L        +E
  gi|2699580   112 AEEY---HRVRVLRSR--DQAVERSLVEET-IPRAFNQLAEEV--GRDEA 153

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L+      vltAHPt + RR++     Ri n La
  gi|2699580   154 LRRLQELEFRPVLTAHPTEARRRAVSRSIRRIGNLLADRDTLRPGGTALA 203

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    E+   L  Ei   +Rt  +R a+Pt  DE++  +  +  t+++  P   R
  gi|2699580   204 EINRHLLAEIDVLWRTQPLRPAKPTVIDEVKSAVGVFDQTLFQTFPEVYR 253
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                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R D  L          P    P ++   W+GGDRDG nP vt +vtR
  gi|2699580   254 RLDDWLLGDDAGRATPLVRPFVRLGTWIGGDRDG-NPNVTADVTRQ---- 298

                    aRmmAanlYisqvEDLmF....ElsmWRCn....dELRvRAEElyrtaar
                    a  +Aa   +  +ED  F++ + l m    ++++d LR     l + +
  gi|2699580   299 AAAVAAEHALAALEDEAFstarKLTMAAGDtppsDALRGLWNRLRQLSGE 348

                    dkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseis
                        +   E      P EP R  L  + +++  tR R   L
  gi|2699580   349 A-AARAEAE-----SPGEPHRAALLVIAERIAATRRRDADL--------- 383

                    EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                        y   E+    L +   sL   G   +A GsL  l+ qv tFG  L
  gi|2699580   384 ---AYPTAEKLEADLRVVQDSLVAAGAPRLAYGSLQKLIWQVQTFGFHLA 430

                    KLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLl
                     L++Rq s+ + + l  i +  ++ s               EL+ +
  gi|2699580   431 ELEVRQHSQVHAEALAEIAEK-GVNS--------------PELSDR---- 461

                    gsDLPktEEvkDvldaf.rvLAELPiDsFGaYiismataPsDvLAv....
                          t Ev D   a++ v A     +   Yi+s + aP    Av +
  gi|2699580   462 ------TREVLDTYRALgAVQARYGERAARRYIVSFTQAPEHLAAVyqla 505

                    ELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinr..idG.
                    EL   +   +  +  +PLFE  ADLe     +e +  +     r  ++G+
  gi|2699580   506 ELAFPDPDERPVIDAIPLFETFADLEGSVEILEAMLELPQVQARlaVNGr 555

                    KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                    K evm+GYsDs KD G ++A   L  Aq  i+  A ++ + L+lFHGRGG
  gi|2699580   556 KVEVMLGYSDSSKDVGPVAATLALHTAQSRIAEWADRHDIELTLFHGRGG 605

                    tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                      GRGGGP   A+L+qPP  ++G  + t qGEvi   +G+  +  r +
  gi|2699580   606 ALGRGGGPANRAVLAQPPHSVDGRFKLTEQGEVILARYGDPVIAMRHIEQ 655

                    FtAAtLEHGmnPPv.....sPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                     +AAtL     P v++++ s    +R+L   + v   E + ++v  E  F
  gi|2699580   656 VAAATL-LASAPSVekrnaSATERFRDLASALDVASRERFHALVRSEG-F 703

                    vEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqtRFH
                      +F   tP  E G + iGsRPaKR  s + ++ LRAiPW+F+W q R
  gi|2699580   704 PQWFAQVTPLEEIGMLAIGSRPAKRGLSVnSLDDLRAIPWVFSWSQARIN 753

                    LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                    L  W G+G A +   +     l  L+  + eWP F   lD +Em  AK D
  gi|2699580   754 LAGWYGLGTALRAYAESRPDGLAELQSAFLEWPLFNTLLDNVEMSIAKTD 803

                    PGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                      iA Ly +L    +L    +++ d+   t++++Lk+ G    LEG   L
  gi|2699580   804 ERIAQLYLQLGDRPDLA---QQVLDELRLTREWVLKVTGNAWPLEGRRVL 850

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                       + LR +Y+  L  +q   L+ +R                A E+s+ a
  gi|2699580   851 GRAVQLRSPYVDALSLLQVRALRALRTDG-------------ASEPSQDA 887

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +   +              L+Lt+ G+ AG+qntG
  gi|2699580   888 AARRERW---------QHLLLLTVNGVSAGLQNTG    913

gi|148556039|ref|YP_001263621.1|: domain 1 of 1, from 24 to 929: score 231.2, E = 2.6e-66
                    *->siDAqLRlLvPGKvsedekLieY.DALLlDkFL.DiLqDLHGedLkE
                       s+D    +     +s    + + +D   l + L+D++    Ge L
  gi|1485560    24    SVDRAFIASQHRAMSSTPPITQNpDIRFLGRLLgDVIRVYGGEALFR 70

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                     +   Y  sA  +  +      E+ + L +L   D++   + ++    LA
  gi|1485560    71 RIE--YIRSASVDRARGIVGSHEIDSGLGALTLDDTLAFVRGFMLFSMLA 118

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
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                nLAE+     R  i                 +D+   l +L   +  s +
gi|1485560   119 NLAED-----RQGIAAEP------------GADVAAALDRLEKEG-ISRA 150

                EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                 v e L    +  vltAHPt   R+s++    +i   ++          D
gi|1485560   151 KVVEMLDRALIVPVLTAHPTEVRRKSMIDHRNKIAELMTLKDIGRTETVD 200

                KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                   +D A+ R i   + t  +RR +    DE+   ++Y+ +      P
gi|1485560   201 GDLIDQAIYRQIALLWQTRPLRRERLYVADEVETALAYLRDIFLPTLPAL 250

                LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                  R   AL            +  +k  sW+GGDRDG nP vt +  R
gi|1485560   251 YSRWQRALGH--------RPASFLKPGSWIGGDRDG-NPFVTADSLRLAL 291

                LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                  +       Y+  + +L  Els+     E+    E l   +  +
gi|1485560   292 SRSAETVIGYYLRELHELGAELSISTELAEVTWEVEKLAEASGDK----- 336

                YiEFWKqvPPtEPYRviLGdvRDKLYntRER.aRHLLAtGiseisEeAvy
                           EPYR  +  +  +L  t E+ +  L A   +  +E   y
gi|1485560   337 -----SSTRSDEPYRRAITGIYSRLSKTYEKlTGRLPARLPATDAEGGAY 381

                tkvEeFLEPLELCYksLCeCGDkviA.DGsLLDlLRqvstFGLsLvKLDi
                 +       L    ++L   G   +A+ G+L  l+R v tFG  L  LD+
gi|1485560   382 EDPAALRADLVEIAHALNRTGADSLAgNGALGRLIRAVETFGFHLATLDM 431

                RqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgsD
                Rq ++ +  v+  + +  ++ ++Y    E  R   L +EL  KR L  +
gi|1485560   432 RQNADVHERVVADLLRVAGVEAdYGALDEPARVALLRSELASKRLLRTPF 481

                LPktEEvkDvldafrvLAELPi....DsFGaYiismataPsDvLAvELLq
                    +E    l  ++  AE   + ++ +   Y+is a + sD+L v +L
gi|1485560   482 GAYADETLSELAIVEAAAEAHRrygpAAITTYLISKAESVSDMLEVNILL 531

                RECgv.......kqtLrvvPLFEkLADLeAAPAavekLFsi..DWYinri
                +E g+  +++++  ++  vPLFE + DL+ AP  + + F++++   i
gi|1485560   532 KEAGLfvpgdppTAAIMAVPLFETIGDLDRAPEVMTQWFALpeVAAITAA 581

                dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                 G qevmvGYsDs KD G l   W L  A   +  v  k    + lFHGR
gi|1485560   582 RGHQEVMVGYSDSNKDGGYLTSVWSLHEASSALKPVFAKANSAIQLFHGR 631

                GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                GG vGRGGG    AiL+qP  t++G +R+t qGEvi   +G  +     L
gi|1485560   632 GGAVGRGGGSSFAAILAQPHGTVQGRIRITEQGEVIAAKYGTRESAAANL 681

                qRFtAAtLEHGmnP.PvsPkPEWRkL..meemAvvAtEEYRsvvvKEPRF
                   + AtL   ++ + + Pk   R    m+e+   A   YR +v+    F
gi|1485560   682 EAMASATLLATLEEdALQPKDAKRFFaaMDEISANAFKAYRGLVYDTEGF 731

                vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                  +FR  tP  E   + iGsRPa R  s  ie LRAiPW+F+W q R  L
gi|1485560   732 RTFFRQMTPIAEIADLKIGSRPASRTKSDRIEDLRAIPWVFSWAQARVML 781

                PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                P W GvG        K  K +  L+Em + WPFF  tl  lEmv AK D
gi|1485560   782 PGWYGVGHGL-----KGFKDIGLLREMLEAWPFFQSTLANLEMVLAKSDM 826

                GiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                 iA  y  L+  E +++  FG+ +Rd ++ t++ LL +     lL   P
gi|1485560   827 DIAERYVALVEDEAMgrDIFGR-IRDGWQRTQEALLSVTRQTRLLQKNPS 875

                LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                L q +RLR +Yi  Ln +q   LKR R                A E+  +
gi|1485560   876 LDQSIRLRLPYIEPLNLLQIELLKRHR----------------AGEDDPR 909

                adeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                  e ++L                +  iA  + n G
gi|1485560   910 VREGIQLS----------------INAIATALRNSG    929
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gi|187476834|ref|YP_784858.1|: domain 1 of 1, from 1 to 936: score 230.5, E = 4.2e-66
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDi.LqDLHGedLkEa
                              P   +   + ++ D  Ll + L i +q   G+ + +
  gi|1874768     1    ----MTATRTPSNLA---EPLRNDIRLLGHQLGIvVQACEGKRVYDT 40

                  vqECYElsAeY..EGK.kDtkKLeELGakLtsLdPaDailvAkailHmLn
                  +      +  +++ GK++D   ++ L  +L + dP    +vA+a++  L
  gi|1874768    41 IETLRRSAVRFrrQGKpEDGLLMQKLVKQLRGTDPN---MVARAFSYFLH 87

                  LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                  L n+AE+ +   R R + +          A     +  t+++L +++  +
  gi|1874768    88 LFNIAEDRDQHRRQRAQALT---------APAPGSLHHTVQQLRSQG-VT 127

                  PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                   e +   L    v  vltAHPt   R+s L  +  i   Laq   + +t
  gi|1874768   128 AERIRRLLAEACVMPVLTAHPTEVQRKSTLDAHREIAALLAQ-RDQTLTA 176

                  eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                  e+  ++D AL   +   + t  +R ++ t  DE+   +sY+  t    +P
  gi|1874768   177 EEIADIDNALLGRVDTLWQTRMLRYTRLTVADEIENALSYYRSTFLPAIP 226

                  KFLRRvDtALKniGinERlPYd.vPLikFssWmGGDRDGknPRvtPEvtR
                  +        L+        P   vP ++  sW+GGDRDG nP v
  gi|1874768   227 RLYTGLSKLLRPESSFSAAPEPlVPFLRMGSWIGGDRDG-NPNVDAGTLE 275

                  DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                     L    +    Y++ v  L  Els+    + +     El   +
  gi|1874768   276 LAMLRQAAVVFEYYLNEVHALGAELSITTLLSHVSDALRELADASGDS-- 323

                  vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE..
                          +q    EPYR  L  +  +L  t   a  L    ++  s ++
  gi|1874768   324 -----SPHRQ---DEPYRRALIGIYARLAAT---ANTLTGRDLARRSTrp 362

                  eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                   A y +    +  L +   sL       iA   L  lL  vs FG  L
  gi|1874768   363 AAPYDHPQALMNDLNVIMDSLSRHHGSPIARLRLSGLLQSVSVFGFHLAT 412

                  LDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaELkGKRPLl
                  LD+Rq s+ +  vl  +    + +  Y    E  R   L  EL   RPL
  gi|1874768   413 LDLRQSSDVHERVLTELFARAGGpPRYDLLDETERVQLLRDELATARPLA 462

                  gsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAvE
                   + L   E+ +  l  +r  A  +++    +    i+s + + sD L v
  gi|1874768   463 SPWLEYSEDTRRELAILRAAAAarrrYGRAALRQTIVSHTESLSDLLEVL 512

                  LLqRECgvkqt......LrvvPLFEkLADLeAAPAavekLFsiDWYinri
                  +Lq+E g+  ++ ++++L vvPLFE + DLe  P  ++    +   + r+
  gi|1874768   513 VLQKETGLIPPtapddgLMVVPLFETISDLERGPDIMAAWLDLPEVRRRV 562

                  ....dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                  +  +d  qevm+GYsDs KD G l   W LY+A  E++ v +   v+L l
  gi|1874768   563 kiaqDDTQEVMLGYSDSNKDGGYLTSNWSLYRAERELVEVFRARQVRLRL 612

                  FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                  FHGRGG vGRGGG    AiL+qPP  + G lR t qGEvi   + + ++
  gi|1874768   613 FHGRGGSVGRGGGSSFDAILAQPPGAVAGQLRLTEQGEVIQSKYKDAEIG 662

                  FrsLqRFtAAtLEHGmnP.PvsPkPEWRk......LmeemAvvAtEEYRs
                     L     A L   + P+P + + E  +++ +++Lm+ +   A   Y s
  gi|1874768   663 RGHLELLVSAVLQASLTPqPAARQAEDAHnelhgpLMQVLSDSARQSYCS 712

                  vvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFa
                  +v+    F +YF  AtP  E   +niGsRPa Rk +  ie LRAiPW F+
  gi|1874768   713 LVYETSGFADYFFAATPISEIAGLNIGSRPASRKQGQRIEDLRAIPWGFS 762

                  WtqtRFHLPvWLGvGAAFKhAidKDiK........nlqkLkEmYkeWPFF
                  W q R  L  W G+G A +  ++   ++ ++++++ l +L+ m ++WP F
  gi|1874768   763 WAQCRLMLTGWYGMGSALQSYLELGAQgaprsrrgRLTQLRAMAQDWPAF 812

                  RvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP..FGksLRdkYvEtkdl
                  R  l  +Emv AK D  iA+ y  L+    L+ + FG  + d+   t
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  gi|1874768   813 RTLLSNMEMVLAKSDLAIASRYAMLVPQRGLREriFG-AISDEHGRTLA- 860

                   LLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvt
                   +Lk+   ++lL   P L   lR R +Yi  Ln +q   ++R R
  gi|1874768   861 MLKLINQRELLADNPTLAASLRERFAYIDPLNYLQIDLIRRHR------- 903

                   lrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqn
                            A+             p +   P L   + Lt+ GiAAG+ n
  gi|1874768   904 ---------AAQC----------QPEKTEDPRLTRAIHLTINGIAAGLRN 934

                   tG<-*
                    G
  gi|1874768   935 SG    936

gi|124268187|ref|YP_001022191.1|: domain 1 of 1, from 1 to 934: score 230.2, E = 5.2e-66
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                         A+    +     ++  Lie D  Ll + L+D++ +  G    E
  gi|1242681     1    MATAKTPRSADRGADKNRPLIE-DIRLLGRILgDVIREQEGALAFEL 46

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   +     l+  Y  K+Dt+    L   L  L    a+ v +a++    LAn
  gi|1242681    47 IERIRQLAVAYRLKRDTQAGRALDRLLKNLSVEQAVSVVRAFSYFSHLAN 96

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   LAE+ +   RR  + +             E  +   + +L  ++     E
  gi|1242681    97 LAEDRHHVRRREHHEQL--------GHVQEGSLAMSFERLAKRG-VRATE 137

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   + e L       vltAHPt   R+s+L  +   R     + A+D  +  +
  gi|1242681   138 IAELLGHAYLSPVLTAHPTEVQRKSVLDAE---RAVAELIGARDTLPTQR 184

                   .kELDEALHRE.iqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                   ++   EA+ R ++   + t  +R ++     E+   +sY+  t  + +P+
  gi|1242681   185 eRAANEAMLRArVTQLWQTRLLRTSKLSVANEIDNALSYYQSTFLRQIPR 234

                   FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                        +  L    +       +P  +   W+GGDRDG nP vt E  R
  gi|1242681   235 LYAELEALLPGFEV-------APFFRMGNWIGGDRDG-NPNVTAETLR-- 274

                   CLLaRmmAanl..YisqvEDLmFElsmWRCndELRvRAE.Elyrtaardk
                     LaR   + l+ Y+  v +L  Els+    + L v   +El+  a r
  gi|1242681   275 LALARHSETVLrfYLTEVHELGAELSI----SALLVQVTpELQALADRS- 319

                   vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                      +           EPYR  L  v  +L  t      L A    e
  gi|1242681   320 -GDHNAHRL-----DEPYRRALIGVYARLAGT------LTALTGTEALRH 357

                   Av.....ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                   Av ++++y   Ee L  L     sL      ++A   L  l+R v  FG
  gi|1242681   358 AVapstpYATAEELLADLRTVEASLASHHGAALAAARLKPLIRAVQVFGF 407

                   sLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK
                    L  +D+Rq s+ +  vl  +     i ++Y   +Ee +   Ll  L
  gi|1242681   408 HLATVDLRQSSDQHEAVLAELMAGARIEAdYAAMPEEAKVALLLGLLNDA 457

                   RPLlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDv
                   R L        E  +  l  f+   E++      +    iis + + sD
  gi|1242681   458 RSLQVRGAVYSERTRGELAIFEAARE gralYGHAAIRHCIISHTETVSDL 507

                   LAvELLqRECgv.........kqtLrvvPLFEkLADLeAAPAavekLFsi
                   L v +Lq+E g+ +++ +++ +  L vvPLFE + DL+ A   +   +++
  gi|1242681   508 LEVLVLQKEAGLlqgtldtdaRCDLIVVPLFETITDLRQAAPIMREFYAL 557

                   DWYinri.......dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKv
                         + +++ ++   q+vm+GYsDs KD G +   W LY+A   ++
  gi|1242681   558 PGVLPLVlrsgadqYCEQDVMLGYSDSNKDGGFFTSNWELYRAETALVEL 607

                   A....KkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvq
                    ++ ++++G  L lFHGRGGtvGRGGGP   AiL+qPP t+nG +R t q
  gi|1242681   608 FeplkREHGLTLRLFHGRGGTVGRGGGPSYQAILAQPPGTVNGQIRLTEQ 657
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                    GEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE.WRkLmeemAv
                    GEvi   +   ++  r L    AAtLE  + PP    P  + +  + +
  gi|1242681   658 GEVIASKYANPEIGRRNLETLVAATLEATLLPPKRHAPKlFLDTADTLSQ 707

                    vAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesL
                         YR +v+  P F +YF  AtP  E   +niGsRPa Rk    ie L
  gi|1242681   708 LSMAAYRKLVYETPGFADYFFAATPIREIAELNIGSRPASRKATRAIEDL 757

                    RAiPWiFaWtqtRFHLPvWLGvGAAFK....hAidKDiKnlqkLkEmYke
                    RAiPW F+W q R  LP W G+G A  +  + A ++    l  L+ m  +
  gi|1242681   758 RAIPWGFSWGQCRVALPGWYGFGSAVEgflgDAPKQRKERLALLQRMHAQ 807

                    WPFFRvtlDLlEmvFAKGDPGiAaLyDkLL.vaEeLkPFGksLRdkYvEt
                    WPFF   l  ++mv AK D  iA+ y +L++     k     + ++++ t
  gi|1242681   808 WPFFGTLLSNIDMVLAKSDLAIATRYVELVpDKRAAKKIFAAVQAEWQRT 857

                    kdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsy
                       L  i G    L G   L   +  R +Yi  Ln +q   ++R R
  gi|1242681   858 DAVLAAITGEPRRLAGNAALARSIEHRLPYIDPLNHLQVELMRRYR---- 903

                    kvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAG
                                 + +     +  +L   erv  G+     + + G+AAG
  gi|1242681   904 -------------AQQ-----GRGELH--ERVQRGIH----MSINGVAAG 929

                    mqntG<-*
                    + n G
  gi|1242681   930 LRNSG    934

gi|284172789|ref|YP_003406171.1|: domain 1 of 1, from 1 to 896: score 229.9, E = 6.3e-66
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                 P         i  D   l   L+++L+D    +  E
  gi|2841727     1    ---------MPTHNR----EISRDVRELGELLgEVLKDQTSRQAFET 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v  C   + eY   +  ++ + L a L +L P    +v +a+     L n
  gi|2841727    35 VESCRQTAVEYRSGERESR-DPLVAELEGLSPHQQRIVVRAFTTYFELIN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAEE     R R++  +    ++  + t E  +      L        +
  gi|2841727    84 LAEE-----RERVRTIR----TESNEGTLEDGLSAAAAELGEED---VDT 121

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v + L    ++  +tAHPt + R+ +  K   i   L  L  + +t  ++
  gi|2841727   122 VHQVLDDVLIEPTFTAHPTEARRKTVKSKLRDISTHLETLDERLLTEKEQ 171

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   +  E+   + t  +R  qP P DE R    Y+  t+++ v
  gi|2841727   172 SQVWRDIDAEVTSLWQTPQVRNRQPEPEDEARNVQWYLENTLFDVVSEVY 221

                    RRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDvC
                         A   i        ++P+L +F sW G DRDG nP vtPEvt
  gi|2841727   222 DELADA---IDAEVDGDLEIPkLFEFRSWAGSDRDG-NPYVTPEVTSNTL 267

                    LLaRmmAanlYisqvEDLmFElsm....WRCndELRvRAEE.lyrtaard
                       R +    Y +q+  L   ls ++++     E  +  EE+  r + +
  gi|2841727   268 ERQREVVLEKYREQLKHLSGVLSQdgsrIDTDGEFEASLEEdRERLPGSA 317

                    kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                                 P EPY       R KL   RER    LA  + ++
  gi|2841727   318 -------RMAEERYPDEPY-------RQKLKLMRER----LAR-VGDVRP 348

                    eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                       y +v+e L  LE+  +sL +     + +  +  + Rqv tFG sL
  gi|2841727   349 GG-YDDVDELLNDLEIIAQSLRNNVAENVVEAHVDPIRRQVATFGFSLAS 397

                    LDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlg
                    LD+R   +++tD +    +  +i  Y + sE  R  +L   +    P+l
  gi|2841727   398 LDLREHQQKHTDAIAEALESEGI-DYYDLSEAERVTFLTDAVLQDEPVL- 445

                    sDLPkt....EEvkDvldafrvLA....ELPiDsFGaYiismataPsDvL
                     DL  t++ +E+ + v + f  LA+ ++E  +++   Y ism+  Ps vL
```

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  gi|2841727   446 -DLSETdglsEDSARVFELFDSLAdwqtEYGVEAIDTYAISMTDEPSHVL 494

                   AvELLqRECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYin
                    v  L    gv + +++  + +vPL E    L  A   +  LF  + Y
  gi|2841727   495 EVLFLADQAGVvslpeHSGIDIVPLLETEYALSGARRIMGTLFENEAYSQ 544

                   ridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                    ++ ++++qe+m+GYsDs K+ G l+A W L+k q  +  +  +y v++
  gi|2841727   545 ALEARgrtQEIMLGYSDSNKENGFLAANWSLFKNQRRLGEICDDYDVQMR 594

                   lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                   lFHGRGG + RGGGP   A+L+ P  ti G ++ t qGE i   +G   +
  gi|2841727   595 LFHGRGGSISRGGGPMNEALLALPNNTITGQVKFTEQGEAIAEKYGNPRI 644

                   CFrsLqRFtAAtL...EHGmnPPvsPkP.EWRkLmeemAvvAtEEYRsvv
                     r +     A L+ +   +n P    P+EW + me mA  A  EYR +
  gi|2841727   645 AERNIEQMLNAQLrarKQAINQPEEEIPsEWTDAMETMADAARQEYRNL- 693

                   vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWt
                   +    Fv YF  AtP +    +n+GsRPa R     +e LRAiPW+F+Wt
  gi|2841727   694 LESDGFVRYFEQATPITVIEDLNLGSRPASRSGERSVEDLRAIPWVFSWT 743

                   qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                   q R  LP W  v      A   D   +  L+EmY+eWPFFR tlD   +
  gi|2841727   744 QSRCILPGWYAVATGIE-AYLEDGGSMETLREMYDEWPFFRTTLDNAALS 792

                   FAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE
                     + D  iAa y ++   +    F  ++ ++++   +l+ +i G +D L
  gi|2841727   793 LSRTDLEIAAQYADIADPDLRERFFSRITAEFERALELITEI-GRRDELH 841

                   GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                      +L   l  R++Y+  Lnv+q   L          t r  +     +E
  gi|2841727   842 PRDWLGENLERRNPYVDPLNVLQVHLLEQ--------THRTDI-----EE 878

                   nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                      tL Lt+KGiAAGm+ntG
  gi|2841727   879 R----------------------TLRLTVKGIAAGMKNTG    896

gi|254525149|ref|ZP_05137204.1|: domain 1 of 1, from 12 to 903: score 229.8, E = 6.7e-66
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      s D  LR          +++ +  AL+ D  ++ +      +d+ E+
  gi|2545251    12    SPDLPLR----------DDVRRLGALVGDLLVEQVSAAFLDDVEEVR 48

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                               ++    L EL   L +  P  a  + +a++    + n+
  gi|2545251    49 ------TRAIARRENQAPLSELAEGLAGRTPQQAETMVRAFSTYFQVVNI 92

                   AEEvelAyRRRikkkkhGDFaDEasAttEsD.iEEtlKkLvlklnKsPeE
                   AE v+   RRR  ++        + A    D++ + l++L +++    +E
  gi|2545251    93 AERVHRIRRRRDYQRA-------GTAAPQPDgLQDALQHLKVQG-VGLDE 134

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     + L    ++ v+tAHPt +vRR+LL K+  +   L        t+ +
  gi|2545251   135 LAQWLPRIDIEPVFTAHPTEAVRRALLEKEQLMVASLVDNLDGQRTPGEA 184

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                             + A + t +    +Pt  DE      Y+   +++ +P
  gi|2545251   185 AADAARFRMALTASWQTTDSSPVRPTVDDEREHVGFYLVQVLYRVIPVLY 234

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                        AL+     E lP    L++F  W+GGD DG nP v     R
  gi|2545251   235 ESLQQALRDTYGGE-LPLPR-LLRFGTWVGGDMDG-NPNVDATTIRNTLD 281

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                     R      Y   +  L          + L    E +    a +  v++Y
  gi|2545251   282 AQRQSVLGRYQKELLQL---------ASLLSQSTERVGVSDALQARVQHY 322

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                       +q+ P    R    d+  +L n R RaR  L   + +   e  y
  gi|2545251   323 ----QQMMPKVQSRPRHADMPYRLLNDRMRAR--LQATLDD--GEGAYAG 364
```

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                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     +e ++ L L  +sL           ++  lL  v tFG  L +LD+RqE
  gi|2545251   365 PDELIDDLQLILHSLRANRGEHAGGFAVQRLLWRVKTFGFHLARLDVRQE 414

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    s  +   l  +    +  ++       R   L    +G  PL   D
  gi|2545251   415 SSVHARALATVLG--GDAAWDGLDAVGRARLLAPHASGEAPLPKGDDEGN 462

                    EEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq
                      +  v  a+ +  A    D+ G Yiisma   sDvLAv  L R  g+ q
  gi|2545251   463 QRLDAVFAALAdARARHGGDALGNYIISMAHDRSDVLAVLALARRGGLVQ 512

                    .....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...qevmv
                    +++  +L + PLFE + DL+   A++  L +   Y+ +++ +++ q vm+
  gi|2545251   513 gdgavPLDIAPLFETVNDLKRGTATLRDLLADPIYRAHLQARddvQMVML 562

                    GYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGG
                    GYsDs KD G  +  W L +Aq E+  vA + G++L+ FHGRGG + RGG
  gi|2545251   563 GYSDSSKDGGIAASRWGLQRAQVELLEVAAEAGIRLTFFHGRGGSISRGG 612

                    GPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtL
                    G t  A+ + P   i+G lRvt qGEvi   +G   L  rsL   t A L
  gi|2545251   613 GKTTHAVDASPRGSIDGRLRVTEQGEVIHRKYGIRALALRSLEQATGAVL 662

                    EHGmnPPvsPkP...EWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAt
                       + P  +P P++++WR +m+ +A    E YR  v     F++YFR At
  gi|2545251   663 RASLRPR-APEPredDWRPVMDAVASASSEVYRGFV-GQAGFMDYFRTAT 710

                    PElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWLGvG
                    P     +m +GsRP++R   +  +  LRAiPW+FaW q R  +P W GvG
  gi|2545251   711 PIDVIERMTLGSRPSRRLGQdAALGNLRAIPWVFAWSQARAVIPGWYGVG 760

                    AAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyD
                       + A+  D    q L+Em ++WPFFR  lD + mv  KGD  iA  +
  gi|2545251   761 SGLQAAV--DAGHEQTLREMARDWPFFRTFLDDIAMVLSKGDITIAEQFS 808

                    kLLvaEeLk.PFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLR
                    kL  + eL++ F  ++  + + t+ +LL +   + lL+ D  L   +RLR
  gi|2545251   809 KL--SGELHgRFFPQVQRELELTRHWLLALMDQQTLLDHDARLALSIRLR 856

                    dsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLn
                    ++Y+  + v+q   L+R R               A     + d+L++
  gi|2545251   857 NPYVDPISVLQVDLLQRWR----------------ASGR--EDDDLLR-- 886

                    ptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                L+  + G+  G+qntG
  gi|2545251   887 -----------ALVACVNGVSQGVQNTG    903

gi|269796282|ref|YP_003315737.1|: domain 1 of 1, from 14 to 900: score 229.8, E = 6.8e-66
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                             R  +   +   ekL     LL D    iL +  G+dL + v
  gi|2697962    14    EATPDDRDDARDEMP--EKLRADVRLLGDLLGTILREAGGPDLLDDV 58

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         l        ++  ++E  + +    P  a  vA+a++    L nL
  gi|2697962    59 ERLRGLVIKARTSPESGAIDEAETLVDTFSPERAEEVARAFSCYFHLVNL 108

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEE    +R R+  ++  + +  a+A     + + l +L   l   P+E
  gi|2697962   109 AEE---HHRVRVVHQHEAEVS-PAEAQAQDYLPDALNRLEAEL--GPDET 152

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L       v+tAHPt + RR++     Ri   La      +    +
  gi|2697962   153 RRRLAGLEFRPVFTAHPTEARRRAIAASIRRITTLLAARDDSSLAGVSRL 202

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    E  + L  Ei   +Rt  +R ++P P DE+R  m  + Et+++  P   R
  gi|2697962   203 ENTDQLLAEIDGLWRTSPLRTTKPSPLDEVRTAMGVFDETLFRVLPEVYR 252

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R D  +         P   P ++   W+GGDRDG nP vt  +tR
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```
  gi|2697962   253 RLDSWVNRDEPGISTPVAPPFVRLGTWIGGDRDG-NPNVTASITRT---- 297

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEEl..yrtaardkvvKy
                   a  +A+   +  +E +   +      d     A E  ++   a+ ++
  gi|2697962   298 AAAIASEHVLIALENVAERVGRTMTLDATTTPASEAldQLWLAQRQLAPE 347

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                            P+EP R  L  v ++L  tR R   L            y
  gi|2697962   348 ITADISSRSPNEPHRRTLLVVAERLRATRRRDADL-----------AYP 385

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                     E+ L  L     sL   G + +A   L  ++ qv tFG  L  L++Rq
  gi|2697962   386 TAEDLLADLQTIQDSLVAAGARRVAYSDLQKFIWQVQTFGFHLAELEVRQ 435

                   EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP.
                    s+ + + l  i +H                            g+D P+
  gi|2697962   436 HSQVHRETLAEIAEH----------------------------GADGPg 456

                   ktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvELLqRE
                     E   +vld+fr +A + +++++ +   Y++s +t+  D   v  L
  gi|2697962   457 LSERAVEVLDTFRAIAAIQkrhgVAAARRYVVSFTTSAEDLGNVYTLAAH 506

                   C..gvkqt..LrvvPLFEkLADLeAAPAavekLFsiDWYinri...dGKq
                     +g  +t+ L vvPLFE  ADL+AAP  ++        + r+  +d +
  gi|2697962   507 AlgGPEHTpvLDVVPLFETFADLQAAPGVLAEYVENPLVVERLaatDRRL 556

                   evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                   evm+GYsDs KD G +sA   LY Aq+ i+  A+   v L+lFHGRGG
  gi|2697962   557 EVMLGYSDSSKDVGPVSATLALYEAQDKIAAWAQAADVTLTLFHGRGGAL 606

                   GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                   GRGGGP   A+L+qPP  ++G  + t qGEvi   +G+  +  r +   +
  gi|2697962   607 GRGGGPANRAVLAQPPGSVDGRFKLTEQGEVIAARYGDPTIATRHIEQVA 656

                   AAtLEHGmnPPvsPk.....PEWRkLmeemAvvAtEEYRsvvvKEPRFvE
                   AAtL   m P v  ++ +    + ++   +  v    +  +v  E  F
  gi|2697962   657 AATLLQSM-PSVGDRnaqaaERFTDVAATLDTVSRKRFFELVHAEG-FPA 704

                   YFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqtRFHLP
                   +F   tP  E G + +GsRPaKR  s + ++ LRAiPW+FaWtq R  L
  gi|2697962   705 WFAQVTPQEEIGLLPLGSRPAKRGLSVnSLDDLRAIPWVFAWTQARINLT 754

                   vWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPG
                    W G+G A        +  l  Lk  Y++WP F   +D +Em  AK D
  gi|2697962   755 GWFGLGTALAA-----VGDLDELKTAYEQWPLFSTMIDNVEMSLAKTDVR 799

                   iAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                   iA  y  L   ++L      + d+   t++++Lki G   +L     L
  gi|2697962   800 IAERYLALGDRDDLATL---VLDEMAVTREWVLKITGKTTMLGNLHVLGR 846

                   rlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkade
                    + LR +Y+  L  +q   L+ +R                A E+
  gi|2697962   847 AVQLRSPYVDALSLIQLRALRALRKG--------------APED------ 876

                   LvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                             P L   L+L + GiAAG+qntG
  gi|2697962   877 ---------QVPQLQRLLLLSVNGIAAGLQNTG    900

gi|291455731|ref|ZP_06595121.1|: domain 1 of 1, from 10 to 917: score 229.5, E = 8.5e-66
                   *->siDAqLRlLvPG.KvsedekLieYDALLlDkFLDiLqDLHGedLkEa
                        DA +     G+K  e+ +L +     +D  L iL D+ Ge   E
  gi|2914557    10    PADAAIVTTGTGrKGPEEHDLPQSLKDDMDLCLKILRDVLGEYNPEL 56

                   v.......qECYElsAe.YEGKkDtk....KLeELGakLtsLdPaDailv
                    ++ ++ +    E sAe++   +D+ + ++ L E   ++  +   Da l+
  gi|2914557    57 LstfdtvrNYSVEASAEhFAELEDPNpaqdGLKEAVNVIDNMTLHDAQLL 106

                   AkailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlK
                   A+a+     LAnL EE    yR  +   +    + E       ++   +
  gi|2914557   107 ARAFATYFHLANLSEE---NYRVSVLHERENNVSGEQAVDPINELTVAYH 153
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                kLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLa
                +L+      P+   e L       v+tAHPt + R+++  K  Ri   L
gi|2914557   154 QLINEM--GPAKAKELLDQLEFHPVFTAHPTEARRKAVEGKIRRISELLG 201

                qLsAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYi
                    K +   DKkE    L  Ei A FRt  i   +PtP +E    +  +
gi|2914557   202 EY--KILGGSDKKECLRRLYNEIDALFRTSPIALKKPTPVEEADTILDIF 249

                HEtvWkGvPKFLRRvDtAL..KniGinERlPYdvPLikFssWmGGDRDGk
                  t+++ +PK  RR D  + +   G+ E  P      +  sW+G DRDG
gi|2914557   250 DNTLFHTIPKVYRRFDDWIlgDQAGLVE--PACPAFFHPGSWIGSDRDG- 296

                nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEE
                nP vt  v R v   aR   +   i  +E+     +       L   AE
gi|2914557   297 NPNVTAKVSRAV---ARKF-SDHVIAALEE-----ATRTVGRNLTMEAET 337

                lyrtaardkvvKyYiEFWKq.......vPPtEPYRviLGdvRDKLYntRE
                    a  + +  +  E     +++   +   E  R ++  + D+L  t E
gi|2914557   338 TPPSAELKNLWSHQKEMSERltdkaalISTKEMHRAVMLVMADRLHYTIE 387

                RaRHLLAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLL
                R   L+            y   ++FL  L +  +sL e G k  A G L
gi|2914557   388 RDADLM------------YHSCDDFLNDLKVVQRSLAEAGAKRSAYGPLQ 425

                DlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRq
                Dl+ q  tFG  +v ++ Rq s  +   l  i +H
gi|2914557   426 DLIWQTETFGFHMVEMEFRQHSVVHARALADIREH--------------- 460

                EWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYi
                      L+G R  l    P+t E   vld+fr L  + ++++  +   Yi
gi|2914557   461 -----GLHGERGDLQ---PMTHE---VLDTFRALGAIQkrngLKAARRYI 499

                ismataPsDvLAvELLqRECgvk....qtLrvvPLFEkLADLeAAPAave
                is + +   +  v  L R    ++++  t+ v+PLFE+L DL+     +e
gi|2914557   500 ISFTKSAQNIKDVYELNRLAFSHpedvPTIDVIPLFEQLEDLQNSVDVLE 549

                kLFsiDWYinridG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiK
                 +  i     r+  +++K evm+GYsDs KDAG  sA   L  AqE i+K
gi|2914557   550 EMIKIPEVQARLKAtgnKLEVMLGYSDSSKDAGPTSATLALHSAQERIAK 599

                vAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEv
                 A  + + L+lFHGRGG vGRGGGP   A+L+qP   ++   + t qGEv
gi|2914557   600 WAESHDIDLTLFHGRGGAVGRGGGPANRAVLAQPVGSVKCRFKLTEQGEV 649

                iEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPk.PEWRkLmeemAvvAt
                i   +G   L  r +   +AAtL     P v  ++ +  k   +mA
gi|2914557   650 IFARYGNPVLAIRHVESVAAATLLQS-APSVEKRnTDMTKKYADMAAQLD 698

                EEY..Rsv.vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.Gies
                E  ++R ++ +    F  +F   tP +E G + iGsRPaKR  + + ++
gi|2914557   699 EAAhnRFLdLLNTDGFAPWFSIVTPLTEIGLLPIGSRPAKRGLGAkSLDD 748

                LRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPF
                LR iPWiF+W q R  L  W G+G A           l  ++  Y+eWP
gi|2914557   749 LRTIPWIFSWAQARINLAAWYGLGTACEK-----FGDLETMRQAYEEWPL 793

                FRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlL
                F   +D +Em  AK D  iA +y  L   E+L    k++ ++ + t++++
gi|2914557   794 FSTFIDNIEMSIAKTDERIAKMYLALGDREDLN---KKVLEEMELTRKWV 840

                LkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtl
                L i G k  L     L q +R+R +Y+  L v q   LK          l
gi|2914557   841 LDIVGDKWPLQHRHVLGQAIRIRSPYVDALSVTQVLALK---------SL 881

                rPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqnt
                r ++ KE       + ++ + L             + t+ G+AAG+qnt
gi|2914557   882 RKKVDKEELSQS--QQAGFIYLI-------------LCTVSGVAAGLQNT 916

                G<-*
                G
gi|2914557   917 G    917
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gi|194364406|ref|YP_002027016.1|: domain 1 of 1, from 12 to 903: score 228.9, E = 1.3e-65
                  *->siDAqLRlLvP..GKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                     s D  LR  v + G     + L+e    +   FLD + D+    +
  gi|1943644    12    SPDLPLRDDVRrlGALV-GDLLVEQ---VSAAFLDDVEDVRTRAIAR 54

                  avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                               ++    L EL   L + +P  a  + +a++    +
  gi|1943644    55 --------------RENQAPLSELADGLAGRAPQQAETMVRAFSTYFQVV 90

                  nLAEEvelAyRRRikkkkhGDFaDEasAttEsD.iEEtlKkLvlklnKsP
                  n+AE v+   RRR  ++        + A    D++ + l++L  ++
  gi|1943644    91 NIAERVHRIRRRRDYQRA-------GTAGAQPDgLQDALQHLKAQG-VGL 132

                  eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                  +E  + L    ++ v+tAHPt +vRR+LL K+  +   L        t+
  gi|1943644   133 DELAQWLPRIDIEPVFTAHPTEAVRRALLEKEQLMVASLVDNLDGQRTPG 182

                  DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                  +           + A + t +    +Pt  DE      Y+   +++ +P
  gi|1943644   183 EAAADAARFRMALTASWQTTDSSPVRPTVDDEREHVGFYLVQVLYRVIPV 232

                  FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                         AL+     E lP    L++F  W+GGD DG nP v     R
  gi|1943644   233 LYESLQQALRDT-YGEELPLPR-LLRFGTWVGGDMDG-NPNVDATTIRNT 279

                  CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      R      Y   +  L          + L    E +    a +  v
  gi|1943644   280 LDAQRQAVLGRYQKELLQL---------ASLLSQSTERVGVSNALQARVA 320

                  yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                  +Y    +q+ P+   R    d+  +L n R RaR  L   + +      y
  gi|1943644   321 HY----QQLLPQVQSRPRHADMPYRLLNDRMRAR--LQATLDD--GAGAY 362

                  tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     +e ++ L L   sL           ++  lL  v tFG  L +LD+R
  gi|1943644   363 AGPDELIDDLQLILDSLRANRGEHAGGFAVQRLLWRVKTFGFHLARLDVR 412

                  qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                  qEs  +   l A+    +  ++       R   L     G  PL   +
  gi|1943644   413 QESSVHARALAAVLG--GDAAWEGLDVLGRARLLAPHAGGEVPLPKGEDE 460

                  ktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                      +  v  a+ +  A    D+ G+Yiisma   sDvLAv  L R  g+
  gi|1943644   461 GNQRLDAVFAALAdARARHGGDALGSYIISMAHDRSDVLAVLALARRGGL 510

                  kq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinri...dGKqev
                    +++  +L + PLFE + DL+   A++  L +   Y+ +++ +d  q v
  gi|1943644   511 VDdndavPLDIAPLFETVDDLKRGTATLRDLLADPVYRAHLrarDDVQMV 560

                  mvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGR
                  m+GYsDs KD G  +  W L +Aq E+  vA + G++L+ FHGRGG + R
  gi|1943644   561 MLGYSDSSKDGGIAASRWGLQRAQVELLEVAAEAGIRLTFFHGRGGSISR 610

                  GGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAA
                  GGG t  A+ + P   i+G lRvt qGEvi   +G   L  rsL   t A
  gi|1943644   611 GGGKTTHAVDASPRGSIDGRLRVTEQGEVIHRKYGIRALALRSLEQATGA 660

                  tLEHGmnP.PvsPkP.EWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlA
                   L   + P+ v P+ ++WR +m+ +A    E YR+ v +   F++YFR A
  gi|1943644   661 VLRASLRPrAVEPREdDWRPVMDVVAGSSSEVYRAFVGQSG-FMDYFRTA 709

                  tPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWLGv
                  tP     +m +GsRP++R   +  +  LRAiPW+FaW q R  +P W Gv
  gi|1943644   710 TPIDVIERMTLGSRPSRRLGQdAALGNLRAIPWVFAWSQARAVIPGWYGV 759

                  GAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLy
                  G   + A+  D    q L+Em ++WPFFR  lD + mv  KGD  iA  +
  gi|1943644   760 GSGLQAAV--DAGHEQTLREMARDWPFFRTFLDDIAMVLSKGDITIAEQF 807

                  DkLLvaEeLk.PFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRL
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                    kL  + eL++ F  ++  + + t+ +LL + G + lL+ D  L   +RL
  gi|1943644   808 SKL--SGELHgRFFPQVQRELELTRHWLLALMGQRTLLDHDARLSLSIRL 855

                    RdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkL
                    R++Y+  + v+q   L+R R               A     + d+L++
  gi|1943644   856 RNPYVDPISVLQVDLLQRWR----------------ASGG--EDDDLLR- 886

                    nptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                L+  + G+  G+qntG
  gi|1943644   887 ------------ALVACVNGVSQGVQNTG    903

gi|94496216|ref|ZP_01302794.1|: domain 1 of 1, from 1 to 899: score 228.8, E = 1.3e-65
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        ++      +P      +  i+Y   Ll    D++    Ge L
  gi|9449621     1    -MESHAQQAAPAITQ--NPDIRYLGRLLG---DVIRAYGGEKLYQ-- 39

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    q  Y  sA  +  +  +  +   + L +L+  D++   + ++    LAnL
  gi|9449621    40 QTEYIRSASVDRARGVQGADLTDTGLDALNLDDTLNFTRGFMLFSMLANL 89

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+           +         A   +D+   lK+L +++    + v
  gi|9449621    90 AED-----------R-----QGVAAEPGADVASALKRLESQG-VGRDAV 121

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     + L    +  vltAHPt   R+s++  + Ri   +    A      D +
  gi|9449621   122 LDLLAHSLIVPVLTAHPTEVRRKSMIDHKNRIADLMHLKDAGRTETADGE 171

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     LDEA+ R i   + t  +RR +    DE+   ++Y+ +      P
  gi|9449621   172 NLDEAIFRQIALLWQTRPLRREKLFVADEIENVLAYFRDSFLPVLPALYA 221

                    RvDtALKniGinERlPYdvP..LikFssWmGGDRDGknPRvtPEvtRDvC
                    R           ER+    P++ ++  sW+GGDRDG nP v
  gi|9449621   222 RW----------ERVLGARPqsFLRVGSWIGGDRDG-NPFVQAPQLQYAL 260

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                          A   Y++ v  L  Els+      +     +l + +  d + +
  gi|9449621   261 KRGAAAAIAYYLDGVHALGAELSLSTELAHVPQAVLDLAQASGDDALSRK 310

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                               EPYR  L  +  +L  t            s +  e  y
  gi|9449621   311 ----------DEPYRRALSGIYARLAATCVSLTGDQPARPSALKGEP-YA 349

                    kvEeFLEPLELCYksLCeCGDkviADGsLL.DlLRqvstFGLsLvKLDiR
                       +    L +  + L   G  ++A G  L+ l+R v tFG  L  LD+R
  gi|9449621   350 SPADLRHDLVVVAQGLASEGNGALASGGALgRLIRAVETFGFHLATLDMR 399

                    qEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgsDL
                    q s  +  v+  + +  ++ ++Y    E  R   L  EL   RPL
  gi|9449621   400 QNSAVHERVVAELLKIAGVEAdYLALDEYARIALLRRELANNRPLGSRFS 449

                    PktEEvkDvldafrvLAELPi....DsFGaYiismataPsDvLAvELLqR
                       +E +  l  ++  AE     ++ +   Yiisma + sD L v +L +
  gi|9449621   450 AYSDETASELAIVHAAAEAHRlygpQCITHYIISMAQSVSDLLEVNILLK 499

                    ECgv.........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                    E g+ + ++++++++ ++  +PLFE + DLeAAP  +   F +      +
  gi|9449621   500 EAGLwrvgdngdppHAAIMAIPLFETIGDLEAAPKIMSAYFGLPEIAGVV 549

                    d..GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                      +G qevm+GYsDs KD G +   W LYkA   +  v  + G  + lFH
  gi|9449621   550 KarGHQEVMIGYSDSNKDGGYITSTWGLYKASKALEPVFAEAGAAMQLFH 599

                    GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                    GRGG vGRGGG    Ai +qP   ++G +R+t qGEvi   FG  ++
  gi|9449621   600 GRGGAVGRGGGSAFAAIQAQPKGSVQGRIRITEQGEVIAAKFGTRDVAMT 649

                    sLqRFtAAtLEHGmnPP.vsPkPEWR..kLmeemAvvAtEEYRsvvvKEP
                     L   t AtL   ++P ++s +   R    m+e+   A   YR +v+
  gi|9449621   650 NLEATTSATLLASLEPEgISQRDAARfaGAMDELSKNAFAAYRDLVYGTE 699
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                    RFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRF
                     F ++FR  tP  E   + iGsRPa Rk s  ie LRAiPW+F+W q R
  gi|9449621   700 GFRDFFRQLTPIQEIAGLKIGSRPASRKKSSRIEDLRAIPWVFSWAQARV 749

                    HLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                     LP W GvG A     dK       L +m + W F +  l  +Emv AK
  gi|9449621   750 MLPGWYGVGQALAGFEDK-----ALLADMAQHWAFLKSALANMEMVLAKS 794

                    DPGiAaLyDkLLvaEeLk..PFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                    D GiAa y  L+    L ++ FG+ +R+ ++  +d LL+  G   lLE
  gi|9449621   795 DLGIAARYLPLVEDQGLAddIFGR-IREGWQAAHDGLLQATGQSRLLESN 843

                    PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                    P L   +RLR +Yi  Ln +q   LKR R                A E+
  gi|9449621   844 PALETSIRLRLPYIEPLNLLQVELLKRHR----------------AGEE- 876

                    kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                 r+  G+E    L +  iA  + n G
  gi|9449621   877 -----------DPRIKEGIE----LSINAIATALRNSG    899

gi|103488557|ref|YP_618118.1|: domain 1 of 1, from 1 to 889: score 228.7, E = 1.5e-65
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                              +  P ++s ++  i+Y    l + L+D++    G+ L  +
  gi|1034885     1    -------MGPPIQIS-QNPDIRY----LGRILgDVIRAYGGDKL--F 33

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                     q  Y  s   +  +     e +   L +L   D+i   + ++    LAn
  gi|1034885    34 RQTEYIRSSSVDRHRGIAGAEAIDPGLDALSLDDTIAFVRGFMLFSMLAN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAE+     R  i                E+ +   l kL   +    +
  gi|1034885    84 LAED-----RQGIAAEP------------EATVAAALEKLKADG-IDSAA 115

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsA.KDvtveD
                    v   L    +  vltAHPt   R+s+L  + Ri   +    A+ D t+e
  gi|1034885   116 VAALLNAALIAPVLTAHPTEVRRKSMLDHKNRIAELMRMRDAgLDETPEG 165

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                       +++A+ R +   + t  +R  +    DE+   + Y+ +     vPK
  gi|1034885   166 -DVVEDAIRRQVVLLWQTRPLRTQKLFVADEIDNALTYLRDVFLPVVPKL 214

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                      R +   K +G        +  ++  sW+GGDRDG nP vt E  R
  gi|1034885   215 YARWE---KELGQR-----PASFLRIGSWIGGDRDG-NPFVTAETLRMAT 255

                    LLaRmmAanl..YisqvEDLmFEls....mWRCndELRvRAEElyrtaar
                       R  Aa +++Yi+qv  L  Els ++++    d + + AE    ta +
  gi|1034885   256 --GRNAAAVIghYIDQVHALGAELSvsstLAPVTDAVEALAEASGDTAPS 303

                    dkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseis
                                    EPYR  L  +  +L  t              +
  gi|1034885   304 R--------------SDEPYRRALSGIYARLSATYAAITGKPPPRPGALK 339

                    EeAvytkvEeFLEPLELCYksLCeCGDkviAD.GsLLDlLRqvstFGLsL
                     e  y    +F   L      L   G   +A  G+L  l+R v  FG  L
  gi|1034885   340 GEP-YAAPGDFRRDLVTIASGLSASGKGQLAGiGALGRLIRAVEVFGFHL 388

                    vKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRP
                      LD+Rq s  +  vl  +    ++ ++Y    E  R   L  EL   RP
  gi|1034885   389 ATLDMRQNSAVHERVLAELFNISGVEAdYLTLDEAARVALLRKELGVNRP 438

                    LlgsDLPktE....EvkDvldafrvLAELPiDsFGaYiismataPsDvLA
                    L  +     E++ +E++ v  a  v   L  D+   +iis a + sD L
  gi|1034885   439 LAAPWHEWSEetagELAIVHAAADVRKRLGKDAIVQWIISKAESLSDLLE 488

                    vELLqRECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                    v +L RE g+ + +++  L vvPLFE +ADL+ APA ++  F++     +
  gi|1034885   489 VHVLAREGGLwsaesRDNLMVVPLFETIADLDDAPAIMAAYFALPEIAPH 538

                    id..GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
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                  +  +G qevm+GYsDs KD G l   W L +A   +  v  +    + lF
  gi|1034885   539 VAarGHQEVMIGYSDSNKDGGYLTSTWGLHQASAALTPVFEQADTAMQLF 588

                  HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                  HGRGG vGRGGG    Ai +qP  t++G +R+t qGEvi   +G  +
  gi|1034885   589 HGRGGAVGRGGGSAFAAIRAQPAGTVQGRIRITEQGEVIAAKYGTIDSAA 638

                  rsLqRFtAAtLEHGmnPPvsPkPEWRkL...meemAvvAtEEYRsvvvKE
                    L     A L   ++P      E  + +  m+ +   A   YR +v+
  gi|1034885   639 TNLEAMVSASLLASLEPEAMGAKEAERFtaaMDALSDTAFAAYRGLVYDT 688

                  PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
                  P F ++FR  tP  E   + iGsRP+ R  s  ie LRAiPW+F+W q R
  gi|1034885   689 PAFRDFFRAMTPIAEIATLKIGSRPSSRTKSTAIEDLRAIPWVFSWAQAR 738

                  FHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAK
                    LP W G G AF    dK       L +m   WPFF   l  +Emv AK
  gi|1034885   739 TMLPGWYGTGEAFAAFADK-----ALLTDMAASWPFFAALLGNMEMVLAK 783

                  GDPGiAaLyDkLL..vaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                   D GiAa y  L +++      FG+ ++d +   +d LL+i G   lLE
  gi|1034885   784 SDMGIAARYAGLAsqIDGHDAIFGR-IKDGWNRAHDGLLEITGQTRLLEK 832

                  DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                   P L   +RLR +Yi  Ln +q   +KR R               A E
  gi|1034885   833 NPALEASIRLRLPYIEPLNLLQIELMKRHR----------------AGET 866

                  skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                  P + + + Lt+  iA  + n G
  gi|1034885   867 ----------------DPRIAEGIQLTINAIATALRNSG    889

gi|213690981|ref|YP_002321567.1|: domain 1 of 1, from 10 to 917: score 227.2, E = 4.1e-65
                  *->siDAqLRlLvPG.KvsedekLieYDALLlDkFLDiLqDLHGedLkEa
                       DA +     G+K  e+ +L e     +D  L+iL  + Ge   E
  gi|2136909    10    PADAAIVTTGTGrKGPEEHDLPESLKYDMDLCLEILRNVLGEYNPEL 56

                  v.......qECYElsAeY..EGKk...DtkKLeELGakLtsLdPaDailv
                   ++ ++ +    E sAe   E K +++D   L E   ++  +   Da l+
  gi|2136909    57 LstfdtvrHYAVEASAEHfaELKDpnpDQDGLKEAVNVIDNMTLHDAQLL 106

                  AkailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlK
                  A+a+     LAnL EE    yR  +   +    + +       ++   +
  gi|2136909   107 ARAFATYFHLANLSEE---NYRVSVLHERENNVSVDQAVDPINELTVAYH 153

                  kLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLa
                  +L+      P+   e L       v+tAHPt + R+++  K  R+   L
  gi|2136909   154 QLINET--GPAKAKELLNQLEFHPVFTAHPTEARRKAVEGKIRRVSELLE 201

                  qLsAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYi
                      K +   DKkE    L  Ei A FRt  i   +PtP +E    +  +
  gi|2136909   202 EY--KRLGGSDKKECLRRLYNEIDALFRTSPIALKKPTPVEEADTILDIF 249

                  HEtvWkGvPKFLRRvDtAL..KniGinERlPYdvPLikFssWmGGDRDGk
                    t+++ +PK  RR D  + +   G+ E  P      +  sW+G DRDG
  gi|2136909   250 DNTLFNTIPKVYRRFDDWVlgDKAGLVE--PACPAFFHPGSWIGSDRDG- 296

                  nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsm.WRCndELRvRAE
                  nP vt  v R v   aR   +   i  +E+    +  +     E
  gi|2136909   297 NPNVTAKVSRAV---ARKF-SDHVIAALEEATRTVGRnLTMEAETTPPSA 342

                  Elyrt.aardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL
                  El++  + ++ +     +    +   E  R ++  + D+L  t ER   L
  gi|2136909   343 ELKSLwSHQKEMSERLTDKAALISTKEMHRAVMLVMADRLHYTIERDADL 392

                  LAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                  +            y   ++FL  L +  +sL   G k  A G L Dl+ q
  gi|2136909   393 M------------YHSCDDFLADLKVVQRSLAAAGAKRSAYGPLQDLIWQ 430

                  vstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLla
                    tFG  +v ++ Rq s  +   l  i +H
  gi|2136909   431 TETFGFHMVEMEFRQHSVVHARALADIREH-------------------- 460
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                    ELkGKRPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismat
                     L+G R  l    P+t E   vld+fr L  + ++++  +   Yiis +
  gi|2136909   461 GLHGERGELQ---PMTHE---VLDTFRALGAIQkrngLKAARRYIISFTK 504

                    aPsDvLAvELLqRECgvk....qtLrvvPLFEkLADLeAAPAavekLFsi
                    +   +  v  L R    ++++  t+ v+PLFE+L DL+     +e +  i
  gi|2136909   505 SAQNIKDVYELNRLAFSHpedvPTIDVIPLFEQLEDLQNSVDVLEEMIKI 554

                    DWYinridG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKky
                         r+  +++K evm+GYsDs KDAG  sA   L  AqE i+K A  +
  gi|2136909   555 PEVQARLKAtgnKLEVMLGYSDSSKDAGPTSATLALHSAQERIAKWAESH 604

                    GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF
                     + L+lFHGRGG vGRGGGP   A+L+qP   ++   + t qGEvi   +
  gi|2136909   605 DIDLTLFHGRGGAVGRGGGPANRAVLAQPVGSVKCRFKLTEQGEVIFARY 654

                    GEEnLCFrsLqRFtAAtLEHGmnPPvsPk.PEWRkLmeemAvvAtEEY..
                    G   L  r +   +AAtL     P v  ++ E  +   +mA    E  ++
  gi|2136909   655 GNPVLAIRHVESVAAATLLQS-APSVEKRnTEMTERYADMAAQLDEAAhn 703

                    Rsv.vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiP
                    R ++ +    F  +F   tP +E G + iGsRPaKR  + + ++ LR iP
  gi|2136909   704 RFLdLLNTDGFAPWFSIVTPLTEIGLLPIGSRPAKRGLGAkSLDDLRTIP 753

                    WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                    WiF+W q R  L  W G+G A           l  ++  Y+eWP F   +
  gi|2136909   754 WIFSWAQARINLAAWYGLGTACEK-----FGDLETMRQAYEEWPLFSTFI 798

                    DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                    D +Em  AK D  iA +y  L   E+L    +++ ++ + t++++L i G
  gi|2136909   799 DNIEMSIAKTDERIARMYLALGDREDLN---EKVLNEMELTRKWVLAIVG 845

                    HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                     k  L     L q +R+R +Y+  L v q   LK          lr ++
  gi|2136909   846 DKWPLQHRHVLGQAIRIRSPYVDALSVTQVLALK---------SLRKKVD 886

                    KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    KE       + ++ + L              + t+ G+AAG+qntG
  gi|2136909   887 KEELSQS--QQAGFIYLI-------------LCTVSGVAAGLQNTG    917

gi|23465189|ref|NP_695792.1|: domain 1 of 1, from 10 to 917: score 226.9, E = 5.1e-65
                    *->siDAqLRlLvPG.KvsedekLieYDALLlDkFLDiLqDLHGedLkEa
                         DA +     G+K  e+ +L e     +D  L+iL  + Ge   E
  gi|2346518    10    PADAAIVTTGTGrKGPEEHDLPESLKYDMDLCLEILRNVLGEYNPEL 56

                    v.......qECYElsAeY..EGKk...DtkKLeELGakLtsLdPaDailv
                     ++ ++ +    E sAe   E K +++D   L E   ++  +   Da l+
  gi|2346518    57 LstfdtvrHYAVEASAEHfaELKDpnpDQDGLKEAVNVIDNMTLHDAQLL 106

                    AkailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlK
                    A+a+     LAnL EE    yR  +   +   + +       ++   +
  gi|2346518   107 ARAFATYFHLANLSEE---NYRVSVLHERENNVSVDQAVDPINELTVAYH 153

                    kLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLa
                    +L+      P+   e L       v+tAHPt + R+++  K  R+   L
  gi|2346518   154 QLINET--GPAKAKELLNQLEFHPVFTAHPTEARRKAVEGKIRRVSELLE 201

                    qLsAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYi
                        K +   DKkE    L  Ei A FRt  i   +PtP +E    +  +
  gi|2346518   202 EY--KRLGGSDKKECLRRLYNEIDALFRTSPIALKKPTPVEEADTILDIF 249

                    HEtvWkGvPKFLRRvDtAL..KniGinERlPYdvPLikFssWmGGDRDGk
                      t+++ +PK  RR D  + +   G+ E  P      +  sW+G DRDG
  gi|2346518   250 DNTLFNTIPKVYRRFDDWVlgDKAGLVE--PACPAFFHPGSWIGSDRDG- 296

                    nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsm.WRCndELRvRAE
                    nP vt  v R v   aR   +   i  +E     +  +     E
  gi|2346518   297 NPNVTAKVSRAV---ARKF-SDHVIAALEQATRTVGRnLTMEAETTPPSA 342

                    Elyrt.aardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL
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                    El++  + ++ +     +    +   E  R ++  + D+L  t ER   L
  gi|2346518   343 ELKSLwSHQKEMSERLTDKAALISTKEMHRAVMLVMADRLHYTIERDADL 392

                    LAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                    +            y   ++FL  L +  +sL   G k  A G L Dl+ q
  gi|2346518   393 M------------YHSCDDFLADLKVVQRSLAAAGAKRSAYGPLQDLIWQ 430

                    vstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLla
                      tFG  +v ++ Rq s  +   l  i +H
  gi|2346518   431 TETFGFHMVEMEFRQHSVVHARALADIREH-------------------- 460

                    ELkGKRPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismat
                     L+G R  l    P+t E   vld+fr L  + ++++  +   Yiis +
  gi|2346518   461 GLHGERGELQ---PMTHE---VLDTFRALGAIQkrngLKAARRYIISFTK 504

                    aPsDvLAvELLqRECgvk....qtLrvvPLFEkLADLeAAPAavekLFsi
                    +   +  v  L R    ++++  t+ v+PLFE+L DL+     +e +  i
  gi|2346518   505 SAQNIKDVYELNRLAFSHpedvPTIDVIPLFEQLEDLQNSVDVLEEMIKI 554

                    DWYinridG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKky
                         r+  +++K evm+GYsDs KDAG  sA   L  AqE i+K A  +
  gi|2346518   555 PEVQARLKAtgnKLEVMLGYSDSSKDAGPTSATLALHSAQERIAKWAESH 604

                    GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF
                     + L+lFHGRGG vGRGGGP   A+L+qP   ++   + t qGEvi   +
  gi|2346518   605 DIDLTLFHGRGGAVGRGGGPANRAVLAQPVGSVKCRFKLTEQGEVIFARY 654

                    GEEnLCFrsLqRFtAAtLEHGmnPPvsPk.PEWRkLmeemAvvAtEEY..
                    G   L  r +   +AAtL     P v  ++ E  +   +mA    E  ++
  gi|2346518   655 GNPVLAIRHVESVAAATLLQS-APSVEKRnTEMTEKYADMAAQLDEAAhn 703

                    Rsv.vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiP
                    R ++ +    F  +F   tP +E G + iGsRPaKR  + + ++ LR iP
  gi|2346518   704 RFLdLLNTDGFAPWFSIVTPLTEIGLLPIGSRPAKRGLGAkSLDDLRTIP 753

                    WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                    WiF+W q R  L  W G+G A           l  ++  Y+eWP F   +
  gi|2346518   754 WIFSWAQARINLAAWYGLGTACEK-----FGDLETMRQAYEEWPLFSTFI 798

                    DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                    D +Em  AK D  iA +y  L   E+L    +++ ++ + t++++L i G
  gi|2346518   799 DNIEMSIAKTDERIARMYLALGDREDLN---EKVLNEMELTRKWVLAIVG 845

                    HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                     k  L     L q +R+R +Y+  L v q   LK          lr ++
  gi|2346518   846 DKWPLQHRHVLGQAIRIRSPYVDALSVTQVLALK---------SLRKKVD 886

                    KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    KE       + ++ + L              + t+ G+AAG+qntG
  gi|2346518   887 KEELSQS--QQAGFIYLI-------------LCTVSGVAAGLQNTG    917

gi|292676674|dbj|BAI98192.1|: domain 1 of 1, from 5 to 905: score 225.9, E = 1e-64
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       si A L       +  ++  i+Y   Ll    D++    Ge +
  gi|2926766     5    SIMATLASSSVPAIT-QNPDIRYLGRLLG---DVIRAYGGEKIYK-- 45

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    q  Y  sA  +  +  +  + + + L +L+  D++   + ++    LAnL
  gi|2926766    46 QTEYIRSASVDRARGLHGADVVDTGLDALNLDDTLSFVRGFMLFSMLANL 95

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AE+            +         A   +D+   + kL + +    + v
  gi|2926766    96 AED------------R-----QGVAAEPGADVASAVEKLQSHG-IGRQAV 127

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     + L    +  vltAHPt   R+s++  + Ri   +          ++ +
  gi|2926766   128 LDLLSHALIVPVLTAHPTEVRRKSMIDHKNRIADLMLLKDGGRTETDEGE 177

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     LDEA+ R i   + t  +RR +    DE+   ++Y+ +      P
  gi|2926766   178 NLDEAIFRQIALLWQTRPLRREKLFVADEIENVLAYFRDVFLPVLPALYA 227
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                    RvDtALKniGinERlPYdvP..LikFssWmGGDRDGknPRvtPEvtRDvC
                    R           ER+    P++ ++   W+GGDRDG nP v     R
  gi|2926766   228 RW----------ERVLGARPqsFLRVGNWIGGDRDG-NPFVQAPQLRLAL 266

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                          A  +Y++ +  L  Els+     EL      +   a
  gi|2926766   267 AKGCEAALGFYMDALHALGAELSL---STELAHVPQAVLDLADAS----- 308

                    YiEFWKqvPP...tEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                           v P+++ EPYR  +  +  +L  t        A   s +  e
  gi|2926766   309 -----GDVSPsrqDEPYRRAISGIYARLAATHRSLVGKAAPRPSALKGEP 353

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLL.DlLRqvstFGLsLvKL
                     y    +    L    + L   G  ++A G  L+ l+R v tFG  L  L
  gi|2926766   354 -YASPADLRRDLVTVAQGLASEGNGALATGGALgRLIRAVETFGFHLATL 402

                    DiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlg
                    D+Rq s+ + Dv+  + +  ++ ++Y    E  R   L  EL   RPL
  gi|2926766   403 DMRQNSDVHQDVVAELLKVAGVEAdYAGLDEYARIALLRRELANNRPLGT 452

                    sDLPktEEvkDvldafrvLAELPi....DsFGaYiismataPsDvLAvEL
                    +     E  +  l  ++  AE     ++ +   Yiis a + sD L v +
  gi|2926766   453 PFFEYSERTASELAIVHAAAEAHRiygpQCITHYIISKAESVSDLLEVNI 502

                    LqRECgv.........kqtLrvvPLFEkLADLeAAPAavekLFsiDWY.
                    + +E g+ + + ++ +++ ++  vPLFE +ADLeAAP  ++  F +   +
  gi|2926766   503 ILKEAGLwragadgappQAAIMAVPLFETIADLEAAPKIMAAYFGLPEVg 552

                    .inridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                    ++ r  G qevm+GYsDs KD G +   W L++A   ++ v  + G  +
  gi|2926766   553 gVVRERGHQEVMIGYSDSNKDGGYITSTWGLFQASKALAPVFAEAGTAMQ 602

                    lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                    lFHGRGG vGRGGG    Ai +qP  t++G +R+t qGEvi   FG  ++
  gi|2926766   603 LFHGRGGAVGRGGGSSFAAIQAQPKGTVQGRIRITEQGEVIAAKFGTRDV 652

                    CFrsLqRFtAAtLEHGmnPPv.sPkPEWR..kLmeemAvvAtEEYRsvvv
                        L   t AtL   ++P v s +   R    m+++   A   YR +v+
  gi|2926766   653 AMTNLEATTSATLLASLEPEVlSDRDAARfaAAMDQLSKTAFAAYRDLVY 702

                    KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                        F E+FR  tP  E   + iGsRPa R  s  ie LRAiPW+F+W q
  gi|2926766   703 GTDGFKEFFRQLTPIQEISGLKIGSRPASRTKSTRIEDLRAIPWVFSWAQ 752

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     R  LP W GvG A     dK       L +m + W F    l  lEmv
  gi|2926766   753 ARVMLPGWYGVGHALSAFEDK-----ALLADMAQHWSFLQSALANLEMVL 797

                    AKGDPGiAaLyDkLL..vaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlL
                    AK D GiAa y  L+++ a     F +++R  +  t+d LL   G   lL
  gi|2926766   798 AKSDLGIAAHYLPLVedQARGAEIF-DRIRGGWDMTHDGLLAATGQSRLL 846

                    EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                    E  P L   +RLR +Yi  Ln +q   +KR R            s E  d
  gi|2926766   847 ERNPKLDTSIRLRLPYIEPLNLLQVELMKRHR-----------SGE--D 882

                    EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    ++              r+  G+E    L +  iA  + n G
  gi|2926766   883 DP--------------RIKEGIE----LSINAIATALRNSG    905

gi|171741712|ref|ZP_02917519.1|: domain 1 of 1, from 37 to 918: score 224.8, E = 2.2e-64
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +D  L +L        e L e+D  Ll  F     ++ G  L
  gi|1717417    37    EMDLCLQILR-------EVLGEFDEQLLASF----DEVRGYALNASA 72

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         +  +     D   L+ +   +  Ld  Da l+A+a+     LAnL
  gi|1717417    73 ERFAGILTD--TNPDQDDLQNVVNTVDKLDMHDAQLLARAFATYFHLANL 120

                    AEEvelAyRRRikkkkhGDFaDEasAtt.EsDiEEtlKkLvlklnKsPeE
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                 EE    yR  +  k+     DE +A  +  ++   + +L+  l   P+
gi|1717417   121 CEE---NYRVSVLHKR-ETAVDENQAVDpVNEMTGAYHQLINEL--GPAK 164

                 vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   + L       v+tAHPt + R+++  K  Ri   L     K +   DK
gi|1717417   165 ARDLLDKLEFHPVFTAHPTEARRKAVEGKIRRISRLLE--AHKLLGGSDK 212

                 kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                 kE    L  Ei A FRt  i   +PtP +E    +  +  t++  +P+
gi|1717417   213 KENSRRLFNEIDALFRTSPIALKKPTPVEEADTILDIFDNTLFYTIPQVY 262

                 RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                 RR D  +         P      +  sW+G DRDG nP vt  v R v
gi|1717417   263 RRFDDWVLGDKAGLVPPMCPAFFHPGSWIGSDRDG-NPNVTAKVSRQVAR 311

                 .LaRmmAanlYisqv...EDLmFElsmWRCndELRvRAEElyrtaardkv
                 + +  +   l i+  + +  L  E       dEL+      +  + r
gi|1717417   312 kFSDHVLGALEIETRtvgKNLTMEAGTTPPSDELKSLWNHQKEMSERL-- 359

                 vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                      +    +   E  R ++  + D+L  t ER   L+
gi|1717417   360 ----TDKAALISTKEMHRAVMLVMADRLHYTIERDADLM----------- 394

                 vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                  y   +eFLE L +  +sL     k  A G + Dl+ q  tFG  +v ++
gi|1717417   395 -YHSCDEFLEDLKIVQRSLAAANAKRSAYGPVQDLIWQTETFGFHMVEME 443

                 iRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
                  Rq s  +   l+ i +H                      L+G R   g+
gi|1717417   444 FRQHSVVHSRALEDIREH--------------------GLHGER---GPL 470

                 LPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvELLq
                  P+t E   vld+fr L  + ++++i +   Yiis + +   +  v  L
gi|1717417   471 QPMTHE---VLDTFRALGAIQkrngIKAARRYIISFTKSAQNIKDVYELN 517

                 RECgvk....qtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid...G
                 R    ++++  t+ v+PLFE+L DL+     +e +  i     r+  ++G
gi|1717417   518 RLAFSHpedvPTIDVIPLFEQLEDLQNSVDVLEDMIKIPEVQARLKatgG 567

                 KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                 K evm+GYsDs KDAG  sA   L  AqE i+K A  + + L+lFHGRGG
gi|1717417   568 KLEVMLGYSDSSKDAGPTSATLALHSAQERIAKWAESHDIDLTLFHGRGG 617

                 tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                  vGRGGGP   A+L+qP   ++   + t qGEvi   +G   L  r +
gi|1717417   618 AVGRGGGPANRAVLAQPVGSVKCRFKLTEQGEVIFARYGNPALAIRHVES 667

                 FtAAtLEHGmnPPvsPk.PEWRkLmeemAvvAtEEY..Rsv.vvKEPRFv
                  +AAtL     P v  ++ +  +   +mA    E  ++R ++ +  P F
gi|1717417   668 VAAATLLQS-APSVEKRnTDMTEKYADMANKLDEAAhnRFLdLLNTPDFA 716

                 EYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqtRFHL
                  +F   tP +E G + iGsRPaKR  + + ++ LR iPWiF+W q R  L
gi|1717417   717 PWFSTVTPLTEIGLLPIGSRPAKRGLGAkSLDDLRTIPWIFSWAQARINL 766

                 PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                   W G+G A           l+ L+  Y+eWP F   +D +Em  AK D
gi|1717417   767 AAWYGLGTAC-----EQFGDLKTLRQAYEEWPLFSTFIDNIEMSLAKTDE 811

                 GiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLK
                  iA +y  L   E+L    k++ d+ + t++++Lki G    L     L
gi|1717417   812 RIAKMYLALGDREDLN---KKVLDEMELTREWVLKIVGDEWPLQHRHVLG 858

                 qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                 q +R+R +Y+  L v q   L  +R             K    E+
gi|1717417   859 QAIRIRSPYVDALSVTQVLALGSLR-------------KQVDKEE----- 890

                 eLvkLnptervaPGLEDtLiL.tmKGiAAGmqntG<-*
                  L +    e++       LiL t+ G+AAG+qntG
gi|1717417   891 -LTHGQ-QENYT-----YLILcTVSGVAAGLQNTG    918
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gi|46190357|ref|ZP_00121597.2|: domain 1 of 1, from 10 to 917: score 224.2, E = 3.3e-64
                  *->siDAqLRlLvPG.KvsedekLieYDALLlDkFLDiLqDLHGedLkEa
                       DA +     G+K  e+ +L e     +D  L+iL  + Ge   E
  gi|4619035    10    PADAAIVTTGTGrKGPEEHDLPESLKYDMDLCLEILRNVLGEYNPEL 56

                  v.......qECYElsAeY..EGKk...DtkKLeELGakLtsLdPaDailv
                   ++ ++ +    E sAe   E K +++D   L E   ++  +   Da l+
  gi|4619035    57 LstfdtvrHYAVEASAEHfaELKDpnpDQDGLKEAVNVIDNMTLHDAQLL 106

                  AkailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlK
                  A+a+     LAnL EE    yR  +   +      +       ++   +
  gi|4619035   107 ARAFATYFHLANLSEE---NYRVSVLHERENNVPVDQAVDPINELTVAYH 153

                  kLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLa
                  +L+      P+   e L       v+tAHPt + R+++  K  R+   L
  gi|4619035   154 QLINET--GPAKAKELLNQLEFHPVFTAHPTEARRKAVEGKIRRVSELLE 201

                  qLsAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYi
                      K +   DKkE    L  Ei A FRt  i   +PtP +E    +  +
  gi|4619035   202 EY--KRLGGSDKKECLRRLYNEIDALFRTSPIALKKPTPVEEADTILDIF 249

                  HEtvWkGvPKFLRRvDtAL..KniGinERlPYdvPLikFssWmGGDRDGk
                    t+++ +PK  RR D  + +   G+ E  P      +  sW+G DRDG
  gi|4619035   250 DNTLFNTIPKVYRRFDDWVlgDKAGLVE--PACPAFFHPGSWIGSDRDG- 296

                  nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsm.WRCndELRvRAE
                  nP vt  v R v   aR   +   i  +E+    +  +     E
  gi|4619035   297 NPNVTAKVSRAV---ARKF-SDHVIAALEEATRTVGRnLTMEAETTPPSA 342

                  Elyrt.aardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL
                  El++  + ++ +     +    +   E  R ++  + D+L  t ER   L
  gi|4619035   343 ELKSLwSHQKEMSERLTDKAALISTKEMHRAVMLVMADRLHYTIERDADL 392

                  LAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                  +            y   ++FL  L +  +sL   G k  A G L Dl+ q
  gi|4619035   393 M------------YHSCDDFLADLKVVQRSLAAAGAKRSAYGPLQDLIWQ 430

                  vstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLla
                    tFG  +v ++ Rq s  +   l  i +H
  gi|4619035   431 TETFGFHMVEMEFRQHSVVHARALADIREH--------------------- 460

                  ELkGKRPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismat
                   L+G R  l    P+t E   vld+fr L  + ++++  +   Yiis +
  gi|4619035   461 GLHGERGELQ---PMTHE---VLDTFRALGAIQkrngLKAARRYIISFTK 504

                  aPsDvLAvELLqRECgvk....qtLrvvPLFEkLADLeAAPAavekLFsi
                  +   +  v  L R    ++++  t+ v+PLFE+L DL+     +e +  i
  gi|4619035   505 SAQNIKDVYELNRLAFSHpedvPTIDVIPLFEQLEDLQNSVDVLEEMIKI 554

                  DWYinridG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKky
                       r+  +++K evm+GYsDs KDAG  sA   L  AqE i+K A  +
  gi|4619035   555 PEVQARLKAtgnKLEVMLGYSDSSKDAGPTSATLALHSAQERIAKWAESH 604

                  GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF
                   + L+lFHGRGG vGRGGGP   A+L+qP   ++   + t qGEvi   +
  gi|4619035   605 DIDLTLFHGRGGAVGRGGGPANRAVLAQPVGSVKCRFKLTEQGEVIFARY 654

                  GEEnLCFrsLqRFtAAtLEHGmnPPvsPk.PEWRkLmeemAvvAtEEY..
                  G   L  r +   +AAtL     P v  ++ E  +   +mA    E  ++
  gi|4619035   655 GNPVLAIRHVESVAAATLLQS-APSVEKRnTEMTEKYADMAAQLDEAAhn 703

                  Rsv.vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiP
                  R ++ +    F  +F   tP +E G + iGsRPaKR  + + ++ LR iP
  gi|4619035   704 RFLdLLNTDGFAPWFSIVTPLTEIGLLPIGSRPAKRGLGAkSLDDLRTIP 753

                  WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                  WiF+W q R  L  W G+G A           l  ++  Y+eWP F   +
  gi|4619035   754 WIFSWAQARINLAAWYGLGTACEK-----FGDLETMRQAYEEWPLFSTFI 798

                  DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                  D +Em  AK D  iA +y  L   E+L    +++ ++ + t++++L i G
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  gi|4619035   799 DNIEMSIAKTDERIARMYLALGDREDLN---EKVLNEMELTRKWVLAIVG 845

                   HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                    k  L     L q +R+R +Y+  L v q   LK          lr ++
  gi|4619035   846 DKWPLQHRHVLGQAIRIRSPYVDALSVTQVLALK---------SLRKKVD 886

                   KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   KE       + ++ + L              + t+ G+AAG+qntG
  gi|4619035   887 KEELSQS--QQAGFIYLI-------------LCTVSGVAAGLQNTG    917

gi|72162953|ref|YP_290610.1|: domain 1 of 1, from 1 to 875: score 224.1, E = 3.7e-64
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            R  +   +   ++L +   LL +    +L +  G+dL + v
  gi|7216295     1    ----MTRDSARQEMP--DQLRRDVRLLGEMLGTVLAESGGQDLLDDV 41

                   qEC.YElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                      +  +    EG  + k + EL   + s     a  vA+a+     L n
  gi|7216295    42 ERLrRAVIGAREGTVEGKEITEL---VASWPLERAKQVARAFTVYFHLVN 88

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   LAEE    +R R  + +     D+a       +   +  +       Pe
  gi|7216295    89 LAEE---HHRMRALRER-----DDAATPQRESLAAAVHSIREDA--GPER 128

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     e +       vltAHPt + RR++     Ri   L  L A
  gi|7216295   129 LRELIAGMEFHPVLTAHPTEARRRAVSTAIQRISAQLERLHAAHPGSGAE 178

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    E    L  Ei   +Rt  +R ++  P DE+R  m+ + Et++  +P
  gi|7216295   179 AEARRRLLEEIDLLWRTSQLRYTKMDPLDEVRTAMAAFDETIFTVIPEVY 228

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                   R  D AL   G   R       +++ sW+GGDRDG nP vt EvtR+
  gi|7216295   229 RSLDRALDPEGCGRRPALAKAFVRYGSWIGGDRDG-NPFVTHEVTREAIT 277

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                   +          +  E +      +       +      + a+     +
  gi|7216295   278 IQSEHVLRALENACERIGRTHTEYTGLTPPSAELRAALSSARAA-YPRLM 326

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                    E  K   P+EP R +L    ++L  tR R   L             y +
  gi|7216295   327 QEIIKR-SPNEPHRQLLLLAAERLRATRLRNADL------------GYPN 363

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    E FL  L     sL   G    A G L  l+ q  tFG  L  L+iRq
  gi|7216295   364 PEAFLADLRTVQESLAAAGAVRQAYGELQNLIWQAETFGFHLAELEIRQH 413

                   seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                   s  +   l  i                R    l+E             +t
  gi|7216295   414 SAVHAAALKEI----------------RAGGELSE-------------RT 434

                   EEvkDvldafrvLAE.LPiDsFGaYiismataPsDvLAv.ELLqREC..g
                   EEv   l  +  + E+  +++    Yi+s + +  D+ Av EL     ++g
  gi|7216295   435 EEVLATLRVVAWIQErFGVEACRRYIVSFTQSADDIAAVyELAEHAMppG 484

                   vkqtLrvvPLFEkLADLeAAPAa...vekLFsiDWYinridGKqevmvGY
                       L v+PLFE  ADL+AAP   +++ +L ++     +   + evm+GY
  gi|7216295   485 KAPILDVIPLFETGADLDAAPQVldgMLRLPAVQRRLEQTGRRMEVMLGY 534

                   sDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGP
                   sDs KD G +sA   LY Aq  ++  A+++ +KL+lFHGRGG  GRGGGP
  gi|7216295   535 SDSAKDVGPVSATLRLYDAQARLAEWAREHDIKLTLFHGRGGALGRGGGP 584

                   tHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtL..
                      A+L+q P  ++G  +vt qGEvi   +G   +  r +     A L
  gi|7216295   585 ANRAVLAQAPGSVDGRFKVTEQGEVIFARYGQRAIAHRHIEQVGHAVLma 634

                   ..EHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtP
                   ++E            +R + +++A  A   YR++v  E  F E+F    P
  gi|7216295   635 stESVQRRAAEAAARFRGMADRIAEAAHAAYRALVDTEG-FAEWFSRVSP 683
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                    ElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAA
                      E   + +GsRPa+R  + G++ LRAiPW+FaWtqtR  LP W G+G
  gi|7216295   684 LEELSELRLGSRPARRSAARGLDDLRAIPWVFAWTQTRVNLPGWYGLGSG 733

                    FKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkL
                       A+d     l  L+  YkeWP F   lD  Em  AK D  iA  y  L
  gi|7216295   734 LA-AVD----DLEALHTAYKEWPLFASLLDNAEMSLAKTDRVIAERYLAL 778

                    LvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsY
                        eL    +++ ++Y  t++l+Lk+  H  lLE    L   + LR++Y
  gi|7216295   779 GGRPELT---EQVLAEYDRTRELVLKVTRHTRLLENRRVLSRAVDLRNPY 825

                    ittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpte
                    +  L  +q   L  +R  +             Ad              +e
  gi|7216295   826 VDALSHLQLRALEALRTGE-------------ADRL------------SE 850

                    rvaPGLEDtLiLtmKGiAAGmqntG<-*
                    +    LE  L+L + G+AAG+qntG
  gi|7216295   851 EDRNHLERLLLLSVNGVAAGLQNTG    875

gi|33599409|ref|NP_886969.1|: domain 1 of 1, from 33 to 982: score 223.9, E = 4.2e-64
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           q+ ++     s   + ++ D  Ll + L++++q   G+ + +
  gi|3359940    33    ----QMNAIRQQSDS--AEPLRHDIRLLGRCLgEVIQACEGKRVYDT 73

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +      +  +    D+     L a++  L   D   vA+a++  L L n
  gi|3359940    74 IETLRRTAVRFRRAGDPADDKLLQARVKQLRGNDPNSVARAFSYFLHLSN 123

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+ +   R R + +        +       +   +  L  ++    +
  gi|3359940   124 IAEDRDQNRRQRDRALA-------GAGPERGSLRQAIESLKAQG-VNNAR 165

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +   L    v  vltAHPt   R+s L  +  i   L q   +++t ++
  gi|3359940   166 IRRLLSEACVMPVLTAHPTEVQRKSTLDVHREISSLLVQ-REReLTADEL 214

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     ELD AL   +   + t  +R ++ t  DE+   +sY+  t  + +P+
  gi|3359940   215 SELDLALIGQVATLWQTRMLRYTRLTVADEIENALSYYRSTFLNVIPRVY 264

                    RRvDtALKniGinERlPYdvPL...ikFssWmGGDRDGknPRvtPEvtRD
                          L    +    P   PL++ ++  sW+GGDRDG nP v
  gi|3359940   265 GDLARLLNREPVKPFTPPPPPLepfLRMGSWIGGDRDG-NPNVDAATLER 313

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                      L    +    Y++ v  L  Els     + L + A+      a
  gi|3359940   314 ALLRQATVLFEHYLQEVHALGAELS----ASTLLIEADPALLALADA--- 356

                    KyYiEFWKqvPP..tEPYRviLGdvRDKLYntRERaRHLLAtGiseisE.
                              P ++ EPYR  L  +  +L  t   aRHL  + ++  +
  gi|3359940   357 -----GGDDSPHrrDEPYRRALIGIYARLAAT---ARHLTGQELARRATv 398

                    .eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                    + A y   +     L +   sL       iA   L  l   v  FG  L
  gi|3359940   399 pAAPYDTPDALAADLAVIAASLSAHHGAPIARLRLSGLQQAVTVFGFHLA 448

                    KLDiRqEseRqtDvlDAittHLeiGs......YReWsEeKRqEWLlaELk
                     +D+Rq s+ +  vl  +    + G +++  +Y    E  R   L  EL
  gi|3359940   449 TVDLRQSSDVHERVLAELFARAGDGIdgqavdYLALDEAARVAVLRRELA 498

                    GKRPLlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPs
                      RPL  + +   EE +  l  +r  A ++ +    +    i+s + + s
  gi|3359940   499 HARPLASPWIAYSEETASELAVLRAAAAgrarYGRQAVLQSIVSHTETLS 548

                    DvLAvELLqRECgvkqt..........LrvvPLFEkLADLeAAPAavekL
                    D L v +Lq+E g+  +++++  ++++L vvPLFE + DL+  P  ++
  gi|3359940   549 DLLEVLVLQKEAGLIAPpgetiapgdgLMVVPLFETIPDLQRGPEIMAAW 598

                    FsiDWYinrid....GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKv
                      +   + r+   ++  qevm+GYsDs KD G l   W LY+A   ++ v
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  gi|3359940   599 LDLPEVRQRVRlaqgDTQEVMLGYSDSNKDGGFLTSNWSLYQAERALVDV 648

                   AKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEvi
                        v+L +FHGRGG vGRGGG    AiL+qPP t+ G lR t qGEvi
  gi|3359940   649 FSARSVRLRMFHGRGGSVGRGGGSSYDAILAQPPGTVAGQLRLTEQGEVI 698

                   EfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPEWRkLmee.......m
                      + + ++    L    AAtLE  + P  +        m+++ +  + m
  gi|3359940   699 QSKYKDAEVGRWHLELLVAATLESSLAPQAAATSAEDAHMQQhapamsfM 748

                   AvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGie
                      A   YR +v+  P F +YF  AtP  E   +niGsRPa Rk +  ie
  gi|3359940   749 SELAQRTYRGLVYDTPGFADYFFAATPISEIAGLNIGSRPASRKKGQHIE 798

                   sLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK........nlqkL
                    LRAiPW F+W q R  L  W G+G A    ++   ++ +++++  l +L
  gi|3359940   799 DLRAIPWGFSWAQCRLMLTGWYGMGSAIEAYLETGAQgaprsrraRLAQL 848

                   kEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL..kPFGksL
                   +Em  +WP FR  l  +Emv AK D  iAa y +L+    L+++ FG  +
  gi|3359940   849 REMASDWPAFRTLLSNMEMVLAKSDLAIAAGYAQLVPRRGLreRVFG-AI 897

                   RdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLK
                    ++   t   +L++   ++lL   P L   lR R +Yi  Ln +q   +K
  gi|3359940   898 TAEHGRTLA-MLRLLTRRELLADNPGLMASLRERFAYIDPLNYLQIELIK 946

                   RiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLt
                   R R                A+      d  +++             + Lt
  gi|3359940   947 RHR----------------AAQRRAGDDADIRVP----------RAIHLT 970

                   mKGiAAGmqntG<-*
                   + GiAAG+ n G
  gi|3359940   971 INGIAAGLRNSG    982

gi|291517702|emb|CBK71318.1|: domain 1 of 1, from 10 to 917: score 221.5, E = 2.1e-63
                   *->siDAqLRlLvPG.KvsedekLieYDALLlDkFLDiLqDLHGedLkEa
                        DA +     G+K  e+ +L e     +D  L+iL  + Ge   E
  gi|2915177    10    PADAAIVTTGTGrKGPEEHDLPESLKYDMDLCLEILRNVLGEYNPEL 56

                   v.......qECYElsAeY..EGKk...DtkKLeELGakLtsLdPaDailv
                    ++ ++ +    E sAe   E K +++D   L E   ++  +   Da l+
  gi|2915177    57 LstfdtvrHYAVEASAEHfaELKDpnpDQDGLKEAVNVIDNMTLHDAQLL 106

                   AkailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlK
                   A+a+     LAnL EE    yR  +   +      +       ++   +
  gi|2915177   107 ARAFATYFHLANLSEE---NYRVSVLHERENNVPVDQAVDPINELTVAYH 153

                   kLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLa
                   +L+      P+   e L       v+tAHPt + R+++  K  R+   L
  gi|2915177   154 QLINET--GPAKAKELLNQLEFHPVFTAHPTEARRKAVEGKIRRVSELLE 201

                   qLsAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYi
                       K +   DKkE    L  Ei A FRt  i   +PtP +E    +  +
  gi|2915177   202 EY--KRLGGSDKKECLRRLYNEIDALFRTSPIALKKPTPVEEADTILDIF 249

                   HEtvWkGvPKFLRRvDtAL..KniGinERlPYdvPLikFssWmGGDRDGk
                     t+++ +PK  RR D  + +   G+ E  P      +  sW+G DRDG
  gi|2915177   250 DNTLFNTIPKVYRRFDDWVlgDKAGLVE--PACPAFFHPGSWIGSDRDG- 296

                   nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsm.WRCndELRvRAE
                   nP vt  v R v   aR   +   i  +E+    +  +     E
  gi|2915177   297 NPNVTAKVSRAV---ARKF-SDHVIAALEEATRTVGRnLTMEAETTPPSA 342

                   Elyrt.aardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL
                   El++  + ++ +     +    +   E  R ++  + D+L  t ER   L
  gi|2915177   343 ELKSLwSHQKEMSERLTDKAALISTKEMHRAVMLVMADRLHYTIERDADL 392

                   LAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                   +            y   ++FL  L +  +sL   G k  A G L Dl+ q
  gi|2915177   393 M------------YHSCDDFLADLKVVQRSLAAAGAKRSAYGPLQDLIWQ 430
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                    vstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLla
                      tFG  +v ++ Rq s  +   l  i +H
  gi|2915177   431 TETFGFHMVEMEFRQHSVVHARALADIREH-------------------- 460

                    ELkGKRPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismat
                     L+G R  l    P+t E   vld+fr L  + ++++  +   Yiis +
  gi|2915177   461 GLHGERGELQ---PMTHE---VLDTFRALGAIQkrngLKAARRYIISFTK 504

                    aPsDvLAvELLqRECgvk....qtLrvvPLFEkLADLeAAPAavekLFsi
                    +   +  v  L R    ++++  t+ v+PLFE+L DL+     +e +  i
  gi|2915177   505 SAQNIKDVYELNRLAFSHpedvPTIDVIPLFEQLEDLQNSVDVLEEMIKI 554

                    DWYinridG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKky
                         r+  +++K evm+GYsDs KDAG  sA   L  AqE i+K A  +
  gi|2915177   555 PEVQARLKAtgnKLEVMLGYSDSSKDAGPTSATLALHSAQERIAKWAESH 604

                    GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF
                     + L+lFHGRGG vGRGGGP   A+L+qP   ++   + t qGEvi   +
  gi|2915177   605 DIDLTLFHGRGGAVGRGGGPANRAVLAQPVGSVKCRFKLTEQGEVIFARY 654

                    GEEnLCFrsLqRFtAAtLEHGmnPPvsPk.PEWRkLmeemAvvAtEEY..
                    G   L  r +   +AAtL     P v  ++ E  +   +mA    E  ++
  gi|2915177   655 GNPVLAIRHVESVAAATLLQS-APSVEKRnTEMTEKYADMAAQLDEAAhn 703

                    Rsv.vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiP
                    R ++ +    F  +F   tP +E G + iGsRPaKR  + + ++ LR iP
  gi|2915177   704 RFLdLLNTDGFAPWFSIVTPLTEIGLLPIGSRPAKRGLGAkSLDDLRTIP 753

                    WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                    WiF+W q R  L  W G+G A           l  ++  Y+eWP F   +
  gi|2915177   754 WIFSWAQARINLAAWYGLGTACEK-----FGDLETMRQAYEEWPLFSTFI 798

                    DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                    D +Em  AK D  iA +y  L   E+L    +++ ++ + t++++L i G
  gi|2915177   799 DNIEMSIAKTDERIARMYLALGDREDLN---EKVLNEMELTRKWVLAIVG 845

                    HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                     k  L     L q +R+R +Y+  L v q   L+          lr ++
  gi|2915177   846 DKWPLQHRHVLGQAIRIRSPYVDALSVTQVLALR---------SLRKKVD 886

                    KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    KE       + ++ + L              + t+ G+AAG+qntG
  gi|2915177   887 KEELSQS--QQAGFIYLI-------------LCTVSGVAAGLQNTG    917

gi|227547454|ref|ZP_03977503.1|: domain 1 of 1, from 10 to 917: score 221.3, E = 2.4e-63
                    *->siDAqLRlLvPG.KvsedekLieYDALLlDkFLDiLqDLHGedLkEa
                         DA +     G+K  e+ +L e     +D  L+iL  + Ge   E
  gi|2275474    10    PADAAIVTTGTGrKGPEEHDLPESLKYDMDLCLEILRNVLGEYNPEL 56

                    v.......qECYElsAeY..EGKk...DtkKLeELGakLtsLdPaDailv
                     ++ ++ +    E sAe   E K +++D   L E   ++  +   Da l+
  gi|2275474    57 LstfdtvrHYAVEASAEHfaELKDpnpDQDGLKEAVNVIDNMTLHDAQLL 106

                    AkailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlK
                    A+a+     LAnL EE    yR  +   +      +       ++   +
  gi|2275474   107 ARAFATYFHLANLSEE---NYRVSVLHERENNVPVDQAVDPINELTVAYH 153

                    kLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLa
                    +L+      P+   e L       v+tAHPt + R+++  K  R+   L
  gi|2275474   154 QLINET--GPAKAKELLNQLEFHPVFTAHPTEARRKAVEGKIRRVSELLE 201

                    qLsAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYi
                        K +   DKkE    L  Ei A FRt  i   +PtP +E    +  +
  gi|2275474   202 EY--KRLGGSDKKECLRRLYNEIDALFRTSPIALKKPTPVEEADTILDIF 249

                    HEtvWkGvPKFLRRvDtAL..KniGinERlPYdvPLikFssWmGGDRDGk
                      t+++ +PK  RR D  + +   G+ E  P      +  sW+G DRDG
  gi|2275474   250 DNTLFNTIPKVYRRFDDWVlgDKAGLVE--PACPAFFHPGSWIGSDRDG- 296

                    nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsm.WRCndELRvRAE
                    nP vt  v R v   aR   +   i  +E+    +  +     E
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  gi|2275474   297 NPNVTAKVSRAV---ARKF-SDHVIAALEEATRTVGRnLTMEAETTPPSA 342

                   Elyrt.aardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL
                   El++  + ++ +     +    +   E  R ++  + D+L  t ER   L
  gi|2275474   343 ELKSLwSHQKEMSERLTDKAALISTKEMHRAVMLVMADRLHYTIERDADL 392

                   LAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq
                   +            y   ++FL  L +  +sL   G k  A G L Dl+ q
  gi|2275474   393 M------------YHSCDDFLADLKVVQRSLAAAGAKRSAYGPLQDLIWQ 430

                   vstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLla
                     tFG  +v ++ Rq s  +   l  i +H
  gi|2275474   431 TETFGFHMVEMEFRQHSVVHARALADIREH-------------------- 460

                   ELkGKRPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismat
                    L+G R  l    P+t E   vld+fr L  + ++++  +   Yiis +
  gi|2275474   461 GLHGERGELQ---PMTHE---VLDTFRALGAIQkrngLKAARRYIISFTK 504

                   aPsDvLAvELLqRECgvk....qtLrvvPLFEkLADLeAAPAavekLFsi
                   +   +  v  L R    ++++  t+ v+PLFE+L DL+     +e +  i
  gi|2275474   505 SAQNIKDVYELNRLAFSHpedvPTIDVIPLFEQLEDLQNSVDVLEEMIKI 554

                   DWYinridG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKky
                        r+  +++K evm+GYsDs KDAG  sA   L  AqE i+K A  +
  gi|2275474   555 PEVQARLKAtgnKLEVMLGYSDSSKDAGPTSATLALHSAQERIAKWAESH 604

                   GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF
                    + L+lFHGRGG vGRGGGP   A+L+qP   ++   + t qGEvi   +
  gi|2275474   605 DIDLTLFHGRGGAVGRGGGPANRAVLAQPVGSVKCRFKLTEQGEVIFARY 654

                   GEEnLCFrsLqRFtAAtLEHGmnPPvsPk.PEWRkLmeemAvvAtEEY..
                   G   L  r +   +AAtL     P v  ++ E  +   +mA    E  ++
  gi|2275474   655 GNPVLAIRHVESVAAATLLQS-APSVEKRnTEMTERYADMAAQLDEAAhn 703

                   Rsv.vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiP
                   R ++ +    F  +F   tP +E G + iGsRPaKR  + + ++ LR iP
  gi|2275474   704 RFLdLLNTDGFAPWFSIVTPLTEIGLLPIGSRPAKRGLGAkSLDDLRTIP 753

                   WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                   WiF+W q R  L  W G+G A           l  ++  Y+eWP F   +
  gi|2275474   754 WIFSWAQARINLAAWYGLGTACEK-----FGDLETMRQAYEEWPLFSTFI 798

                   DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                   D +Em  AK D  iA +y  L   E+L    +++ ++ + t++++L i G
  gi|2275474   799 DNIEMSIAKTDERIARMYLALGDREDLN---EKVLNEMELTRKWVLAIVG 845

                   HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                    k  L     L q +R+R +Y+  L v q   L+          lr ++
  gi|2275474   846 DKWPLQHRHVLGQAIRIRSPYVDALSVTQVLALR---------SLRKKVD 886

                   KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   KE       + ++ + L              + t+ G+AAG+qntG
  gi|2275474   887 KEELSQS--QQAGFIYLI-------------LCTVSGVAAGLQNTG    917

gi|20196786|emb|CAC86365.1|: domain 1 of 1, from 1 to 396: score 221.2, E = 2.7e-63
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2019678     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2019678     - ---------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2019678     - ---------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                          +vDLvltAHPtqs RRsLL+K+++iRnCL+qL+AKD+  +DKk
  gi|2019678     1 -------TVDLVLTAHPTQSLRRSLLKKHTKIRNCLTQLYAKDISEDDKK 43
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                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL REiqAAFRtDEiRRaqPtPqDEmR+Gm YiHEt+WkGvP FLR
  gi|2019678    44 ELDEALQREIQAAFRTDEIRRAQPTPQDEMRYGMNYIHETIWKGVPNFLR 93

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALK iGi ERlPYdvPLikFssWmGGDRDG n RvtPEvtRDvCLL
  gi|2019678    94 RVDTALKKIGIDERLPYDVPLIKFSSWMGGDRDG-NLRVTPEVTRDVCLL 142

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmAanlYisq+E+LmFElsmWRCndELR++AEEl+   a++kvvKyY
  gi|2019678   143 ARMMAANLYISQIEELMFELSMWRCNDELRAKAEELHD--ASKKVVKYYT 190

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFWK +P +EPYRv+L  vR KL ntRER+R LLA G+sei+E A +t+v
  gi|2019678   191 EFWKEIPINEPYRVVLASVRNKLHNTRERSRDLLANGFSEIPESAAFTNV 240

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    eFLEPLELCYksLC+ GDk iADGsLLD++Rqv tFGLsL KLDiRqEs
  gi|2019678   241 KEFLEPLELCYKSLCDSGDKTIADGSLLDFMRQVATFGLSLTKLDIRQES 290

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   +R+t+v+D ittHL+iGsYR+W+EeKR EWL++EL+GKRPLl +DLP+ E
  gi|2019678   291 DRHTEVIDTITTHLGIGSYRSWPEEKRVEWLVSELQGKRPLLSPDLPQSE 340

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+D l++fr LAELP DsFG+YiismataPsDvLA ELLqREC++  +L
  gi|2019678   341 EVADALGTFRALAELPRDSFGPYIISMATAPSDVLAAELLQRECKIADPL 390

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLF
  gi|2019678   391 PVVPLF---------------------------------------------- 396

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|2019678     - ------------------------------------------------- -

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

  gi|2019678     - ------------------------------------------------- -

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|2019678     - ------------------------------------------------- -

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|2019678     - ------------------------------------------------- -

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|2019678     - ------------------------------------------------- -

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|2019678     - ------------------------------------------------- -

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|2019678     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|2019678     - -------------    -

gi|163858843|ref|YP_001633141.1|: domain 1 of 1, from 1 to 951: score 221.0, E = 3.2e-63
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           ++++ P       + ++ D  Ll + L+ ++q   Ge + +
  gi|1638588     1    -----MKAIRPQSAT--AEPLRHDIRLLGRLLgQVIQACEGERVYDT 40

                   vqECYElsAeY..EGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                   +      +  +++EG +   KL  L  ++  L   D   vA+a++  L L
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gi|1638588    41 IETLRRTAVRFrrEGNEADGKL--LEQRVKRLRGNDPNSVARAFSYFLHL 88

                 AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                  n+AE+     R  ++ ++    aD++ A     + E +  L  ++
gi|1638588    89 SNIAED-----RDQNRAQRMRALADDTPA--RGSLREAVALLKEQG-VGT 130

                 eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                 + +   L    v  vltAHPt   R+s L  +  i   L q     +t e
gi|1638588   131 ARIRRLLAEARVVPVLTAHPTEVQRKSTLDVHREISTLLLQREG-PLTAE 179

                 DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                 +  +LD AL   +   + t  +R ++ t  DE+   +sY+  t  + +P
gi|1638588   180 EIADLDLALLGRVATLWQTRMLRYTRLTVADEIENALSYYRSTFLNVIP- 228

                 FLRRvDtAL.KniGinERlPYdv......PLikFssWmGGDRDGknPRvt
                    Rv   L++ +G     P+ +++ + +P ++  sW+GGDRDG nP v
gi|1638588   229 ---RVYGELsRLLGRDSAKPFAAppaplePFLRMGSWIGGDRDG-NPNVD 274

                 PEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE.Elyrt
                         L    +    Y++ v  L  Els+      L + A++ l+
gi|1638588   275 ASTLELALLRQATVLFEYYLQEVHALGAELSI----TTLLIDADpALQAL 320

                 aardkvvKyYiEFWKqvPP..tEPYRviLGdvRDKLYntRERaRHLLAtG
                 a +              P ++ EPYR  L  +  +L  t   a  L
gi|1638588   321 ADSG---------GDNSPHrrDEPYRRALVGIYARLAAT---AQQLTGRD 358

                 is.eisEeA.vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvs
                 +++ +   A+ y    e    L +   sL       iA   L  l   v
gi|1638588   359 LArRVTHPApAYGAPQELAQDLAIIAASLSAHHAAPIARLRLTGLQQAVE 408

                 tFGLsLvKLDiRqEseRqtDvlD.....AittHLei.GsYReWsEeKRqE
                  FG  L  +D+Rq s+ +  vl +  ++A  +H + +  Y    E+ R
gi|1638588   409 VFGFHLATVDLRQSSDVHERVLTelfkrAGAQHDGKpVDYARLDEDARVA 458

                 WLlaELkGKRPLlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYii
                  L aEL   RPL+ + L   EE    l  +r  A ++ +    +    i+
gi|1638588   459 LLRAELALARPLVSPWLTYSEETTRELAVLRAAAAgrarYGKLAVQQTIV 508

                 smataPsDvLAvELLqRECgvk.............qtLrvvPLFEkLADLe
                 s + + sD L v +Lq+E g+  +++++ +  ++  L vvPLFE + DL+
gi|1638588   509 SHTETLSDLLEVLVLQKETGLIvdpepgasiasgDGLMVVPLFETIPDLQ 558

                 AAPAavekLFsiDWYinri....dGKqevmvGYsDsGKDAGRlsAAWqLY
                   P  ++    +   + r+++ +dG qevm+GYsDs KD G l   W LY
gi|1638588   559 RGPEIMAAWLDLPEVRQRVkqaqDGTQEVMLGYSDSNKDGGFLTSNWALY 608

                 kAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGsl
                 +A   ++ v    Gv+L lFHGRGG vGRGGG    AiL+qPP t+ G l
gi|1638588   609 QAERALVDVFSARGVRLRLFHGRGGSVGRGGGSSFDAILAQPPGTVAGQL 658

                 RvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP.......kP
                 R t qGEvi   + + ++    L    AAtLE  + P  + ++ ++ +
gi|1638588   659 RLTEQGEVIQSKYKDAEVGRWHLELLVAATLESTLAPRAAAtsaedahMA 708

                 EWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPa
                  +   m  m   A   YR +v+  P F EYF  AtP  E   +niGsRPa
gi|1638588   709 HYGPAMSFMSDTAQRSYRGLVYDTPGFAEYFFAATPISEIAGLNIGSRPA 758

                 KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi.....
                  Rk +  i+ LRAiPW F+W q R  L  W G+G A    ++    + ++
gi|1638588   759 SRKQGQRIDDLRAIPWGFSWAQCRLMLTGWYGMGSAIEAYLETGAagapr 808

                 ...KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL
                 +++  l +L+Em +eWP FR  l  +Emv AK D  iAa y +L+    L
gi|1638588   809 srrARLAQLREMAREWPAFRTLLSNMEMVLAKSDLSIAARYAQLVPNRAL 858

                 ..kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittL
                 +++ FG ++ ++   t   +L++   ++lL   P L   lR R +Yi  L
gi|1638588   859 rnRIFG-QISAEHGRTIA-MLRLLTQRELLADNPALLASLRERFAYIDPL 906

                 nvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaP
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                    n +q   ++R R  +          ++   E+ k+    ++L
  gi|1638588   907 NYLQIELIRRYRSAQ----------RDGDGEPDKRVRSAIHLT------- 939

                    GLEDtLiLtmKGiAAGmqntG<-*
                             + GiAAG+ n G
  gi|1638588   940 ---------INGIAAGLRNSG    951

gi|227988853|ref|ZP_04035945.1|: domain 1 of 1, from 1 to 892: score 220.4, E = 4.5e-63
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedlkEav
                               +v       ++L +   LL       ++ L Ge L
  gi|2279888     1    --------MVSDPLY--DQLKREVDLLGRALGQAIKTLSGERLYHLE 37

                    qECYElsAeYEGK.kDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                     E   l       + D++  e +   + +   a+a  + +a+     L n
  gi|2279888    38 EEVRALTKHLRQNpGDAEAREKMQRLIRGASLAEAEGLVRAFATYFHLVN 87

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnK....
                    LAEE     R R++  +    a Ea+ t  s   E +  Lv  l K ++
  gi|2279888    88 LAEE-----RQRVRVNR----AREAESTPISPRSESFLGLVGSL-Kaqgl 127

                    sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt
                    s e v   L      L +tAHPt   RR +    + i      L A++
  gi|2279888   128 SYEQVVRVLSELRLHLTFTAHPTETRRRTVRYHLGEIERL---LEAREQG 174

                    veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGv
                      D   +  A+       + t E+RR++ t  DE++ G+ Y+  t+W  +
  gi|2279888   175 QPDADCIN-AIEAHTMLLWGTLELRRTRMTVEDEVKGGLFYLPRTLWASI 223

                    PKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                    P+ +   + A+       R     PL+ F sW+GGDRDG nP vtP+vt
  gi|2279888   224 PRLVEGLERAVEA-HYGARPDLSPPLV-FRSWIGGDRDG-NPNVTPDVTL 270

                    DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                         aR +A   +++ ++ L+  ls+    d L    E    t    k
  gi|2279888   271 WAQRYARELALQRFVEEIDGLIRALSL--SEDRLPTPREIRLATEEASKK 318

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                          F       EPYR  L   R KL       R LL
  gi|2279888   319 LPLPDRF-----AGEPYRRYLMIPRYKL-------RSLLGE-----QPGP 351

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                     y    e +  L      L + G k +A   +         +GL Lv LD
  gi|2279888   352 GYASGGELVAELRAIEAGLAQLGLKKVAQTLVKPARVRAEAYGLDLVSLD 401

                    iRqEseRqtDvlDAittHLeiG....sYReWsEeKRqEWLlaELkGKRPL
                    +R Es  +    +A+ + L +G++++ Y e s e R   L  EL+  RPL
  gi|2279888   402 LREESRQHA---EAVAELLRVGggseNYLELSPEEREALLTQELHSARPL 448

                    lgsDL.PktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELL
                     +   +P+t  +   l+a++        + GaY++sm+  PsD L v LL
  gi|2279888   449 APVGYrPQTRALSVALGALH-----NWQARGAYVVSMTHHPSDLLEVFLL 493

                    qRECgvkq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK
                     RE g+ +++++ +  vvPLFE L DLeAAP  v+ L     +  +++G+
  gi|2279888   494 AREVGLYRpgrplPFDVVPLFETLSDLEAAPRVVAELLENPIFQAHVQGR 543

                    ..qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRG
                    ++ evm+GYsDs KDAG lsA W LY+AqE +++vA+  Gv++  FHGRG
  gi|2279888   544 ggMEVMIGYSDSNKDAGFLSANWALYRAQEQVAQVAQGRGVRVYFFHGRG 593

                    GtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLq
                        RGGG    Ai s PP t+   +R+t qGE +   +   +L +r L
  gi|2279888   594 TSTARGGGSAGRAIASLPPGTVGTRMRITEQGEALADRYQHPELAYRNLE 643

                    RF......tAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEP
                          + +AA    G +  v P+ EW++ +e+ A      YR++ + EP
  gi|2279888   644 QMlyymglAAARDAYGQKDTV-PQ-EWKDALEHAARESERVYRAL-LAEP 690

                    RFvEYFRlAtPElEYGkmniGsRPaKRk.PsGGiesLRAiPWiFaWtqtR
                    RF E++   tP  E G +ni sRP  R +    i+ LRAiPW+ +Wtq R
  gi|2279888   691 RFFEFYEAFTPIREIGALNIASRPVYRSgRVREITDLRAIPWVMSWTQVR 740
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                    FHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAK
                      LP W G+ A            +   +EmY+ WPFF+ tl+      AK
  gi|2279888   741 LLLPGWYGIDAGLGQV------PMELRREMYRGWPFFKSTLEAAAEALAK 784

                    GDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDP
                     D GiA  y +L+  E    F   + + ++   + +L+      lL   P
  gi|2279888   785 ADLGIAREYLRLVSPELAEAFFPPIAQAFERSVK-VLEETFQGSLLHNRP 833

                    YLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnsk
                     L  +  LR++Y+               DP  +v  + +l   y   +
  gi|2279888   834 ILARQTELRNPYV---------------DPISHV--QVELLARYRRTP-- 864

                    kadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                             p     PGLE  L+L + GiAAG+ n G
  gi|2279888   865 ---------PEHPERPGLERALMLSILGIAAGLRNAG    892

gi|183602906|ref|ZP_02964265.1|: domain 1 of 1, from 37 to 918: score 220.3, E = 5e-63
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +D  L +L        + L eYD  Ll  F  + q     +   +
  gi|1836029    37    DMDLCLNILR-------QVLSEYDENLLKTFDTVRQYAVDASAERFS 76

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         +  +    +D   Le     + +++  Da l+A+a+     LAnL
  gi|1836029    77 ----GVLTDTHPERDD--LEMAVKTIDAMNLHDAQLLARAFATYFHLANL 120

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     EE    yR  +   +     D        ++   + +L++     P+
  gi|1836029   121 CEE---NYRVAVLHEREAKVDDTQAIDPVNEMTKAYHQLISEM--GPAKA 165

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt.veDK
                     e L       v+tAHPt + R+++   +++iR     L A  + +  DK
  gi|1836029   166 KELLERLEFHPVFTAHPTEARRKAV---EGKIRRIAQLLEAHRLLgGSDK 212

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    kE    L  Ei A FRt  i   +PtP +E    +  +  t+++ +P
  gi|1836029   213 KEDSRRLYSEIDALFRTSPIALKKPTPVEEADTILDIFDNTLFHTIPMVY 262

                    RRvDtAL..KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    RR D  + +   Gi    P      +  sW+G DRDG nP vt  v R v
  gi|1836029   263 RRFDDWMlgDKAGIEP--PACPAFFHPGSWIGSDRDG-NPNVTAKVSRQV 309

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk.vv
                       aR     +     E            +E     +El     ++k++
  gi|1836029   310 ---ARKFSDHVLAALEEATRTVGRNMTVESETTPPSDELRALWNQQKeIS 356

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                             +   E  R +L  + D+L  t  R   L+
  gi|1836029   357 ERLTGKASLISTKELHRAVLLVMADRLHYTIKRDTDLM------------ 394

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y + ++FL  L +  +sL e GDk  A G L Dl+ q  tFG  +v ++
  gi|1836029   395 YHNCDDFLADLRVVQRSLAEAGDKRAAYGPLQDLIWQTETFGFHMVEMEF 444

                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    Rq s  +   lD i +H                    L+G R   g+
  gi|1836029   445 RQHSVVHARALDDIREH-------------------GLHGER---GPLQ 471

                    PktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvELLqR
                    P+t E   vld+fr L  + +++++ +   Yiis + +   v  v  L R
  gi|1836029   472 PMTHE---VLDTFRALGAIQkrngVKAARRYIISFTKSAKNVRDVYELNR 518

                    ECgvk....qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG...K
                         +++   + v+PLFE+L DLe     ++ +  i     r+  +++K
  gi|1836029   519 LAFSNpddaPVIDVIPLFEQLEDLEHSVSVLDEMLKIPEVQARLKQtgrK 568

                    qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                     evm+GYsDs KDAG   A   L  AqE i+K A +  + L+lFHGRGG
  gi|1836029   569 MEVMLGYSDSSKDAGPTTATLALHSAQERIAKWADENDIDLTLFHGRGGA 618

                    vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
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                    vGRGGGP   A+L+qP   ++   + t qGEvi   +G   L  r +
  gi|1836029   619 VGRGGGPANRAVLAQPKGSVKCRFKLTEQGEVIFARYGNPVLAIRHVESV 668

                    tAAtLEHGmnPPvsPkPEWRk....LmeemAvvAtEEYRsvvvKEPRFvE
                    +AAtL            E  ++ +++ +++  v  E +  +   E  F
  gi|1836029   669 AAATLLQSAPSVEKTNTEMTEkykpMANQLSEVSHETFLDLLNSED-FAP 717

                    YFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqtRFHLP
                    +F   tP +E G + iGsRPaKR  + + ++ LR iPWiF+W q R  L
  gi|1836029   718 WFSIVTPLTEIGLLPIGSRPAKRGLGAkSLDDLRTIPWIFSWAQARINLA 767

                    vWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPG
                     W G+G A           l  L+  Y+eWP F   +D +Em  AK D
  gi|1836029   768 AWYGLGSAC-----ESFGDLATLRKAYEEWPLFSTFIDNIEMSLAKTDER 812

                    iAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                    iA +y  L    +L    k++ d+ + t++++Lki G    L     L q
  gi|1836029   813 IAKMYLALGDRPDLS---KKVLDEMELTRKWVLKIVGDEWPLQHRHVLGQ 859

                    rlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkade
                     +R+R +Y+  L v q   L+          lr ++ KE   E   + ++
  gi|1836029   860 AIRIRSPYVDALSVTQVLALR---------SLRKKVDKEELSES--QQAG 898

                    LvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     + L              + t+ G+AAG+qntG
  gi|1836029   899 FIYLI-------------LCTVSGVAAGLQNTG    918

gi|289177836|gb|ADC85082.1|: domain 1 of 1, from 67 to 948: score 220.3, E = 5e-63
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +D  L +L        + L eYD  Ll  F  + q     +   +
  gi|2891778    67    DMDLCLNILR-------QVLSEYDENLLKTFDTVRQYAVDASAERFS 106

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         +  +    +D   Le     + +++  Da l+A+a+     LAnL
  gi|2891778   107 ----GVLTDTHPERDD--LEMAVKTIDAMNLHDAQLLARAFATYFHLANL 150

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     EE    yR  +   +     D        ++   + +L++     P+
  gi|2891778   151 CEE---NYRVAVLHEREAKVDDTQAIDPVNEMTKAYHQLISEM--GPAKA 195

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt.veDK
                     e L       v+tAHPt + R+++   +++iR     L A  + +  DK
  gi|2891778   196 KELLERLEFHPVFTAHPTEARRKAV---EGKIRRIAQLLEAHRLLgGSDK 242

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    kE    L  Ei A FRt  i   +PtP +E    +  +  t+++ +P
  gi|2891778   243 KEDSRRLYSEIDALFRTSPIALKKPTPVEEADTILDIFDNTLFHTIPMVY 292

                    RRvDtAL..KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    RR D  + +   Gi    P      +  sW+G DRDG nP vt  v R v
  gi|2891778   293 RRFDDWMlgDKAGIEP--PACPAFFHPGSWIGSDRDG-NPNVTAKVSRQV 339

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk.vv
                       aR     +     E            +E     +El     ++k++
  gi|2891778   340 ---ARKFSDHVLAALEEATRTVGRNMTVESETTPPSDELRALWNQQKeIS 386

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                             +   E  R +L  + D+L  t  R   L+
  gi|2891778   387 ERLTGKASLISTKELHRAVLLVMADRLHYTIKRDTDLM------------ 424

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y + ++FL  L +  +sL e GDk  A G L Dl+ q  tFG  +v ++
  gi|2891778   425 YHNCDDFLADLRVVQRSLAEAGDKRAAYGPLQDLIWQTETFGFHMVEMEF 474

                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    Rq s  +   lD i +H                    L+G R   g+
  gi|2891778   475 RQHSVVHARALDDIREH-------------------GLHGER---GPLQ 501

                    PktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvELLqR
                    P+t E   vld+fr L  + +++++ +   Yiis + +   v  v  L R
  gi|2891778   502 PMTHE---VLDTFRALGAIQkrngVKAARRYIISFTKSAKNVRDVYELNR 548
```

```
                    ECgvk....qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG...K
                         +++   + v+PLFE+L DLe     ++ +  i     r+  +++K
  gi|2891778   549 LAFSNpddaPVIDVIPLFEQLEDLEHSVSVLDEMLKIPEVQARLKQtgrK 598

                    qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                     evm+GYsDs KDAG   A   L  AqE i+K A +  + L+lFHGRGG
  gi|2891778   599 MEVMLGYSDSSKDAGPTTATLALHSAQERIAKWADENDIDLTLFHGRGGA 648

                    vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                    vGRGGGP   A+L+qP   ++   + t qGEvi   +G   L  r +
  gi|2891778   649 VGRGGGPANRAVLAQPKGSVKCRFKLTEQGEVIFARYGNPVLAIRHVESV 698

                    tAAtLEHGmnPPvsPkPEWRk....LmeemAvvAtEEYRsvvvKEPRFvE
                    +AAtL            E  ++ +++ +++  v  E +  +   E  F
  gi|2891778   699 AAATLLQSAPSVEKTNTEMTEkykpMANQLSEVSHETFLDLLNSED-FAP 747

                    YFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqtRFHLP
                    +F   tP +E G + iGsRPaKR  + + ++ LR iPWiF+W q R  L
  gi|2891778   748 WFSIVTPLTEIGLLPIGSRPAKRGLGAkSLDDLRTIPWIFSWAQARINLA 797

                    vWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPG
                     W G+G A           l  L+  Y+eWP F   +D +Em  AK D
  gi|2891778   798 AWYGLGSAC-----ESFGDLATLRKAYEEWPLFSTFIDNIEMSLAKTDER 842

                    iAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                    iA +y  L    +L    k++ d+ + t++++Lki G    L     L q
  gi|2891778   843 IAKMYLALGDRPDLS---KKVLDEMELTRKWVLKIVGDEWPLQHRHVLGQ 889

                    rlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkade
                     +R+R +Y+  L v q   L+          lr ++ KE   E   + ++
  gi|2891778   890 AIRIRSPYVDALSVTQVLALR---------SLRKKVDKEELSES--QQAG 928

                    LvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     + L              + t+ G+AAG+qntG
  gi|2891778   929 FIYLI-------------LCTVSGVAAGLQNTG    948

gi|94984768|ref|YP_604132.1|: domain 1 of 1, from 3 to 831: score 219.6, E = 7.9e-63
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                     s        D  +l + L+ +L++  Ge   E
  gi|9498476     3    -------------LS-------HDVNVLGRTLgQVLKEQEGEGFFEL 29

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     l  +     D   L  L   +  Ld   a  + +a++    L n
  gi|9498476    30 VERTRALVRDVRAGGDDTELRGL---IERLDQRTAENLVRAFSWYFQLVN 76

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAEE e     R++ +         +      i   l  L  ++  + eE
  gi|9498476    77 LAEEYE-----RVRVLS------GIQGVRPQSIAQALTELKAQG-VTAEE 114

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                        L+     L +tAHPt   RR        +Rn L  + A+D+   D
  gi|9498476   115 AEALLQRLDLGLTFTAHPTEMRRRT-------VRNHLVEV-ARDIPHLDG 156

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + L E +   i A + t E+RR +Pt  DE++ G+ Y+   + +  P
  gi|9498476   157 EGL-ERVAAHIEAMWGTPELRRLKPTVLDEVKGGLNYV-SSIAQALPELQ 204

                    RRvDtALKni.GinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R    A   + G     P   PL  FssWmGGDRDG nP vtP  tRD
  gi|9498476   205 RDLVRAFHQVyGRATQAP--LPL-SFSSWMGGDRDG-NPFVTPQATRDTL 250

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     L R  A  l +  +     +ls     ++L    EE  + + r
  gi|9498476   251 ALHRERARELLLGVLRQAYTDLS----QEDL----EEPEQAPYRA----E 288

                    YiEFWKqvPPtEPYRvi..LGdvRDKLYntRERaRHLLAtGiseisEeAv
                      E  + v   EP   +++L + R +LY
  gi|9498476   289 LRELHQAVREGEPVDLVprLEALRARLYAD------------------- 318

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
```

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                                    G +  AD  L  lL     FG  Lv LD+
  gi|9498476   319 ----------------------GQHRSADLLLTPLLTVARVFGQHLVSLDL 347

                   RqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgsD
                   R  s      +  +    ++  +Y + +E  +qE L  EL+ +RPL ++
  gi|9498476   348 REHSAQTGAAVARLLAEAGVETdYLNLPEHAKQEVLTRELRSRRPLWPAG 397

                   LPktEEvkDvldafr.vLAELPiD...sFGaYiismataPsDvLAvELLq
                        E++  ++ +r+v A   + ++++FG Yiism+ + sDvL   LL
  gi|9498476   398 EALPAELENAIGPIReVQAATRVSgprAFGRYIISMSESVSDVLEPLLLA 447

                   RECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri.dGKqevmv
                   RE g +  L+ vPLFE LADL+ AP  v  L s+  Y+  ++d  qe+m+
  gi|9498476   448 REVGFR-ILP-VPLFETLADLDRAPQVVWELLSVPEYRAVLgDDVQEIML 495

                   GYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGG
                   GYsDs KDAG l+A W L  Aq  i  v ++ Gv+   FHGRG  +GRGG
  gi|9498476   496 GYSDSNKDAGFLAANWALHEAQRKISEVCRRAGVRWRFFHGRGTSIGRGG 545

                   GPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtL
                   GP   AiL qP  ti+  lR+t qGE +   +    L  r L       L
  gi|9498476   546 GPAARAILGQPAGTIDAGLRITEQGEALADKYSHPVLARRNLEQALYGLL 595

                   EHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPEl
                        P   P  EW + + + A      YR++v  +P F  +F   tP
  gi|9498476   596 LAAARPAENPPAEWTQALTRAAEASAAAYRALV-HDPDFLPFFEAVTPIH 644

                   EYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFK
                   E  ++ni sRP +R  +  +  LRAiPW+ +Wtq R  LP W G+    +
  gi|9498476   645 EIARLNIASRPVRRPGAPSLGNLRAIPWVMSWTQNRANLPGWYGLAEGLR 694

                   hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLv
                     i  D       + mY+eWPFFR  lD   m  AK D  i a y +L
  gi|9498476   695 E-IGPDLA-----RQMYQEWPFFRTVLDNAQMSLAKSDFLIFAEYLRLSG 738

                   aEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYit
                      L    ++LR+ Y Et   L++ A   +lL  +P L+  ++LR++Yi
  gi|9498476   739 EQRLA---EQLRAAYDETVR-LVQEAVGAELLTNEPRLRASIKLRNPYID 784

                   tLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpterv
                    +  +q   L+R R            +   Ad+            t+++
  gi|9498476   785 PIHRIQVELLRRARS-----------AAGSADDS-----------GTDEY 812

                   aPGLEDtLiLtmKGiAAGmqntG<-*
                       E  L+L ++GiAAG+ ntG
  gi|9498476   813 ----ERPLLLSLQGIAAGVRNTG    831

gi|257052544|ref|YP_003130377.1|: domain 1 of 1, from 1 to 898: score 219.2, E = 1e-62
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       +    R L    v e  +L+            i+      d  E v
  gi|2570525     1    -MTLHGRELTQ-DVRELGELLG----------TIIEAQDSTDAYETV 35

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    E    sA    + D +  e +   L  L P    +vA+a+     L nL
  gi|2570525    36 -ETIRNSAIAYRRGDGESREPIHDELDRLSPEMQDVVARAFTTYFELINL 84

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEE e     R   +  GD +D         +EE +  L       P+ v
  gi|2570525    85 AEERERVREIREGVQS-GDLSDT--------VEEAVETLDAED-VDPDTV 124

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    e L    ++  +tAHPt + R+ +  K   +   +  L    +t  +K+
  gi|2570525   125 EEILEDVMIEPTFTAHPTEARRKTIKAKLWSVGKIIQDLDQIRLTDREKR 174

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    +   L  E+   + t  +R  +P   DE      Y+   +++ +
  gi|2570525   175 RMKRELQAEVTSLWQTPQVRDRRPDVTDETLNIQWYLENSLFDIISEVYD 224

                   RvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDvCL
                     + AL      E    dvP+L +F sW G DRDG nP vtPEvt +
  gi|2570525   225 ELEHALSETYDGE---VDVPkLYEFRSWAGSDRDG-NPYVTPEVTEETLE 270
```

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                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                      R +A  lY + +  L   ls    n E+    EE +   ++
  gi|2570525   271 RQRSVALELYRDDLKSLSGVLSQDVENLEMSDAFEESHEAHKQR--LPGV 318

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                     +      P EPY       R KL   RE         + ++   A y +
  gi|2570525   319 ADGIEERYPDEPY-------RQKLKLMRESVLR-----VDDVRSGA-YDN 355

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     +e L  LE+   sL e     i D  +  l+R+v tFG sL  LD+R
  gi|2570525   356 DDELLADLEIIAESLRENDADEIVDAHVKPLIRKVDTFGFSLANLDLRDH 405

                    seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPL..lgsDLP
                     e++t  l    +  +i  Y + sE+ R E+L   +    P+ ++  D
  gi|2570525   406 REKHTNALVETLKREGI-DYESMSEDERVEFLTEAILQDDPVidIEDDEG 454

                    ktEEvkDvldafrvLA....ELPiDsFGaYiismataPsDvLAvELLqRE
                      EE + vl  f   A+ ++E  +D+   Y is     s  L v  L
  gi|2570525   455 LSEESAKVLTLFSDAAgwqrEYGVDAIDTYAISWFEESSHALEVLFLGDQ 504

                    Cgvkqt.....LrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...
                     g+   ++  +  +vPLFE    L      +  LF  + Y   ++ ++++
  gi|2570525   505 AGIVDLpgycgFDIVPLFESEYALTRVREMLGTLFENEAYSQALEARnnt 554

                    qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                    qe+++GYsDs K+ G l+A W LY+ q  ++ +  ++Gv L lFHGRGG
  gi|2570525   555 QEILLGYSDSSKENGYLAANWELYRNQKRMANICDDFGVTLRLFHGRGGS 604

                    vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL.qR
                    + RGG P H A+L+ P  t+nG ++ t qGE i   +G  ++  r L+q
  gi|2570525   605 ISRGGVPMHEAMLALPNQTVNGQIKFTEQGEAIAEKYGNPDIAERNLeQM 654

                    FtAAtLEH..GmnPPvsPkP.EWRkLmeemAvvAtEEYRsvvvKEPRFvE
                      A  L   + m+ Pv   P+EW +  e  A  A  EYR + +    FvE
  gi|2570525   655 LNAQVLARynAMENPVEDIPeEWIEAFETAAEHASAEYRDL-LETDGFVE 703

                    YFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPv
                    YF  AtP +    +n+GsRPa R     +e LR iPW+F+Wtq R  +P
  gi|2570525   704 YFEQATPITVIENLNMGSRPASRTEDRSLEDLRSIPWVFSWTQARCIVPG 753

                    WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                    W  v    +  +d +   +  LkEmY+eWP+F   lD   m  AK D  i
  gi|2570525   754 WFSVATGIQGYLD-EGGDMETLKEMYEEWPYFGTILDHAGMALAKSDMEI 802

                    AaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                    A+ y +L   E    F   +R +Y+   +l+ +i G   lL    ++
  gi|2570525   803 ATEYADLADDELRERFFPWIRSEYENSVELIQEISGRETLLN-RSWMEEN 851

                    lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                    l  R++Y+  Ln +q   L                    +
  gi|2570525   852 LQRRNPYVDPLNLLQTRLL----------------------AQS------- 873

                    vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     +L  ter a      L Lt+ GiAAGm+ntG
  gi|2570525   874 -HLTETERRA------LRLTVHGIAAGMKNTG    898

gi|254419270|ref|ZP_05032994.1|: domain 1 of 1, from 1 to 901: score 219.1, E = 1.1e-62
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            + ++ P   + d+ L e   LL     +++    G+dL + v
  gi|2544192     1    -----MPMMTP---AADDALREEVRLLGGILGEVIRQEGGQDLFDHV 39

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          s  Y     ++    L   Lt++    a  +A+ +     LAn+
  gi|2544192    40 EAVRQASVAYHRDPASHPAKRLEKLLTAMTVDQAAGLAHGFALFSLLANI 89

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDi.EEtlKkLvlklnKsPeE
                    AE+   A RRR + +          A    D +E  l++L  +     +
  gi|2544192    90 AEDR--ATRRRAQGQV--------VAGARPDTpEGALQRLAEQK-VDKAA 128

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCL.aqLsAKDvtveD
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                    v   L    v  vltAHP    R+s++ + a +   L+a   A D
  gi|2544192   129 VRALLDEALVSPVLTAHPSEVRRKSVIDRIAAVSDMLdACDKAGDACSA- 177

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                       +   L R i   + t  +R      qDE+   +s++     +  PK
  gi|2544192   178 -AQINQPLRRQIVILWATRLVRTQGLVVQDEIDTVVSFLDRIFLRVAPKQ 226

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    L      L         P   P ++   W+GGDRDG nP v   v
  gi|2544192   227 LSAWRRLLDA-------PDLQPFMRVGTWVGGDRDG-NPNVDGAVLAAAF 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                              Y++ v  L  Els+     EL     El   a       +
  gi|2544192   269 RTQSRAVLGYYLEEVHALGAELSL---AAELAQVSPELAVLADAA----H 311

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv..
                         +     EPYR  L  v  +L  t E      A G    +  Av
  gi|2544192   312 DPSPHRA---DEPYRRALTGVYGRLAATYE------ARGGTPPPRRAVva 352

                    ...ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                     ++y   + F   L +   sL      v AD  L Dl+  v  FG  +
  gi|2544192   353 aepYPGPDAFEADLKIMRDSLVAYNGEVFADDRLSDLVTAVEIFGFHMAT 402

                    LDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLl
                    LD+Rq s+ +  v+  + +  ++ ++Y    Ee R   L aEL   R L+
  gi|2544192   403 LDLRQNSDVHERVVADLLKTAGVCAdYSGLDEEGRLSVLAAELASPRLLF 452

                    gsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAv
                     +      E     + ++  AE    +FG++  ++ i+s + a sD L v
  gi|2544192   453 SPYAEYAAETLKERGILQAAAE-ALAAFGPqairtHIVSKTDAASDLLEV 501

                    ELLqRECgvkq.......tLrvvPLFEkLADLeAAPAavekLFs..iDWY
                     LL +E g+ +++++   +++  PLFE + DL+A   ++e+L  ++
  gi|2544192   502 YLLLKEVGLYRpedpaacPIQAAPLFETIEDLRASRPTLERLLKepSALA 551

                    inridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                    + +  G qevm+GYsDs KD   l   W L  A   ++ v K  G KL l
  gi|2544192   552 VAKARGVQEVMIGYSDSNKDGSYLTSGWELHEASRALVEVTKAAGLKLQL 601

                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                    FHGRGGtvGRGGG     +L+qP  t++G +R t qGEvi   +GE ++
  gi|2544192   602 FHGRGGTVGRGGGSSFAGVLAQPEGTVQGRIRTTEQGEVIANKYGEPEIA 651

                    FrsLqRFtA....AtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvv
                     r L   t +   A L+ G +       +    + ++       YR +v+
  gi|2544192   652 LRNLDALTCgavlASLDQGKDHVFT--ADHGATLSDLSARSMAAYRKLVY 699

                    KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                        Fv+Y+R AtP  E   + iGsRP+ R  s  ie LRAiPW+F+W q
  gi|2544192   700 ETDGFVDYYRAATPIAEIADLKIGSRPSSRTASTRIEDLRAIPWVFSWSQ 749

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     R  LP W G+G A +       + +  Lk m + WPFFR  +  +Emv
  gi|2544192   750 SRVMLPGWFGFGSAVQ------GQDMAELKAMAEVWPFFRTLVQNMEMVM 793

                    AKGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlL
                    AK D  +A  y  L+    L  + +G+ +Rd+++ t+d +L i GH  lL
  gi|2544192   794 AKSDMTVARRYATLVPDPALaaRIYGE-IRDEWQRTHDAVLAITGHDRLL 842

                    EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                     G P L   +RLR +Y+  Ln +q   ++R R                 d
  gi|2544192   843 GGQPELDRLIRLRMPYVEPLNHVQIELIRRRRA---------------GD 877

                    EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    E+                 P + + ++L + G+AAG+ n G
  gi|2544192   878 ED-----------------PRVREGILLAINGVAAGLRNSG    901

gi|33595127|ref|NP_882770.1|: domain 1 of 1, from 33 to 982: score 219.0, E = 1.2e-62
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           q+ ++     s   + ++ D  Ll + L++++q   G+ + +
  gi|3359512    33    ----QMNAIRQQSDS--AEPLRHDIRLLGRCLgEVIQACEGKRVYDT 73
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                vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                +      +  +    D+     L a++  L   D   vA+a++  L L n
gi|3359512     74 IETLRRTAVRFRRAGDPADDKLLQARVKQLRGNDPNSVARAFSYFLHLSN 123

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                +AE+ +   R R + +        +       +   +  L  ++    +
gi|3359512    124 IAEDRDQNRRQRDRALA-------GAGPERGSLRQAIESLKAQG-VNNAR 165

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                +   L    v  vltAHPt   R+s L  +  i   L q   +++t ++
gi|3359512    166 IRRLLSEACVMPVLTAHPTEVQRKSTLDVHREISSLLVQ-RERELTADEL 214

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                 ELD AL   +   + t  +R ++ t  DE+   +sY+  t  + +P+
gi|3359512    215 SELDLALIGQVATLWQTRMLRYTRLTVADEIENALSYYRSTFLNVIPRVY 264

                RRvDtALKniGinERlPYdvPL...ikFssWmGGDRDGknPRvtPEvtRD
                      L    +    P   PL++ ++  sW+GGDRDG nP v
gi|3359512    265 GDLARLLNREPVKPFTPPPPPLepfLRMGSWIGGDRDG-NPNVDAATLER 313

                vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                  L    +    Y++ v  L  Els     + L + A+      a
gi|3359512    314 ALLRQATVLFEHYLQEVHALGAELS----ASTLLIEADPALLALADA--- 356

                KyYiEFWKqvPP..tEPYRviLGdvRDKLYntRERaRHLLAtGiseisE.
                          P ++ EPYR  L  +  +L  t   aRHL  + ++  +
gi|3359512    357 -----GGDDSPHrrDEPYRRALIGIYARLAAT---ARHLTGQELARRATv 398

                .eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                + A y   +     L +   sL       iA   L  l   v  FG  L
gi|3359512    399 pAAPYDTPDALAADLAVIAASLSAHHGAPIARLRLSGLQQAVTVFGFHLA 448

                KLDiRqEseRqtDvlDAittHLeiGs......YReWsEeKRqEWLlaELk
                 +D+Rq s+ +  vl  +    + G +++  +Y    E  R   L  EL
gi|3359512    449 TVDLRQSSDVHERVLAELFARAGDGIdgqavdYLALDEAARVAVLRRELA 498

                GKRPLlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPs
                  RPL  + +   EE +  l  +r  A ++ +    +    i+s + + s
gi|3359512    499 HARPLASPWIAYSEETASELAVLRAAAAgrarYGRQAVLQSIVSHTETLS 548

                DvLAvELLqRECgvkqt..........LrvvPLFEkLADLeAAPAavekL
                D L v +Lq+E g+  +++++  ++++L vvPLFE + DL+  P  ++
gi|3359512    549 DLLEVLVLQKEAGLIAPpgetiapgdgLMVVPLFETIPDLQRGPEIMAAW 598

                FsiDWYinrid....GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKv
                  +   + r+   ++  qevm+GYsDs KD G l   W LY+A   ++ v
gi|3359512    599 LDLPEVRQRVRlaqgDTQEVMLGYSDSNKDGGFLTSNWSLYQAERALVDV 648

                AKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEvi
                     v+L +FHGRGG vGRGGG    AiL+qPP t+ G lR t qGEvi
gi|3359512    649 FSARSVRLRMFHGRGGSVGRGGGSSYDAILAQPPGTVAGQLRLTEQGEVI 698

                EfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPEWRkLmee.......m
                   + + ++    L    AAtLE  + P  +        m+++ +  + m
gi|3359512    699 QSKYKDAEVGRWHLELLVAATLESSLAPQAAATSAEDAHMQQhapamsfM 748

                AvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGie
                   A   YR +v+  P F +YF  AtP  E   +niGsRPa Rk +  ie
gi|3359512    749 SELAQRTYRGLVYDTPGFADYFFAATPISEIAGLNIGSRPASRKKGQHIE 798

                sLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK........nlqkL
                 LRAiPW F+W q R  L  W G+G A    ++   ++ +++++  l +L
gi|3359512    799 DLRAIPWGFSWAQCRLMLTGWYGMGSAIEAYLETGAQgaprsrraRLAQL 848

                kEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL..kPFGksL
                +Em  +WP FR  l  +Emv AK D  iAa y +L+    L+++ FG  +
gi|3359512    849 REMASDWPAFRTLLSNMEMVLAKSDLAIAAGYAQLVPRRGLreRVFG-AI 897

                RdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLK
                 ++   t   +L++   ++lL   P L   lR R +Yi  Ln +q   +K
```

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  gi|3359512   898 TAEHGRTLA-MLRLLTRRELLADNPGLMASLRERFAYIDPLNYLQIELIK 946

                   RiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLt
                   R R                A+      d  +++             + Lt
  gi|3359512   947 RHR----------------AAQRRAGDDADIRVP----------RAIHLT 970

                   mKGiAAGmqntG<-*
                   + GiAAG+ n
  gi|3359512   971 INGIAAGLRNSD    982

gi|241761565|ref|ZP_04759652.1|: domain 1 of 1, from 1 to 885: score 218.2, E = 2.1e-62
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                             +  P  + ++ +L  +  LL      ++++  Ge+L   +
  gi|2417615     1    -------MTKPRTINQNPDLRYFGNLL----GQVIKEQGGESLFNQI 36

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         sA     +      EL ++L  Ld  D    A+a+l    LAnL
  gi|2417615    37 EQIR--SAAIRRHRGIVDSTELSSRLADLDLNDMFSFAHAFLLFSMLANL 84

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   A++            + GD  D      ++ +   lK +  k+  s + +
  gi|2417615    85 ADD------------RQGDALD-----PDANMASALKDIKAKG-VSQQAI 116

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    + +    +  vltAHPt   R+s+L    Ri   +    A     eD
  gi|2417615   117 IDMIDKACIVPVLTAHPTEVRRKSMLDHYNRIAGLMRLKDAGQTVTEDGL 166

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    +++AL   i   + t  +   + t  DE+   +s++ Et     P+
  gi|2417615   167 PIEDALIQQITILWQTRPLMLQKLTVADEIETALSFLRETFLPVLPQLYA 216

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     +  L        +P     i+   W+GGDRDG      P v  D  +L
  gi|2417615   217 EWEKLL-----GSSIP---SFIRPGNWIGGDRDG-----NPNVNADTIML 253

                   aRmmAanl....YisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                   +    +    ++Y++ ++ L+  ls+     ++    +++ r a +
  gi|2417615   254 SLKRSSETvltdYLNRLDKLLSNLSV---STDMVSVSDDILRLADKS--- 297

                   KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                            +   EPYR  L  + D+L  t            +  s eA
  gi|2417615   298 ----GDDAAIRADEPYRRALNGIYDRLAATYRQIAGRNPSRPALRSAEA- 342

                   ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                   y +  e L  L    k L e G   +A+Gs   l+R v tFG  L  LD+
  gi|2417615   343 YKRPQELLADL----KTLAE-GLGKLAEGSFKALIRSVETFGFHLATLDL 387

                   RqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgsD
                   Rq s+ +  v+  + +   + ++Y + sEe R   L  EL+  R L+ +
  gi|2417615   388 RQNSQVHERVVNELLRTAVVEAdYLSLSEEDRVKLLRRELSQPRTLFVPR 437

                   LPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvELL
                       EE +  ld ++  A    + FG+++ ++Y+is   + sD+L v LL
  gi|2417615   438 ADYSEETRSELDIIQAAAR-AHEIFGPesittYLISNGESISDILEVYLL 486

                   qRECgv.......kqtLrvvPLFEkLADLeAAPAavekLFsi..DWYinr
                    +E g+ +++ ++k ++   PLFE +ADLe AP  +e  F +++   i +
  gi|2417615   487 LKEAGLyqggakpKAAIEAAPLFETVADLENAPKVMEEWFKLpeAQAIAK 536

                   idGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                     G qevmvGYsDs KD G l   W LYkA   ++ +  k Gv++  FHG
  gi|2417615   537 AHGVQEVMVGYSDSNKDGGYLTSVWGLYKACLALVPIFEKAGVQIQFFHG 586

                   RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                   RGG vGRGGG    AiLsqP   ++G +R t qGEv+   +G  +
  gi|2417615   587 RGGSVGRGGGSNFNAILSQPAGAVKGRIRYTEQGEVVAAKYGTHESAIAH 636

                   LqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEEYRsvvvKEPR
                   L    AAtL   ++ P    PE +++Rk ++++   A   YR +v+
  gi|2417615   637 LDEAVAATLITSLEAPTIVEPEfsrYRKALDQISDSAFQTYRQLVYGTKG 686
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                    FvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFH
                    F  +F   tP  E   + iGsRP  Rk s  ie LRAiPW+F+W q R
  gi|2417615   687 FRKFFSEFTPLPEIALLKIGSRPPSRKKSDRIEDLRAIPWVFSWSQVRVM 736

                    LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                    LP W G+G A       D      L+Em   WPFFR t+  +E v A+ D
  gi|2417615   737 LPGWFGFGQAL-----YDFEDTELLQEMASRWPFFRTTIRNMEQVMARSD 781

                    PGiAaLyDkLLvaE.eLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                      iA  y  L+   ++     +s+ d +    + LLk      lLE  P
  gi|2417615   782 MTIAKHYLALVEDQtNGEAIYDSIADGWNKGCEGLLKATQQNWLLERFPA 831

                    LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                    +   + +R +Y+  Ln +q   LK+ R
  gi|2417615   832 VDNSVQMRRPYLEPLNYLQVELLKKWR---------------------- 858

                    adeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                             +    P + + + Lt+  iA  + n G
  gi|2417615   859 ---------GGDTNPHILESIQLTINAIATALRNSG    885

gi|260753930|ref|YP_003226823.1|: domain 1 of 1, from 1 to 885: score 217.3, E = 3.9e-62
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                             +  P  + ++ +L  +  LL      ++++  Ge+L   +
  gi|2607539     1    -------MTKPRTINQNPDLRYFGNLL----GQVIKEQGGESLFNQI 36

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          sA     +      EL ++L  Ld  D    A+a+l    LAnL
  gi|2607539    37 EQIR--SAAIRRHRGIVDSTELSSRLADLDLNDMFSFAHAFLLFSMLANL 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    A++            + GD  D      ++ +   lK +  k+  s + +
  gi|2607539    85 ADD------------RQGDALD-----PDANMASALKDIKAKG-VSQQAI 116

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     + +    +  vltAHPt   R+s+L    Ri   +    A     eD
  gi|2607539   117 IDMIDKACIVPVLTAHPTEVRRKSMLDHYNRIAGLMRLKDAGQTVTEDGL 166

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +++AL   i   + t  +   + t  DE+   +s++ Et     P+
  gi|2607539   167 PIEDALIQQITILWQTRPLMLQKLTVADEIETALSFLRETFLPVLPQIYA 216

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                      +  L        +P     i+   W+GGDRDG      P v  D  +L
  gi|2607539   217 EWEKLL-----GSSIP---SFIRPGNWIGGDRDG-----NPNVNADTIML 253

                    aRmmAanl....YisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                    +    +    ++Y++ ++ L+  ls+     ++    +++ r a +
  gi|2607539   254 SLKRSSETvltdYLNRLDKLLSNLSV---STDMVSVSDDILRLADKS--- 297

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                             +   EPYR  L  + D+L  t            +  s eA
  gi|2607539   298 ----GDDAAIRADEPYRRALNGIYDRLAATYRQIAGRNPSRPALRSAEA- 342

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y +  e L  L    k L e G   +A+Gs   l+R v tFG  L  LD+
  gi|2607539   343 YKRPQELLADL----KTLAE-GLGKLAEGSFKALIRSVETFGFHLATLDL 387

                    RqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgsD
                    Rq s+ +  v+  + +   + ++Y + sEe R   L  EL+  R L+ +
  gi|2607539   388 RQNSQVHERVVNELLRTATVEAdYLSLSEEDRVKLLRRELSQPRTLFVPR 437

                    LPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvELL
                        EE +  ld ++  A    + FG+++ ++Y+is   + sD+L v LL
  gi|2607539   438 ADYSEETRSELDIIQAAAR-AHEIFGPesittYLISNGESISDILEVYLL 486

                    qRECgv.......kqtLrvvPLFEkLADLeAAPAavekLFsi..DWYinr
                     +E g+ +++ ++k ++   PLFE +ADLe AP  +e  F +++   i +
  gi|2607539   487 LKEAGLyqggakpKAAIEAAPLFETVADLENAPKVMEEWFKLpeAQAIAK 536

                    idGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                      G qevmvGYsDs KD G l   W LYkA   ++ +  k Gv +  FHG
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  gi|2607539   537 AHGVQEVMVGYSDSNKDGGYLTSVWGLYKACLALVPIFEKAGVPIQFFHG 586

                    RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                    RGG vGRGGG    AiLsqP   ++G +R t qGEv+   +G  +
  gi|2607539   587 RGGSVGRGGGSNFNAILSQPAGAVKGRIRYTEQGEVVAAKYGTHESAIAH 636

                    LqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEEYRsvvvKEPR
                    L    AAtL   ++ P    PE +++Rk ++++   A   YR +v+
  gi|2607539   637 LDEAVAATLITSLEAPTIVEPEfsrYRKALDQISDSAFQTYRQLVYGTKG 686

                    FvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFH
                    F  +F   tP  E   + iGsRP  Rk s  ie LRAiPW+F+W q R
  gi|2607539   687 FRKFFSEFTPLPEIALLKIGSRPPSRKKSDRIEDLRAIPWVFSWSQVRVM 736

                    LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                    LP W G+G A       D      L+Em   WPFFR t+  +E v A+ D
  gi|2607539   737 LPGWFGFGQAL-----YDFEDTELLQEMASRWPFFRTTIRNMEQVMARSD 781

                    PGiAaLyDkLLvaE.eLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                      iA  y  L+   ++     +s+ d +    + LLk      lLE  P
  gi|2607539   782 MTIAKHYLALVEDQtNGEAIYDSIADGWNKGCEGLLKATQQNWLLERFPA 831

                    LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                    +   + +R +Y+  Ln +q   LK+ R
  gi|2607539   832 VDNSVQMRRPYLEPLNYLQVELLKKWR---------------------- 858

                    adeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                             +    P + + + Lt+  iA  + n G
  gi|2607539   859 ---------GGDTNPHILESIQLTINAIATALRNSG    885

gi|56552392|ref|YP_163231.1|: domain 1 of 1, from 1 to 885: score 217.3, E = 4e-62
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                              +  P  + ++ +L  +  LL      ++++  Ge+L   +
  gi|5655239     1    -------MTKPRTINQNPDLRYFGNLL----GQVIKEQGGESLFNQI 36

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          sA     +      EL ++L  Ld  D    A+a+l    LAnL
  gi|5655239    37 EQIR--SAAIRRHRGIVDSTELSSRLADLDLNDMFSFAHAFLLFSMLANL 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    A++            + GD  D      ++ +   lK +  k+  s + +
  gi|5655239    85 ADD------------RQGDALD-----PDANMASALKDIKAKG-VSQQAI 116

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     + +    +  vltAHPt   R+s+L    Ri   +    A     eD
  gi|5655239   117 IDMIDKACIVPVLTAHPTEVRRKSMLDHYNRIAGLMRLKDAGQTVTEDGL 166

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     +++AL   i   + t  +   + t  DE+   +s++ Et     P+
  gi|5655239   167 PIEDALIQQITILWQTRPLMLQKLTVADEIETALSFLRETFLPVLPQIYA 216

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                      +  L        +P     i+   W+GGDRDG      P v  D  +L
  gi|5655239   217 EWEKLL-----GSSIP---SFIRPGNWIGGDRDG-----NPNVNADTIML 253

                    aRmmAanl....YisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                    +    +    ++Y++ ++ L+  ls+     ++    +++ r a +
  gi|5655239   254 SLKRSSETvltdYLNRLDKLLSNLSV---STDMVSVSDDILRLADKS--- 297

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                             +   EPYR  L  + D+L  t             +  s eA
  gi|5655239   298 ----GDDAAIRADEPYRRALNGIYDRLAATYRQIAGRNPSRPALRSAEA- 342

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y +  e L  L    k L e G   +A+Gs   l+R v tFG  L  LD+
  gi|5655239   343 YKRPQELLADL----KTLAE-GLGKLAEGSFKALIRSVETFGFHLATLDL 387

                    RqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgsD
                    Rq s+ +  v+  + +   + ++Y + sEe R   L  EL+  R L+ +
  gi|5655239   388 RQNSQVHERVVNELLRTATVEAdYLSLSEEDRVKLLRRELSQPRTLFVPR 437
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                    LPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAvELL
                        EE +  ld ++  A    + FG+++ ++Y+is   + sD+L v LL
  gi|5655239   438 ADYSEETRSELDIIQAAAR-AHEIFGPesittYLISNGESISDILEVYLL 486

                    qRECgv.......kqtLrvvPLFEkLADLeAAPAavekLFsi..DWYinr
                     +E g+ +++ ++k ++   PLFE +ADLe AP  +e  F +++   i +
  gi|5655239   487 LKEAGLyqggakpKAAIEAAPLFETVADLENAPKVMEEWFKLpeAQAIAK 536

                    idGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                      G qevmvGYsDs KD G l   W LYkA   ++ +  k Gv +  FHG
  gi|5655239   537 AHGVQEVMVGYSDSNKDGGYLTSVWGLYKACLALVPIFEKAGVPIQFFHG 586

                    RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                    RGG vGRGGG    AiLsqP   ++G +R t qGEv+   +G  +
  gi|5655239   587 RGGSVGRGGGSNFNAILSQPAGAVKGRIRYTEQGEVVAAKYGTHESAIAH 636

                    LqRFtAAtLEHGmnPPvsPkPE...WRkLmeemAvvAtEEYRsvvvKEPR
                    L    AAtL   ++ P    PE +++Rk ++++   A   YR +v+
  gi|5655239   637 LDEAVAATLITSLEAPTIVEPEfsrYRKALDQISDSAFQAYRQLVYGTKG 686

                    FvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFH
                    F  +F   tP  E   + iGsRP  Rk s  ie LRAiPW+F+W q R
  gi|5655239   687 FRKFFSEFTPLPEIALLKIGSRPPSRKKSDRIEDLRAIPWVFSWSQVRVM 736

                    LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                    LP W G+G A       D      L+Em   WPFFR t+  +E v A+ D
  gi|5655239   737 LPGWFGFGQAL-----YDFEDTELLQEMASRWPFFRTTIRNMEQVMARSD 781

                    PGiAaLyDkLLvaE.eLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                      iA  y  L+   ++     +s+ d +    + LLk      lLE  P
  gi|5655239   782 MTIAKHYLALVEDQtNGEAIYDSIADGWNKGCEGLLKATQQNWLLERFPA 831

                    LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                    +   + +R +Y+  Ln +q   LK+ R
  gi|5655239   832 VDNSVQMRRPYLEPLNYLQVELLKKWR---------------------- 858

                    adeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                             +    P + + + Lt+  iA  + n G
  gi|5655239   859 ---------GGDTNPHILESIQLTINAIATALRNSG    885

gi|190572823|ref|YP_001970668.1|: domain 1 of 1, from 12 to 903: score 216.9, E = 5.4e-62
                    *->siDAqLRlLvP..GKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                       s D  LR  v + G     + L+e    +   FLD + D+    +
  gi|1905728    12    SPDLPLRDDVRrlGALV-GDLLVEQ---VSAAFLDDVEDVRTRAIAR 54

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                                  ++    L EL   L +  P  a  + +a++    +
  gi|1905728    55 --------------RENQAPLSELADGLAGRTPQQAETMVRAFSTYFQVV 90

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsD.iEEtlKkLvlklnKsP
                    n+AE v+   RRR  ++        + A    D++ + l++L  ++
  gi|1905728    91 NIAERVHRIRRRRDYQRA-------GTAGAQPDgLQDALQHLKAQG-VGL 132

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    +E  + L    ++ v+tAHPt +vRR+LL K+  +   L        t+
  gi|1905728   133 DELAQWLPRIDIEPVFTAHPTEAVRRALLEKEQLMVASLVDNLDGQRTPG 182

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    +           + A + t +    +Pt  DE      Y+   +++ +P
  gi|1905728   183 EAAADAARFRMALTASWQTTDSSPVRPTVDDEREHVGFYLVQVLYRVIPV 232

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                           AL+     E lP    L++F  W+GGD DG nP v     R
  gi|1905728   233 LYESLQQALRDT-YGEELPLPR-LLRFGTWVGGDMDG-NPNVDAHTIRNT 279

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                        R      Y   +  L   ls     +  Rv   +  +    +
  gi|1905728   280 LDAQRQAVLGRYQKELLQLASLLS----QSTERVGVSDALQARVAQ---- 321

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                         ++q+ P+   R    d+  +L n R RaR L At   +    A y
```

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  gi|1905728   322 -----YQQLLPQVQSRPRHADMPYRLLNDRMRAR-LQAT--LDNGGGA-Y 362

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                        e ++ L L   sL           ++  lL  v tFG  L +LD+R
  gi|1905728   363 AGPAELIDDLQLILDSLLANRGEHAGGFAVQRLLWRVKTFGFHLARLDVR 412

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs  +   l A+    e  ++       R   L    +G   L   D
  gi|1905728   413 QESSVHARALAAVLGGEE--AWQALDVAGRARLLSPHASGETALPNGDDE 460

                    ktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                        +  v  a+ +  A   +D+ G+Yiisma   sDvLAv  L R  g+
  gi|1905728   461 GNQRLDAVFAALAdARARHGSDALGSYIISMAHDRSDVLAVLALARRGGL 510

                    kq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...qev
                     +++++ +L + PLFE + DL+   A++  L +   Y+ +++ +++ q v
  gi|1905728   511 VEengsvPLDIAPLFETVDDLKRGTATLRDLLADPIYRAHLQARddvQMV 560

                    mvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGR
                    m+GYsDs KD G  +  W L +Aq E+  vA + G++L+ FHGRGG + R
  gi|1905728   561 MLGYSDSSKDGGIAASRWGLQRAQVELLEVAAEAGIRLTFFHGRGGSISR 610

                    GGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAA
                    GGG t  A+ + P   i+G lRvt qGEvi   +G   L  rsL   t A
  gi|1905728   611 GGGKTTHAVDASPRGSIDGRLRVTEQGEVIHRKYGIRALALRSLEQATGA 660

                    tLEHGmnPPvs.PkP.EWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlA
                     L   + P  ++P+ ++WR +m+ +A    E YR+ v     F++YFR A
  gi|1905728   661 VLRASLRPRAAePREdDWRPVMDAVAGASSEVYRAFV-GQAGFMDYFRTA 709

                    tPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWLGv
                    tP     +m +GsRP++R   +  +  LRAiPW+FaW q R  +P W Gv
  gi|1905728   710 TPIDVIERMTLGSRPSRRLGQdAALGNLRAIPWVFAWSQARAVIPGWYGV 759

                    GAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLy
                    G   + A+  D    q L++m ++WPFFR  lD + mv  KGD  iA  +
  gi|1905728   760 GSGLQAAV--DAGHEQTLRDMARDWPFFRTFLDDISMVLSKGDITIAEQF 807

                    DkLLvaEeLk.PFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRL
                     +L  + eL++ F  ++  + + t+ +LL +   + lL+ D  L   +RL
  gi|1905728   808 SQL--SGELHgRFFPQVQRELELTRHWLLALMDQQTLLDHDARLALSIRL 855

                    RdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkL
                    R++Y+  + ++q   L+R R               A     + d+L++
  gi|1905728   856 RNPYVDPISMLQVDLLQRWR----------------ASGR--EDDDLLR- 886

                    nptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                L+  + G+  G+qntG
  gi|1905728   887 ------------ALVACVNGVSQGVQNTG    903

gi|117927606|ref|YP_872157.1|: domain 1 of 1, from 47 to 915: score 216.2, E = 8.5e-62
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       si  q R   P +          D  Ll   L+ +L +  G++L +
  gi|1179276    47    SIREQARQEMPEQLR-------RDVRLLGELLgQVLREYGGQQLLDD 86

                    vqEC.YElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    v   +  + A   G    + +eEL a+   L  a+   vA+a+     LA
  gi|1179276    87 VEALrRAVIAARTGAGRIEDVEELVARW-PLSRAEE--VARAFTVYFHLA 133

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    nLAEE    +R R+ + +      ++  t    +   +  +  +     e
  gi|1179276   134 NLAEE---HHRVRVLRSR------DGLGTAGDSLAASVSEVRALY--GEE 172

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                       e L    v  vltAHPt + RR+++   aR    L  L        +
  gi|1179276   173 RLAELLAGLRVHPVLTAHPTEARRRAVVSAIARAGEQLDRLDDPRAGESE 222

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    + +    L  Ei   +Rt  +R +   P DE+R  ms + Et+++ +P
  gi|1179276   223 RADARRRLLEEIDILWRTAHLRSTAVDPLDEVRTAMSAFDETLFRVMPAL 272
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                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                     R  D  L       R P     ++  sW+GGDRDG nP vt  vtR
  gi|1179276   273 YRGLDHLLLGEESGARRPAAPAFLRLGSWVGGDRDG-NPLVTASVTR--- 318

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE.........Elyrt
                          Aa         L  E +  R    L + AE++++++  ++
  gi|1179276   319 ------AAMAIQAEHVLLALERAATRIGRTLTASAEttppntalqDALAE 362

                    aardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLY.ntRERaRHLLAtGi
                    a+r       +E      P EP Rv        LY   R RaR
  gi|1179276   363 ARRR--LPSVVEELEIRAPGEPHRVY------TLYaAARVRARRR----- 399

                    seisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFG
                        E   y +  eFL  L L   sL + G + +A G L  l+ qv tFG
  gi|1179276   400 ---GEPTGYRHAGEFLADLRLVQESLVQSGAHRLAFGELQHLIWQVETFG 446

                    LsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGK
                      L  L+iRq s  +   l      L+ G
  gi|1179276   447 FHLAELEIRQHSAIHAKAL----ADLDSG---------------------- 471

                    RPLlgsDLPktEEvkDvldafrvLA.ELPiDsFGaYiismataPsDvLAv
                        g+   +t+Ev +   ++r L +E  +D+   Y+is + +  D+ Av
  gi|1179276   472 ----GPRWEMTDEVLETFRTIRWLQdEYGVDACRRYVISFTRSAEDIAAV 517

                    .ELLqRECgvkqt.LrvvPLFEkLADLeAAPAavekLFsiDWYinri..d
                      L  R      + L vvPLFE   DL+    ++e    i   + r+  +
  gi|1179276   518 yRLADRATDGSPPvLDVVPLFETEEDLRHCVPTLEAALDIPEVRARLaaN 567

                    GKq.evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    G+  evm+GYsDs KD G +sA   LY Aq  ++  A+++ v+L+lFHGR
  gi|1179276   568 GRRmEVMLGYSDSAKDVGPVSATLALYDAQQALADFARRHDVQLTLFHGR 617

                    GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                    GG  GRGGGP   AiLsq P  ++G  +vt qGEvi   +G   +  r L
  gi|1179276   618 GGALGRGGGPANRAILSQAPGSVDGRFKVTEQGEVIFARYGNPVIARRHL 667

                    qRFtAAtLEHG....mnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPR
                       tAA L   ++  m+   +    +R + e +   A  EYR +v   P
  gi|1179276   668 DQVTAAVLLAStpavMERVAAAERKYRPVFEAVSRAARTEYRGLV-ETPG 716

                    FvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFH
                    F EYF    P  E G + iGsRP +R  +  +  LRAiPW F+W qtR
  gi|1179276   717 FAEYFAAVSPLPEIGALRIGSRPVRRSAGTDLADLRAIPWNFSWAQTRVN 766

                    LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                    LP W G+G  F    d D      L+  Y eWP F   +D +Em  AK D
  gi|1179276   767 LPGWYGIGSGFAAVGDVDA-----LRAAYAEWPLFTTMVDNVEMSLAKTD 811

                    PGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                      iA  +  L    ++    +++ ++Y    +++L++ G   lLE    L
  gi|1179276   812 RDIAQRHLALGNRPDIA---DRILAEYDRSVEWVLRVLGTTRLLETHRVL 858

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                     q + LR++Y+  L  +q   L  +R             +   dE   +
  gi|1179276   859 GQAVQLRNPYVDALSHLQLRALAALR-------------RGIPDEA--ER 893

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    d  ++L              +L + G+AAG+qntG
  gi|1179276   894 DRTLRLL-------------LLSINGVAAGLQNTG    915

gi|229821216|ref|YP_002882742.1|: domain 1 of 1, from 4 to 888: score 215.7, E = 1.2e-61
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                       s          G v e  + ++ D  Ll   L+++L +  G++L +
  gi|2298212     4    SSNGR-----GGAVHEMPDELRADVRLLGELLgEVLSETGGPELLDD 45

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     l     G  +++ +    a + s  P  a  vA+a+     L n
  gi|2298212    46 VERLRGLTIAAYGAGEASAITQAEALVDSFTPERAADVARAFTCYFHLVN 95

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAEE +     R + +  G+   E+ A  +s +   l +L        eE
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gi|2298212    96 LAEEYHRVRTLRQRDRERGE--SEGPASADS-LPGALAQLRAEV--GEEE 140

                 vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     L       vltAHPt + RR++     Ri   +a      +
gi|2298212   141 TSRRLAGLEFRPVLTAHPTEARRRAVAAAIRRISELVAERDDPRLGATTL 190

                 kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  E+   +  Ei   +Rt  +R ++P P DE+R  m  + Et+++  P+
gi|2298212   191 AEIRRRMLGEIDTLWRTSPLRTSKPSPLDEVRTAMGVFDETLFQVLPQVY 240

                 RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                 R  D  L         P     ++  sW+G DRDG nP vt  vtR
gi|2298212   241 RILDDHLLGADAGRVAPRAPAFVRLGSWIGADRDG-NPNVTAKVTR---- 285

                 LaRmmAanlYisqvEDLmFElsmWRCndELRvRAE......Elyrtaard
                      Aa +  + v  L  E +  R    L   A ++++++El    +r+
gi|2298212   286 ----AAASIAAEHVL-LGLERAATRIGRALTLDATstppsgELLALWRRQ 330

                 kvvKyYiEFWKqv...PPtEPYRviLGdvRDKLYntRERaRHLLAtGise
                 + v    E    +  + P EPYR ++  + +++  tR R   L
gi|2298212   331 QSVDE--ELTAEIaarAPDEPYRRVVLVIAERIAATRRRDADL------- 371

                 isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                       y + Ee L  L++   sL   GD   A G L  l+ qv tFG
gi|2298212   372 -----AYADPEELLADLDVVQASLVAAGDARGAYGELQHLIWQVRTFGFH 416

                 LvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRP
                 L  L++Rq s  +     A+t                    laE++ K
gi|2298212   417 LAELEVRQHSKVH-----ALT-------------------LAEIEAK-- 439

                 LlgsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPsDvL
                   g D        +vl+ frv+A +    +G    ++Yi+s + +  D+
gi|2298212   440 --GVDGDLDPVAVEVLEVFRVIATI-QQRYGQlaarrYIVSFTMSADDIA 486

                 Av....ELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                 Av +  EL     +    L vvPLFE  ADLeA    ++ +        r
gi|2298212   487 AVyrlaELALGSAEAAPVLDVVPLFETFADLEASTDVLDAMVTQPQVQAR 536

                 idG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                 +  ++++ evm+GYsDs KD G +sA   LY Aq  i++ A++  + L+l
gi|2298212   537 LAAtgrRLEVMLGYSDSAKDVGPVSATLALYDAQSRIARWAQDNDIVLTL 586

                 FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                 FHGRGG  GRGGGP   A+L+qPP  ++G  + t qGEvi   +G  ++
gi|2298212   587 FHGRGGALGRGGGPANRAVLAQPPNSVDGRFKLTEQGEVIFARYGNPHIA 636

                 FrsLqRFtAAtLEHGmnPPv.....sPkPEWRkLmeemAvvAtEEYRsvv
                  r +   +AAtL     P ++++++s    + ++  +m  v    +  +v
gi|2298212   637 TRHIEQVAAATL-LASAPSIeernsSAAATYADVAARMDTVSRSRFYDLV 685

                 vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaW
                   E  F  +F   tP  E G + +GsRPaKR  s + +e LRAiPW+FaW
gi|2298212   686 QAEG-FPQWFAEVTPQEEVGLLALGSRPAKRGLSVnSLEDLRAIPWVFAW 734

                 tqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEm
                 tq R  L  W G+GAA        +  l  L+  Y eWP F   +D +Em
gi|2298212   735 TQARINLTGWFGLGAALDA-----VGDLELLRRAYAEWPLFTTMIDNVEM 779

                 vFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlL
                   AK D  iA  y +L   E+L      + d+   t+ ++L i GH  lL
gi|2298212   780 SLAKTDERIARRYLELGDREDLAAL---VLDELALTRRWVLDITGHERLL 826

                 EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                      L   + LR +Y+  L  +q   L+ +R              E Ad
gi|2298212   827 ATSRVLGRAVQLRSPYVDALSLIQLRALRALR--------------EGAD 862

                 EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                 E   k  eL +L              +L + G+AAG+qntG
gi|2298212   863 EA--KVPELQRLL-------------LLSVNGVAAGLQNTG    888

gi|289580156|ref|YP_003478622.1|: domain 1 of 1, from 1 to 898: score 215.6, E = 1.3e-61
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                *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          L    v   +++ e  ALL     D+L D    +  E v
gi|2895801     1    ------MQLHNRDVR--QDVRELGALL----GDVLEDQTSRQAFETV 35

                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                  C   + +Y   +  ++ e L + L +L P    +vA+ +     L nL
gi|2895801    36 ESCRRAAIDYRAGELESR-ESLITELEGLSPHQQRIVARGFTSYFELINL 84

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AEE     R R++  +      E++A t  D  Et      +++   e v
gi|2895801    85 AEE-----RERVRSIR-----TESQAGTLEDSLET--AAAELGEEDIETV 122

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                 + L    ++  +tAHPt + R+ +  K   i   L  L  + +t  +
gi|2895801   123 QQVLDDVLIEPTFTAHPTEARRKTVKSKLRAISMALETLDERLLTDKESG 172

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                 +  A+  E+   + t  +R  qP P DE R    Y+  t+++ v
gi|2895801   173 QIWAAIDSEVTSLWQTPQVRNRQPEPEDEARNVQWYLQNTLFDVVGEIYD 222

                RvDtALKniGinERlP..YdvP.LikFssWmGGDRDGknPRvtPEvtRDv
                    A     i E + ++ d+P+L +F sW G DRDG nP vtP+vt
gi|2895801   223 EFADA-----IDEEVAsdIDIPkLFEFRSWAGSDRDG-NPYVTPDVTART 266

                CLLaRmmAanlYisqvEDLmFElsm..WRCn..dELRvRAEElyrtaard
                    R +    Y +q+  L   ls ++ R  +++E  +  E
gi|2895801   267 LERQRSVVLDRYREQLKRLSGVLSQdgSRIDpgSEFQAALESDRERLPGA 316

                kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                   K   E +    P EPYR  L  +R++L    +R   +   G
gi|2895801   317 --AKTAAERY----PDEPYRQKLKLMRERL----DRVGDVRPGG------ 350

                eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                   y + Ee    L     sL + G   + +  +  + Rqv tF  sL
gi|2895801   351 ---YDDAEELRADLTTIATSLRDNGAASVVEAHVDPIRRQVATFDFSLAS 397

                LDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlg
                LD+R   +++tD +    +  +i  Y   sEe R E L   +    P++
gi|2895801   398 LDLRDHQQKHTDAIAEALESEGI-DYHALSEEERAELLTDAILQDEPVID 446

                sDLPktEEvkD....vldafrvLA....ELPiDsFGaYiismataPsDvL
                      +++ D++ +vl  f  LA+ ++E  +++   Y ism+  Ps vL
gi|2895801   447 LADAVSDDLSDdsarVLRLFDSLAdwqrEYGVEAIDTYCISMTEEPSHVL 496

                AvELLqRECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYin
                 v  L    gv + +++  + vvPL E    L  A   +  LF  + Y
gi|2895801   497 EVLFLADQAGVvslpeHCGIDVVPLLETEYALSGARRIMGSLFENEAYAQ 546

                ridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                 ++ ++++qe+m+GYsDs K+ G l+A W LYk q  +  +  ++ v++
gi|2895801   547 ALEARgrtQEIMLGYSDSNKENGFLAANWSLYKNQRRLGEICDDHDVRMR 596

                lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                lFHGRGG + RGGGP   A+L+ P  t+ G ++ t qGE i   +    +
gi|2895801   597 LFHGRGGSISRGGGPMNEALLALPNSTVTGQVKFTEQGEAIAEKYANPRI 646

                CFrsLqRFtAAtLEHGm....nPPvsPkPEWRkLmeemAvvAtEEYRsvv
                  r +     A L   +  +++P    + EW + me mA  A  EYR +
gi|2895801   647 AERNIEQMLNAQLRARLyakdQPEDEIREEWIEAMETMADAARREYRDL- 695

                vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWt
                +    Fv YF  AtP +    + +GsRPa R     +e LRAiPW+F+Wt
gi|2895801   696 LESDGFVRYFEQATPITVIEDLDLGSRPASRSGERTVEDLRAIPWVFSWT 745

                qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                q R  LP W  +       +d D   +  L+ mY+eWPFFR tlD   +
gi|2895801   746 QSRCILPGWYAIATGIDAYLD-DGGDVETLQTMYEEWPFFRTTLDNAALS 794

                FAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE
                  + +  iA  y  L   +    F  +L  +Y+   dl+ +i G +D L
gi|2895801   795 LSRTELEIAEQYAALADDDLREQFFPRLTGEYERAADLITEI-GQRDQLH 843
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                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                       +L    l  R++Y+  Ln +q   L          t r  +     +E
  gi|2895801   844 TRDWLGENLERRNPYVDPLNLLQTHLLDQ--------THRTDI-----EE 880

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                      tL Lt+KGiAAGm+ntG
  gi|2895801   881 R----------------------TLRLTVKGIAAGMKNTG    898

gi|270284604|ref|ZP_05966403.2|: domain 1 of 1, from 12 to 918: score 214.9, E = 2.1e-61
                    *->siDAqLRlLvPGKvsedekLieYDA...LLlDkFLDiLqDLHGedLk
                        ++    + +P  v e+e  ++  A+ +L l     +L++   + L
  gi|2702846    12    QVESTSSAAAPAVVEEQELPVKLKAdmdLCLGILRQVLKEFDENLLT 58

                    Ea...vqECYElsAe.YEGKk.....DtkKLeELGakLtsLdPaDailvA
                     +++  q   + sAe++ G  +++++D   Le     + s++  Da l+A
  gi|2702846    59 QFdtvRQYAVDASAErFSGVLtdtnpDQDDLENAVRTIDSMNLHDAQLLA 108

                    kailHmLnLAnLAEE...velAyRRRikkkkhGDFaDEasAttEsDiEEt
                    +a+     LAnL EE+ +v + + R  +        D  +A t +
  gi|2702846   109 RAFATYFHLANLCEEnyrVSVLHQREAEVDE-TAAVDPVNAMTKA----- 152

                    lKkLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnC
                    + +L+      P+   e L       v+tAHPt + R+++   +++iR
  gi|2702846   153 YHQLIGEM--GPAKAKELLNQLEFHPVFTAHPTEARRKAV---EGKIRRI 197

                    LaqLsAK.DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGm
                       L A   +   D+kE    L  Ei A FRt  i   +PtP +E    +
  gi|2702846   198 AVLLEANaQLGGSDRKENMRRLYNEIDALFRTSPIALKKPTPVEEADTIL 247

                    sYiHEtvWkGvPKFLRRvDtAL..KniGinERlPYdvPLikFssWmGGDR
                      +  t+++ +P   RR D  + +   G+ E  P      +  sW+G DR
  gi|2702846   248 DIFDNTLFHTIPMVYRRFDDWVlgDQAGLVE--PECPAFFHPGSWIGSDR 295

                    DGknPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFEl..smWRCndELR
                    DG nP vt  v R v   aR   +   i  +E+    +++ m    +
  gi|2702846   296 DG-NPNVTAKVSRQV---ARKF-SDHVIAALEEAARTVgrNMTMESETTP 340

                    vRAEElyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERa
                      AE  +   +++ +          +  +E  R +L  + D+L  t  R
  gi|2702846   341 PSAELRQLWNQQKEISERLTSKAALISTQELHRAVLLVMADRLHYTIKRD 390

                    RHLLAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDl
                      L+            y   E+F+  L +  +sL e GD+  A G L Dl
  gi|2702846   391 TDLM-----------YHTCEDFIADLRVVQRSLAEAGDRRAAYGPLQDL 428

                    LRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEW
                    + q  tFG  +v ++ Rq s  +   l  i +H
  gi|2702846   429 IWQAETFGFHMVEMEFRQHSVVHARALADIREH----------------- 461

                    LlaELkGKRPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiis
                        L+G R   g+  P+t E   vld+fr L  + +++++ +   Yiis
  gi|2702846   462 ---GLHGER---GPLQPMTHE---VLDTFRALGAIQkrngVKAARRYIIS 502

                    mataPsDvLAvELLqRECgvkqt....LrvvPLFEkLADLeAAPAavekL
                     + +   v  v  L R      ++ + + v+PLFE+L DLe     ++ +
  gi|2702846   503 FTKSAQNVRDVYELNRMSFANPAdcpvIDVIPLFEQLEDLENSVNVLDEM 552

                    FsiDWYinridG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvA
                      i     r+  +++K evm+GYsDs KDAG  sA   L  Aq  i++ A
  gi|2702846   553 LKIPEVQARLKQtgrKMEVMLGYSDSSKDAGPTSATLALHEAQQRIAQWA 602

                    KkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviE
                     +  + L+lFHGRGG vGRGGGP   A+L+qP   ++   + t qGEvi
  gi|2702846   603 EDNDIDLTLFHGRGGAVGRGGGPANRAVLAQPAGSVKCRFKLTEQGEVIF 652

                    fsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPk.PEWRkLmeemA..vvAt
                      +G   L  r +   +AAtL     P v  ++ +  +  e++A++   t
  gi|2702846   653 ARYGNPVLAIRHVESVAAATLLQS-APSVEKRnTDMTEEFEDLAnkLDET 701

                    EEYRsvvvKEPR.FvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLR
```

```
                      R + + E  +F  +F   tP +E G + iGsRPaKR  + + ++ LR
  gi|2702846   702 SHARYLDLLETDgFAPWFSTVTPLTEVGLLPIGSRPAKRGLGAkSLDDLR 751

                   AiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFR
                    iPWiF+W q R  L  W G+G A        +  l  L+  YkeWP F
  gi|2702846   752 TIPWIFSWAQARINLAAWYGLGSACEA-----VGDLELLQRAYKEWPLFS 796

                   vtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLk
                     +D +Em   K D  iA +y  L   ++L+   +++ d+ + t++++Lk
  gi|2702846   797 TFIDNIEMSLTKTDERIAKMYLALGDRDDLR---DKVLDEMELTRKWVLK 843

                   iAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrP
                   i G    L     L q +R+R +Y+  L   q   L+          lr
  gi|2702846   844 IVGDEWPLQHRHVLGQAIRIRSPYVDALSLTQVLALR---------SLRK 884

                   hlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<
                   ++ KE   E   + ++ + L              + t+ G+AAG+qntG
  gi|2702846   885 KVDKEELSES--QQAGFIYLI-------------LCTVSGVAAGLQNTG  918

                   -*

  gi|2702846     -    -

gi|229816951|ref|ZP_04447233.1|: domain 1 of 1, from 10 to 915: score 213.6, E = 5.3e-61
                   *->siDAqLRlLvPG.KvsedekL...ieYDALLlDkFL.DiLqDLHGed
                        DA +     G+K  e+ +L+++++YD  L  k L+D+L +   +
  gi|2298169    10    PADASIVETGTGrKAPEEHDLpenLKYDMDLCLKILrDVLNEYDPKL 56

                   LkEa.vqECYElsAeYE.....GKkDtkKLeELGakLtsLdPaDailvAk
                   L  ++    Y + A  E+ +++   D   L E    +  ++  Da l+A+
  gi|2298169    57 LTTFdTVRKYAVEASDEhfggnTNTDEDGLAEAVKIIDEMNLHDAQLLAR 106

                   ailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkL
                   a+     LAnL EE    yR  + + +  +  D        ++   + kL
  gi|2298169   107 AFATHFHLANLSEE---NYRVSVLRERESEVDDINAVDPVNELTVAYHKL 153

                   vlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqL
                   +      P+   e L       v+tAHPt + R+++  K  Ri   L q
  gi|2298169   154 INEM--GPAKAKELLDRLEFHPVFTAHPTEARRKAVEGKIRRISELLEQ- 200

                   sAKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHE
                       +   DKkE    L  Ei A FRt  i   +PtP +E    +  +
  gi|2298169   201 -HNKLGGSDKKENSRRLYNEIDALFRTSPIALKKPTPVEEADTILDIFDS 249

                   tvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRv
                   t+++ +P+  RR D  L         P      +  sW+G DRDG nP v
  gi|2298169   250 TLFHTIPQVYRRFDDWLLGDKAGLEPPVCPAFFHPGSWIGSDRDG-NPNV 298

                   tPEvtRDvCLLaRmmAanlYisqvED....LmFElsmWRCndELRvRAEE
                   t  v R v   aR   +   +s +E+ ++++   l m            +
  gi|2298169   299 TAKVSRQV---ARKF-SDHVVSALEEatrtVGRNLTMEAGTTPASTELKD 344

                   lyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLA
                   l    +         E    +   E  R ++  + D+L  t  R   L+
  gi|2298169   345 LWNHQKEM--SERLTEKAALISSKELHRAVMLVMADRLHYTVVRDADLM- 391

                   tGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvs
                              y   E+F+  L    +sL   G k  A G L Dl+ q
  gi|2298169   392 -----------YHSCEDFIADLKTVQRSLAAAGAKRSAYGPLQDLIWQAE 430

                   tFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaEL
                   tFG  +v ++ Rq s  +   l+ i +H                    L
  gi|2298169   431 TFGFHMVEMEFRQHSVVHSRALEDIREH--------------------GL 460

                   kGKRPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismataP
                   +G R  l    P+t E   vld+fr L  + +++++ +   Yiis + +
  gi|2298169   461 HGERGELQ---PMTHE---VLDTFRALGSIQkrngMKAARRYIISFTKSA 504

                   sDvLAvELLqRECgvk....qtLrvvPLFEkLADLeAAPAavekLFsiDW
                     +  v  L R    ++++  t+ v+PLFE+L DL+     +e +  i
  gi|2298169   505 QNIKDVYELNRLAFAHpedvPTIDVIPLFEQLEDLQNSVNVLEEMIKIPE 554
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                    Yinrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGv
                       r+  ++GK evm+GYsDs KDAG  sA   L  AqE i+K A  + +
  gi|2298169   555 VQARLKatgGKLEVMLGYSDSSKDAGPTSATLALHSAQERIAKWAESHDI 604

                    KLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGE
                     L+lFHGRGG vGRGGGP   A+L+qP   ++   + t qGEvi   +G
  gi|2298169   605 DLTLFHGRGGAVGRGGGPANRAVLAQPVGSVKCRFKLTEQGEVIFARYGN 654

                    EnLCFrsLqRFtAAtLEHGmnPPvsPk.PEWRkLmeemAvv...AtEEYR
                      L  r +   +AAtL     P v  ++ +  +   +mA   ++A  E
  gi|2298169   655 PTLAIRHVESVAAATLLQS-APSVEKRnTDMTEKYADMASKldeAAHERF 703

                    svvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWi
                       +    F  +F   tP +E G + iGsRPaKR  + + ++ LR iPWi
  gi|2298169   704 LDLLNTDGFAPWFSTVTPLTEIGLLPIGSRPAKRGLGAkSLDDLRTIPWI 753

                    FaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDL
                    F+W q R  L  W G+G A     d D      L+  Y+eWP F   +D
  gi|2298169   754 FSWAQARINLAAWYGLGTACEKFGDLDT-----LRKAYEEWPLFSTFIDN 798

                    lEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHk
                    +Em  AK D  iA +y  L   E+L    +++  + + t++++L i G k
  gi|2298169   799 IEMSIAKTDERIARMYLALDDREDLP---EKVLTEMKLTRKWVLAIVGDK 845

                    DlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKE
                      L     L   +R+R +Y+  L   q   LK          lr ++ KE
  gi|2298169   846 WPLQHRHVLGRAVRIRSPYVDVLSLTQVLALK---------SLRKKVDKE 886

                    yAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                           k ++   L              + t+ G+AAG+qntG
  gi|2298169   887 ELSHG--KREGYTYLI-------------LCTVSGVAAGLQNTG    915

gi|78046414|ref|YP_362589.1|: domain 1 of 1, from 3 to 904: score 213.2, E = 6.8e-61
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedL.kEa
                            L    P     d+         + +   ++ DL  e+++ E+
  gi|7804641     3    EYRSSLVFATPDLPLRDD---------VRRLGALVGDLLAEQVsAEF 40

                    vqECYElsAeYEGKkDtkK.LeELGakLtsLdPaDailvAkailHmLnLA
                      E   +      ++++  +   L  +Lt+ +P Da  + +a++    +
  gi|7804641    41 LDEIERVRTTAISRRESDApPSTLSEQLTGRQPRDAEALVRAFSTYFQVV 90

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsD.iEEtlKkLvlklnKsP
                    n+AE v+   RRR  ++        +  t   D++ + l++L  ++  +
  gi|7804641    91 NIAERVHRIRRRREYQRS-------GTDTPQPDgLHDALRRLKAQG-VTL 132

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    +E  + L    v+ v+tAHPt +vRR+LL K+  +   L        t++
  gi|7804641   133 DELSQWLPRIDVEPVFTAHPTEAVRRALLEKEQLMVASLVDNLDGMRTPN 182

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++          + A + t +    +Pt  DE      Y+   +++ +P
  gi|7804641   183 ERASDAARFRMALTASWQTADSSPVRPTVDDEREHVGFYLTQVLYRVIPV 232

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                         + A+        +P    L++F  W+GGD DG nP v
  gi|7804641   233 MYETLEHAIEE--TYGSVPALPRLLRFGTWVGGDMDG-NPNVD------- 272

                    CLLaRmmAanlYisqvEDL.mFElsmWRCndELRvRAEElyrtaardkvv
                       a+ +A  l  +    L+ +   +W   + L      ++  a
  gi|7804641   273 ---AKTIAGTLDAQRRAVLdRYQKELWQLASLLSQSTTLVQVSAELT--- 316

                    KyYiEFWKqvPPtEPYRv..iLGdvRDKLYntRERaRHLLAtGiseisEe
                       +E ++ + P    R ++  Gd+  +L n   RaR  L   + +   e
  gi|7804641   317 -AQLERYRALLPDAAARSrpRHGDMPYRLLNDLMRAR--LQATLDD--AE 361

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y    e    L L   sL           ++  lL  v  FG  L +L
  gi|7804641   362 GAYSAPSELEHDLQLILDSLQANKGLHAGWFAVRRLLWRVRSFGFHLARL 411

                    DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
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                    D+RqEs  +     A+   L+   +      +R   L     G+ PL
  gi|7804641   412 DVRQESSVHA---RAVADALGQTDWDAQDATQRAAVLGPYAAGQEPLPRV 458

                    DLPktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLqRE
                    D      +  v  a+ +       D+ G+Yiisma   +DvL v  L R
  gi|7804641   459 DDEGNARLDAVFAALAdARTRHGADALGSYIISMAHNRADVLTVLALARR 508

                    Cgvkq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...
                     g+  + +  +L +vPLFE + DL+    +v+ L +   Y+ ++  ++++
  gi|7804641   509 GGLVDdagavPLDIVPLFETVDDLRGGTGTVQDLLADPVYRQHLAARgdt 558

                    qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                    q vm+GYsDsGKD G  +  W L +Aq E+   A + Gv+L+ FHGRGG
  gi|7804641   559 QMVMLGYSDSGKDGGIAASRWGLQRAQVELLEAAAELGVRLTFFHGRGGS 608

                    vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                    + RGGG t  A+ + P   ++G lRvt qGEvi   +G   L  rsL
  gi|7804641   609 IARGGGKTSRALDAAPRGSVDGRLRVTEQGEVIHRKYGIRALALRSLEQM 658

                    tAAtLEHGmnP..PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                    t A L   + P+ P      WR +m+ +A   t  YR+ v   P F+ YF
  gi|7804641   659 TGAVLLSSLRPraPEPREAHWRPVMDLVAERSTVAYRAFV-GAPEFMQYF 707

                    RlAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvW
                    RlAtP     +m +GsRP++R   +  +  LRAiPW+FaW q R  +P W
  gi|7804641   708 RLATPIDVIERMTLGSRPSRRLGQdAALSNLRAIPWVFAWSQARAVIPGW 757

                    LGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiA
                     GvG   + A+d        L+Em ++WPFFR  lD + mv  KGD  iA
  gi|7804641   758 YGVGSGLQAAVDAGHED--TLREMAQDWPFFRTFLDDIAMVLSKGDLNIA 805

                    aLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                     L+ +L  + +L+ +F   +Rd+   tk ++  +   + lL  DP L
  gi|7804641   806 ELFSRL--SGDLHTrFFPLIRDELALTKAWVKALLQQQSLLQHDPRLALS 853

                    lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                    +RLR++Yi  + v+q   L+R R            + +  dE
  gi|7804641   854 IRLRNPYIDPISVLQVDLLQRWR------------ATDGEDEA------- 884

                    vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      L            L+  + G+  G+qntG
  gi|7804641   885 -LLR-----------ALVACVNGVSQGVQNTG    904

gi|163797958|ref|ZP_02191900.1|: domain 1 of 1, from 1 to 876: score 213.1, E = 7.4e-61
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           +    P    e +  ++YD  Ll + L++ +    Ge++ +
  gi|1637979     1    -----MESASPSESPEKDAPLRYDIRLLGRILgETIRIQEGEEVFDT 42

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v      s  +          EL   L +L    ai v + +     LAn
  gi|1637979    43 VERIRQTSVRFHRDAHEAARRELQGILAGLSNEQAITVIRGYGYFSHLAN 92

                    LAEEvelAyRRRikkkkhGDFaDEasAt.tEsDiEEtlKkLvlklnKsPe
                    +AE+ +   R R +          a At+ E  +   l +    +  s +
  gi|1637979    93 IAEDQHHIRRTRAHAMS-------AGATpREGTMARALDRARRAG-VSGA 134

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                       e         vltAHPt   R s + ++  i   L       +t  +
  gi|1637979   135 QLQEFFDHALCSPVLTAHPTEIRRTSSMDREMEIARLLDERDRVRLTQAE 184

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                          AL R +   + t  +R ++    DE+  G++ +  t  +  P+
  gi|1637979   185 LTVNRKALRRNVLILWQTSLLRSTRLHVLDEVTNGLAHYDHTFLRELPRL 234

                    LRRvDtALKniGinE...RlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                       +          ++ R+P     ++  sW+GGDRDG nP vt +v R
  gi|1637979   235 YADFEDQFAAFDPDQpsvRVP---SFLRIGSWIGGDRDG-NPYVTADVLR 280

                    DvCLLaRmmAanlYisqvEDLmFEls....mWRCndELRvRAEEl.yrta
                        L    A  +Y++ +  L  Els +++m    d L + AE  + r +
  gi|1637979   281 SALRLQSERALRFYLDELHQLGGELSldgrMVAVSDSLTALAERSpDRSP 330
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                    ardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGise
                     r+                EPYR  +  +  +L  t  R    +
  gi|1637979   331 HRQ---------------HEPYRRAVTGMYARLAAT-TRILDDVEAPRHA 364

                    isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                    +     y   EeF   L++   sL   G   +A G L  l R v  FG
  gi|1637979   365 VGAAPAYSSAEEFRADLDVLIDSLTAGGSPSLARGRLSLLRRAVDVFGFH 414

                    LvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKR
                    L  +D+Rq s+ +  v+    +  +   +Y    E  R   LlaEL   R
  gi|1637979   415 LATIDLRQNSDVHERVVAEFLEAAGTSNrYEPADEGGRTALLLAELTSAR 464

                    PLlgsDLPktEEvkDvldafrvLAELPi....DsFGaYiismataPsDvL
                    PL  + L   E  +  l  +r  AE     ++D+   Yiis +   sD+L
  gi|1637979   465 PLASPHLAYSELAAGELAILRAAAEARRlygpDAVRHYIISKTDEVSDIL 514

                    AvELLqRECgvkqt......LrvvPLFEkLADLeAAPAavekLFsiDWYi
                       +L +E g+ ++++ + ++ +vPLFE +ADL+     +++L s+  Y+
  gi|1637979   515 EAAVLLKEVGLLHPrearldVDIVPLFETIADLRRCGDVMDRLLSLPEYR 564

                    nri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                      + ++d  qevm+GYsDs KD G l   W LYkAq  +i   +++Gv+L
  gi|1637979   565 RLLasrDETQEVMLGYSDSNKDGGYLTSIWELYKAQITLIDTFRHHGVRL 614

                    vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                     lFHGRGG vGRGGGP   AiL+qP   i+ ++Rvt qGEvi   +   +
  gi|1637979   615 RLFHGRGGSVGRGGGPSYQAILAQPAGAIQAAIRVTEQGEVIAAKYSNAE 664

                    LCFrsLqRFtAAtLEHGmnPP..vsPkPEWRkLmeemAvvAtEEYRsvvv
                    +  r L   +AAtLE  +  P++ +P+  +  +me++   A   YR +v+
  gi|1637979   665 VGRRNLETLAAATLEATILAPdqAAPQANYLTIMERLSATAYAAYRGLVY 714

                    KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                        F  YFR  t   E   +niGsRPa R  s  ie LRAiPW+F+W q
  gi|1637979   715 ETDGFERYFRESTVIGEIANLNIGSRPASRTKSSRIEDLRAIPWVFSWSQ 764

                    tRFHLPvWLGvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                     R  LP W G+GAA K +  +     l  L+ mY++WPFFR  l  l+mv
  gi|1637979   765 CRLMLPGWFGFGAAVKaWIAEHPDDGLATLRAMYRDWPFFRTALSNLDMV 814

                    FAKGDPGiAaLyDkLLvaEeLk.PFGksLRdkYvEtkdlLLkiAGHkDlL
                     AK D  iA+ y +L+   eL++   ++LR ++++  d +L +    +lL
  gi|1637979   815 LAKSDIAIASRYAELVTDTELRtTIFDRLRGEWQDSIDAVLAVMEQGELL 864

                    EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                    EG
  gi|1637979   865 EG------------------------------------------------ 866

                    EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     n        ++n
  gi|1637979   867 -N-----RCCHVN-------------------------SSS    876

gi|33591459|ref|NP_879103.1|: domain 1 of 1, from 33 to 980: score 212.4, E = 1.2e-60
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                           q+ ++     s   + ++ D  Ll + L++++q   G+ + +
  gi|3359145    33    ----QMNAIRQQSDS--AEPLRHDIRLLGRCLgEVIQACEGKRVYDT 73

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +      +  +    D+     L a++  L   D   vA+a++  L L n
  gi|3359145    74 IETLRRTAVRFRRAGDPADDKLLQARVKQLRGNDPNSVARAFSYFLHLSN 123

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AE+ +   R R + +        +       +   +  L  ++    +
  gi|3359145   124 IAEDRDQNRRQRERALA-------GAGPERGSLRQAIESLKAQG-VNNAR 165

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +   L    v  vltAHPt   R+s L  +  i   L q   +++t ++
  gi|3359145   166 IRRLLSEACVMPVLTAHPTEVQRKSTLDVHREISSLLVQ-REReLTADEL 214

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
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                    ELD AL   +   + t  +R ++ t  DE+   +sY+  t  + +P+
  gi|3359145   215 SELDLALIGQVATLWQTRMLRYTRLTVADEIENALSYYRSTFLNVIPRVY 264

                    RRvDtALKniGinERlPYdvPL...ikFssWmGGDRDGknPRvtPEvtRD
                          L    +    P   PL++ ++  sW+GGDRDG nP v
  gi|3359145   265 GDLARLLNREPVKPFTPPPPPLepfLRMGSWIGGDRDG-NPNVDAATLER 313

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                      L    +    Y++ v  L  Els     + L + A+      a
  gi|3359145   314 ALLRQATVLFEHYLQEVHALGAELS----ASTLLIEADPALLALADA--- 356

                    KyYiEFWKqvPP..tEPYRviLGdvRDKLYntRERaRHLLAtGiseisE.
                              P ++ EPYR  L  +  +L  t   aRHL  + ++  +
  gi|3359145   357 -----GGDDSPHrrDEPYRRALIGIYARLAAT---ARHLTGQKLARRATv 398

                    .eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                    + A y   +     L +   sL       iA   L  l   v  FG  L
  gi|3359145   399 pAAPYDTPDALAADLAVIAASLSARHGAPIARLRLSGLQQAVTVFGFHLA 448

                    KLDiRqEseRqtDvlDAittHLeiGs......YReWsEeKRqEWLlaELk
                     +D+Rq s+ +  vl  +    + G +++  +Y    E  R      EL
  gi|3359145   449 TVDLRQSSDVHERVLAELFARAGDGIdgqavdYLALDEAARVAG--RELA 496

                    GKRPLlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPs
                      RPL  + +   EE +  l  +r  A ++ +    +    i+s + + s
  gi|3359145   497 HARPLASPWIAYSEETASELAVLRAAAAgrarYGRQAVLQSIVSHTETLS 546

                    DvLAvELLqRECgvkqt..........LrvvPLFEkLADLeAAPAavekL
                    D L v +Lq+E g+  +++++  ++++L vvPLFE + DL+  P  ++
  gi|3359145   547 DLLEVLVLQKEAGLIAPpgetiapgdgLMVVPLFETIPDLQRGPEIMAAW 596

                    FsiDWYinrid....GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKv
                      +   + r+   ++  qevm+GYsDs KD G l   W LY+A   ++ v
  gi|3359145   597 LDLPEVRQRVRlaqgDTQEVMLGYSDSNKDGGFLTSNWSLYQAERALVDV 646

                    AKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEvi
                         v+L +FHGRG  vGRGGG    AiL+qPP t+ G lR t qGEvi
  gi|3359145   647 FSARSVRLRMFHGRGDSVGRGGGSSYDAILAQPPGTVAGQLRLTEQGEVI 696

                    EfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPEWRkLmee.......m
                       + + ++    L    AAtLE  + P  +        m+++ +  + m
  gi|3359145   697 QSKYKDAEVGRWHLELLVAATLESSLAPQAAATSAEDAHMQQhapamsfM 746

                    AvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGie
                       A   YR +v+  P F +YF  AtP  E   +niGsRPa Rk +  ie
  gi|3359145   747 SELAQRTYRGLVYDTPGFADYFFAATPISEIAGLNIGSRPASRKKGQHIE 796

                    sLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiK........nlqkL
                     LRAiPW F+W q R  L  W G+G A    ++   ++ +++++  l +L
  gi|3359145   797 DLRAIPWGFSWAQCRLMLTGWYGMGSAIEAYLETGAQgaprsrraRLAQL 846

                    kEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL..kPFGksL
                    +Em  +WP FR  l  +Emv AK D  iAa y +L+    L+++ FG  +
  gi|3359145   847 REMASDWPAFRTLLSNMEMVLAKSDLAIAAGYAQLVPRRGLreRVFG-AI 895

                    RdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLK
                     ++   t   +L++   +DlL   P L   lR R +Yi  Ln +q   +K
  gi|3359145   896 TAEHGRTLA-MLRLLTRRDLLADNPGLMASLRERFAYIDPLNYLQIELIK 944

                    RiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLt
                    R R                A+      d  +++             + Lt
  gi|3359145   945 RHR----------------AAQRRAGDDADIRVP----------RAIHLT 968

                    mKGiAAGmqntG<-*
                    + GiAAG+ n G
  gi|3359145   969 INGIAAGLRNSG    980

gi|289670989|ref|ZP_06492064.1|: domain 1 of 1, from 3 to 904: score 212.1, E = 1.4e-60
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedL.kEa
                            L    P     d+         + +   ++ DL  e+++ E+
  gi|2896709     3    EYRSSLVFATPDLPLRDD---------VRRLGALVGDLLAEQVsAEF 40
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                vqECYElsAeYEGKkDtkK.LeELGakLtsLdPaDailvAkailHmLnLA
                  E   +      ++++  +   L  +Lt+ +P Da  + +a++    +
gi|2896709    41 LDEIERVRTTAISRRESDApPSTLSEQLTGREPRDAEALVRAFSTYFQVV 90

                nLAEEvelAyRRRikkkkhGDFaDEasAttEsD.iEEtlKkLvlklnKsP
                n+AE v+   RRR  ++        +  t   D++ + l++L  ++  +
gi|2896709    91 NIAERVHRIRRRREYQRS-------GTDTPQPDgLHDALRRLKAQG-VTL 132

                eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                +E  + L    v+ v+tAHPt +vRR+LL K+  +   L        t++
gi|2896709   133 DELSQWLPRIDVEPVFTAHPTEAVRRALLEKEQLMVASLVDNLDGMRTPN 182

                DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                ++          + A + t +    +Pt  DE      Y+   +++ +P
gi|2896709   183 ERASDAARFRMALTASWQTADSSPVRPTVDDEREHVGFYLTQVLYRVIPV 232

                FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     + A+        +P    L++F  W+GGD DG nP v
gi|2896709   233 MYETLEHAIEE--TYGSVPVLPRLLRFGTWVGGDMDG-NPNVDANTIAGT 279

                CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                    R      Y            +W   + L      ++  +
gi|2896709   280 LDAQRRAVLDRYQKE---------LWQLASLLSQSTTLVQVSPELT---- 316

                yYiEFWKqvPPtEPYRv..iLGdvRDKLYntRERaRHLLAtGiseisEeA
                  +E ++ + P+   R ++  Gd+  +L n   RaR  L   + +   +
gi|2896709   317 AQLERYRALLPEAAARSrpRHGDMPYRLLNDLMRAR--LQATLDD--ADG 362

                vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                 y    e    L L   sL           ++  lL  v  FG  L +LD
gi|2896709   363 AYAAPSELEHDLQLILDSLQANKGLHAGWFAVRRLLWRVRSFGFHLARLD 412

                iRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
                +RqEs  +     A+   L+   +      +R   L     GK PL
gi|2896709   413 VRQESSVHA---RAVADALGQTDWDVQDATQRAAVLGPYAAGKEPLPRVQ 459

                LPktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLqREC
                      +  v  a+ +       D+ G+Yiisma   +DvL v  L R
gi|2896709   460 DEGNARLDAVFAALAdARTRHGADALGSYIISMAHNRADVLTVLTLARRG 509

                gvkq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                g+  + +  +L +vPLFE + DL+    +v+ L +   Y+ ++  ++++q
gi|2896709   510 GLVDdagavPLDIVPLFETVDDLRGGTGTVQDLLADPVYRQHLAARsdtQ 559

                evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                 vm+GYsDsGKD G  +  W L +Aq E+   A + Gv+L+ FHGRGG +
gi|2896709   560 MVMLGYSDSGKDGGIAASRWGLQRAQVELLEAAAELGVRLTFFHGRGGSI 609

                GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                 RGGG t  A+ + P   ++G lRvt qGEvi   +G   L  rsL   t
gi|2896709   610 ARGGGKTSRALDAAPRGSVDGRLRVTEQGEVIHRKYGIRALALRSLEQMT 659

                AAtLEHGmnPPv.sPkPE.WRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                 A L   + P  + P+ E+WR  m+ +A   t  YR+ v   P F+ YFR
gi|2896709   660 GAVLLSSLRPRApEPREErWRPAMDLVAERSTVAYRAFV-GAPDFMQYFR 708

                lAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWL
                lAtP     +m +GsRP++R   +  +  LRAiPW+FaW q R  +P W
gi|2896709   709 LATPIDVIERMTLGSRPSRRLGQdAALSNLRAIPWVFAWSQARAVIPGWY 758

                GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                GvG   + A+d        L+Em ++WPFFR  lD + mv  KGD  iA
gi|2896709   759 GVGSGLQAAVDAGHED--TLREMAQDWPFFRTFLDDIAMVLSKGDLNIAE 806

                LyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrl
                L+ +L  + +L+ +F   +Rd+   tk ++  +   + lL  DP L   +
gi|2896709   807 LFSRL--SGDLHTrFFPLIRDELALTKGWVKALLQQQSLLQHDPRLALSI 854

                RLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLv
                RLR++Yi  + v+q   L+R R               A +   + +eL+
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  gi|2896709   855 RLRNPYIDPISVLQVDLLQRWR----------------ATDG--EDEELL 886

                   kLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   +              L+  + G+  G+qntG
  gi|2896709   887 R-------------ALVACVNGVSQGVQNTG    904

gi|289663604|ref|ZP_06485185.1|: domain 1 of 1, from 3 to 904: score 212.0, E = 1.5e-60
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedL.kEa
                           L    P     d+         + +   ++ DL  e+++ E+
  gi|2896636     3    EYRSSLVFATPDLPLRDD---------VRRLGALVGDLLAEQVsAEF 40

                   vqECYElsAeYEGKkDtkK.LeELGakLtsLdPaDailvAkailHmLnLA
                     E   +      ++++  +   L  +Lt+ +P Da  + +a++    +
  gi|2896636    41 LDEIERVRTTAISRRESDApPSTLSEQLTGREPRDAEALVRAFSTYFQVV 90

                   nLAEEvelAyRRRikkkkhGDFaDEasAttEsD.iEEtlKkLvlklnKsP
                   n+AE v+   RRR  ++        +  t   D++ + l++L  ++  +
  gi|2896636    91 NIAERVHRIRRRREYQRS-------GTDTPQPDgLHDALRRLKAQG-VTL 132

                   eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                   +E  + L    v+ v+tAHPt +vRR+LL K+  +   L        t++
  gi|2896636   133 DELSQWLPRIDVEPVFTAHPTEAVRRALLEKEQLMVASLVDNLDGMRTPN 182

                   DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                   ++          + A + t +    +Pt  DE      Y+   +++ +P
  gi|2896636   183 ERASDAARFRMALTASWQTADSSPVRPTVDDEREHVGFYLTQVLYRVIPV 232

                   FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                        + A+        +P    L++F  W+GGD DG nP v
  gi|2896636   233 MYETLEHAIEE--TYGSVPVLPRLLRFGTWVGGDMDG-NPNVDANTIAGT 279

                   CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                       R      Y            +W   + L      ++  +
  gi|2896636   280 LDAQRRAVLDRYQKE---------LWQLASLLSQSTTLVQVSPELT---- 316

                   yYiEFWKqvPPtEPYRv..iLGdvRDKLYntRERaRHLLAtGiseisEeA
                     +E ++ + P+   R ++  Gd+  +L n   RaR  L   + +   +
  gi|2896636   317 AQLERYRALLPEAAARSrpRHGDMPYRLLNDLMRAR--LQATLDD--ADG 362

                   vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                    y    e    L L   sL           ++  lL  v  FG  L +LD
  gi|2896636   363 AYAAPSELEHDLQLILDSLQANKGLHAGWFAVRRLLWRVRSFGFHLARLD 412

                   iRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
                   +RqEs  +     A+   L+   +      +R   L     GK PL
  gi|2896636   413 VRQESSVHA---RAVADALGQTDWDVQDATQRAAVLGPYAAGKEPLPRVQ 459

                   LPktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLqREC
                         +  v  a+ +       D+ G+Yiisma   +DvL v  L R
  gi|2896636   460 DEGNARLDAVFAALAdARTRHGADALGSYIISMAHNRADVLTVLALARRG 509

                   gvkq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                   g+  + +  +L +vPLFE + DL+    +v+ L +   Y+ ++  ++++q
  gi|2896636   510 GLVDdagavPLDIVPLFETVDDLRGGTGTVQDLLADPVYRQHLAARsdtQ 559

                   evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                    vm+GYsDsGKD G  +  W L +Aq E+   A + Gv+L+ FHGRGG +
  gi|2896636   560 MVMLGYSDSGKDGGIAASRWGLQRAQVELLEAAAELGVRLTFFHGRGGSI 609

                   GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                    RGGG t  A+ + P   ++G lRvt qGEvi   +G   L  rsL   t
  gi|2896636   610 ARGGGKTSRALDAAPRGSVDGRLRVTEQGEVIHRKYGIRALALRSLEQMT 659

                   AAtLEHGmnPPv.sPkPE.WRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                    A L   + P  + P+ E+WR  m+ +A   t  YR+ v   P F+ YFR
  gi|2896636   660 GAVLLSSLRPRApEPREErWRPAMDLVAERSTVAYRAFV-GAPDFMQYFR 708

                   lAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWL
                   lAtP     +m +GsRP++R   +  +  LRAiPW+FaW q R  +P W
  gi|2896636   709 LATPIDVIERMTLGSRPSRRLGQdAALSNLRAIPWVFAWSQARAVIPGWY 758
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                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    GvG   + A+d        L+Em ++WPFFR  lD + mv  KGD  iA
  gi|2896636   759 GVGSGLQAAVDAGHED--TLREMAQDWPFFRTFLDDIAMVLSKGDLNIAE 806

                    LyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrl
                    L+ +L  + +L+ +F   +Rd+   tk ++  +   + lL  DP L   +
  gi|2896636   807 LFSRL--SGDLHTrFFPLIRDELALTKGWVKALLQQQSLLQHDPRLALSI 854

                    RLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLv
                    RLR++Yi  + v+q   L+R R               A +   + +eL+
  gi|2896636   855 RLRNPYIDPISVLQVDLLQRWR---------------ATDG--EDEELL 886

                    kLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +             L+  + G+  G+qntG
  gi|2896636   887 R-------------ALVACVNGVSQGVQNTG    904

gi|224283986|ref|ZP_03647308.1|: domain 1 of 1, from 35 to 918: score 211.5, E = 2.2e-60
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s D  L l    ++   + L eYD  Ll  F D +     +   E
  gi|2242839    35    SNDMSLCL----RIL-RDVLGEYDPQLLATF-DTVRNYAVKASAEHF 75

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                           A  +   D   L    a + +++  Da l+A+a+     LAnL
  gi|2242839    76 A-----GATADPHPDEDGLAKAVATIDAMNLHDAQLLARAFATYFHLANL 120

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     EE    yR  +  ++     D+       ++   + +L       P+
  gi|2242839   121 SEE---NYRVSVLHQRENQVEDDEAVDPVNELTTAYHQLLTEM--GPAKA 165

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L       v+tAHPt + R+++  K  Ri   L     K +   DKk
  gi|2242839   166 KALLEKLEFHPVFTAHPTEARRKAVEGKIRRIAELLEE--NKRLGGSDKK 213

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    E    L  Ei A FRt  i   +PtP +E    +  +  t++  +PK
  gi|2242839   214 ENVRRLYNEIDALFRTSPIALKKPTPVEEADTILDIFDNTLFTTIPKVYH 263

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R    L         P      +  sW+G DRDG nP vt  v R v
  gi|2242839   264 RFNDWLLGDKAGLEQPQCPAFFHPGSWIGSDRDG-NPNVTAKVSRQV--- 309

                    aRmmAanlYisqvEDLmFElsm.WRCndELRvRAEElyrt.aardkvvKy
                    aR   +   i  +E+    +  +    +E      El++  + ++ +
  gi|2242839   310 ARKF-SDHVIGALEEATRTVGRnLTMESETTPASAELKSLwSHQKEMSER 358

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                      +    +   E  R ++  + D+L  t ER   L+            y
  gi|2242839   359 LTDKAALISTKELHRAVMLVMADRLRYTIERDADLM-----------YH 396

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                      ++F+  L +  +sL e G k  A G L Dl+ q  tFG  +v ++ Rq
  gi|2242839   397 SCDDFIADLQVVQRSLAEAGAKRSAYGPLQDLIWQAQTFGFHMVEMEFRQ 446

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                     s  +   l+ i +H                     L+G R  l    P+
  gi|2242839   447 HSVVHARALEDIREH-------------------GLHGERGELQ---PM 473

                    tEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvELLqREC
                    t E   vld+fr L  + ++++i +   Yiis + +   v  v  L R
  gi|2242839   474 THE---VLDTFRALGAIQkrngIKAARRYIISFTKSAQNVRDVYELNR-L 519

                    gvkqt.....LrvvPLFEkLADLeAAPAavekLFsiDWYinridG...Kq
                       ++++ + + v+PLFE+L DL+     +e +  i     r+  +++K
  gi|2242839   520 AFSHPedvpvIDVIPLFEQLEDLQNCVNVLEEIVKIPEVQARLKAtgnKM 569

                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                    e+m+GYsDs KDAG   A   L  A   i+  A k+ + L+lFHGRGG v
  gi|2242839   570 EIMLGYSDSSKDAGPTTATLALHSAESRIVAWAAKHDIDLTLFHGRGGAV 619

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                    GRGGGP   A+L+qP   +n   + t qGEvi   +G   L  r L   +
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  gi|2242839   620 GRGGGPANRAVLAQPKGSVNCRFKLTEQGEVIFARYGNPVLAIRHLESVA 669

                    AAtLEHGmnPPvsPkPEWRkLmeemAvv...AtEEYRsvvvKEPRFvEYF
                    AAtL            E  +   +m  v ++A  E     +  P F  +F
  gi|2242839   670 AATLLQSAPSVEKTNTEMTEKYAQMTEVldnASHERFLDLLNTPDFAPWF 719

                    RlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqtRFHLPvW
                       tP +E G + iGsRPaKR  + + ++ LR iPW+F+W q R  L  W
  gi|2242839   720 SIVTPLTEVGLLPIGSRPAKRGLGAkSLDDLRTIPWVFSWAQARINLAAW 769

                    LGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiA
                     G+G A     d D      L+E Y+eWP F   +D +Em  AK D  iA
  gi|2242839   770 YGLGSACEKFGDLDT-----LREAYEEWPLFSTFIDNIEMSLAKTDERIA 814

                    aLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrl
                     +y  L   E+L    k++ d+ + t +++Lki      L     L q +
  gi|2242839   815 KMYLALGDDENLS---KKVLDEMKLTTKWVLKIVNDEWPLQHRHVLGQAI 861

                    RLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLv
                    R+R +Y+  L v q   L+          lr ++ KE       + ++ +
  gi|2242839   862 RIRSPYVDALSVTQVLALR---------SLRKKVDKEELSKS--QQAGFI 900

                    kLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     L              + t+ G+AAG+qntG
  gi|2242839   901 YLI-------------LCTVSGVAAGLQNTG    918

gi|209965727|ref|YP_002298642.1|: domain 1 of 1, from 1 to 902: score 210.3, E = 5.1e-60
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                             l     v   +   + D  Ll + L+D++    G++L +
  gi|2099657     1    ------MLNESDGVG--DWPARNDVRLLGRLLgDVIRQHDGQELFDR 39

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    +      s              L a+L +L+  D +   + +l    LAn
  gi|2099657    40 IEAIRKASIAAHREPGVANDAHLAAQLHALELDDMLRFVRGFLWFSLLAN 89

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAE+ +    RR    +h     ++ A         +  L  k+  s +
  gi|2099657    90 LAEDRQA---RRDATERHVPGRPDTLA-------RAVEVLEAKG-VSRAA 128

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v e L    +  vltAHPt   R+s++ ++a i   +  L A     e +
  gi|2099657   129 VAELLDHALISPVLTAHPTEVRRKSVIDREAAIGQLMQALDAA-ADRETR 177

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      +   L REi   + t  +R a+ t  DE+   +sY+  t  +  P+
  gi|2099657   178 DGILADLYREIAILWNTRALREARITVADEIDTALSYFRATFLEVLPRLH 227

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRv.tPEvtRDvC
                     R +  L     n  lP     ++  sW+GGDRDG nP v+    t
  gi|2099657   228 ARWEGVLG----NGPLP---AFLRLGSWIGGDRDG-NPNVsAATLTQALK 269

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                      aR  A   Y++ +  L   ls+  C d          + +  +    +
  gi|2099657   270 QQAR-RALGHYLEELHALGGQLSI--CAD---------ISPPSAE--LEH 305

                    YiEFWKqvPP...tEPYRviLGdvRDKLYn.tRERaRHLL..AtGiseis
                      E      P++  EPYR  L      LY +t    R L+++A   s
  gi|2099657   306 LAEISGDTSPhraDEPYRRALTG----LYArTAATYRQLVgeAPPRSPAV 351

                    EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                        y +    L  L +   sL   G   i D  L +l+  v  FG  L
  gi|2099657   352 PGDPYPDAAALLADLRVVRDSLAR-GSAPIVDRRLNELINAVDLFGFHLA 400

                    KLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPL
                     LD+Rq ++ +  v+  + +  ++ + Y   +E  R   L  EL   R L
  gi|2099657   401 TLDLRQNADVHGRVVAELLRVAGVEdNYLGLPEPARVALLRRELAHLRLL 450

                    lgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAv
                      +     +E +  l+ +r LA ++++    +   Yi+s +   s  L v
  gi|2099657   451 CNPFAGYSDETRRELEILRTLAAsherYGAGCVRQYIVSKTSGVSNLLEV 500
```

```
                    ELLqRECgvkqt.......LrvvPLFEkLADLeAAPAavekLF...siDW
                     LL +E g+ ++++++ + +  vPLFE + DL AAP  +    + + i
  gi|2099657   501 HLLLKEAGMFRPgdppfgaVMAVPLFETIEDLAAAPLVMREYLgfpEIRA 550

                    YinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                          G qevm+GYsDs KD G l   W L  A   +  v  + Gv+L
  gi|2099657   551 LALSCWGFQEVMLGYSDSNKDGGYLTSNWSLHEAACALRHVFDEAGVRLQ 600

                    lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                    lFHGRGG vGRGGG    Ai +qP  t+ G +R+t qGEvi   +G   +
  gi|2099657   601 LFHGRGGAVGRGGGSAFAAIRAQPSGTVGGRIRITEQGEVIAAKYGNTTV 650

                    CFrsLqRFtAAtLEHGmnPP..vsPkPEWRkLmeemAvvAtEEYRsvvvK
                       sL    AA +   ++P +       +R  m+ m   A   YR++v+
  gi|2099657   651 GTASLETMVAAVVLASLEPGglREDMSRFRLAMQGMSRSAFHAYRALVYD 700

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                     P F ++FR AtP  E   + iGsRPa R     ie LRAiPW+F+Wtq
  gi|2099657   701 TPGFKDFFRAATPIAEIADLKIGSRPASRTTLDRIEDLRAIPWVFSWTQA 750

                    RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                    R  LP W GvG A     d+       L+ mY+ WPF    l  lEmv A
  gi|2099657   751 RIMLPGWYGVGTALESFPDRGL-----LEAMYEGWPFLQAALSNLEMVLA 795

                    KGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEG
                    K D  +Aa y  L+  E L+ +    +R +++ t+d LL + G  +lL
  gi|2099657   796 KTDMDVAATYAGLVPDEALRTrVFSAIRSEWQRTHDQLLALTGQSELLQH 845

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                     P +   +RLR +Y+  Ln +q   ++R R                A E
  gi|2099657   846 APAVARSIRLRLPYVEPLNLLQVELIRRHR----------------AGET 879

                    skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                    aP + D + Lt+ GiA  + n G
  gi|2099657   880 ----------------APEIRDGIHLTINGIATSLRNSG    902

gi|15806301|ref|NP_295007.1|: domain 1 of 1, from 1 to 829: score 208.7, E = 1.5e-59
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                    ++     ++ D   l + L+ +L++  Ge
  gi|1580630     1    -------------MA-----LNNDVNRLGRILgQVLKEQEGEAFFNL 29

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v     l  e     D+ +L+ L   L sL   Da  +A+a+     L n
  gi|1580630    30 VEQTRTLVREVRAGGDPAQLNAL---LGSLSENDASNLARAFTWYFQLVN 76

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AEE e   R R+ + +        s      +   l  L  ++  s e+
  gi|1580630    77 IAEEYE---RVRVLQSR--------SGVRSQSLAQALADLREQG-LSAED 114

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    v + L     +L +tAHPt   RR +      i   L      D+  e
  gi|1580630   115 VENLLARVNLELTFTAHPTEMRRRTVRSHLEHIARELP-----DLGRESA 159

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +E   A    + A +Rt E+RR +Pt  DE++ G+ Yi  t+ +  PK
  gi|1580630   160 QERVAA---HVEALWRTPELRRLKPTVLDEVKGGLNYI-STIAQALPKLE 205

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    R    A +     E     vPL +FssWmGGDRDG nP vtPE tR+
  gi|1580630   206 RDLSDAFQATYGRETAAH-VPL-RFSSWMGGDRDG-NPFVTPEATREALQ 252

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    L R  A  l +  +     +ls     +E    AE  yrt  r
  gi|1580630   253 LHRERARELLLAALRQAYTDLS----QEEEEDAAEGTYRTELRA------ 292

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                                  +  +vRD                       e v
  gi|1580630   293 ---------------LHNAVRD--------------------GEPV--- 303

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      e L  LE     L   G    A   L+ lL     FG  Lv LDiR
```

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  gi|1580630   304 --ELLPRLEALNARLHADGQERTAWQLLMPLLSVARVFGQHLVSLDIREH 351

                   seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   s      +  + +  ++ ++Y   sE+ + E L  EL+  RPL ++
  gi|1580630   352 SGQTGAAVAELLKAAGVEAdYLGLSEDAKLELLTRELRSHRPLWPAGATF 401

                   tEEvkDvldafr.vLAE...LPiDsFGaYiismataPsDvLAvELLqREC
                   tE ++ v++ +r+v A  +++   +FG Y+ism+ + sD+L   +L RE
  gi|1580630   402 TETLEAVIGPIReVQAAarrVGPLAFGHYVISMSESVSDILEPLILAREV 451

                   gvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri.dGKqevmvGYs
                   g +  L+ vPLFE L DL+ AP  v  L ++  Y+  ++d  qe+m+GYs
  gi|1580630   452 GFR-VLP-VPLFETLDDLQHAPRIVTDLLALPEYRAVLgDDMQEIMIGYS 499

                   DsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPt
                   Ds KDAG l+A W L  Aq  i  v ++ Gv+   FHGRG  +GRGGGP
  gi|1580630   500 DSNKDAGFLAANWALHEAQRTISDVCRRAGVRWRFFHGRGTSIGRGGGPA 549

                   HLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHG
                     AiL qP  ti+  +R+t qGE +   +    L  r L       L
  gi|1580630   550 SRAILGQPAGTIDAGVRITEQGEALADKYSHPVLARRNLEQALYGVLLAA 599

                   mnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYG
                     P   P  ++   m + A      YR  v  +P F  +F   tP  E
  gi|1580630   600 ARPVGDPPADFMAAMTRAAEASATAYRDFV-HDPDFLPFFERVTPIHEIS 648

                   kmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAi
                   ++ni sRP +R  +  +  LRAiPW+ +Wtq R  LP W G+
  gi|1580630   649 RLNIASRPVRRPGAPTLGNLRAIPWVMSWTQNRANLPGWYGLAEGLAEI- 697

                   dKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEe
                                mY eWPFF   lD   m  AK DP + a y  LL
  gi|1580630   698 -----GPELAAKMYAEWPFFHSMLDNAQMSLAKSDPLVFAEYLTLLEGAS 742

                   LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLn
                    +   + LR+ Y  t   +  + G   +L G+  LK  + LR++Yi  +
  gi|1580630   743 TR-LADHLRESYARTVAAVESVIGGELML-GEQRLKESIALRNPYIDPIH 790

                   vfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPG
                    +q   L+R R            s E   ++
  gi|1580630   791 RLQVELLRRSR------------SHEGGLDE------------------- 809

                   LEDtLiLtmKGiAAGmqntG<-*
                    E  L+Lt++GiAAG+ ntG
  gi|1580630   810 YERPLLLTLQGIAAGVRNTG    829

gi|212715167|ref|ZP_03323295.1|: domain 1 of 1, from 37 to 918: score 208.1, E = 2.4e-59
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       +D  L +L        e L e+D  LlDkF ++       + k +
  gi|2127151    37    EMDLCLQILR-------EVLGEFDEKLLDKFDEVREHALNASAKRFS 76

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        +  +    +D   L+ +   +   d  +a l+A+a+     LAnL
  gi|2127151    77 ----GILTDTNPNQDD--LQKVVDIIDKTDVHEAQLLARAFTTYFHLANL 120

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    EE    yR  +   +     D        ++   + +L+      P+
  gi|2127151   121 CEE---NYRVSVLHSREAAVDDTQAVDPVNEMTCAYHQLINEM--GPAKA 165

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    e L       v+tAHPt + R+++  K  Ri   La    K +   DKk
  gi|2127151   166 KELLDKLEFHPVFTAHPTEARRKAVEGKIRRISQLLA--THKLLGGSDKK 213

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   E    L  Ei A FRt  i   +PtP +E    +  +  t++  +P+  R
  gi|2127151   214 ENSRRLFNEIDALFRTSPIALKKPTPVEESETILDIFDNTLFYTIPQVYR 263

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   R D  +         P      +  sW+G DRDG nP vt  v R v
  gi|2127151   264 RFDDWVLGDKAGLVPPVCPAFFHPGSWIGSDRDG-NPNVTAKVSRQV--- 309
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                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aR     +          E+   R    L   AE     a  + +  +
  gi|2127151   310 ARKFSDHVLGA------LEIETRRVGKNLTMEAETTPPSAELKSLWNHQK 353

                    EFWKq.......vPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                    E     +++   +   E  R ++  + D+L  t +R   L+
  gi|2127151   354 EMSERltdkaalISTKELHRAVMLVMADRLKATIDRDADLM--------- 394

                    eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                       y   E+++  L +  +sL e   k  A G L Dl+ q  tFG  +v
  gi|2127151   395 ---YHSCEDYIADLKVVQRSLAEANAKRSAYGPLQDLIWQAETFGFHMVE 441

                    LDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlg
                    ++ Rq s  +   l+ i +H                     L+G R  l
  gi|2127151   442 MEFRQHSVVHSRALEDIREH--------------------GLHGERGELQ 471

                    sDLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvEL
                       P+t E   vld+fr L  + ++++i +   Yiis + +   +  v
  gi|2127151   472 ---PMTHE---VLDTFRALGSIQkrngIKAARRYIISFTKSAQNIKDVYE 515

                    LqREC..gvkq..tLrvvPLFEkLADLeAAPAavekLFsiDWYinrid..
                    L R   ++ k  +t+ v+PLFE+L DL+     +e +  i     r+  +
  gi|2127151   516 LNRLAfsHPKDvpTIDVIPLFEQLEDLQNSVDVLEEMIKIPEVQARLKat 565

                    .GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    +GK evm+GYsDs KDAG  sA   L  AqE i+K A  + + L+lFHGR
  gi|2127151   566 gGKMEVMLGYSDSSKDAGPTSATLALHSAQERIAKWAESHDIDLTLFHGR 615

                    GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                    GG vGRGGGP   A+L+qP   ++   + t qGEvi   +G   L  r +
  gi|2127151   616 GGAVGRGGGPANRAVLAQPVGSVKCRFKLTEQGEVIFARYGNPALAIRHV 665

                    qRFtAAtLEHGmnPPvsPk.PEWRkLmeemAvvAtEEY..Rsv.vvKEPR
                       +AAtL     P v  ++ +      +mA    E  ++R ++ +
  gi|2127151   666 ESVAAATLLQS-APSVEKRnTDMTAKYADMASKLDEAAhnRFLdLLNTDG 714

                    FvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqtRF
                    F  +F   tP +E G + iGsRPaKR  + + ++ LR iPWiF+W q R
  gi|2127151   715 FAPWFSTVTPLTEIGLLPIGSRPAKRGLGAkSLDDLRTIPWIFSWAQARI 764

                    HLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                     L  W G+G A           l  L+  Y+eWP F   +D +Em  AK
  gi|2127151   765 NLAAWYGLGTAC-----EQFGDLNTLRQAYEEWPLFSTFIDNIEMSLAKT 809

                    DPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                    D  iA +y  L   E+L    k++ d+ + t++++L+i G k  L
  gi|2127151   810 DERIAKMYLALGDREDLN---KKVLDEMELTRKWVLEIVGDKWPLQHRHV 856

                    LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                    L q +R+R +Y+  L   q   L  +R             K    E+
  gi|2127151   857 LGQAIRIRSPYVDALSATQVLALGSLR-------------KRVDKEE--- 890

                    adeLvkLnptervaPGLEDtLiL.tmKGiAAGmqntG<-*
                       L +    e++       LiL t+ G+AAG+qntG
  gi|2127151   891 ---LTHGQ-KENYT-----YLILcTVSGVAAGLQNTG    918

gi|16125740|ref|NP_420304.1|: domain 1 of 1, from 7 to 909: score 208.0, E = 2.5e-59
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siD      v    s   ++ +   LL D  ++ +  L Ge+  E v
  gi|1612574     7    SID------VDRPTS--RHVRQNAHLLSDLLIEAITYLEGEEKAELV 45

                    qECYE.lsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                          s e     D+  L+ L + Lt      a+ +A+a+     LAn
  gi|1612574    46 AKARKaASREDVVNGDAPLLDHLFSDLTT---EQAVFLARAFASHSLLAN 92

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + E+v  A RRR          DE   t    + + +K L   + Ks +E
  gi|1612574    93 IGEDV--AGRRRHAEAD-AQPGDERPRT----LIDAVKALKAAG-KSDAE 134

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                             v  vltAHPt   RRs++ +++ i   L  L    + ++
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  gi|1612574   135 LAKIFAAMNVVPVLTAHPTEVRRRSMVDRETEISR-LMALRRHHLPPDLE 183

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    E+ E L REi   +Rt   R  + t +DE+R  +s +   +    P  +
  gi|1612574   184 AEIRESLFREIALMWRTRLYRPERITVKDEIRNALSIVRTSI---LPAII 230

                   RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                            iG    l   +PL+k  sW+GGDRDG +P v     +
  gi|1612574   231 DLYGDWTGKIGQHGQL---APLLKMGSWLGGDRDG-HPGVNGQTLKLALS 276

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                       +    Y   v  L   l++        v  E l   a+ +    +
  gi|1612574   277 SQSRVILDWYAGEVRKLWSNLAV--STAYTPVSDELLALAAQAKDPSVHR 324

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                   i+        EPYR  L  + D+L     +         s +     y +
  gi|1612574   325 ID--------EPYRLALELIFDRLTAVSQKLTGAPVAFASGVTSVEPYAH 366

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                    + F+  L +   sL   G   +   +L  l+      G  L+ LD+Rq
  gi|1612574   367 PDAFVADLSVIIDSLERNGGERLVGSALRTLVEVAKACGFHLMSLDLRQN 416

                   seRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgsDLPk
                   ++ +   lD + +  + G +Y +  E+ R   L+ EL+ +RPL+ +
  gi|1612574   417 ADVHERTLDELFRRAGTGVeYLKLDEDARCKVLIDELSHQRPLVSPFTAY 466

                   tEEvkDvldafrvLAELPiD....sFGaYiismataPsDvLAvELLqREC
                    EE    l +++  A    D ++++ GaYiis + + sD+L   +L +
  gi|1612574   467 GEETSKELATMEAAAQAVRDyghgCLGAYIISKSATLSDMLEPLVLLKQV 516

                   gv.......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK..
                   g+  ++  ++ +++v PLFE + DLe  PA + +   +   +  +  ++
  gi|1612574   517 GLvwggaapRASVKVAPLFETIGDLENGPAVLRQWLELPLSRTILGDRpv 566

                   qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                   qe+m+GYsDs KD G ++    +      ++  A + Gv L lFHGRGG
  gi|1612574   567 QEIMLGYSDSNKDGGYVASRRGVATGASALAHEADRMGVGLQLFHGRGGS 616

                   vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                   vGRGGGP   A+L+qP  t++G +R+t qGE+i   FG+     r L
  gi|1612574   617 VGRGGGPAAEAVLAQPAGTVQGRIRMTEQGEMIARRFGDQPTARRNLDGL 666

                   tAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRl
                   +AA L     P     P     m  +A    E YR++v+ +  F ++F +
  gi|1612574   667 AAAVLMASERPIPKRDPKVEGAMTALAQSSFEGYRALVYDDAAFEDFFWS 716

                   AtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGv
                    tP  E   +niGsRPa R  s  ie LRAiPW+F+W q RF LP W G
  gi|1612574   717 VTPISEIVGLNIGSRPASRTASRKIEDLRAIPWVFSWSQARFMLPGWYG- 765

                   GAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLy
                      F   +++    + +L+++  ++ FF   l  +E+  A+   GiAa y
  gi|1612574   766 ---FASGVERAGLSVEQLRDLAGNFDFFASLLSNMELALAQSQMGIAARY 812

                   DkLL..vaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                     L ++ a   + F   +R + +    l L i G   lL+  P L   +
  gi|1612574   813 VALSpdKANAERIF-ATIRREHEAATGLALAIRGGAALLDNQPDLAESVA 861

                   LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                   L    +  Ln +q   L R R                A +     de ++
  gi|1612574   862 LASRSVDPLNHLQLELLSRRR----------------AGDI----DEELR 891

                   LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   L             + Lt+ GiAAG+ ntG
  gi|1612574   892 LA------------IQLTVAGIAAGLRNTG    909

gi|167645723|ref|YP_001683386.1|: domain 1 of 1, from 4 to 905: score 207.3, E = 4.1e-59
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      s+D        G      ++ +   LL     + +  L Ge+    v
  gi|1676457     4    SLD--------GDRPTSRHVRQNASLLSNLLNEAIAYLDGEEAAKLV 42
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                      + +     ++ +L+ L a L s     ai +A+a+     LAn+
gi|1676457    43 ATARKAASQEALDGEAVRLDHLFADLSS---DQAIFLARALASHSMLANI 89

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                 E+v  A RRR          DE   t    + + ++kLv  + KsP+E
gi|1676457    90 GEDV--AGRRRHAEAD-AAPGDERPRT----LVDAVRKLVADG-KSPAEL 131

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   L    v  vltAHPt   RRs++ +++ i   L  L    + +
gi|1676457   132 TRILAAMNVVPVLTAHPTEVRRRSMVDRETEISR-LMALRRHHLPPAMDA 180

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                E+ E L REi   +Rt   R  + t +DE+R  +s +   +   +
gi|1676457   181 EIRERLFREIALMWRTRLYRPERITVKDEIRNALSIVRTSILPAIIDLYG 230

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                  D  L+ iG    +   +PL+k  sW+GGDRDG +P v  + t    L
gi|1676457   231 --DWSLQ-IGEHGQM---APLLKMGSWLGGDRDG-HPGVNGD-TLKLALA 272

                aRm.mAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                +  ++    Y   v  L   l++      +    EE+   a +
gi|1676457   273 SQArVILDWYAGEVRKLWSNLAVSTAYAPV---SEEVLALASQT--KDPS 317

                iEFWKqvPPtEPYRviLGdvRDKLYntRERaR...HLLAtGiseisEeAv
                i         EPYR  L  + D+L     +  +++   A G  ++
gi|1676457   318 IHRL-----DEPYRLALELIFDRLTAVSQKLTgqpVAFANGTTDVDP--- 359

                ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                y + E F+  L +   sL   G   +   +L  l+      G  L+ LD+
gi|1676457   360 YGHPEAFVADLKIVIDSLERNGGERLVGSALRTLVEVAQACGFHLMSLDL 409

                RqEseRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGKRPLlgsD
                Rq ++ +   l  + +  + G +Y +  Ee R   L++EL+ +RPL+ +
gi|1676457   410 RQNADVHERTLHELFQRAGSGVkYLDLDEEARSALLISELSHQRPLVSPF 459

                LPktEEvkDvldafrvLAELPiD....sFGaYiismataPsDvLAvELLq
                    EE    l ++   A +  D ++++ GaY+is + + sD+L   +L
gi|1676457   460 TAYGEETTKELATMGAAAQMVRDyghgCLGAYVISKSATLSDILEPLVLL 509

                RECgv.......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                +  g+  ++  ++ ++++ PLFE + DLe  P  + +   +   +  +
gi|1676457   510 KQVGLvwggaapRASVKISPLFETIGDLENGPRVLRQWLELPISRTILGD 559

                K..qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                ++ qe+m+GYsDs KD G ++    + +    ++  A + Gv L lFHGR
gi|1676457   560 RpvQEIMLGYSDSNKDGGYVASRRGVARGASALAFEAERMGVGLQLFHGR 609

                GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                GG vGRGGGP   A+++qP  t++G +R+t qGE+i   FG+     r L
gi|1676457   610 GGSVGRGGGPAAEAVMAQPAGTVQGRIRMTEQGEMIARRFGDQPTARRNL 659

                qRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEY
                   +AAtL     P   P P     m  +A      +R++v+ +  F ++
gi|1676457   660 DGLAAATLMASERPVQQPDPKVEAAMTALAEASFHGFRALVYDDRAFEDF 709

                FRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvW
                F +AtP  E   +niGsRPa R  s  ie LRAiPW+F+W qtRF LP W
gi|1676457   710 FWSATPIGEIVGLNIGSRPASRTASRKIEDLRAIPWVFSWSQTRFMLPGW 759

                LGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiA
                 G    F   +++      +L+++   + FF   l  +E+  A+   GiA
gi|1676457   760 YG----FASGVERAGLSTGQLQDLAGGFDFFASLLSNMELALAQSHMGIA 805

                aLyDkLL.vaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                a y +L +   + +   + +  +     ++ L i G   lL+  P L
gi|1676457   806 ARYKDLSpDKADAQRIFDTIQREHDNASQIALAIRGGSALLDNQPELAES 855

                lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                + L    +  Ln +q   L R R               A ++    de
gi|1676457   856 VALAGLSVDPLNHLQLELLARRR----------------AGDQ----DEN 885
```

```
                  vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                  v+L             + Lt+ GiAAG+ ntG
  gi|1676457   886 VRLA------------IQLTVAGIAAGLRNTG    905

gi|254671854|emb|CBA04047.1|: domain 1 of 1, from 1 to 821: score 207.3, E = 4.2e-59
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2546718     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                                                                   n+
  gi|2546718     1 ----------------------------------------------MNI 3

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AE+v+   RR i+          +    E  + Et+++L        + v
  gi|2546718     4 AEDVHHERRRQIHEEA-------GRGGAEGSLTETVRRLKAGK-ADGKSV 45

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtve
                     L n sv  vltAHPt   R  +L  n RiR  L q+++    D
  gi|2546718    46 QRQLDNTSVTAVLTAHPTEVQRQTVLNFNRRIRALLPQrerCTNADALAR 95

                  DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                   ++E+D  L    q    t E RR +    DE+  G+s +    ++  PK
  gi|2546718    96 LRREIDTILLGLWQ----TSETRRHKLSVNDEINNGVSIFPMSFFEALPK 141

                  FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    R+++   +      R+P    ++k   W+GGDRDG nP v  E  R
  gi|2546718   142 LYRKMEHDFQTAYPDVRVP---NILKIGGWIGGDRDG-NPFVSAETLRFA 187

                  CLLaRmmAanlYisqvEDLmFE..lsmWRCndELRvRAEElyrtaardkv
                            +Y   ++ L  E +ls+ R      v A    +
  gi|2546718   188 FRRHADAVFRFYRGELDKLYRElpLSIRRVKVNDDVMALAALSPDEEL-- 235

                  vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEe
                              +EPYR  +  +   +     +aR L+L  G      e
  gi|2546718   236 ----------ARTEEPYRRAIAYI---MARAMGKARALgLGMGCKFGFLE 272

                  AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                    y    eFL+ L    +sL + G + +A+G L Dl+R vs FG  ++ L
  gi|2546718   273 P-YASAQEFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPL 321

                  DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                  D+Rq + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL+ +RPL+ +
  gi|2546718   322 DLRQHAGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELSHQRPLYSP 371

                  DLPktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAvELL
                   +   +  +  l  f++ +++  E   D+    iis +  PsD LA  LL
  gi|2546718   372 FITYSDHTRHELAIFNearkIKDEFGEDAVTQSIISNCEQPSDLLALALL 421

                  qRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                   +E g+   ++++++  + +vPLFE +  Le A   +e +F +DWY   +
  gi|2546718   422 LKESGLlavengkpRSRINIVPLFETIEALENACPVMETMFRLDWYDALL 471

                  dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                  +  ++ qe+m+GYsDs KD G +   W LY+A   ++   Kky v++ lF
  gi|2546718   472 ESCgniQEIMLGYSDSNKDGGYVTSSWCLYQAELGLVELFKKYDVRMRLF 521

                  HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                  HGRGG vGRGGGP   AiL+qP   + G +R+t qGEvi   + +
  gi|2546718   522 HGRGGSVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQ 571

                  rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRF
                  r L    AAtLE  + P    k    kLm+ +  v    YR ++   P F
  gi|2546718   572 RNLETLVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDF 618

                  vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                  ++YF    P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  L
  gi|2546718   619 IDYFLQTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLML 668

                  PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
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                    P W G+G A     +     l  L+E  +  PFF   l  +E v AK D
  gi|2546718   669 PAWYGFGSAVETLCEDKPETLAALREHAQSNPFFQAMLSNMEQVMAKTDI 718

                    GiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     +A  y  L  ++E        ++++Y+  ++ LL +    +lL     L
  gi|2546718   719 TLAENYAGLSESpEKAAVIFGMIKEEYQRSRKALLDLLQTEELLRDNRSL 768

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                       l LR +Y+  Ln +q   LKR+R                  E+   +
  gi|2546718   769 ARSLALRIPYLNALNGLQVAMLKRLR-----------------KEP-DNP 800

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      L+ +              Lt+ G+A G+ ntG
  gi|2546718   801 HALLMVH--------------LTINGVAQGLRNTG    821

gi|55377433|ref|YP_135283.1|: domain 1 of 1, from 1 to 898: score 206.8, E = 5.8e-59
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                               L    +   +++ e  ALL     ++L      +  + v
  gi|5537743     1    ------MTLHAREIN--QDVRELGALL----GEVLEAQTSTEAFDTV 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                            +Y  + D++  +E+   L  L+P    +vA+a+     L nL
  gi|5537743    36 ETIRNSCIDYR-RGDAETRDEVHRALNRLNPETQDIVARAFTTYFELINL 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEE     R R++  + G   D         +EE ++ L  ++   PeE
  gi|5537743    85 AEE-----RERVREIREGSQGD----VLADSVEEAVRDLAERG-ADPEEF 124

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     + L    +   +tAHPt + R+ +  K   +   +  L  + +t  ++k
  gi|5537743   125 EQVLEDVLIQPTFTAHPTEARRKTVKAKLRSVARDIERLDERRLTEREQK 174

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     ++  L  E+   + t  +R  +P   DE      Y+   +++ +
  gi|5537743   175 RIERNLDAEVTSLWQTPQVRDRRPEVTDEALNVQWYLENVLFDVIDEVYD 224

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                      +  L  +   E +  d  L +F sW G DRDG nP vt +vt +
  gi|5537743   225 ELEHTLEDV-YDEDIDIDT-LYEFRSWAGSDRDG-NPFVTTDVTEETLER 271

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk..vvKy
                     R     lY  ++ +L   ls    n    +   E     +++ ++v K
  gi|5537743   272 QRETVLPLYRTKLKELSGVLSQDASNIATDALFNERLDRHKSKLpgVAKE 321

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                      E +    P EPY       R KL   RE          +s++     y
  gi|5537743   322 AEERY----PDEPY-------RQKLRLMRESVIR-----VSDVRQGG-YE 354

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                      Ee L  L +   sL e    viA+  +  l+R+v tFG  L  LD+R
  gi|5537743   355 SEEELLTDLRVIADSLRENDAEVIAEAHVDPLIRKVETFGFTLASLDLRD 404

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                        +tD +       +i  Y +  E+ R E+L   +     ++  D+
  gi|5537743   405 HRKMHTDAIAEAVDRQGI-DYASMDEDERVEFLTEAILQDNTVI--DMED 451

                    tEEvkD....vldafrvLA....ELPiDsFGaYiismataPsDvLAvELL
                    tE + ++ ++vld fr  A+ ++E  iD+   Y is +  Ps  L v  L
  gi|5537743   452 TEGLSEdatrVLDRFRATAdwqnEFGIDAIDTYAISWCEEPSHALEVLFL 501

                    qRECgvkqt.....LrvvPLFEkLADLeAAPAavekLFsiDWYinridGK
                         +   ++  +  vvPL E    L  A   +  LF  + Y   ++ +
  gi|5537743   502 ADQVDIVDLpgycgFDVVPLLESEYALSGARRIMGTLFENEAYSQALEAR 551

                    ...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    ++ qe+m+GYsDs K+ G l+A W LY  q  ++ +  +y v + lFHGR
  gi|5537743   552 dniQEIMLGYSDSNKENGFLAANWSLYNNQKRLADITDDYDVEMRLFHGR 601

                    GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                    GG + RGGGP   A+L+ P +t+ G ++ t qGE i   +   ++  r L
  gi|5537743   602 GGSISRGGGPMNDAMLALPNETVTGQIKFTEQGEAIAEKYANHDIAERNL 651
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                    qRFtAAtL...EHGmnPPvsPkP.EWRkLmeemAvvAtEEYRsvvvKEPR
                         A ++ +   ++ Pv   P+EW + me  A  A +EY  + +
  gi|5537743   652 EQMLNAQIrarQNAIEEPVEEIPdEWAEAMETAADAARDEYQDL-LETDG 700

                    FvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFH
                    FvE+F  AtP +    +n+GsRPa R     +e LRAiPW+F+Wtq R
  gi|5537743   701 FVEFFEQATPITVIENLNMGSRPASRSEDRSVEDLRAIPWVFSWTQARCI 750

                    LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                    +P W  +      A       +  L+EmY++WPFFR  lD   +  A+ D
  gi|5537743   751 IPGWYSISTGLD-AYLENGGDMETLQEMYENWPFFRTKLDNASLALARTD 799

                    PGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     GiA  y +L   E       ++ ++Y+ t   +L+i G   lL  D +L
  gi|5537743   800 LGIAEEYADLADPELRERIYPRIVEEYENTVAKVLEITGQDGLLSRD-WL 848

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                    K  l  R++Y+  Ln +q   LK               s     E
  gi|5537743   849 KENLERRNPYVDPLNLLQVRLLKQ--------------SHRTETER---- 880

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                  tL Lt++GiAAGm+ntG
  gi|5537743   881 -----------------RTLRLTVQGIAAGMKNTG    898

gi|148271562|ref|YP_001221123.1|: domain 1 of 1, from 16 to 910: score 206.8, E = 5.9e-59
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                         D    ++ P   s        D   l   L+ +L +  G+dL
  gi|1482715    16    TRDGTRDAVEPALRS--------DVSHLGGLLgQVLRESGGDDLLRD 54

                    vqECYElsAe.YEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    v    El  + YE  +D++ +++    +    P  a  vA+a+     LA
  gi|1482715    55 VERLRELVIDaYESARDAS-IDDAERLVATFTPERAEQVARAFTCYFHLA 103

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsD.iEEtlKkLvlklnKsP
                    nLAEE    +R R+ + +      Ea A    D+i + + kL   l
  gi|1482715   104 NLAEE---HHRVRVLRER------EAAAGFVPDsIPDAVGKLTEEL--GR 142

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    eE    L       vltAHPt + RR++     Ri   L+
  gi|1482715   143 EEAMRRLGEMRFHPVLTAHPTEARRRAVATGIRRIGDLLTERDGAMAGTL 192

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                       ++D  L  Ei   +Rt  +R ++PtP DE+R  m  +  t+++ vP+
  gi|1482715   193 TGADVDRRLLEEIDGLWRTTPLRTTRPTPLDEVRTAMGVFDQTLFEVVPR 242

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R  D  L       R        +   W+  DRDG nP vt  vt +
  gi|1482715   243 VYRLLDDWLLGDEAGVRDAVAPAFFRLGNWIAADRDG-NPYVTAAVTEE- 290

                    CLLaRmmAanlYisqvEDLmFEl..smWRCndELRvRAEElyrtaardkv
                       a  +A+   +  +E +   +++s+     +    AE     aa+d +
  gi|1482715   291 ---AAGIASEHILLGLERVALRVgrSLTLGDADTPPSAELRELAAAQDAL 337

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                      +         P E  R +L  +  +L  tRER    +A
  gi|1482715   338 APHLTARIGTRAPAELHRRVLLVIAGRLSATRERHDDPIA---------- 377

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                     y    e L  L +   sL   G + iA G L  l+ q  tFG  L  ++
  gi|1482715   378 -YPSAAELLADLRVLQASLRSAGAHRIAGGELQGLVWQAETFGFHLAEME 426

                    iRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
                    +Rq s+ +    +A+ + L + +              a+ +G     +
  gi|1482715   427 VRQHSQVHR---EALREVLAVAA--------------ADASGDQA--PEL 457

                    LPktEEvkDvldafrvLAE.LPiDsFGaYiismataPsDvLAv.ELLqRE
                     P+t Ev Dv  ++  L E+  +  F  +i+s + +  D+  v+EL
  gi|1482715   458 APMTVEVLDVFRTLARLQErHGVAPFSRFIVSFTQSADDIRTVhELAALA 507

                    Cgvkqt...LrvvPLFEkLADLeAAPAa...vekLFsiDWYinridGKqe
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                    g  ++ + L v+PLFE  ADL+A     +++ +L  +     +   K e
  gi|1482715   508 LGSAEAapvLDVIPLFETFADLNASTEIldgMIRLPQVAARLAQTGRKLE 557

                    vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                    vm+GYsDs KD G +sA + L+ Aq  i+  A++  + L+lFHGRGG  G
  gi|1482715   558 VMLGYSDSSKDVGPVSATFALFDAQARIAAWARENDIELTLFHGRGGALG 607

                    RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                    RGGGP   A+ +qPP  ++G  + t qGEvi   +G+  +  r +   +A
  gi|1482715   608 RGGGPADRAVRAQPPGSVDGRFKLTEQGEVIFAHYGDKRIAARHIEQMAA 657

                    AtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsv...vvKEPRFvEYFR
                    AtL              +   em     E  R+   + vK P F  +F
  gi|1482715   658 ATLLASAPSNEERNAVAAEGSAEMVRTMDEASRARffeLVKAPGFAPWFA 707

                    lAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWL
                      tP  E G + +GsRPa+R  s   +e LRAiPW+FaWtq R  L  W
  gi|1482715   708 QVTPMEEIGLLALGSRPARRGLSvESLEDLRAIPWVFAWTQARINLTGWF 757

                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    G+G A     d  +     L+  Y+eWP F   +D +Em  AK D  +A
  gi|1482715   758 GLGSALAAVGDEAV-----LRKAYEEWPLFTSMIDNVEMSLAKTDGRLAE 802

                    LyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                     y  L    +L      + ++ + t++++ k  G  ++LEG P L+  +R
  gi|1482715   803 RYLALGDRPDLAAL---VTEEMERTREWVRKATGRGEILEGRPVLRRAVR 849

                    LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                    LR +Y+  L  +q   L+ +R      t   + +   A  ++ + d
  gi|1482715   850 LRSPYVDALSLLQLRALRALR------TSASEAAGQGAPGQADPTD---- 889

                    LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      p  r        L+Lt+ GiAAG+qntG
  gi|1482715   890 --PDHRL-------LLLTVNGIAAGLQNTG    910

gi|166710682|ref|ZP_02241889.1|: domain 1 of 1, from 3 to 904: score 206.2, E = 8.7e-59
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedL.kEa
                            L    P     d+         + +   ++ DL  e+++ E+
  gi|1667106     3    EYRSSLVFATPDLPLRDD---------VRRLGALVGDLLAEQVsAEF 40

                    vqECYElsAeYEGKkDtkK.LeELGakLtsLdPaDailvAkailHmLnLA
                      E   +      ++++  +   L  +Lt+ +P Da  + +a++    +
  gi|1667106    41 LDEIERVRTTAISRRESDApPSTLSEQLTGREPRDAEALVRAFSTYFQVV 90

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsD.iEEtlKkLvlklnKsP
                    n+AE v+   RRR  ++        +  t   D++ + l++L  ++  +
  gi|1667106    91 NIAERVHRIRRRREYQRS-------GTDTPQPDgLHDALRRLKAQG-VTL 132

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    +E  + L    v+ v+tAHPt +vRR+LL K+  +   L        t++
  gi|1667106   133 DELSQWLPRIDVEPVFTAHPTEAVRRALLEKEQLMVASLVDNLDGMRTPN 182

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++          + A + t +    +Pt  DE      Y+   +++ +P
  gi|1667106   183 ERTSDAARFRMALTASWQTADSSPVRPTVGDEREHVGFYLTQVLYRVIPV 232

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                         + A+        +P    L++F  W+GGD DG nP v
  gi|1667106   233 MYETLEHAIEE--TYGSVPALPRLLRFGTWVGGDMDG-NPNVDANTIAGT 279

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                        R      Y            +W   + L      ++  +
  gi|1667106   280 LDAQRRAVLDRYQKE---------LWQLASLLSQSTTLVQVSPELM---- 316

                    yYiEFWKqvPPtEPYRv..iLGdvRDKLYntRERaRHLLAtGiseisEeA
                      +E ++ + P    R ++  Gd+  +L n   RaR  L   + +   +
  gi|1667106   317 TQLERYRALLPDAAARSrpRHGDMPYRLLNDLMRAR--LQATLDD--ADG 362

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                     yt   e  + L L   sL           ++  lL  v  FG  L +LD
  gi|1667106   363 AYTAPSELEDDLQLILDSLQANKGLHAGWFAVRRLLWRVRSFGFHLARLD 412
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                    iRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
                    +RqEs  +     A+   L+   +      +R   L     G+  L  +
  gi|1667106   413 VRQESSVHA---RAVADALGQTDWDGQDATRRAAVLGPYACGQEALPRAQ 459

                    LPktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLqREC
                          +  v  a+ +       D+ G+Yiisma   +DvL v  L R
  gi|1667106   460 DEGNARLDAVFAALAdARTRHGADALGSYIISMAHNRADVLTVLALARRG 509

                    gvkq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                    g+    ++ +L +vPLFE + DL+    +v+ L +   Y+ ++  ++++q
  gi|1667106   510 GLVDaagtvPLDIVPLFETVDDLRGGTGTVQDLLADPVYRQHLAARgdtQ 559

                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                     vm+GYsDsGKD G  +  W L +Aq E+   A + Gv+L+ FHGRGG +
  gi|1667106   560 MVMLGYSDSGKDGGIAASRWGLQRAQVELLEAAADLGVRLTFFHGRGGSI 609

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                     RGGG t  A+ + P   ++G lRvt qGEvi   +G   L  rsL   t
  gi|1667106   610 ARGGGKTSRALDAAPRGSVDGRLRVTEQGEVIHRKYGIRALALRSLEQMT 659

                    AAtLEHGmnP..PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                     A L   + P+ P      WR +m+ +A   t  YR+ v   P F+ YFR
  gi|1667106   660 GAVLLSSLRPraPEPREARWRPVMDLVAERSTVAYRAFVA-APEFMQYFR 708

                    lAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWL
                    lAtP     +m +GsRP++R   +  +  LRAiPW+FaW q R  +P W
  gi|1667106   709 LATPIDVIERMTLGSRPSRRLGQdAALSNLRAIPWVFAWSQARAVIPGWY 758

                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    GvG   + A+d        L+Em ++WPFFR  lD + mv  KGD  iA
  gi|1667106   759 GVGSGLQAAVDAGHED--TLREMAQDWPFFRTFLDDVAMVLSKGDLNIAE 806

                    LyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrl
                    L+ +L  + +L+ +F   +Rd+   tk ++  +   + lL  DP L   +
  gi|1667106   807 LFSRL--SGDLHTrFFPLIRDELALTKGWVKALLQQQSLLQHDPRLALSI 854

                    RLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLv
                    RLR++Yi  + v+q   L+R R            + +  dE
  gi|1667106   855 RLRNPYIDPISVLQVDLLQRWR------------ATDGEDEA-------- 884

                    kLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     L             L+  + G+  G+qntG
  gi|1667106   885 LLR-----------ALVACVNGVSQGLQNTG    904

gi|154486362|ref|ZP_02027769.1|: domain 1 of 1, from 37 to 918: score 205.6, E = 1.3e-58
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +D  L +L        e L e+D  Ll kF     ++    Lk
  gi|1544863    37    EMDLCLQILR-------EVLGEFDENLLAKF----DEVREHALKASD 72

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         +  +     D   L+ +   +  +d  Da l+A+a+     LAnL
  gi|1544863    73 ERFSGILTD--TNPDQDDLQKVVDIVDKVDVHDAQLLARAFTTYFHLANL 120

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     EE    yR  +  ++     ++       ++   + +L+      P+
  gi|1544863   121 CEE---NYRVSVLHQREAAVNEDQAVDPVNEMTCAYHQLINEM--GPARA 165

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     e L       v+tAHPt + R+++  K  Ri   L     K +   DKk
  gi|1544863   166 KELLDQLEFHPVFTAHPTEARRKAVEGKIRRISQLLE--AHKLLGGSDKK 213

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    E    L  Ei A FRt  i   +PtP +E    +  +  t++  +P+  R
  gi|1544863   214 ENSRRLFNEIDALFRTSPIALKKPTPVEEADTILDIFDNTLFYTIPQVYR 263

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R D  +         P      +  sW+G DRDG nP vt  v R v
  gi|1544863   264 RFDDWVLGDKAGLVPPVCPAFFHPGSWIGSDRDG-NPNVTAKVSRQV--- 309

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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                    aR     +          E+   R    L   AE     a  + +  +
  gi|1544863   310 ARKFSDHVLGA------LEIETRRVGKNLTMEAETTPPSAELKSLWNHQK 353

                    EFWKq.......vPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                    E     +++   +   E  R ++  + D+L  t +R   L+
  gi|1544863   354 EMSERltdkaalISTKELHRAVMLVMADRLKATIDRDADLM--------- 394

                    eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                       y   E+++  L    +sL e   k  A G L Dl+ q  tFG  +v
  gi|1544863   395 ---YHSCEDYIADLKTVQRSLAEANAKRSAYGPLQDLIWQAETFGFHMVE 441

                    LDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlg
                    ++ Rq s  +   l+ i +H                    L+G R  l
  gi|1544863   442 MEFRQHSVVHSRALEDIREH-------------------GLHGERGELQ 471

                    sDLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvEL
                       P+t E   vld+fr L  + ++++i +   Yiis + +   +  v
  gi|1544863   472 ---PMTHE---VLDTFRALGSIQkrngIKAARRYIISFTKSAQNIKDVYE 515

                    LqRECgvk....qtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid..
                    L R    ++++  t+ v+PLFE+L DL+     +e +  i     r+  +
  gi|1544863   516 LNRLAFSHpedvPTIDVIPLFEQLEDLQNSVDVLEEMIKIPEVQARLKat 565

                    .GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    +GK evm+GYsDs KDAG  sA   L  AqE i+K A  + + L+lFHGR
  gi|1544863   566 gGKMEVMLGYSDSSKDAGPTSATLALHSAQERIAKWAESHDIDLTLFHGR 615

                    GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                    GG vGRGGGP   A+L+qP   ++   + t qGEvi   +G   L  r +
  gi|1544863   616 GGAVGRGGGPANRAVLAQPVGSVKCRFKLTEQGEVIFARYGNPVLAIRHV 665

                    qRFtAAtLEHGmnPPvsPk.PEWRkLmeemAvvAtEEY..Rsv.vvKEPR
                       +AAtL     P v  ++ +  k   +mA    E  ++R ++ +
  gi|1544863   666 ESVAAATLLQS-APSVEKRnTDMTKKYADMASKLDEAAhnRFLdLLNTDG 714

                    FvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqtRF
                    F  +F   tP +E G + iGsRPaKR  + + ++ LR iPWiF+W q R
  gi|1544863   715 FAPWFSTVTPLTEIGLLPIGSRPAKRGLGAkSLDDLRTIPWIFSWAQARI 764

                    HLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                     L  W G+G A           l  L+  Y+eWP F   +D +Em  AK
  gi|1544863   765 NLAAWYGLGTAC-----EQFGDLNTLRQAYEEWPLFSTFIDNIEMSLAKT 809

                    DPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                    D  iA +y  L   E+L    k++ d+ + t++++Lki G    L
  gi|1544863   810 DERIAKMYLALGDREDLN---KKVLDEMELTRKWVLKIVGDEWPLQHRHV 856

                    LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                    L q +R+R +Y+  L v q   L  +R             K    E+
  gi|1544863   857 LGQAIRIRSPYVDALSVTQVLALGSLR-------------KRVDKEE--- 890

                    adeLvkLnptervaPGLEDtLiL.tmKGiAAGmqntG<-*
                       L +    e++       LiL t+ G+AAG+qntG
  gi|1544863   891 ---LTHGQ-KENYT-----YLILcTVSGVAAGLQNTG    918

gi|66769781|ref|YP_244543.1|: domain 1 of 1, from 3 to 904: score 205.6, E = 1.3e-58
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            L    P  v   +++ +  AL+     D+L +    d  E +
  gi|6676978     3    EYRSSLVFATP-DVPLRDDVRRLGALV----GDLLAEQVSADFLEEI 44

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E     A      Dt   + L + L + +P  a  + +a++    + n+
  gi|6676978    45 -ERIRTTAIARRESDTPPAGLL-SLLEGREPRAAEALVRAFSTYFQVVNI 92

                    AEEvelAyRRRikkkkhGDFaDEasAttEsD.iEEtlKkLvlklnKsPeE
                    AE v+   RRR  ++        +  t   +++ + l++L  ++  + +E
  gi|6676978    93 AERVHRIRRRRDYQRS-------GTDTPQPEgLHDALRRLKAQG-VTLDE 134

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      e L    v+ v+tAHPt +vRR+LL K+  +   L        t++++
  gi|6676978   135 LSEWLPRIDVEPVFTAHPTEAVRRALLEKEQLMVASLVDNLDGMRTPNER 184
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                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                              + A + t +    +Pt  DE      Y+   +++ +P
  gi|6676978   185 ATDAARFRMALTASWQTADSSPVRPTVEDEREHVGFYLTQVLYRVIPVMY 234

                    RRvDtALKn.iGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                       + A+  + G    lP    L++F  W+GGD DG nP v
  gi|6676978   235 ETLEHAIEEtYGSTLALP---RLLRFGTWVGGDMDG-NPNVDAHTIAGTL 280

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                       R      Y++          +W   + L      +   +a
  gi|6676978   281 DAQRRAVLDRYLNE---------LWQLASLLSQSTTLVAVSPALS----A 317

                    YiEFWKqvPPtEPYRv..iLGdvRDKLYntRERaRHLLAtGiseisEeAv
                     +E ++ + P    R ++  Gd+  +L n   RaR  L   + +   +
  gi|6676978   318 QLERYQALLPDAAARSrpRHGDMPYRLLNDLMRAR--LQATLDD--ADGA 363

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y    e    L L   sL           ++  lL  v  FG  L +LD+
  gi|6676978   364 YAAPAELEHDLQLILDSLQANKGLHAGWFAVRRLLWRVRSFGFHLARLDV 413

                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    RqEs  +     A+   L+   + +     R   L    +G   L   D
  gi|6676978   414 RQESSVHA---RAVADALGQADWDSQDATHRAGLLGPYASGEQALPQVDD 460

                    PktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLqRECg
                         +  v  a+ +       D+ G+Yiisma   +DvL v  L R  g
  gi|6676978   461 EGNARLDAVFAALAdARTRHGADALGSYIISMAHNRADVLTVLALARRGG 510

                    vkq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...qe
                    +  + +  +L +vPLFE + DL+    +v+ L +   Y+ ++  ++++q
  gi|6676978   511 LVDdagavPLDIVPLFETVDDLRGGTGTVQDLLADPVYRQHLRARgdtQM 560

                    vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                    vm+GYsDsGKD G  +  W L +Aq E+   A + Gv+L+ FHGRGG +
  gi|6676978   561 VMLGYSDSGKDGGIAASRWGLQRAQVELLEAAAELGVRLTFFHGRGGSIV 610

                    RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                    RGGG t  A+ + P   ++G lRvt qGEvi   +G   L  rsL   t
  gi|6676978   611 RGGGKTTRALDAAPRGSVDGRLRVTEQGEVIHRKYGIRALALRSLEQMTG 660

                    AtLEHGmnPPvsPkP...EWRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                    A L   + P  +P P+++ WR +m+ +A   t  YR  v   P F+ YFR
  gi|6676978   661 AVLLSSLRPR-APEPredAWRPVMDLVAERSTVAYRGFV-GAPDFMQYFR 708

                    lAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWL
                    lAtP     +m +GsRP++R   +  +  LRAiPW+FaW q R  +P W
  gi|6676978   709 LATPIDVIERMTLGSRPSRRLGQdAALSNLRAIPWVFAWSQARAVIPGWY 758

                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    GvG   + A++        L+Em ++WPFFR  lD + mv  KGD  iA
  gi|6676978   759 GVGSGLQAAVEAGHED--SLREMAQDWPFFRTFLDDIAMVLSKGDLNIAE 806

                    LyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrl
                    L+ +L  a  L+ +F  ++Rd+   tk ++  + G + lL  DP L   +
  gi|6676978   807 LFSRL--AGPLHArFFPRIRDELALTKHWVKTLLGQRSLLQHDPRLALSI 854

                    RLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLv
                    RLR++Yi  + v+q   L+R R               A +   + +eL+
  gi|6676978   855 RLRNPYIDPISVLQVDLLQRWR----------------ATDG--EDEELL 886

                    kLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +             L+  + G+A G+qntG
  gi|6676978   887 R-------------ALVACVNGVAQGVQNTG    904

gi|1705591|sp|P51060.1|CAPP_THES7: domain 1 of 1, from 1 to 857: score 205.4, E = 1.5e-58
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                  +s+  + ++ +  Ll + L++ +  + Ge
  gi|1705591     1    -------------MSDPFEALKAEVDLLGRLLgEAIRKVSGERFFAL 34

                    vqECYEls.AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
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```
                v E   ls+A   G  D    e L  ++  +   +   + +a+ H   L
gi|1705591    35 VEEVRLLSkARRQG--DGAAAEVLSQRVERMPVEEMEALVRAFTHYFHLV 82

                nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnK...
                nLAEE    +R R+ +++      E++ t E    E +  L   l K+++
gi|1705591    83 NLAEE---RHRVRVNRLR-----TEGE-TLENPRPEGFLALAKAL-Kerg 122

                .sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                 s eE    L   +  L +tAHPt   RR L     R+      L   D
gi|1705591   123 lSLEEAEAHLNRLALLLTFTAHPTETRRRTLRHHLERLQE---ELEGGD- 168

                tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                         E L   +   + t+E+R+a+P   DE++ G+ Y+  t+W+
gi|1705591   169 --------RERLLARVVLLYATEEVRKARPSVEDEIKGGLYYLPTTLWRA 210

                vPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                +PK +   + AL    +  + P     ++F sWmGGDRDG nP vtPEvt
gi|1705591   211 IPKVVEGLEAALER--VYGKRPHLRSPVRFRSWMGGDRDG-NPYVTPEVT 257

                RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk
                      aR +A   Y++ +E L+ +ls+    +E R+      r
gi|1705591   258 AFAGRYAREVAKGRYLEELEALVRDLSL----SEARIPVPKEVREGGEG- 302

                vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                v ++         P EPYR    +    LY   E               e
gi|1705591   303 VERF---------PGEPYRRYFAA----LYRALE--------------GE 325

                AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                A  t  E     L +  k L   G   +A   L  l    s FGL L  L
gi|1705591   326 ALST--EGLARALKVAEKGLEGVGLAQVAQAFLRPLEARLSAFGLELAPL 373

                DiRqEseRqtDvlDAittHLeiGs....YReWsEeKRqEWLlaELkGKRP
                D+R Es +    l+A  + L +G  ++++   s e +   L  ELk  RP
gi|1705591   374 DLREESGK---LLEAAAELLRLGGvhpdFLALSPEEKEALLTEELKTARP 420

                Llgs.DLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvEL
                Ll+ +++P+ E ++  l+a+r   +      Ga ++sm+  P+D LAv L
gi|1705591   421 LLPVgEVPQGEALRVALGALRAWGDK-----GAHVVSMTHHPADLLAVFL 465

                LqRECgvkq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                L RE g+ +++++ +  vvPLFE L DLe AP  + +L +   ++ + +G
gi|1705591   466 LAREVGLYRpgkplPFDVVPLFETLEDLERAPEVLRRLLANPVFRAHAQG 515

                K..qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                +++ evm+GYsDs KDAG l A   LY+AqE +  v    G+ +  FHGR
gi|1705591   516 RggVEVMIGYSDSNKDAGFLMANLALYQAQEALHAVGEAQGIPVFFFHGR 565

                GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                G    RGGGP   Ai   PP  +   lR t qGE +   +   +L  r L
gi|1705591   566 GTSTARGGGPAGRAIAGLPPKSVGHRLRLTEQGEALADRYAHPDLAVRHL 615

                qRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEY
                           +   v Pk  WR+ + e        YR++  +E  F  +
gi|1705591   616 EQLLYHFAQAALGDGVEPKAHWREALGEAGERSMARYRALLSQEG-FFPF 664

                FRlAtPElEYGkmniGsRPaKRk.PsGGiesLRAiPWiFaWtqtRFHLPv
                F   tP  E G + i sRP  R++    i  LRAiPW+ aWtq R  LP
gi|1705591   665 FEAFTPIREIGELPIASRPVYRHgRVRDIRDLRAIPWVMAWTQVRLLLPG 714

                WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                W G+ A        +   +  L+EmY+eWPFF  tl+   m  AK D Gi
gi|1705591   715 WYGLSAL-------EGLPMPLLREMYREWPFFATTLESAAMALAKADLGI 757

                AaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                A  y k Lv E L+ F + L ++Y  t  lL  i     lL     L  +
gi|1705591   758 AERYLK-LVPEGLQGFYHHLAEEYRRTVALLEAIF-EAPLLHNQKTLERQ 805

                lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                + LR++Y+  +n +q   L R R P
gi|1705591   806 IALRNPYVDPINFVQVELLARYRAP------------------------ 830
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                    vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                         + r   G+   L+L + G+AAG+ n G
  gi|1705591   831 -----GGREDEGVRRALLLSLLGVAAGLRNAG    857

gi|58583419|ref|YP_202435.1|: domain 1 of 1, from 3 to 904: score 205.2, E = 1.8e-58
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedL.kEa
                            L    P     d+         + +   ++ DL  e+++ E+
  gi|5858341     3    EYRSSLVFATPDLPLRDD---------VRRLGALVGDLLAEQVsAEF 40

                    vqECYElsAeYEGKkDtkK.LeELGakLtsLdPaDailvAkailHmLnLA
                      E   +      ++++  +   L  +Lt+ +P Da  + +a++    +
  gi|5858341    41 LDEIERVRTTAISRRESDApPSTLSEQLTGREPRDAEALVRAFSTYFQVV 90

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsD.iEEtlKkLvlklnKsP
                    n+AE v+   RRR  ++        +  t   D++ + l++L  ++  +
  gi|5858341    91 NIAERVHRIRRRREYQRS-------GTDTPQPDgLHDALRRLKAQG-VTL 132

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    +E  + L    v+ v+tAHPt +vRR+LL K+  +   L        t++
  gi|5858341   133 DELSQWLPRIDVEPVFTAHPTEAVRRALLEKEQLMVASLVDNLDGMRTPN 182

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++          + A + t +    +Pt  DE      Y+   +++ +P
  gi|5858341   183 ERTSDAARFRMALTASWQTADSSPVRPTVGDEREHVGFYLTQVLYRVIPV 232

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                         + A+        +P    L++F  W+GGD DG nP v
  gi|5858341   233 MYETLEHAIEE--TYGSVPALPRLLRFGTWVGGDMDG-NPNVDANTIAGT 279

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                        R      Y            +W   + L      ++  +
  gi|5858341   280 LDAQRRAVLDRYQKE---------LWQLASLLSQSTTLVQVSPELM---- 316

                    yYiEFWKqvPPtEPYRv..iLGdvRDKLYntRERaRHLLAtGiseisEeA
                      +E ++ + P    R ++  Gd+  +L n   RaR  L   + +   +
  gi|5858341   317 TQLERYRALLPDAAARSrpRHGDMPYRLLNDLMRAR--LQATLDD--ADG 362

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                     yt   e  + L L   sL           ++  lL  v  FG  L +LD
  gi|5858341   363 AYTAPSELEDDLQLILDSLQANKGLHAGWFAVRRLLWRVRSFGFHLARLD 412

                    iRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
                    +RqEs  +     A+   L+   +      +R   L     G+  L
  gi|5858341   413 VRQESSVHA---RAVADALGQTDWDAQDATRRAAVLGPYACGQEALPRVQ 459

                    LPktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLqREC
                          +  v  a+ +       D+ G+Yiisma   +DvL v  L R
  gi|5858341   460 DEGNARLDAVFAALAdARTRHGADALGSYIISMAHNRADVLTVLALARRG 509

                    gvkq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                    g+    +  +L +vPLFE + DL+    +v+ L +   Y+ ++  ++++q
  gi|5858341   510 GLVDaagavPLDIVPLFETVDDLRGGTGTVQDLLADPVYRQHLAARgdtQ 559

                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                     vm+GYsDsGKD G  +  W L +Aq E+   A + Gv+L+ FHGRGG +
  gi|5858341   560 MVMLGYSDSGKDGGIAASRWGLQRAQVELLEAAADLGVRLTFFHGRGGSI 609

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                     RGGG t  A+ + P   ++G lRvt qGEvi   +G   L  rsL   t
  gi|5858341   610 ARGGGKTSRALDAAPRGSVDGRLRVTEQGEVIHRKYGIRALALRSLEQMT 659

                    AAtLEHGmnP..PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                     A L   + P+ P      WR +m+ +A   t  YR+ v   P F+ YFR
  gi|5858341   660 GAVLLSSLRPraPEPREARWRPVMDLVAERSTVAYRAFVA-APEFMQYFR 708

                    lAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWL
                    lAtP     +m +GsRP++R   +  +  LRAiPW+FaW q R  +P W
  gi|5858341   709 LATPIDVIERMTLGSRPSRRLGQdAALSNLRAIPWVFAWSQARAVIPGWY 758

                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    GvG   + A+d        L+Em ++WPFFR  lD + mv  KGD  iA
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  gi|5858341   759 GVGSGLQAAVDAGHED--SLREMAQDWPFFRTFLDDVAMVLSKGDLNIAE 806

                   LyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrl
                   L+ +L  + +L+ +F   +Rd+   tk ++  +   + lL  DP L   +
  gi|5858341   807 LFSRL--SGDLHTrFFPLIRDELALTKGWVKALLQQQSLLQHDPRLALSI 854

                   RLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLv
                   RLR++Yi  + v+q   L+R R            + +  dE
  gi|5858341   855 RLRNPYIDPISVLQVDLLQRWR------------ATDGEDEA-------- 884

                   kLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    L             L+  + G+  G+qntG
  gi|5858341   885 LLR-----------ALVACVNGVSQGLQNTG    904

gi|73920190|sp|Q8PP82.2|CAPP_XANAC: domain 1 of 1, from 3 to 904: score 204.9, E = 2.2e-58
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedL.kEa
                           L    P     d+         + +   ++ DL  e+++ E+
  gi|7392019     3    EYRSSLVFATPDLPLRDD---------VRRLGALVGDLLAEQVsAEF 40

                   vqECYElsAeYEGKkDtkK.LeELGakLtsLdPaDailvAkailHmLnLA
                     E   +      ++++  +   L  +L + +P Da  + +a++    +
  gi|7392019    41 LDEIERVRTTAISRRESDApPSTLSEQLAGRQPRDAEALVRAFSTYFQVV 90

                   nLAEEvelAyRRRikkkkhGDFaDEasAttEsD.iEEtlKkLvlklnKsP
                   n+AE v+   RRR  ++        +  t   D++ + l++L  ++  +
  gi|7392019    91 NIAERVHRIRRRREYQRS-------GTDTPQPDgLHDALRRLKAQG-VTL 132

                   eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                   +E  + L    v+ v+tAHPt +vRR+LL K+  +   L        t++
  gi|7392019   133 DELSQWLPRIDVEPVFTAHPTEAVRRALLEKEQLMVASLVDNLDGMRTPN 182

                   DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                   ++          + A + t +    +Pt  DE      Y+   +++ +P
  gi|7392019   183 ERASDAARFRMALTASWQTADSSPVRPTVDDEREHVGFYLTQVLYRVIPV 232

                   FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                        + A+        +P    L++F  W+GGD DG nP v
  gi|7392019   233 MYETLEHAIEE--TYGSVPALPRLLRFGTWVGGDMDG-NPNVD------- 272

                   CLLaRmmAanlYisqvEDL.mFElsmWRCndELRvRAEElyrtaardkvv
                      a+ +A  l  +    L+ +   +W   + L      ++
  gi|7392019   273 ---AKTIAGTLDAQRRAVLdRYQKELWQLASLLSQSTTLVQVSGELT--- 316

                   KyYiEFWKqvPPtEPYRv..iLGdvRDKLYntRERaRHLLAtGiseisEe
                      +E ++ + P    R ++  Gd+  +L n   RaR  L   + +   +
  gi|7392019   317 -AQLERYRALLPDAAARSrpRHGDMPYRLLNDLMRAR--LQATLDD--AD 361

                   AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                     y    e    L L   sL           +   lL  v  FG  L +L
  gi|7392019   362 GAYAAPSELEHDLQLILDSLQANKGLHAGWFAARRLLWRVRSFGFHLARL 411

                   DiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgs
                   D+RqEs  +     A+   L+   +      +R   L     G+ PL
  gi|7392019   412 DVRQESSVHA---RAVADALGQTDWDAQDATQRAAVLGPYAAGQDPLPRV 458

                   DLPktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLqRE
                   D      +  v  a+ +       D+ G+Yiisma   +DvL v  L R
  gi|7392019   459 DDEGNARLDAVFAALAdARTRHGADALGSYIISMAHNRADVLTVLALARR 508

                   Cgvkq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...
                    g+  + +  +L +vPLFE + DL+    +v+ L +   Y+ ++  ++++
  gi|7392019   509 GGLVDdagavPLDIVPLFETVDDLRGGTGTVQDLLADPVYRQHLAARgdt 558

                   qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                   q vm+GYsDsGKD G  +  W L +Aq E+   A + Gv+L+ FHGRGG
  gi|7392019   559 QMVMLGYSDSGKDGGIAASRWGLQRAQVELLEAAAELGVRLTFFHGRGGS 608

                   vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                   + RGGG t  A+ + P   ++G lRvt qGEvi   +G   L  rsL
  gi|7392019   609 IARGGGKTSRALDAAPRGSVDGRLRVTEQGEVIHRKYGIRALALRSLEQM 658
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                    tAAtLEHGmnP..PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                    t A L   + P+ P      WR +m+ +A   t  YR+ v   P F+ YF
  gi|7392019   659 TGAVLLSSLRPraPEPREARWRPVMDLVAERSTVAYRAFV-GAPEFMQYF 707

                    RlAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvW
                    RlAtP     +m +GsRP++R   +  +  LRAiPW+FaW q R  +P W
  gi|7392019   708 RLATPIDVIERMTLGSRPSRRLGQdAALSNLRAIPWVFAWSQARAVIPGW 757

                    LGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiA
                     GvG   + A+d        L+Em ++WPFFR  lD + mv  KGD  iA
  gi|7392019   758 YGVGSGLQAAVDAGHEE--TLREMAQDWPFFRTFLDDIAMVLSKGDLNIA 805

                    aLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                     L+ +L  + +L+ +F   +Rd+   tk ++  +   + lL  DP L
  gi|7392019   806 ELFSRL--SGDLHTrFFPLIRDELALTKGWVKALLQQQSLLQHDPRLALS 853

                    lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                    +RLR++Yi  + v+q   L+R R            + +  dE
  gi|7392019   854 IRLRNPYIDPISVLQVDLLQRWR------------ATDGEDEA------- 884

                    vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      L             L+  + G+  G+qntG
  gi|7392019   885 -LLR-----------ALVACVNGVSQGVQNTG    904

gi|1581933|prf||2117330A: domain 1 of 1, from 1 to 857: score 204.4, E = 2.9e-58
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                    +s+  + ++ +  Ll + L++ +  + Ge
  gi|1581933     1    -------------MSDPFEALKAEVDLLGRLLgEAIRKVSGERFFAL 34

                    vqECYEls.AeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    v E   ls+A   G  D    e L  ++  +   +   + +a+ H   L
  gi|1581933    35 VEEVRLLSkARRQG--DGAAAEVLSQRVERMPVEEMEALVRAFTHYFHLV 82

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnK...
                    nLAEE    +R R+ +++      E++ t E    E +  L   l K+++
  gi|1581933    83 NLAEE---RHRVRVNRLR-----TEGE-TLENPRPEGFLALAKAL-Kerg 122

                    .sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                     s eE    L   +  L +tAHPt   RR L     R+      L   D
  gi|1581933   123 lSLEEAEAHLNRLALLLTFTAHPTETRRRTLRHHLERLQE---ELEGGD- 168

                    tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                             E L   +   + t+E+R+a+P   DE++ G+ Y+  t+W+
  gi|1581933   169 --------RERLLARVVLLYATEEVRKARPSVEDEIKGGLYYLPTTLWRA 210

                    vPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                    +PK +   + AL    +  + P     ++F sWmGGDRDG nP vtPEvt
  gi|1581933   211 IPKVVEGLEAALER--VYGKRPHLRSPVRFRSWMGGDRDG-NPYVTPEVT 257

                    RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk
                          aR +A   Y++ +E L+ +ls+    +E R+      r
  gi|1581933   258 AFAGRYAREVAKGRYLEELEALVRDLSL----SEARIPVPKEVREGGEG- 302

                    vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                    v ++         P EPYR    +    LY   E               e
  gi|1581933   303 VERF---------PGEPYRRYFAA----LYRALE--------------GE 325

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                    A  t  E     L +  k L   G   +A   L  l    s FGL L  L
  gi|1581933   326 ALST--EGLARALKVAEKGLEGVGLAQVAQAFLRPLEARLSAFGLELAPL 373

                    DiRqEseRqtDvlDAittHLeiGs....YReWsEeKRqEWLlaELkGKRP
                    D+R Es +    l+A  + L +G  ++++   s e +   L  ELk  RP
  gi|1581933   374 DLREESGK---LLEAAAELLRLGGvhpdFLALSPEEKEALLTEELKTARP 420

                    Llgs.DLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvEL
                    Ll+ +++P+ E ++  ++a+r   +      Ga ++sm+  P+D LAv L
  gi|1581933   421 LLPVgEVPQGEALRVAIGAIRAWGDK-----GAHVVSMTHHPADLLAVFL 465

                    LqRECgvkq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                    L RE g+ +++++ +  vvPLFE L DLe AP  + +L +   ++ + +G
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  gi|1581933   466 LAREVGLYRpgkplPFDVVPLFETLEDLERAPEVLRRLLANPVFRAHAQG 515

                   K..qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                   +++ evm+GYsDs KDAG l A   LY+AqE +  v    G+ +  FHGR
  gi|1581933   516 RggVEVMIGYSDSMKDAGFLMANLALYQAQEALHAVGEAQGIPVFFFHGR 565

                   GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                   G    RGGGP   Ai   PP  +   lR t qGE +   +   +L  r L
  gi|1581933   566 GTSTARGGGPAGRAIAGLPPKSVGHRLRLTEQGEALADRYAHPDLAVRHL 615

                   qRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEY
                             +   v Pk  WR+ + e        YR++  +E  F  +
  gi|1581933   616 EQLLYHFAQAALGDGVEPKAHWREALGEAGERSMARYRALLSQEG-FFPF 664

                   FRlAtPElEYGkmniGsRPaKRk.PsGGiesLRAiPWiFaWtqtRFHLPv
                   F   tP  E G + i sRP  R++    i  LRAiPW+ aWtq R  LP
  gi|1581933   665 FEAFTPIREIGELPIASRPVYRHgRVRDIRDLRAIPWVMAWTQVRLLLPG 714

                   WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                   W G+ A        +   +  L+EmY+eWPFF  tl+   m  AK D Gi
  gi|1581933   715 WYGLSAL-------EGLPMPLLREMYREWPFFATTLESAAMALAKADLGI 757

                   AaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                   A  y k Lv E L+ F + L ++Y  t  lL  i     lL     L  +
  gi|1581933   758 AERYLK-LVPEGLQGFYHHLAEEYRRTVALLEAIF-EAPLLHNQKTLERQ 805

                   lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                   + LR++Y+  +n +q   L R R P
  gi|1581933   806 IALRNPYVDPINFVQVELLARYRAP------------------------ 830

                   vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        + r   G+   L+L + G+AAG+ n G
  gi|1581933   831 -----GGREDEGVRRALLLSLLGVAAGLRNAG    857

gi|21230228|ref|NP_636145.1|: domain 1 of 1, from 3 to 904: score 203.7, E = 4.8e-58
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           L    P  v   +++ +  AL+     D+L +    d  E +
  gi|2123022     3    EYRSSLVFATP-DVPLRDDVRRLGALV----GDLLAEQVSADFLEEI 44

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    E     A      Dt   + L + L + +P  a  + +a++    + n+
  gi|2123022    45 -ERIRTTAIARRESDTPPAGLL-SLLEGREPRAAEALVRAFSTYFQVVNI 92

                   AEEvelAyRRRikkkkhGDFaDEasAttEsD.iEEtlKkLvlklnKsPeE
                   AE v+   RRR  ++        +  t   +++ + l++L  ++  + +E
  gi|2123022    93 AERVHRIRRRRDYQRS-------GTDTPQPEgLHDALRRLKAQG-VTLDE 134

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     e L    v+ v+tAHPt +vRR+LL K+  +   L        t++++
  gi|2123022   135 LSEWLPRIDVEPVFTAHPTEAVRRALLEKEQLMVASLVDNLDGMRTPNER 184

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                             + A + t +    +Pt  DE      Y+   +++ +P
  gi|2123022   185 ATDAARFRMALTASWQTADSSPVRPTVEDEREHVGFYLTQVLYRVIPVMY 234

                   RRvDtALKn.iGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                      + A+  + G    lP    L++F  W+GGD DG nP v
  gi|2123022   235 ETLEHAIEEtYGSTLALP---RLLRFGTWVGGDMDG-NPNVDAHTIAGTL 280

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                      R      Y++          +W   + L      +   +a
  gi|2123022   281 DAQRRAVLDRYLNE---------LWQLASLLSQSTTLVAVSPALS----A 317

                   YiEFWKqvPPtEPYRv..iLGdvRDKLYntRERaRHLLAtGiseisEeAv
                    +E ++ + P    R ++  Gd+  +L n   RaR  L   + +   +
  gi|2123022   318 QLERYQALLPDAAARSrpRHGDMPYRLLNDLMRAR--LQATLDD--ADGA 363

                   ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                   y    e    L L   sL           ++  lL  v  FG  L +LD+
  gi|2123022   364 YAAPAELEHDLQLILDSLEVNKGLHAGWFAVRRLLWRVRSFGFHLARLDV 413
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                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    RqEs  +     A+   L+   + +     R   L    +G   L   D
  gi|2123022   414 RQESSVHA---RAVADALGQADWDSQDATHRAGLLGPYASGEQALPQVDD 460

                    PktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLqRECg
                         +  v  a+ +       D+ G+Yiisma   +DvL v  L R  g
  gi|2123022   461 EGNARLDAVFAALAdARTRHGADALGSYIISMAHNRADVLTVLALARRGG 510

                    vkq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...qe
                    +  + +  +L +vPLFE + DL+    +v+ L +   Y+ ++  ++++q
  gi|2123022   511 LVDdagavPLDIVPLFETVDDLRGGTGTVQDLLADPVYRQHLRARgdtQM 560

                    vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                    vm+GYsDsGKD G  +  W L +Aq E+   A + Gv+L+ FHGRGG +
  gi|2123022   561 VMLGYSDSGKDGGIAASRWGLQRAQVELLEAAAELGVRLTFFHGRGGSIV 610

                    RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                    RGGG t  A+ + P   ++G lRvt qGEvi   +G   L  rsL   t
  gi|2123022   611 RGGGKTTRALDAAPRGSVDGRLRVTEQGEVIHRKYGIRALALRSLEQMTG 660

                    AtLEHGmnPPvsPkP...EWRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                    A L   + P  +P P+++ WR +m+ +A   t  YR  v   P F+ YFR
  gi|2123022   661 AVLLSSLRPR-APEPredAWRPVMDLVAERSTVAYRGFV-GAPDFMQYFR 708

                    lAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWL
                    lAtP     +m +GsRP++R   +  +  LRAiPW+FaW q R  +P W
  gi|2123022   709 LATPIDVIERMTLGSRPSRRLGQdAALSNLRAIPWVFAWSQARAVIPGWY 758

                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    GvG   + A++        L+Em ++WPFFR  lD + mv  KGD  iA
  gi|2123022   759 GVGSGLQAAVEAGHED--SLREMAQDWPFFRTFLDDIAMVLSKGDLNIAE 806

                    LyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrl
                    L+ +L  a  L+ +F  ++Rd+   tk ++  + G + lL  DP L   +
  gi|2123022   807 LFSRL--AGPLHArFFPRIRDELALTKHWVKTLLGQRSLLQHDPRLALSI 854

                    RLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLv
                    RLR++Yi  + v+q   L+R R                A +   + +eL+
  gi|2123022   855 RLRNPYIDPISVLQVDLLQRWR----------------ATDG--EDEELL 886

                    kLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +              L+  + G+A G+qntG
  gi|2123022   887 R-------------ALVACVNGVAQGVQNTG    904

gi|188575328|ref|YP_001912257.1|: domain 1 of 1, from 4 to 896: score 203.3, E = 6.4e-58
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         D  LR          +++ +  AL+ D    +   +  e L E+
  gi|1885753     4    TPDLPLR----------DDVRRLGALVGDL---LAEQVSAEFLDEIE 37

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                              E    ++ L E   +Lt+ +P Da  + +a++    + n+
  gi|1885753    38 RVRTTAISRRESDAPPSTLSE---QLTGREPRDAEALVRAFSTYFQVVNI 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsD.iEEtlKkLvlklnKsPeE
                    AE v+   RRR  ++        +  t   D++ + l++L  ++  + +E
  gi|1885753    85 AERVHRIRRRREYQRS-------GTDTPQPDgLHDALRRLKAQG-VTLDE 126

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      + L    v+ v+tAHPt +vRR+LL K+  +   L        t++++
  gi|1885753   127 LSQWLPRIDVEPVFTAHPTEAVRRALLEKEQLMVASLVDNLDGMRTPNER 176

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                              + A + t +    +Pt  DE      Y+   +++ +P
  gi|1885753   177 TSDAARFRMALTASWQTADSSPVRPTVGDEREHVGFYLTQVLYRVIPVMY 226

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                       + A+        +P    L++F  W+GGD DG nP v
  gi|1885753   227 ETLEHAIEE--TYGSVPALPRLLRFGTWVGGDMDG-NPNVDANTIAGTLD 273

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                      R      Y  q E       +W   + L      ++  +
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  gi|1885753   274 AQRRAVLDRY--QRE-------LWQLASLLSQSTTLVQVSPELM----TQ 310

                   iEFWKqvPPtEPYRv..iLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                   +E ++ + P    R ++  Gd+  +L n   RaR  L   + +   +  y
  gi|1885753   311 LERYRALLPDAAARSrpRHGDMPYRLLNDLMRAR--LQATLDD--ADGAY 356

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                   t   e  + L L   sL           ++  lL  v  FG  L +LD+R
  gi|1885753   357 TAPSELEDDLQLILDSLQANKGLHAGWFAVRRLLWRVRSFGFHLARLDVR 406

                   qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                   qEs  +     A+   L+   +      +R   L    +G+  L  +
  gi|1885753   407 QESSVHA---RAVADALGQTDWDGQDATRRAAVLGPYASGQEALPRAQDE 453

                   ktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                       +  v  a+ +       D+ G+Yiisma   +DvL v  L R  g+
  gi|1885753   454 GNARLDAVFAALAdARTRHGADALGSYIISMAHNRADVLTVLALARRGGL 503

                   kq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...qev
                       +  +L +vPLFE + DL+    +v+ L +   Y+ ++  ++++q v
  gi|1885753   504 VDaagavPLDIVPLFETVDDLRGGTGTVQDLLADPVYRQHLAARgdtQMV 553

                   mvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGR
                   m+GYsDsGKD G  +  W L +Aq E+   A + Gv+L+ FHGRGG + R
  gi|1885753   554 MLGYSDSGKDGGIAASRWGLQRAQVELLEAAADLGVRLTFFHGRGGSIAR 603

                   GGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAA
                   GGG t  A+ + P   ++G lRvt qGEvi   +G   L  rsL   t A
  gi|1885753   604 GGGKTSRALDAAPRGSVDGRLRVTEQGEVIHRKYGIRALALRSLEQMTGA 653

                   tLEHGmnPPvsPkPE...WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRl
                    L   + P  +P P +  WR +m+ +A   t  YR+ v   P F+ YFRl
  gi|1885753   654 VLLSSLRPR-APEPReacWRPVMNLVAERSTVAYRAFV-GAPEFMQYFRL 701

                   AtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWLG
                   AtP     +m +GsRP++R   +  +  LRAiPW+FaW q R  +P W G
  gi|1885753   702 ATPIDVIERMTLGSRPSRRLGQdAALSNLRAIPWVFAWSQARAVIPGWYG 751

                   vGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaL
                   vG   + A+d        L+Em ++WPFFR  lD + mv  KGD  iA L
  gi|1885753   752 VGSGLQAAVDAGHED--TLREMAQDWPFFRTFLDDVAMVLSKGDLNIAEL 799

                   yDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                   + +L  + +L+ +F   +Rd+   tk ++  +   + lL  DP L   +R
  gi|1885753   800 FSRL--SGDLHTrFFPLIRDELALTKGWVKALLQQQSLLQHDPRLALSIR 847

                   LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                   LR++Yi  + v+q   L+R R            + +  dE
  gi|1885753   848 LRNPYIDPISVLQVDLLQRWR------------ATDGEDEA--------L 877

                   LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   L             L+  + G+  G+qntG
  gi|1885753   878 LR-----------ALVACVNGVSQGLQNTG    896

gi|225352396|ref|ZP_03743419.1|: domain 1 of 1, from 37 to 918: score 203.2, E = 7.2e-58
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       +D  L +L        e L e+D  Ll kF     ++    L
  gi|2253523    37    EMDLCLQILR-------EVLGEFDEKLLAKF----DEVREHALNASA 72

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        +  +    +D   L+ +   +   d  +a l+A+a+     LAnL
  gi|2253523    73 ERFSGILTDTNPNQDD--LQKVVDIIDKTDVHEAQLLARAFTTYFHLANL 120

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    EE    yR  +   +     D        ++   + +L+      P+
  gi|2253523   121 CEE---NYRVSVLHSREAAVDDTQAVDPVNEMTCAYHQLINEM--GPAKA 165

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    e L       v+tAHPt + R+++  K  Ri   La    K +   DKk
  gi|2253523   166 KELLDQLEFHPVFTAHPTEARRKAVEGKIRRISQLLA--THKLLGGSDKK 213
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                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    E    L  Ei A FRt  i   +PtP +E    +  +  t++  +P+  R
  gi|2253523   214 ENSRRLFNEIDALFRTSPIALKKPTPVEESETILDIFDNTLFYTIPQVYR 263

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R D  +         P      +  sW+G DRDG nP vt  v R v
  gi|2253523   264 RFDDWILGDKAGLVPPVCPAFFHPGSWIGSDRDG-NPNVTAKVSRQV--- 309

                    aRmmAanlY.isqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    aR     + +  q+E         R    L   AE     a  + +  +
  gi|2253523   310 ARKFSDHVLgALQIE-------TRRVGKNLTMEAETTPPSAELKSLWNHQ 352

                    iEFWKq.......vPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseis
                     E     +++   +   E  R ++  + D+L  t +R   L+
  gi|2253523   353 KEMSERltdkaalISTKELHRAVMLVMADRLKATIDRDADLM-------- 394

                    EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                        y   E+++  L +  +sL e   k  A G L Dl+ q  tFG  +v
  gi|2253523   395 ----YHSCEDYIADLKVVQRSLAEANAKRSAYGPLQDLIWQAETFGFHMV 440

                    KLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLl
                     ++ Rq s  +   l+ i +H                    L+G R  l
  gi|2253523   441 EMEFRQHSVVHSRALEDIREH--------------------GLHGERGEL 470

                    gsDLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvE
                        P+t E   vld+fr L  + ++++i +   Yiis + +   +  v
  gi|2253523   471 Q---PMTHE---VLDTFRALGSIQkrngIKAARRYIISFTKSAQNIRDVY 514

                    LLqREC..gvkq..tLrvvPLFEkLADLeAAPAavekLFsiDWYinrid.
                     L R   ++ k  +t+ v+PLFE+L DL+     +e +  i     r+
  gi|2253523   515 ELNRLAfsHPKDvpTIDVIPLFEQLEDLQNSVDVLEEMIKIPEVQARLKa 564

                    ..GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                    ++GK evm+GYsDs KDAG  sA   L  AqE i+K A  + + L+lFHG
  gi|2253523   565 tgGKMEVMLGYSDSSKDAGPTSATLALHSAQERIAKWAESHDIDLTLFHG 614

                    RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                    RGG vGRGGGP   A+L+qP   ++   + t qGEvi   +G   L  r
  gi|2253523   615 RGGAVGRGGGPANRAVLAQPVGSVKCRFKLTEQGEVIFARYGNPALAIRH 664

                    LqRFtAAtLEHGmnPPvsPk.....PEWRkLmeemAvvAtEEYRsvvvKE
                    +   +AAtL     P v  ++++ +  + ++ +++   A   +  +   +
  gi|2253523   665 VESVAAATLLQS-APSVEKRntdmtAKYADMANKLDEAAHNRFLDLLNTD 713

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqt
                      F  +F   tP +E G + iGsRPaKR  + + ++ LR iPWiF+W q
  gi|2253523   714 G-FAPWFSTVTPLTEIGLLPIGSRPAKRGLGAkSLDDLRTIPWIFSWAQA 762

                    RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                    R  L  W G+G A           l  L+  Y+eWP F   +D +Em  A
  gi|2253523   763 RINLAAWYGLGTAC-----EQFGDLNTLRQAYEEWPLFSTFIDNIEMSLA 807

                    KGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                    K D  iA +y  L   E+L    k++ d+ + t++++L+i G k  L
  gi|2253523   808 KTDERIAKMYLALGDREDLN---KKVLDEMELTRKWVLEIVGDKWPLQHR 854

                    PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                      L q +R+R +Y+  L   q   L  +R             K    E+
  gi|2253523   855 HVLGQAIRIRSPYVDALSATQVLALGSLR-------------KRVDKEE- 890

                    kkadeLvkLnptervaPGLEDtLiL.tmKGiAAGmqntG<-*
                         L +    e++       LiL t+ G+AAG+qntG
  gi|2253523   891 -----LTHGQ-KENYT-----YLILcTVSGVAAGLQNTG    918

gi|170782299|ref|YP_001710632.1|: domain 1 of 1, from 16 to 910: score 202.1, E = 1.5e-57
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                         D    ++ P   s        D   l   L+ +L +  GedL
  gi|1707822    16    TRDGTRDAVEPALRS--------DVSHLGGLLgQVLRESGGEDLLRD 54

                    vqECYElsAe.YEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    v    El  + YE  +D++ +++    +    P  a  vA+a+     LA
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gi|1707822    55 VERLRELVIDaYESARDAS-IDDAERLVATFTPERAEQVARAFTCYFHLA 103

                 nLAEEvelAyRRRikkkkhGDFaDEasAttEsD.iEEtlKkLvlklnKsP
                 nLAEE    +R R+ + +      Ea A    D+i + +  L   l
gi|1707822   104 NLAEE---HHRVRVLRER------EAAAGFVPDsIPDAVGTLTEEL--GR 142

                 eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                 eE    L       vltAHPt + RR++     Ri   L+
gi|1707822   143 EEAMRRLGEMRFHPVLTAHPTEARRRAVATGIRRIGDLLTERDGAMAGTL 192

                 DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++D  L  Ei   +Rt  +R ++PtP DE+R  m  +  t+++ vP+
gi|1707822   193 TGADIDRRLLEEIDGLWRTSPLRTTRPTPLDEVRTAMGVFDQTLFEVVPR 242

                 FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                   R  D  L       R        +   W+  DRDG nP vt  vt +
gi|1707822   243 VYRLLDDWLLGEEAGVRDAVAPAFFRLGNWIAADRDG-NPYVTAAVTEE- 290

                 CLLaRmmAanlYisqvEDLmFEl..smWRCndELRvRAEElyrtaardkv
                    a  +A+   +  +E +   +++s+     +     E     aa+d +
gi|1707822   291 ---AAGIASEHILLGLERVALRVgrSLTLGDADTPPSPELRELAAAQDAL 337

                 vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                   +         P E  R +L  +  +L  tRER    +A
gi|1707822   338 APHLTARIGTRAPAELHRRVLLVIAGRLAATRERHDDPIA---------- 377

                 vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                  y    e L  L +   sL   G + iA G L  l+ q  tFG  L  ++
gi|1707822   378 -YPSAAELLADLRVLQGSLRSAGAHRIAGGELQGLIWQAETFGFHLAEME 426

                 iRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
                 +Rq s+ + + l                   R    +a         ++
gi|1707822   427 VRQHSQVHREAL-------------------REVLAVAAADASGDAVPEL 457

                 LPktEEvkDvldafrvLAE.LPiDsFGaYiismataPsDvLAv.ELLqRE
                  P+t Ev  v  a+  L E+  +  F  +i+s + +  D+  v+EL
gi|1707822   458 APMTVEVLYVFRALARLQErHGVAPFCRFIVSFTQSADDIRTVhELAALA 507

                 Cgvkq...tLrvvPLFEkLADLeAAPAa...vekLFsiDWYinridGKqe
                  g  ++ + L v+PLFE  ADL+A     +++ +L  +     +   K e
gi|1707822   508 LGSAEdapVLDVIPLFETFADLNASTEIldgMIRLPQVAARLEQTGRKLE 557

                 vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                 vm+GYsDs KD G +sA + L+ Aq  i+  A++  + L+lFHGRGG  G
gi|1707822   558 VMLGYSDSSKDVGPVSATFALFDAQARIAAWARENDIELTLFHGRGGALG 607

                 RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                 RGGGP   A+ +qPP  ++G  + t qGEvi   +G+  +  r +   +A
gi|1707822   608 RGGGPADRAVRAQPPGSVDGRFKLTEQGEVIFAHYGDKRIAARHIEQMAA 657

                 AtL.......EHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFv
                 AtL  + +++E           E  + m+e       E     vK P F
gi|1707822   658 ATLlasapsnEERNAAAAQGSAEMVRTMDEASRARFFE----LVKAPGFA 703

                 EYFRlAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHL
                  +F   tP  E G + +GsRPa+R  s   +e LRAiPW+FaWtq R  L
gi|1707822   704 PWFTQVTPMEEIGLLALGSRPARRGLSvESLEDLRAIPWVFAWTQARINL 753

                 PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                   W G+G A     d  +     L+  Y+eWP F   +D +Em  AK D
gi|1707822   754 TGWFGLGSALAAVGDEAV-----LRKAYDEWPLFTSMIDNVEMSLAKTDG 798

                 GiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLK
                  +A  y  L    +L      + ++ + t++++ k  G  D+LEG P L+
gi|1707822   799 RLAERYLALGDRPDLAAL---VTEEMELTREWVRKATGRGDILEGRPVLR 845

                 qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                   +RLR +Y+  L  +q   L+ +R      t +    +  Ad
gi|1707822   846 RAVRLRSPYVDALSLLQLRALRALRTTASAATGQAAPGQ--ADPT----- 888

                 eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
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                       p  r        L+Lt+ GiAAG+qntG
  gi|1707822   889 -----DPDHRL-------LLLTVNGIAAGLQNTG    910

gi|218295525|ref|ZP_03496338.1|: domain 1 of 1, from 1 to 857: score 201.9, E = 1.7e-57
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                    + e  +L++ +  Ll + L++ +  + Ge
  gi|2182955     1    -------------MTEPFELLKAEVDLLGRLLgEAIRRVSGERFFAL 34

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v E   l A    + D    e L  ++  L   +a  + +a+ H   L n
  gi|2182955    35 VEEV-RLLAKARRQGDEGAGEALWKRVGTLSTEEAEALVRAFTHYFHLVN 83

                    LAEEvelAyRRRikkkkhGDFaDEasAtt.EsDiEEtlKkLvlklnK...
                    LAEE    +R R+ + +       a+A t+E    E +  L   l K+++
  gi|2182955    84 LAEE---RHRVRVNRMR-------AQAETpENPRPEGFLALAQAL-Kgrg 122

                    .sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                     s eE    L      L +tAHPt   RR L       R  L  L
  gi|2182955   123 lSLEEAEAHLNRLELLLTFTAHPTETRRRTL-------RHHLEALQG--- 162

                    tveDKkELDEA....LHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEt
                          EL+E ++++L   +   + t+E+R+a+P   DE++ G+ Y+  t
  gi|2182955   163 ------ELEEGertrLEARVALLYATEEVRKARPSVEDEIKGGLYYLPTT 206

                    vWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvt
                    +W+ +PK +   +tAL  +    R     P ++F sW+GGDRDG nP vt
  gi|2182955   207 LWRAIPKVVEGLETALERV-YGKRPRLKSP-VRFRSWIGGDRDG-NPFVT 253

                    PEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrta
                    PEvtR     aR +A    ++ +  L+ +ls+    +E +v      r
  gi|2182955   254 PEVTRFAARYAREVAKEKVLEELGALVRDLSL----SEAKVPVPREVRAG 299

                    ardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGise
                        v ++         P EPY                  R   A+ +
  gi|2182955   300 GEG-VERF---------PGEPY-----------------RRFFAQIYRK 321

                    isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                    +s +   t  Ee L  L +    L   G   +    L  l    s FGL
  gi|2182955   322 VSQDEATT--EELLSALKVAEGGLRAVGLEEVGKSFLRPLEARLSAFGLE 369

                    LvKLDiRqEseRqtDvlDAittHLeiGs....YReWsEeKRqEWLlaELk
                    L  LD+R Es +    l A  + L +G  ++++ + s e     L  ELk
  gi|2182955   370 LAPLDLREESGK---LLLAAAELLRLGGvhpdFLSLSPEAQEALLTEELK 416

                    GKRPLlgs.DLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvL
                      RPLl+ ++ P+ E ++  l+a+r   +      Ga ++sm+  P+D L
  gi|2182955   417 TARPLLPVgEEPQEEALRVALGALRAWRDK-----GAHVVSMTHHPADLL 461

                    AvELLqRECgvkq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYin
                     v LL RE g+ +++++ +  vvPLFE L DL+ AP  + +L     +
  gi|2182955   462 SVFLLAREVGLYRpgkplPFDVVPLFETLEDLRRAPLVLRRLLENPVFLA 511

                    ridGK..qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                    +  G+++ evm+GYsDs KDAG l A   LY AqE + +v  + G  +
  gi|2182955   512 HARGRggVEVMIGYSDSNKDAGFLMANLALYEAQEALSRVGEERGLPVHF 561

                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                    FHGRG    RGGGP   Ai s PP  +   lR t qGE +   +G  +L
  gi|2182955   562 FHGRGTSTARGGGPAGRAIASLPPRSVGRRLRLTEQGEALADRYGHPDLA 611

                    FrsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPR
                     r L           +   v PkP WR+ +          YR++   E
  gi|2182955   612 VRHLEQLLFHFAQAALGDGVEPKPHWREALSWAGERSMAHYRALLAEEG- 660

                    FvEYFRlAtPElEYGkmniGsRPaKRk.PsGGiesLRAiPWiFaWtqtRF
                    F  +F   tP  E G + i sRP  R++    i  LRAiPW+ aWtq R
  gi|2182955   661 FFPFFEALTPIREIGELPIASRPVYRHgRVRDIGDLRAIPWVMAWTQVRL 710

                    HLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                     LP W G+          +   l  L+EmY+eWPFF  tl+   m  AK
  gi|2182955   711 LLPGWYGLSTL-------EELPLELLREMYREWPFFATTLESAAMALAKA 753
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                    DPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                    D G+A Ly + Lv E L+P  +++ ++Y  t+ lL  i     lL
  gi|2182955   754 DLGVARLYLR-LVPEALHPLFHRIAEEYLRTQALLEAIF-QAPLLHNQRT 801

                    LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                    L  ++ LR++Y+  +n++q   L+R R P  +            dE
  gi|2182955   802 LERQIALRNPYVDPINIVQVELLRRYRAPGGR-----------EDEA--- 837

                    adeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                   L   L+L + G+AAG+ n G
  gi|2182955   838 ----------------LRKALLLSILGVAAGLRNAG    857

gi|119025042|ref|YP_908887.1|: domain 1 of 1, from 37 to 918: score 201.7, E = 2e-57
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +D  L +L        e L e+D  Ll kF     ++    Lk
  gi|1190250    37    EMDLCLQILR-------EVLGEFDENLLAKF----DEVREHALKASD 72

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         +  +     D   L+ +   +   d  +a l+A+a+     LAnL
  gi|1190250    73 ERFSGILTD--TNPDQDDLQKVVDIIDKTDVHEAQLLARAFTTYFHLANL 120

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     EE    yR  +   +     D        ++   + +L+      P+
  gi|1190250   121 CEE---NYRVSVLHSRENAVDDTQAVDPVNEMTCAYHQLINEM--GPARA 165

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     e L       v+tAHPt + R+++  K  Ri   L     K +   DKk
  gi|1190250   166 KELLDQLEFHPVFTAHPTEARRKAVEGKIRRISQLLE--AHKLLGGSDKK 213

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    E    L  Ei A FRt  i   +PtP +E    +  +  t++  +P+  R
  gi|1190250   214 ENSRRLFNEIDALFRTSPIALKKPTPVEEADTILDIFDNTLFYTIPQVYR 263

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R D  +         P      +  sW+G DRDG nP vt  v R v
  gi|1190250   264 RFDDWVLGDKAGLVPPVCPAFFHPGSWIGSDRDG-NPNVTAKVSRQV--- 309

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aR     +          E+   R    L   AE     a  + +  +
  gi|1190250   310 ARKFSDHVLGA------LEIETRRVGKNLTMEAETTPPSAELKSLWNHQK 353

                    EFWKq.......vPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                    E     +++   +   E  R ++  + D+L  t +R   L+
  gi|1190250   354 EMSERltdkaalISTKELHRAVMLVMADRLKATIDRDADLM--------- 394

                    eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                       y   E+++  L    +sL e   k  A G L Dl+ q  tFG  +v
  gi|1190250   395 ---YHSCEDYIADLKTVQRSLAEANAKRSAYGPLQDLIWQAETFGFHMVE 441

                    LDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlg
                    ++ Rq s  +   l+ i +H                    L+G R  l
  gi|1190250   442 MEFRQHSVVHSRALEDIREH-------------------GLHGERGELQ 471

                    sDLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvEL
                       P+t E   vld+fr L  + ++++i +   Yiis + +   +  v
  gi|1190250   472 ---PMTHE---VLDTFRALGSIQkrngIKAARRYIISFTKSAQNIKDVYE 515

                    LqRECgvk....qtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid..
                    L R    ++++  t+ v+PLFE+L DL+     +e +  i     r+  +
  gi|1190250   516 LNRLAFSHpedvPTIDVIPLFEQLEDLQNSVDVLEEMIKIPEVQARLKat 565

                    .GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    +GK evm+GYsDs KDAG  sA   L  AqE i+K A  + + L+lFHGR
  gi|1190250   566 gGKMEVMLGYSDSSKDAGPTSATLALHSAQERIAKWAESHDIDLTLFHGR 615

                    GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                    GG vGRGGGP   A+L+qP   ++   + t qGEvi   +G   L  r +
  gi|1190250   616 GGAVGRGGGPANRAVLAQPVGSVKCRFKLTEQGEVIFARYGNPVLAIRHV 665

                    qRFtAAtLEHGmnPPvsPk.PEWRkLmeemAvvAtEEY..Rsv.vvKEPR
```

```
                     +AAtL     P v  ++ +  k   +mA    E  ++R ++ +
  gi|1190250   666 ESVAAATLLQS-APSVEKRnTDMTKKYADMASKLDEAAhnRFLdLLNTDG 714

                     FvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqtRF
                     F  +F   tP +E G + iGsRPaKR  + + ++ LR iPWiF+W q R
  gi|1190250   715 FAPWFSTVTPLTEIGLLPIGSRPAKRGLGAkSLDDLRTIPWIFSWAQARI 764

                     HLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                      L  W G+G A           l  L+  Y+eWP F   +D +Em  AK
  gi|1190250   765 NLAAWYGLGTAC-----EQFGDLNTLRQAYEEWPLFSTFIDNIEMSLAKT 809

                     DPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                     D  iA +y  L   E+L    k++ d+ + t++++Lki G    L
  gi|1190250   810 DERIAKMYLALGDREDLN---KKVLDEMELTRKWVLKIVGDEWPLQHRHV 856

                     LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                     L q +R+R +Y+  L v q   L  +R             K    E+
  gi|1190250   857 LGQAIRIRSPYVDALSVTQVLALGSLR-------------KRVDKEE--- 890

                     adeLvkLnptervaPGLEDtLiL.tmKGiAAGmqntG<-*
                        L +    e++       LiL t+ G+AAG+qntG
  gi|1190250   891 ---LTHGQ-KENYT-----YLILcTVSGVAAGLQNTG    918

gi|292606014|gb|EFF49287.1|: domain 1 of 1, from 3 to 904: score 199.8, E = 7.5e-57
                     *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedL.kEa
                             L    P     d+         + +   ++ DL  e+++ E+
  gi|2926060     3    EYRSSLVFATPDLPLRDD---------VRRLGALVGDLLAEQVsAEF 40

                     vqECYElsAeYEGKkDtkK.LeELGakLtsLdPaDailvAkailHmLnLA
                       E   +      ++++  +   L  +L + +P Da  + +a++    +
  gi|2926060    41 LDEIERVRTTAISRRESDApPSTLSEQLAGREPRDAEALVRAFSTYFQVV 90

                     nLAEEvelAyRRRikkkkhGDFaDEasAttEsD.iEEtlKkLvlklnKsP
                     n+AE v+   RRR  ++        +  t   D++ + l++L  ++  +
  gi|2926060    91 NIAERVHRIRRRREYQRS-------GTDTPQPDgLHDALRRLKAQG-VTL 132

                     eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                     +E  + L    v+ v+tAHPt +vRR+LL K+  +   L        t++
  gi|2926060   133 DELSQWLPRIDVEPVFTAHPTEAVRRALLEKEQLMVASLVDNLDGMRTPN 182

                     DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     ++          + A + t +    +Pt  DE      Y+   +++ vP
  gi|2926060   183 ERASDAARFRMALTASWQTADSSPVRPTVDDEREHVGFYLTQVLYRVVPV 232

                     FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                          + A+        +P    L++F  W+GGD DG nP v  + t
  gi|2926060   233 MYETLEHAIEE--TYGSVPALPRLLRFGTWVGGDMDG-NPNV--DATTIA 277

                     CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                       L     a l   q E       +W   + L      ++
  gi|2926060   278 GTLDAQRRAVLDRYQKE-------LWQLASLLSQSTTLVQVSGELT---- 316

                     yYiEFWKqvPPtEPYRv..iLGdvRDKLYntRERaRHLLAtGiseisEeA
                       +E ++ + P    R ++  Gd+  +L n   RaR  L   + +   +
  gi|2926060   317 AQLERYRALLPDAAARSrpRHGDMPYRLLNDLMRAR--LQATLDD--ADG 362

                     vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                      y    e    L L   sL           ++  lL  v  FG  L +LD
  gi|2926060   363 AYAAPSELEHDLQLILDSLQANKGLHAGWFAVRRLLWRVRSFGFHLARLD 412

                     iRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
                     +RqEs  +     A+   L+   +      +R   L     G+ PL   +
  gi|2926060   413 VRQESSVHA---RAVADALDQTDWDAQDAAQRAAVLGPYAAGQDPLPRVE 459

                     LPktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLqREC
                           +  v  a+ +       D+ G+Yiisma   +DvL v  L R
  gi|2926060   460 DEGNARLDAVFAALAdARTRHGADALGSYIISMAHNRADVLTVLALARRG 509

                     gvkq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                     g+  + +  +L +vPLFE + DL+    +v+ L +   Y+ ++  ++++q
  gi|2926060   510 GLVDdagavPLDIVPLFETVDDLRGGTGTVQDLLADPVYRQHLAARgdtQ 559
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                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                     vm+GYsDsGKD G  +  W L +Aq E+   A + Gv+L+ FHGRGG +
  gi|2926060   560 MVMLGYSDSGKDGGIAASRWGLQRAQVELLEAAAELGVRLTFFHGRGGSI 609

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                     RGGG t  A+ + P   ++G lRvt qGEvi   +G   L  rsL   t
  gi|2926060   610 ARGGGKTSRALDAAPRGSVDGRLRVTEQGEVIHRKYGIRALALRSLEQMT 659

                    AAtLEHGmnP..PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                     A L   + P+ P      WR +m+ +A   t  YR+ v   P F+ YFR
  gi|2926060   660 GAVLLSSLRPraPEPREARWRPVMDLVAERSTVAYRAFV-GAPEFMQYFR 708

                    lAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWL
                    lAtP     +m +GsRP++R   +  +  LRAiPW+FaW q R  +P W
  gi|2926060   709 LATPIDVIERMTLGSRPSRRLGQdAALSNLRAIPWVFAWSQARAVIPGWY 758

                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    GvG   + A+d        L+Em ++WPFFR  lD + mv  KGD  iA
  gi|2926060   759 GVGSGLQAAVDAGHED--TLREMAQDWPFFRTFLDDIAMVLSKGDLNIAE 806

                    LyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrl
                    L+ +L  + +L+ +F   + d+   tk ++  +   + lL  DP L   +
  gi|2926060   807 LFSRL--SGDLHTrFFPLIGDELALTKGWVKALLQQRSLLQHDPRLALSI 854

                    RLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLv
                    RLR++Yi  + v+q   L+R R               A +     ++
  gi|2926060   855 RLRNPYIDPISVLQVDLLQRWR----------------ATDG----EDQA 884

                    kLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     L             L+  + G+  G+qntG
  gi|2926060   885 LLR-----------ALVACVNGVSQGVQNTG    904

gi|162451699|ref|YP_001614066.1|: domain 1 of 1, from 1 to 913: score 199.6, E = 8.4e-57
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                                P +  e ++ ++ +  Ll + L+++L +  Ge+L  +
  gi|1624516     1    ---------MPPRRREVDRPLRKEVRLLGRLLgEVLIEQEGEELFAI 38

                    vqECYElsA.eYEGKkD..tkKLeELGakLtsLdPaDail.vAkailHmL
                          l+ +   G  D++++   EL   L  L P D + +v +a+
  gi|1624516    39 EERIRTLAIrRRRGPSDgrAHAAAELSKLLAEL-PHDRLEpVIRAFTVYF 87

                    nLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnK
                     L nLAE        Ri++ +    +D +       iE  +  L   +
  gi|1624516    88 RLVNLAEQ-----HHRIRRAR-AYATDPGARPQRGSIEAAMHTLKKAG-- 129

                    sPeE.vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                     P+E+v  AL+   v L ltAHPt ++RR +L K  Ri   L       +
  gi|1624516   130 VPAErVRAALRTLDVTLTLTAHPTEAARRTVLEKLYRIAKNLEERDRCQL 179

                    tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                    t+++       +  Ei A + tDE+RR +Pt  DE++    Yi E +W+
  gi|1624516   180 TPDESARKLAEIREEITALWQTDEVRRDRPTVGDEVKNVAWYIEEILWDL 229

                    vPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                     P     +  A       E l  ++  ++  sW+G D DG nP v P v
  gi|1624516   230 LPDLPTVIGRAFEA-AYGEPLDAEIAPLRIHSWVGADMDG-NPLVVPAVL 277

                    RDvCLLaRmmAanlYisqvEDLmFElsmWRCndE....LRvRAEElyrta
                     D     R+      +  v DL   ls       +++ L +  EE    a
  gi|1624516   278 EDALFAYRIRGLRRLVRAVRDLGGALSQSVRHVTpppwLLASIEE--DAA 325

                    ardkvvKyYiEFWKqvPPt..EPYRviLGdvRDKLYntRERaRHLLAt..
                    a   v  ++       P t++EP+R  L  +  +L  t E a H  A  +
  gi|1624516   326 AMPEVAAHFG------PRTegEPWRRKLHFIEARLTATLEHAEHGRAEar 369

                    ...GiseisEeAvytkvEe......FLEPLELCYksLCeCGDkviADGs.
                     ++G     E   + + Ee++   ++ EP EL  + L    D   A
  gi|1624516   370 arsGQGPAREGRAFVRPEEptlavpYREPAEL-ERDLAVVADSLRAARCa 418

                    ......LLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYR
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                    ++++++   lL qv   G +L  L++R  +e      DA      +   R
  gi|1624516   419 ssgerrARALLSQVRALGFALAELEMRAPAE------DARAAAASLAEGR 462

                    eWsEeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiD..
                      + +                      +t E + v +a++ +A    D++
  gi|1624516   463 VEPAQ----------------------MTPEARRVFEALQRIAAAQRDgg 490

                    ..sFGaYiismataPsDvLAvEL......LqRECgvkqtLrvvPLFEkLA
                    ++s    ++sm+ +  DvLA   + +  +L  E      + vvPLFE LA
  gi|1624516   491 esSCRTLVLSMTHSEDDVLAALAsakaagLWDEARSCARIDVVPLFESLA 540

                    DLeAAPAavekLFsiDWYinri..dGKqevmvGYsDsGKDAGRlsAAWqL
                     L+     +  L +   Y+ ++   G qevm+GYsDsGK+ G l+A   L
  gi|1624516   541 ALNDSARILRALLAHPEYRPHVlaRGVQEVMIGYSDSGKEVGLLAASAAL 590

                    YkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGs
                     + qE + K+A +    L +FHGRG  v RGGGP H A+L+ P   + G
  gi|1624516   591 RRVQETLPKIAAEAELPLRVFHGRGESVARGGGPAHQALLALPAGSVGGR 640

                    lRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm....nPPvsPkPEW
                     + t qGE ++  +   +L  r+L       L H ++ ++ PP +    +
  gi|1624516   641 YKATEQGEALDHKYARPELAMRTLEIMLSGVLLHTLgaqpRPPAASELRY 690

                    RkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKR
                        +e+A      YR++v  EP+FvE+F   tP  E  ++ +GsRP+KR
  gi|1624516   691 AAAFDELAETGRRAYRALVWEEPKFVEFFTAVTPIDEIARLPLGSRPSKR 740

                    kPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLk
                    + +GG+esLRAiPW+FaWtq R  LP W GvG     A+ +       Lk
  gi|1624516   741 R-AGGLESLRAIPWVFAWTQNRAILPGWYGVGSGLE-AMGQRPEGAELLK 788

                    EmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdk
                    Em   WPFFR  +D +Emv AK D  i a y +L  a   k    ++ ++
  gi|1624516   789 EMMASWPFFRAVIDNVEMVLAKADMTIFAGYAELAPAAARKAVAPRIIAE 838

                    YvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiR
                    Y+ t+ +L ++ G + lLEG P L+  + LR++Y+  L  +q   L+  R
  gi|1624516   839 YKRTRSWLKRLTGNRRLLEGNPTLQRSISLRNPYVDPLSFLQVELLRASR 888

                    DPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKG
                                  +                   G +  L+Lt+ G
  gi|1624516   889 ----------------GGDS------------------GRDRSLLLTLNG 904

                    iAAGmqntG<-*
                    iAAGm ntG
  gi|1624516   905 IAAGMRNTG    913

gi|21241576|ref|NP_641158.1|: domain 1 of 1, from 7 to 888: score 199.6, E = 8.8e-57
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        + A +  L   +vs               FLD +  +    +
  gi|2124157     7    RLGALVGDLLAEQVS-------------AEFLDEIERVRTTAI---- 36

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                              E    ++ L E   +L + +P Da  + +a++    + n+
  gi|2124157    37 -------SRRESDAPPSTLSE---QLAGRQPRDAEALVRAFSTYFQVVNI 76

                    AEEvelAyRRRikkkkhGDFaDEasAttEsD.iEEtlKkLvlklnKsPeE
                    AE v+   RRR  ++        +  t   D++ + l++L  ++  + +E
  gi|2124157    77 AERVHRIRRRREYQRS-------GTDTPQPDgLHDALRRLKAQG-VTLDE 118

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      + L    v+ v+tAHPt +vRR+LL K+  +   L        t++++
  gi|2124157   119 LSQWLPRIDVEPVFTAHPTEAVRRALLEKEQLMVASLVDNLDGMRTPNER 168

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                              + A + t +    +Pt  DE      Y+   +++ +P
  gi|2124157   169 ASDAARFRMALTASWQTADSSPVRPTVDDEREHVGFYLTQVLYRVIPVMY 218

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                       + A+        +P    L++F  W+GGD DG nP v
  gi|2124157   219 ETLEHAIEE--TYGSVPALPRLLRFGTWVGGDMDG-NPNVD--------- 256
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                    LaRmmAanlYisqvEDL.mFElsmWRCndELRvRAEElyrtaardkvvKy
                     a+ +A  l  +    L+ +   +W   + L      ++
  gi|2124157   257 -AKTIAGTLDAQRRAVLdRYQKELWQLASLLSQSTTLVQVSGELT----A 301

                    YiEFWKqvPPtEPYRv..iLGdvRDKLYntRERaRHLLAtGiseisEeAv
                     +E ++ + P    R ++  Gd+  +L n   RaR  L   + +   +
  gi|2124157   302 QLERYRALLPDAAARSrpRHGDMPYRLLNDLMRAR--LQATLDD--ADGA 347

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y    e    L L   sL           +   lL  v  FG  L +LD+
  gi|2124157   348 YAAPSELEHDLQLILDSLQANKGLHAGWFAARRLLWRVRSFGFHLARLDV 397

                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    RqEs  +     A+   L+   +      +R   L     G+ PL   D
  gi|2124157   398 RQESSVHA---RAVADALGQTDWDAQDATQRAAVLGPYAAGQDPLPRVDD 444

                    PktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLqRECg
                         +  v  a+ +       D+ G+Yiisma   +DvL v  L R  g
  gi|2124157   445 EGNARLDAVFAALAdARTRHGADALGSYIISMAHNRADVLTVLALARRGG 494

                    vkq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...qe
                    +  + +  +L +vPLFE + DL+    +v+ L +   Y+ ++  ++++q
  gi|2124157   495 LVDdagavPLDIVPLFETVDDLRGGTGTVQDLLADPVYRQHLAARgdtQM 544

                    vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                    vm+GYsDsGKD G  +  W L +Aq E+   A + Gv+L+ FHGRGG +
  gi|2124157   545 VMLGYSDSGKDGGIAASRWGLQRAQVELLEAAAELGVRLTFFHGRGGSIA 594

                    RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                    RGGG t  A+ + P   ++G lRvt qGEvi   +G   L  rsL   t
  gi|2124157   595 RGGGKTSRALDAAPRGSVDGRLRVTEQGEVIHRKYGIRALALRSLEQMTG 644

                    AtLEHGmnP..PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRl
                    A L   + P+ P      WR +m+ +A   t  YR+ v   P F+ YFRl
  gi|2124157   645 AVLLSSLRPraPEPREARWRPVMDLVAERSTVAYRAFV-GAPEFMQYFRL 693

                    AtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWLG
                    AtP     +m +GsRP++R   +  +  LRAiPW+FaW q R  +P W G
  gi|2124157   694 ATPIDVIERMTLGSRPSRRLGQdAALSNLRAIPWVFAWSQARAVIPGWYG 743

                    vGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaL
                    vG   + A+d        L+Em ++WPFFR  lD + mv  KGD  iA L
  gi|2124157   744 VGSGLQAAVDAGHEE--TLREMAQDWPFFRTFLDDIAMVLSKGDLNIAEL 791

                    yDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                    + +L  + +L+ +F   +Rd+   tk ++  +   + lL  DP L   +R
  gi|2124157   792 FSRL--SGDLHTrFFPLIRDELALTKGWVKALLQQQSLLQHDPRLALSIR 839

                    LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                    LR++Yi  + v+q   L+R R            + +  dE
  gi|2124157   840 LRNPYIDPISVLQVDLLQRWR------------ATDGEDEA--------L 869

                    LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    L             L+  + G+  G+qntG
  gi|2124157   870 LR-----------ALVACVNGVSQGVQNTG    888

gi|292601213|gb|EFF45267.1|: domain 1 of 1, from 3 to 904: score 199.1, E = 1.2e-56
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedL.kEa
                           L    P     d+         + +   ++ DL  e+++ E+
  gi|2926012     3    EYRSSLVFATPDLPLRDD---------VRRLGALVGDLLAEQVsAEF 40

                    vqECYElsAeYEGKkDtkK.LeELGakLtsLdPaDailvAkailHmLnLA
                      E   +      ++++  +   L  +L + +P Da  + +a++    +
  gi|2926012    41 LDEIERVRTTAISRRESDApPSTLSEQLAGREPRDAEALVRAFSTYFQVV 90

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsD.iEEtlKkLvlklnKsP
                    n+AE v+   RRR  ++        +  t   D++ + l++L  ++  +
  gi|2926012    91 NIAERVHRIRRRREYQRS-------GTDTPQPDgLHDALRRLKAQG-VTL 132

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
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                    +E  + L    v+ v+tAHPt +vRR+LL K+  +   L        t++
  gi|2926012   133 DELSQWLPRIEVEPVFTAHPTEAVRRALLEKEQLMVASLVDNLDGMRTPN 182

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    ++          + A + t +    +Pt  DE      Y+   +++ vP
  gi|2926012   183 ERASDAARFRMALTASWQTADSSPVRPTVDDEREHVGFYLTQVLYRVVPV 232

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                         + A+        +P    L++F  W+GGD DG nP v  + t
  gi|2926012   233 MYETLEHAIEE--TYGSVPALPRLLRFGTWVGGDMDG-NPNV--DATTIA 277

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      L     a l   q E       +W   + L      ++
  gi|2926012   278 GTLDAQRRAVLDRYQKE-------LWQLASLLSQSTTLVQVSGELT---- 316

                    yYiEFWKqvPPtEPYRv..iLGdvRDKLYntRERaRHLLAtGiseisEeA
                      +E ++ + P    R ++  Gd+  +L n   RaR  L   + +   +
  gi|2926012   317 AQLERYRALLPDAAARSrpRHGDMPYRLLNDLMRAR--LQATLDD--ADG 362

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                     y    e    L L   sL           ++  lL  v  FG  L +LD
  gi|2926012   363 AYATPSELEHDLQLILDSLQANKGLHAGWFAVRRLLWRVRSFGFHLARLD 412

                    iRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
                    +RqEs  +     A+   L+   +      +R   L     G+ PL   +
  gi|2926012   413 VRQESSVHA---RAVADALDQTDWDVQDAAQRAAVLGPYAAGQDPLPRVE 459

                    LPktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLqREC
                          +  v  a+ +       D+ G+Yiisma   +DvL v  L R
  gi|2926012   460 DEGNARLDAVFAALAdARTRHGADALGSYIISMAHNRADVLTVLALARRG 509

                    gvkq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                    g+  + +  +L +vPLFE + DL+    +v+ L +   Y+ ++  ++++q
  gi|2926012   510 GLVDdagavPLDIVPLFETVDDLRGGTGTVQDLLADPVYRQHLAARgdtQ 559

                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                     vm+GYsDsGKD G  +  W L +Aq E+   A + Gv+L+ FHGRGG +
  gi|2926012   560 MVMLGYSDSGKDGGIAASRWGLQRAQVELLEAAAELGVRLTFFHGRGGSI 609

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                     RGGG t  A+ + P   ++G lRvt qGEvi   +G   L  rsL   t
  gi|2926012   610 ARGGGKTSRALDAAPRGSVDGRLRVTEQGEVIHRKYGIRALALRSLEQMT 659

                    AAtLEHGmnP..PvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                     A L   + P+ P      WR +m+ +A   t  YR+ v   P F+ YFR
  gi|2926012   660 GAVLLSSLRPraPEPREARWRPVMDLVAERSTVAYRAFV-GAPEFMQYFR 708

                    lAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWL
                    lAtP     +m +GsRP++R   +  +  LRAiPW+FaW q R  +P W
  gi|2926012   709 LATPIDVIERMTLGSRPSRRLGQdAALSNLRAIPWVFAWSQARAVIPGWY 758

                    GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                    GvG   + A+d        L+Em ++WPFFR  lD + mv  KGD  iA
  gi|2926012   759 GVGSGLQAAVDAGHED--TLREMAQDWPFFRTFLDDIAMVLSKGDLNIAE 806

                    LyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrl
                    L+ +L  + +L+ +F   + d+   tk ++  +   + lL  DP L   +
  gi|2926012   807 LFSRL--SGDLHTrFFPLIGDELALTKGWVKALLQQRSLLQHDPRLALSI 854

                    RLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLv
                    RLR++Yi  + v+q   L+R R                A +     ++
  gi|2926012   855 RLRNPYIDPISVLQVDLLQRWR----------------ATDG----EDQA 884

                    kLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     L             L+  + G+  G+qntG
  gi|2926012   885 LLR-----------ALVACVNGVSQGVQNTG    904

gi|20196792|emb|CAC86368.1|: domain 1 of 1, from 1 to 381: score 198.9, E = 1.4e-56
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2019679     -    ---------------------------------------------- -
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|2019679     - ------------------------------------------------ -

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|2019679     - ------------------------------------------------ -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                                  qsvRRsLLqK+aRiR CL+qL AKD+t +DKk
gi|2019679     1 -----------------QSVRRSLLQKHARIRSCLTQLDAKDITEDDKK 32

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                ELDEAL REiqAAFRtDEiRRaqPtPqDEmR+GmsY+HEt+WkGvPKFLR
gi|2019679    33 ELDEALQREIQAAFRTDEIRRAQPTPQDEMRYGMSYFHETIWKGVPKFLR 82

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                RvDtALKniGi ER PY +PLikFssWmGGDRDG nPRvtP+vtRDv LL
gi|2019679    83 RVDTALKNIGIDERFPYRAPLIKFSSWMGGDRDG-NPRVTPDVTRDVVLL 131

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                aRmmAa lY+sq+EDLmFElsmWRCndELR+RAEEly  +++   +K+Yi
gi|2019679   132 ARMMAADLYYSQIEDLMFELSMWRCNDELRARAEELYGASKKA-ATKHYI 180

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                EFWKq+PP EPYRv+LGdvRDKLY tRER+RHLL  G sei+E+A +t+v
gi|2019679   181 EFWKQIPPSEPYRVVLGDVRDKLYYTRERSRHLLTSGSSEIPEDATFTDV 230

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                E+FLEPLELCY+sL  CGDk iADGsLLD+LRqv tFGLsLvKLDiRqEs
gi|2019679   231 EQFLEPLELCYRSLVACGDKPIADGSLLDFLRQVATFGLSLVKLDIRQES 280

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                eR+tDv+DAittHL+iGsYR+WsEeKRqEWLl+EL+GKRPLl +D+P+ +
gi|2019679   281 ERHTDVIDAITTHLGIGSYRSWSEEKRQEWLLSELSGKRPLLAPDMPQSD 330

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                Ev+D +++frvLAELP DsFG+YiismataPsDvLAvELLqREC+++++L
gi|2019679   331 EVADAIGTFRVLAELPADSFGPYIISMATAPSDVLAVELLQRECQIRKPL 380

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                +
gi|2019679   381 P------------------------------------------------- 381

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

gi|2019679     - ------------------------------------------------ -

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

gi|2019679     - ------------------------------------------------ -

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

gi|2019679     - ------------------------------------------------ -

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

gi|2019679     - ------------------------------------------------ -

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

gi|2019679     - ------------------------------------------------ -

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

gi|2019679     - ------------------------------------------------ -

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
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  gi|2019679     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|2019679     - -------------    -

gi|20196794|emb|CAC86369.1|: domain 1 of 1, from 1 to 395: score 198.0, E = 2.7e-56
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2019679     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2019679     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2019679     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                          +v+LvltAHPtqs RRsLLqK+++iRnCL+qL+AKD+t ++Kk
  gi|2019679     1 -------TVELVLTAHPTQSLRRSLLQKHTKIRNCLTQLYAKDITDDEKK 43

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL  Ei AAFRtDEiRR+qPtPqDEmR+GmsY+HEt+WkGvPKFLR
  gi|2019679    44 ELDEALQAEIHAAFRTDEIRRSQPTPQDEMRYGMSYFHETIWKGVPKFLR 93

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALK iGi ERlPYdvP+ikFssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2019679    94 RVDTALKSIGISERLPYDVPVIKFSSWMGGDRDG-NPRVTPEVTRDVCLL 142

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRmmAanlY+s +EDLmFElsm RCndELR+RA+E       +   K+Yi
  gi|2019679   143 ARMMAANLYVSSIEDLMFELSMRRCNDELRARADEHLASRETK---KHYI 189

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFW+ +P tEPYRv+LG vRDKLYntRERa H+L +G+sei Ee   t v
  gi|2019679   190 EFWRAIPATEPYRVLLGYVRDKLYNTRERALHMLTKGYSEIKEESTITTV 239

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   EeF+EPLE+CYksLC+CGDk iADG LLD++Rqv tFGLsL KLDiRqEs
  gi|2019679   240 EEFMEPLEVCYKSLCDCGDKTIADGLLLDFMRQVNTFGLSLAKLDIRQES 289

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   eR+tD +DAittHL+iGsY+eW+EeKRqEWLl+EL+GKRPLl +D+P  E
  gi|2019679   290 ERHTDAVDAITTHLGIGSYKEWPEEKRQEWLLSELQGKRPLLVPDMPVSE 339

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+ vl+ f+vLAELP DsFG+YiismataPsDvLAvELLqRECgv+q+L
  gi|2019679   340 EVEAVLGCFKVLAELPRDSFGPYIISMATAPSDVLAVELLQRECGVRQPL 389

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLF
  gi|2019679   390 PVVPLF---------------------------------------- 395

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|2019679     - ------------------------------------------------ -

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

  gi|2019679     - ------------------------------------------------ -

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|2019679     - ------------------------------------------------ -

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|2019679     - ------------------------------------------------ -
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                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|2019679     - ------------------------------------------------- -

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|2019679     - ------------------------------------------------- -

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|2019679     - ------------------------------------------------- -

                  tmKGiAAGmqntG<-*

  gi|2019679     - -------------    -

gi|266627058|ref|ZP_06119989.1|: domain 1 of 1, from 3 to 909: score 196.6, E = 6.6e-56
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          L + v    s  +++ +   LL D  ++ +  L Ge+    v
  gi|2666270     3    --NPALSIEVDRPTS--QHVRKNANLLSDLLVEAIAYLEGEEAAALV 45

                  qECYEl.sAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                       + s e     D+  L+ L + L s+d  +a+ +A+a+     LAn
  gi|2666270    46 ARARRVaSHEDVANGDAPVLDRLFSDL-SID--EAVFLARAFASQSLLAN 92

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  + E+v  A RRR          DE   t    + + +K L  ++ K+ e+
  gi|2666270    93 IGEDV--AGRRRHAEAD-AQPGDERPRT----LVDAVKLLKRQG-KTDED 134

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                           v  vltAHPt   RRs++ +++ i   L  L    + ++
  gi|2666270   135 LAKTFAAMNVVPVLTAHPTEVRRRSMVDRETEISR-LMALRRHHLPPDLE 183

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   E+ E L REi   +Rt   R  + t +DE+R  +s +   +    P  +
  gi|2666270   184 AEIRESLFREIALMWRTRLYRPERITVKDEIRNALSIVRTSI---LPAII 230

                  RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                           iG    l   +PL+k  sW+GGDRDG +P v  E  +
  gi|2666270   231 DLYGDWTGKIGQHGHL---APLLKLGSWLGGDRDG-HPGVNGETLKLAFA 276

                  LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv.vKy
                      +    Y   v  L   l++      +    EEl   aa+ + +  +
  gi|2666270   277 SQSRVILDWYAGEVRKLWSNLAVSTAYTPV---SEELLALAAQTRDpSVH 323

                  YiEFWKqvPPtEPYRviLGdvRDKLYntRERaR...HLLAtGiseisEeA
                   ++        EPYR  L  + D+L     +  +++   A G  ++
  gi|2666270   324 RLD--------EPYRLALELIFDRLTAVSQKLTgqpVAFANGDTDVEP-- 363

                  vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                   y + + F+  L +   sL   G   +   +L  l+  v   G  L+ LD
  gi|2666270   364 -YGHPDAFVADLSVIIDSLERNGGERLVGTALRTLVDVVKACGFHLMSLD 412

                  iRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgs
                  +Rq ++ +   +  + +  + G +Y +  E+ R   L+ EL+ +RPL+ +
  gi|2666270   413 LRQNADVHERTIHELYERAGSGvAYLKLDEDARCKLLIEELSHQRPLVSP 462

                  DLPktEEvkDvldafrvLAELPiD....sFGaYiismataPsDvLAvELL
                       EE    l ++   A    D ++++ GaYiis + + sD+L   +L
  gi|2666270   463 FTAYSEETTRELATMTAAAQAVRDyghgCLGAYIISKSATLSDILEPLVL 512

                  qRECgv.......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                   +  g+  ++  ++ +++v PLFE + DLe  PA + +   +   +  +
  gi|2666270   513 LKQVGLvwggaapRASVKVAPLFETIGDLENGPAVLRQWLELPLARSILG 562

                  GK..qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                   ++ qe+m+GYsDs KD G ++    + +    +++ A + Gv L lFHG
  gi|2666270   563 DRpvQEIMLGYSDSNKDGGYVASRRGVAVGASALAREADRMGVGLQLFHG 612

                  RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                  RGG vGRGGGP   A+L+qP  t++G +R+t qGE+i   FG+     r
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  gi|2666270   613 RGGSVGRGGGPAAEAVLAQPAGTVQGRIRMTEQGEMIARRFGDQPTARRN 662

                   LqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvE
                   L   +AA +     P     P     m  +A      +R++v+ +P F +
  gi|2666270   663 LDGLAAAVMMASDRPVQKLDPKIDAAMTALADASFHGFRALVYDDPAFED 712

                   YFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPv
                   +F + tP  E   +niGsRPa R  s  ie LRAiPW+F+W q RF LP
  gi|2666270   713 FFWSVTPISEIVGLNIGSRPASRTASRKIEDLRAIPWVFSWSQSRFMLPG 762

                   WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                   W G+ A     +d+    + +L+++   + FF   l  +E+  A+    i
  gi|2666270   763 WFGFAA----GVDRAGLSVEQLRDLAGSFDFFASLLSNMELALAQSHMPI 808

                   AaLyDkLLvaEe.LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                   A+ y +L    ++ +     +R + +   +l L i G   lL+  P L
  gi|2666270   809 ASRYVELSPDKDnAQRIFATIRREHERAAELALAIRGGSSLLDNQPDLAE 858

                   rlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkade
                    + L    +  Ln +q   L R R                A ++    +e
  gi|2666270   859 SVALAGRVVDPLNHLQLELLSRRR----------------AGDQ----NE 888

                   LvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    ++L             + Lt+ GiAAG+ ntG
  gi|2666270   889 ELRLA------------IQLTVAGIAAGLRNTG    909

gi|285019549|ref|YP_003377260.1|: domain 1 of 1, from 12 to 904: score 196.3, E = 8.3e-56
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        D  LR  v    +           L+   L     + G  L E+
  gi|2850195    12    TPDLPLRDDVRRLGA----------LVGELLA--EQVSGAFLEEIE 45

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          A  E +  ++ L  L   L +  P +a  + +a++    + n+
  gi|2850195    46 RIRIAAIARRE-RNAPSSL--LSQSLSGRTPREAEALVRAFSTYFQVVNI 92

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AE v+   RRR  ++        a+      + + l +L  ++  s +E
  gi|2850195    93 AERVHRIRRRRDYQRS------SADTPQPDGLHDALYRLKAQG-VSVQEL 135

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    + L    v+ v+tAHPt +vRR+LL K+  +   L        t+ ++
  gi|2850195   136 SDWLPRLDVEPVFTAHPTEAVRRALLEKEQLMVASLVDHLDGMRTPGEQA 185

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                        L   + A + t +    +Pt  DE      Y+   +++ +P
  gi|2850195   186 TDAARLRMALTATWQTADSSPVRPTVEDEREHVGFYLNQVLYRVIPVMYE 235

                   RvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                     + A+++  G    lP    L++F  W+GGD DG nP v
  gi|2850195   236 TLEHAIeQTYGQSLHLP---RLLRFGTWVGGDMDG-NPNVDATTMTATLD 281

                   LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                     R      Y+  +  L   ls     + + v      + +  +
  gi|2850195   282 AQRRAVLERYLKELRQLASLLS----QSIILVGV----SAPLLE-----Q 318

                   iEFWKqvPPtEPYRv..iLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                   +E ++q+ P+   R ++   d+  +L n   RaR  L   + + +    y
  gi|2850195   319 LERYRQLLPQAAARSrpRHADMPYRLLNDLMRAR--LQATLDDAPGG--Y 364

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                       e    L L   sL           ++  lL  v  FG  L +LD+R
  gi|2850195   365 AAPSELEHDLQLILDSLRANKGLHAGWFAVRRLLWRVRSFGFHLARLDVR 414

                   qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                   qEs  +     A+   L++  +   +   R   L     G  PL
  gi|2850195   415 QESSVHA---RAVAAALGVQEWEALPAAERARLLGPYAGGETPLPACADA 461

                   ktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLqRECgv
                       +  v  a+ +  A    D+ G+Yiisma   +DvL v  L R  g+
  gi|2850195   462 GNARLDAVFAALAdARARHGADALGSYIISMAHDRADVLTVLALARRGGL 511
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                    kq.....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...qev
                        +  +L +vPLFE + DL+   A++  L +   Y+ ++d +++ q v
  gi|2850195   512 VDaadavPLDIVPLFETVDDLRGGTATLRDLLADPVYRRHLDARgdvQMV 561

                    mvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGR
                    m+GYsDsGKD G  +  W L +Aq E+   A + G++L+ FHGRGG + R
  gi|2850195   562 MLGYSDSGKDGGIAASRWGLQRAQVELLEAAGESGIRLTFFHGRGGSIVR 611

                    GGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAA
                    GGG t  A+ + PP  ++G lRvt qGEvi   +G   L  rsL   t A
  gi|2850195   612 GGGKTTRALEAAPPGSVDGRLRVTEQGEVIHRKYGIRALALRSLEQMTGA 661

                    tLEHGmnP.PvsPk.PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlA
                     L   + P+Pv  ++  WR +m+++A      YR  v  +  F+ YFRlA
  gi|2850195   662 VLLSSLRPrPVDAReAQWRPVMDRVAEHSSQAYRHFV-GDAEFMRYFRLA 710

                    tPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWLGv
                    tP     +m +GsRP++R   +  +  LRAiPW+FaW q R  +P W Gv
  gi|2850195   711 TPIDVIERMTLGSRPSRRLGQdAALSNLRAIPWVFAWSQARAVIPGWYGV 760

                    GAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLy
                    G   + A+d        L+ m  +WPFFR  lD + mv  KGD  iA ++
  gi|2850195   761 GSGLQAAVDAGHEA--ALRAMAIDWPFFRTFLDDIAMVLSKGDLNIAEMF 808

                    DkLL..vaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                     +L ++  E   P   ++Rd+   tk ++  + G   lL  DP L   +R
  gi|2850195   809 SHLAgpLHERFFP---RIRDELALTKHWVKALTGQASLLQHDPRLALSIR 855

                    LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                    LR++Yi  + v+q   L+R R               A +   + +eL++
  gi|2850195   856 LRNPYIDPISVLQVDLLQRWR----------------ATDG--EDEELLR 887

                    LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                 L+  + G+A G+qntG
  gi|2850195   888 -------------ALVACVNGVAQGLQNTG    904

gi|229243257|ref|ZP_04367569.1|: domain 1 of 1, from 3 to 891: score 192.1, E = 1.5e-54
                    *->siDAqLRlLvP.GKvs.edekLieYDALLlDkFL.DiLqDLHGedLk
                          A +   vP+G vs+e  +L++ D  Ll   L+ +L +  GedL
  gi|2292432     3    --QAEIGPDVPrGVVShEVPELLRNDVRLLGELLgRVLREAGGEDLL 47

                    EavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnL
                      v    El+         + L E    + +     a  vA+a+     L
  gi|2292432    48 ADVERLRELAIASHSEPNGHALAEAEQLVAGFGHERAEQVARAFTCYFHL 97

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                    AnLAEE    +R R+ + +    +    A  +s +   +++Lv      P
  gi|2292432    98 ANLAEEY---HRVRVLRDRESRLSPHELAPDDS-LPAAYQQLVDEI--GP 141

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                    +     L       v+tAHPt + RR++     Ri   +a      +
  gi|2292432   142 DAARRRLHELEFRPVFTAHPTEARRRAVSRAIRRIAELVAERDTLHIGGT 191

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                       E +  L  Ei   +Rt  +R  +Pt  DE+   +s +  t+ +  P
  gi|2292432   192 TLAENERRLLAEIDTLWRTSPLRAEKPTVLDEVATVLSIFDATLADVLPT 241

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      RR D  L         P  +P  +  sW+GGDRDG nP vt EvtR
  gi|2292432   242 VYRRLDDWLLEDEAGTTAPTVAPFARLGSWIGGDRDG-NPNVTAEVTRA- 289

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE......Elyrtaa
                       a  mA+      ++ L+  +s  R  d L   A ++++++El    +
  gi|2292432   290 ---AAAMASE---HALDALL--VSARRTADGLTLDAAgtppstELSALWQ 331

                    rdkvvKyYiE.FWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGise
                    r++     i +      P+EP R  L  + +++  tR R   L   G  e
  gi|2292432   332 RQRSLSDAITsRIADAAPNEPHRRALLGIVERVAATRRRDADLAYAGADE 381

                    isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                    +  +            L +   sL   G +  A G L  l+ qv tFG
```

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  gi|2292432   382 LEAD------------LLIVQESLRAAGAHRAAFGDLQRLVWQVQTFGFH 419

                   LvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRP
                   L  L++Rq s+ +   l  i  H   G                EL+
  gi|2292432   420 LAELEVRQHSQVHEAALADIEAHGVDG----------------ELQ---- 449

                   LlgsDLPktEEvkDvldaf.rvLAELPiDsFGaYiismataPsDvLAvEL
                         P+t Ev D   a++ v   L + +   Yi+s + +P    Av
  gi|2292432   450 ------PMTVEVLDTFRALgTVQRRLGVKAARRYIVSFTQSPEHLAAVYT 493

                   LqREC....gvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri..d
                   L     ++++    +  +PLFE  ADL+     +e          r+  +
  gi|2292432   494 LADLAfggpEHAPVIDAIPLFETFADLQNSVDILEAALEHPRVQERLaaN 543

                   GKq.evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                   G+  evm+GYsDs KD G lsA   L  Aq  i+  A+++ + L+lFHGR
  gi|2292432   544 GRRvEVMLGYSDSSKDVGPLSATLALDDAQRRIAEWARRHDIVLTLFHGR 593

                   GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                   GG  GRGGGP   A+L+qPP  ++G  + t qGEvi   +G+ ++  r +
  gi|2292432   594 GGALGRGGGPANRAVLAQPPGSVDGRFKLTEQGEVIFARYGDPDIAARHI 643

                   qRFtAAtLEHGmnPPvsPkPEWRkLmeemAv...vAtEEYRsvvvKEPRF
                      tAAtL       v           ++A + +vA  E     v+   F
  gi|2292432   644 EQVTAATLLADAPSVVQRNDTAAARFADLAArldVASREHFHRLVRADGF 693

                   vEYFRlAtPElEYGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFH
                     +F   tP  E G + iGsRPa+R  s   ++ LRAiPW+F+W q R
  gi|2292432   694 PAWFAQVTPLEELGLLPIGSRPARRGLSvSSLDDLRAIPWVFSWSQARIN 743

                   LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                   L  W G+G A     d +      L+  Y eWP F   +D +Em  AK D
  gi|2292432   744 LAGWYGLGTALEAVGDAEA-----LRVAYAEWPLFATIIDNVEMSLAKTD 788

                   PGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     iAa y  L   ++L    + + d+   t+ ++L + G   +L     L
  gi|2292432   789 ERIAARYLALGDRDDLA---QLVLDELRRTRTWVLAVTGSTGVLSRRRIL 835

                   KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                      + LR +Y+  L  +q   L+ +R                  E+   a
  gi|2292432   836 GRAVQLRSPYVDALSLLQLRALRGLR----------------TGEPNESA 869

                   deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   d+L +L              +Lt+ G+AAG+qntG
  gi|2292432   870 DDLRRLL-------------LLTVNGVAAGLQNTG    891

gi|229206299|ref|ZP_04332755.1|: domain 1 of 1, from 4 to 853: score 191.8, E = 1.9e-54
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                             +L+                      D+L D+  e L+ av
  gi|2292062     4    ------TVLAESGGE----------------DLLADV--EKLRRAV 25

                   qECYElsAeYEGKkDtkKL.eELGakLtsLdPaDailvAkailHmLnLAn
                              G +D +  +eE+ a + +     a  vA+a+     LAn
  gi|2292062    26 I----------GARDGSVTgEEITAIVAAWPLERAKQVARAFTVYFHLAN 65

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   LAEE +   R R  + +     D a+   Es       + +  ++   e
  gi|2292062    66 LAEEHQ---RMRALRER----DDAANPPRESLAAAV--RAIREGEGGEER 106

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     e +       v+tAHPt + RR++     R+    aqL A     e
  gi|2292062   107 LDELIAGMEFHPVVTAHPTEARRRAVSTSILRVS---AQLEAWHSSHEGS 153

                   kELDEALHR...EiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                       EA  R  +Ei   +Rt  +R ++  P DE+R  ++ + Et++  +P
  gi|2292062   154 SAAAEAHRRlleEIDLLWRTSQLRYTRLNPLDEVRTALAAFDETIFSVIP 203

                   KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                   +  R  D A+   G   R P   P +++ sW+GGDRDG nP vt ++tR+
  gi|2292062   204 QVYRSLDAAIDPEGTGVRPPRATPFVRYGSWIGGDRDG-NPYVTSDITRE 252
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                    vCLLaRmmAanlYisqvEDLmFEls.mWRCndELRvRAEElyrtaardkv
                      L+     +   +  +E     +++     + L      l    a+ k
  gi|2292062   253 AVLIQ----SEHVLRGLEASCTKVArTLTAYSNLTPASPALLDALASAKA 298

                    vKyYiEFWKqv...PPtEPYRviLGdvRDKLYntRERaRHLLAtGiseis
                     +   E    ++ + P+EP R +L     +L  tRER   L
  gi|2292062   299 GQP--ELTAEIgarSPNEPHRQLLLLAAARLRATRERDADL--------- 337

                    EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                        y + + FL  L     sL e G    A G L  l+ q  tFG  L
  gi|2292062   338 ---AYPDADAFLADLRTVQESLAEAGAVRQAYGELQHLVWQAQTFGFHLA 384

                    KLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLl
                     L+iRq se +   l  +         Re  E       l+E
  gi|2292062   385 ELEIRQHSEVHAAALAEL---------REGGE-------LSE-------- 410

                    gsDLPktEEvkDvldafrvLAE.LPiDsFGaYiismataPsDvLAv.ELL
                         +tEEv   +  +  + E+  +++   Y++s + +  D+ Av EL
  gi|2292062   411 -----RTEEVLATIRVIAWIQErFGVEACRRYVVSFTRSAEDIAAVyELA 455

                    qRE..CgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG...K
                        + g    L vvPLFE  ADL+A P  ++ +  +     r+d ++++
  gi|2292062   456 AHAlpAGRVPVLDVVPLFETGADLDASPHVLDGMLKLPQVNKRLDEtgrR 505

                    qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                     evm+GYsDs KD G +sA   LY Aq  ++  A ++ v+L+lFHGRGG
  gi|2292062   506 IEVMLGYSDSAKDVGPVSATLRLYDAQARLAAWAEEHDVRLTLFHGRGGS 555

                    vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                     GRGGGP   A+L+q P  + G  +vt qGEvi   +G   +  r +
  gi|2292062   556 LGRGGGPASRALLAQAPGSVGGRFKVTEQGEVIFARYGQPAIARRHIEQV 605

                    tAAtLEHGmnPPv....sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvE
                      A L    +   ++++s    +R   + +A  A E Y  ++  E  F
  gi|2292062   606 GHAVLMASTDAVQererSAERRYRAHADTIARAAQEAYLELINTED-FAV 654

                    YFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPv
                    +F    P  E G + +GsRP++R  + G+  LRAiPW+FaWtqtR  LP
  gi|2292062   655 WFSRVSPLEELGELRLGSRPSRRGAARGLGDLRAIPWVFAWTQTRVNLPG 704

                    WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                    W G+G          +  l  L+  Y+eWP F   lD  Em  AK D  i
  gi|2292062   705 WFGLGTGLAA-----VEDLGVLQAAYREWPMFSSLLDNAEMSLAKTDRDI 749

                    AaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                    A  y  L    eL    +++ ++Y  t+dl+Lk+ GH  lLE    L
  gi|2292062   750 AQRYLALGGRPELT---ERVLAEYDRTRDLVLKVTGHSRLLENRAVLSRA 796

                    lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                    + LR++Y+  L  +q   L  +R                  E+   ad L
  gi|2292062   797 VDLRNPYVDALSHLQLRALEALR-----------------GEE---ADSL 826

                    vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                         +e+    LE  L+L + G+AAG+qntG
  gi|2292062   827 -----SEEDQQHLERLLLLSVNGVAAGLQNTG    853

gi|20196796|emb|CAC86370.1|: domain 1 of 1, from 1 to 396: score 189.7, E = 8.3e-54
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2019679     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2019679     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2019679     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                           +v+LvltAHPtqs RRsLLqK+++iRn L+qL+AKD+t ++Kk
```

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  gi|2019679     1 -------TVELVLTAHPTQSLRRSLLQKHTKIRNYLTQLYAKDITEDEKK 43

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL  EiqAAFRtDE+RRaqPtPqDEmR+GmsY+ E +WkGvPK LR
  gi|2019679    44 ELDEALQAEIQAAFRTDEVRRAQPTPQDEMRYGMSYFQENIWKGVPKSLR 93

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALK iGi ERlPYd+PLikFssWmGGDRDG nPRvtPEvtRDvCLL
  gi|2019679    94 RVDTALKSIGIDERLPYDAPLIKFSSWMGGDRDG-NPRVTPEVTRDVCLL 142

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRm+AanlYis +EDLmFElsmWRCndELR+RA+El + +++    K+Yi
  gi|2019679   143 ARMIAANLYISEIEDLMFELSMWRCNDELRARADELLSAPKKA--SKHYI 190

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFW+ +P tEPYRv+LGd RDKLYnt ER R LLAtG+se++E      +
  gi|2019679   191 EFWRAIPSTEPYRVLLGDLRDKLYNTSERWRDLLATGFSEVPEKPTIKSI 240

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    eFLEPLE+CY+sL e GDk iADG LLD++RqvstFGL L KLDiRqEs
  gi|2019679   241 QEFLEPLEVCYRSLVEVGDKTIADGVLLDFMRQVSTFGLTLAKLDIRQES 290

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   eR+tD +DAittHL+iGsYReW+EeKRqEWLl+EL+GKRPLl +DLP  E
  gi|2019679   291 ERHTDAIDAITTHLGIGSYREWPEEKRQEWLLSELQGKRPLLVADLPVSE 340

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl+ frvLAELP+DsFG+YiismataPsDvLAvELLqRECg++++L
  gi|2019679   341 EVADVLGCFRVLAELPSDSFGPYIISMATAPSDVLAVELLQRECGIRNPL 390

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLF
  gi|2019679   391 PVVPLF------------------------------------------- 396

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|2019679     - ------------------------------------------------- -

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

  gi|2019679     - ------------------------------------------------- -

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|2019679     - ------------------------------------------------- -

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|2019679     - ------------------------------------------------- -

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|2019679     - ------------------------------------------------- -

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|2019679     - ------------------------------------------------- -

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|2019679     - ------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|2019679     - -------------    -

gi|262189851|ref|ZP_06048182.1|: domain 1 of 1, from 1 to 585: score 188.4, E = 2.1e-53
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2621898     -    ------------------------------------------- -
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|2621898    - ------------------------------------------------- -

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|2621898    - ------------------------------------------------- -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|2621898    - ------------------------------------------------- -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|2621898    - ------------------------------------------------- -

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|2621898    - ------------------------------------------------- -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                                     m +Cn+ +R+ A E       +
gi|2621898    1 --------------------MTKCNEAVRALAGE-------E------- 15

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                         EPYR iL  +R  L  t E     L      ++  A
gi|2621898   16 --------HEPYRAILKPIRSLLQETIEILDAKLNG--QKLAVKAPLQTA 55

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                ++  EPL  CY+sL eCG  viADGsLLD LR +  FG+ Lv+LD+RqEs
gi|2621898   56 DQLWEPLYACYQSLHECGMGVIADGSLLDTLRRIKAFGVHLVRLDVRQES 105

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                 R+ +v+  +t+HL+iG Y +WsE+ +  +L +EL  KRPLl+ D
gi|2621898  106 SRHAEVISELTRHLGIGDYNQWSEQDKIAFLTTELNSKRPLLPRDWQPSP 155

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                 vk+vld+ +++A    ++FGaY+isma + sDvLAv LL  E g    +
gi|2621898  156 QVKEVLDTCKIIAAQSKEAFGAYVISMARTASDVLAVHLLLQEAGCPYRM 205

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                 v PLFE L DL+ A   + +L  iD Y+  i+  q vm+GYsDs KDAG
gi|2621898  206 DVCPLFETLDDLNNAESVIRQLMNIDLYRGFIQNHQMVMIGYSDSAKDAG 255

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 ++A W  Y+A E ++Kv  + G+ L+lFHGRGGt+GRGG P H A+Lsq
gi|2621898  256 VMAAGWAQYRAMEALVKVGEEAGIELTLFHGRGGTIGRGGAPAHAALLSQ 305

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PP  ++G lRvt qGE+i f  G  ++   s   ++ A LE  + PP  P
gi|2621898  306 PPKSLKGGLRVTEQGEMIRFKLGLPEVAVNSFNMYASAILEANLLPPPEP 355

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                k EWR Lm+ +  +    YR vv  EP Fv YFR AtPElE Gk+ +GsR
gi|2621898  356 KNEWRALMDILSEISCNAYRKVVRGEPDFVPYFRQATPELELGKLPLGSR 405

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                PaKR P GG+esLRAiPWiF+W q R  LP WLG G A + Ai+   + l
gi|2621898  406 PAKRNPTGGVESLRAIPWIFSWSQNRLILPAWLGAGEAIQIAINEGHQAL 455

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  L+Em +eWPFF   l +lEmv+ K    iA  yD+ Lv   L+P G++
gi|2621898  456 --LEEMCREWPFFSTRLGMLEMVYTKCSVSIARHYDERLVEPTLRPLGEK 503

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR++ +   + +L +     l+  DP+ +  +RLR+ Yi  Ln++qA  L
gi|2621898  504 LRAQLQQDIKVVLNVENNENLMQSDPWGQESIRLRNIYIEPLNMLQAELL 553

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                 R R  +               +               aP LE+ L++
gi|2621898  554 YRTRQSEL---------------P----------------APELEEALMV 572
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                  tmKGiAAGmqntG<-*
                  t+ GiAAGm ntG
  gi|2621898   573 TIAGIAAGMRNTG    585

gi|15022444|dbj|BAB62259.1|: domain 1 of 1, from 1 to 368: score 186.0, E = 1e-52
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1502244     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1502244     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1502244     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1502244     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1502244     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1502244     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1502244     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1502244     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1502244     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1502244     - ---------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                                                     LLqREC+vk++L
  gi|1502244     1 -------------------------------------LLQRECHVKKPL 12

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  rvvPLFEkLADLeAAPAa+++LFs+DWY+nridGKqevm+GYsDsGKDAG
  gi|1502244    13 RVVPLFEKLADLEAAPAALARLFSVDWYRNRIDGKQEVMIGYSDSGKDAG 62

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  R+sAAW LYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1502244    63 RFSAAWELYKAQEELIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 112

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFt AtLEHGm+PP+sP
  gi|1502244   113 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTCATLEHGMHPPISP 162

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+emA vAt EYRs+v++E RFvEYFRlAtPElEYG+mniGsR
  gi|1502244   163 KPEWRALMDEMAAVATKEYRSIVFQEARFVEYFRLATPELEYGRMNIGSR 212

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|1502244   213 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLQKDIRNL 262

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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                    q L+EmY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+PFG +
  gi|1502244   263 QILQEMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWPFGAR 312

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Etk+lLL++AGHkDlLEGDPYL+qrlR+RdsYit Lnv+qA t
  gi|1502244   313 LRANYEETKQLLLQVAGHKDLLEGDPYLRQRLRIRDSYITALNVCQACTA 362

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    K    P
  gi|1502244   363 KAYQGP---------------------------------------------- 368

                    tmKGiAAGmqntG<-*

  gi|1502244     - -------------    -

gi|227516707|ref|ZP_03946756.1|: domain 1 of 1, from 66 to 949: score 184.8, E = 2.4e-52
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s+   L l     v     + eYD  L   F  +L D    d +Ea
  gi|2275167    66    SLKSNLTLFLH-LVR--KVIQEYDENLCTTFDMLLSDFIEADNQEAH 109

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          sA          L++    + +L+  +a ++A+a+     LAn+
  gi|2275167   110 HPSQTCSA----------LQDAVRIINGLEIHEATMLARAFASYFHLANI 149

                    AEE.velAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     EE+ ++A  R  +k       D   A    D+   +  ++    K  +
  gi|2275167   150 CEEnYRVAALRAREKSTPVSKKDNPFANPNNDLSAAYHEIMRECGKDKAN 199

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKD.vtveD
                      e L        v+tAHPt + R+ +   +aRiRn  + L  + ++
  gi|2275167   200 --ELLHRLEFHPVFTAHPTEARRKTV---EARIRNIATLLEKRArLGGAS 244

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                      E D  +  Ei A FRt  i   +PtP +E    +  +  t+++ vP
  gi|2275167   245 LAENDRRMLEEIEALFRTSPIALKKPTPVEEADTIIDIFDHTLFEMVPDV 294

                    LRRvDtALKniGinE.RlPYdvP.LikFssWmGGDRDGknPRvtPEvtRD
                     RR D     +G   +++P   P   k  sW+G DRDG nP vt  v R
  gi|2275167   295 YRRFDD--WELGDDAgKVPPLCPaFFKPGSWIGTDRDG-NPNVTAKVSRK 341

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                    v    R        +    +   l +             l
  gi|2275167   342 VAEKFRTHMLTKLAEETKKVARSLTLDTVSTPASKQLRNLWNHQVEM--S 389

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                            qv   E    +L  +  +L  t  R+  L+
  gi|2275167   390 EVLSARAYQVSASELHHAVLKVMANRLEATITRTADLM------------ 427

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    yt  E+F+  L +   sL + G    A G +  l+ q  tFG sLv+++
  gi|2275167   428 YTTAEDFISDLRIVQESLAQAGAVRAAYGVVQRLIWQAETFGFSLVQMEF 477

                    RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    Rq s  +t  l+ i  H        W E         EL
  gi|2275167   478 RQHSLVHTRALEDIRAH------GRWGER-------GELA---------- 504

                    PktEEvkDvldaf.rvLAELPiDsFGaYiismataPsDvLAvELLqRECg
                    P+t Ev D   a++ +     +++   Yiis + +P  +  v  L
  gi|2275167   505 PMTKEVLDTFRAIgSIQRRNGVEAARRYIISFTQSPQNIEDVYTLAHLAF 554

                    vkq....tLrvvPLFEkLADLeAAPAavekLFsiDWYinri...dGKqev
                     + ++ +tL v+PLFE++ DL+ A  +++++  i     r+ +++ + ev
  gi|2275167   555 AHDkdvpTLDVIPLFEQVEDLNNAIDTLNHMIEIPAVQKRLaqtNRRLEV 604

                    mvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGR
                    m+GYsDs KDAG  sA   L   q  i++ AK++ + L+l HGRGG vGR
  gi|2275167   605 MLGYSDSSKDAGPTSATLVLHETQARIAQWAKDHNINLILMHGRGGAVGR 654

                    GGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAA
                    GGGP   A+LsqP   +n   + t qGEvi   +G+  L  r +   + A
  gi|2275167   655 GGGPANRAVLSQPMGSVNAFFKLTEQGEVIFARYGDPVLARRHVESVAGA 704
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                    tLEHGmnPPv.....sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                    tL     P +++ ++     +  L ee+   A   +  ++  E  F E+F
  gi|2275167   705 TLLQS-APSIeklntETTQSYLGLAEELDRAAHARFLRLIHTEG-FPEWF 752

                    RlAtPElEYGkmniGsRPaKRkPsGG.iesLRAiPWiFaWtqtRFHLPvW
                       tP  E G m iGsRPaKR  +  ++  LR iPWiF+W q R  L  W
  gi|2275167   753 STVTPLAEIGMMPIGSRPAKRGLGATsLADLRTIPWIFSWSQARTNLAAW 802

                    LGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiA
                     G+G A       +i  l +L+  Yk+WP F   +D +Em  AK D  iA
  gi|2275167   803 YGLGTAC-----EEIGDLARLRSAYKQWPLFTTFIDNIEMSLAKTDTRIA 847

                    aLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrl
                     +y  L   ++L      + d+ + tk+++L i G +  LE    L   +
  gi|2275167   848 KMYLALGKRDDLTAL---VLDEMELTKKWVLSITGNQWPLEHRRVLGPLI 894

                    RLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLv
                    R+R +++  L v qA  L  +R      t    ls E   E     +  +
  gi|2275167   895 RMRSPFVDVLSVTQAHALSVLR------TRGQDLSPE---EK----EKFI 931

                    kLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     L              + t+ G+AAG+qntG
  gi|2275167   932 YLI-------------LCTVSGVAAGLQNTG    949

gi|257388564|ref|YP_003178337.1|: domain 1 of 1, from 7 to 898: score 184.5, E = 3.1e-52
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        i   +R L  G      ++ie                  +  E v
  gi|2573885     7    EINEDVREL--GELL--GEVIEAQT--------------STEGFETV 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          s +Y  + D+   +++   L  L P    +vA+a+     L nL
  gi|2573885    36 ENIRTSSIDYR-RGDADDRDDVERTLDRLSPDMQDIVARAFTTYFELINL 84

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEE     R R++  +  + + E+    E  + + + kL  ++   Pe
  gi|2573885    85 AEE-----RQRVREIR--EGSQEG--VLEDSVTDAVEKLSERG-ADPETL 124

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L    ++  +tAHPt + R+ +  K   +   L  L    +t  +++
  gi|2573885   125 ERVLDDVLIEPTFTAHPTEARRKTVKAKLRSVAGDLEVLDEVRLTDSEQE 174

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ++++ L  E+   + t  +R  +P   DE      Yi   +++ +
  gi|2573885   175 DIEDDLAAEVTSLWQTPQVRDRRPEVTDEALNVQWYIENVLFEVIDEVYD 224

                    RvDtALKniGinERl..PYdvP.LikFssWmGGDRDGknPRvtPEvtRDv
                      + A     i E  ++  dvP+L +F sW G DRDG nP vtPE+t +
  gi|2573885   225 ELEDA-----IDEEYdgDVDVPkLYEFRSWAGSDRDG-NPFVTPEITEET 268

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                        R +   lY + + +L   ls    n +     +E  r a  +
  gi|2573885   269 LERQRDVVLPLYRDRLKELSGVLSQDASNIDTTDAFDE--RLADHKEALP 316

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                              P EPYR  L  +R+ +     R   +   G+s+ s
  gi|2573885   317 GVASEAEERYPDEPYRQKLKLMREGVL----RVGDVRSGGYSDSS----- 357

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                        + L  L      L      viA+  +  l+R+v tFG  L  LD+R
  gi|2573885   358 ----DLLADLRAIADDLRANDADVIAEAHVDPLVRKVDTFGFTLAGLDMR 403

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLl.aELkGKRPLlgsDL
                         +tD +       +i  Y +  E+ R E+L +a L+    +   D+
  gi|2573885   404 DHRKMHTDAIAETVDRDGI-DYADMDEDERVEFLTeAILQDGQIVDMEDV 452

                    P.ktEEvkDvldafrvLA....ELPiDsFGaYiismataPsDvLAvELLq
                     +  ++ + v+  fr LA+ ++E  +D+   Y is +   s vL v  L
  gi|2573885   453 DgLSDDSARVIRRFRKLAdwqrEFGVDAIDTYAISWCEEASHVLEVLFLG 502

                    RECgvkqt.....LrvvPLFEkLADLeAAPAavekLFsiDWYinri...d
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                      g+   ++  +L +vPL E    L+ A   +  LF  D Y   +  ++
  gi|2573885   503 DQAGIVDLpgycgLDIVPLLESKYALDGARRIMGTLFENDAYEEALaarN 552

                   GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRG
                   G qe+m+GYsDs K+ G l+A W LY+ q  ++ +  ++ v + lFHGRG
  gi|2573885   553 GVQEIMLGYSDSNKENGYLAANWSLYRNQKRLAAITDDFDVEMRLFHGRG 602

                   GtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLq
                   G + RGGGP   A+L+ P +t+ G ++ t qGE i   +  E +  r L
  gi|2573885   603 GSISRGGGPMNDAMLALPNETVTGQIKFTEQGEAIAEKYANEAIAERNLE 652

                   RFtAAtLE...HGmnPPvsPkPE.WRkLmeemAvvAtEEYRsvvvKEPRF
                       A + ++   ++ Pv   PE W + me     A   Y s+   E  F
  gi|2573885   653 QMLNAQVRsryNALEEPVEEVPEaWEDAMETASEAARQKYESLLQTEG-F 701

                   vEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHL
                   v++F  AtP      +n+GsRPa R     +e LRAiPW+F+Wtq R  +
  gi|2573885   702 VDFFEQATPISVIENLNMGSRPASRSGDRSVEDLRAIPWVFSWTQARCII 751

                   PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                   P W  +    +  +d D   +  L+EmY+eWPFF   lD   +  A+ D
  gi|2573885   752 PGWYSIATGLQAYLD-DGGDVETLQEMYEEWPFFQTKLDNASLALARTDF 800

                   GiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLK
                    iA  y  L   +       ++R++Y++t d++ +i G   lL  + +L
  gi|2573885   801 DIAEEYAALADDDLRERIFPDIRQEYEDTVDIVTEITGRDSLLKRE-WLE 849

                   qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                   q l  R++Y+  Ln +q   L                    +
  gi|2573885   850 QNLDRRNPYVDPLNLLQVRLL----------------------AQS----- 873

                   eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      +L  ter       tL Lt++GiAAGm+ntG
  gi|2573885   874 ---HLTETERR------TLRLTVQGIAAGMKNTG    898

gi|114706303|ref|ZP_01439205.1|: domain 1 of 1, from 15 to 930: score 184.0, E = 4.4e-52
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         Aq R  +      +++      LLl +   ++   H +dL  +v
  gi|1147063    15    TERAQTRESAMADAGLEQNGQGIRGLLLAQLSTVVRRRH-PDLARVV 60

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                              G    + L+E    L +L         +ai     L  +
  gi|1147063    61 ----------NGAMSVRELDE-SLWLDGL---------QAIAAWFQLLAI 90

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEE     RRR   +k       a+A   s     + + +  + +s eE+
  gi|1147063    91 AEEYTATSRRRAVERK-----GSADAILGS-FSNVVGQCMADG-QSGEEI 133

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      L    v   +tAHPt   R  +L  + Ri   L+    +   + +++
  gi|1147063   134 RRVLGALRVGPTMTAHPTETKRVTVLEIHRRIYRTLTEAEQQRWSPRERE 183

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   EL + L  Ei   + t E+R  +P    E+  G+ ++ E +++ vPK
  gi|1147063   184 ELIDRLRGEIELLWLTGELRLEKPSVDQEVAWGLHFFREILFETVPKLGD 233

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                       ALK     E      P ++Fs W+GGDRDG nP vt + tR
  gi|1147063   234 VLSAALKR-HAPENATAVSPNLRFSTWIGGDRDG-NPFVTADLTRKSLKE 281

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    R  A   Y+  +  L  Els+      +    E       +
  gi|1147063   282 YRRAALESYLVPLQRLTVELSV---STNVCTIPETFREALNSAMDLSGER 328

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv..yt
                   +      P+EP+R  + +vR +L       R  L     e  E A ++y
  gi|1147063   329 DGIANRNPNEPFRQFVCAVRARL-------RATLSAENGEKRESAAtpYR 371

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                      e    +    + L e G  ++A+  +  l+ q   FG     LD+Rq
  gi|1147063   372 SPAEMRGEILALNQGLIEIGAIAVAERLVRPLIWQLEIFGFHTAALDVRQ 421
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                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELk.GKRPLlgsDLP
                     +   t v   + + L++G   e   eK  E   a L++  R    +D+
  gi|1147063   422 NA---TIVNKVVAELLNLGVDEEKRIEKGDEGWGARLReALRSDSKPDIS 468

                    ktE...EvkDvldafrvLAELPiD...sFGaYiismataPsDvLAvELLq
                      E +++ ++ ++ frv+ E    +++s Ga+i+sm+ +  D++A  LL
  gi|1147063   469 GHElsdDAQETVNLFRVMREAKLKdnrSIGAFILSMTESAEDMIACHLLA 518

                    RECgvkq........tLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                    R  g+  +++++  +tL +vPLFE + DL+AAP  ++ + si   +  +
  gi|1147063   519 RWGGITAgddpsaatTLAIVPLFETIDDLRAAPDILDEMISIPAIRRSLR 568

                    G...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                      +++qevm+GYsDs KD G +   W L kAq  +  +  k  vK+  FH
  gi|1147063   569 EcgdRQEVMLGYSDSNKDGGFFTSNWELSKAQRTLHEIGVKRRVKVSFFH 618

                    GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                    GRGG v RGG Pt  Ai +qPP+t++G+lR t qGEv+   F       +
  gi|1147063   619 GRGGSVSRGGAPTGRAIAAQPPETVDGALRLTEQGEVVSSKFANKGTALH 668

                    sLqRFtAAtLEHGmnPP....vsPkPEWRkLmeemAvvAtEEYRsvvvKE
                     L   tA  L H ++ P+++++    E+ + me +       Y  ++  E
  gi|1147063   669 NLEILTASVLAHTLKSPhekeLKDNAEFNEAMEALSGLSQTAYADLIGTE 718

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsG..GiesLRAiPWiFaWtq
                      F++YF  A P  E G +niGsRPa+R  + ++ +  LRAiPW+FaW q
  gi|1147063   719 G-FIDYFNQASPVEELGLLNIGSRPARRFGGSpkDLSELRAIPWVFAWSQ 767

                    tRFHLPvWLGvGAAFKhAid.KDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                     R  +  W G+G AF   ++ +    ++ Lk m+++   FR  +D +E
  gi|1147063   768 NRHLMTGWYGIGTAFDSFVKvRGDDGMKLLKSMFRNSRLFRLIVDEVEKQ 817

                    FAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtkdlLLkiAGHkDlL
                      +    iA  y  L+  E +++   +++ ++Y+ tk +L+++ G  Dl
  gi|1147063   818 HYQCNLDIAREYVALVENETVrRAIFEKIEAEYELTKTMLIEVTGADDLS 867

                    EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                    E  P  K ++    + +t +  +q   L R+R
  gi|1147063   868 ERFPVHKRQIDRVAPQLTGVHDLQVKLLSRVR------------------ 899

                    EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     n       vk        P   D L+L +    AG+  tG
  gi|1147063   900 -N----TAKVKDS-----DPRTLDALLLSIHCTSAGLGWTG    930

gi|10241562|emb|CAC09415.1|: domain 1 of 1, from 1 to 389: score 183.4, E = 6.3e-52
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1024156     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1024156     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1024156     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                                +tAHPtqs RRsLLqK+++iRnCL+qL+AKD+t ++Kk
  gi|1024156     1 ------------FTAHPTQSLRRSLLQKHTKIRNCLTQLYAKDITEDEKK 38

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL  EiqAAFRtDEiRR+qPtPqDEmR+GmsY+HEt+WkGvPKFLR
  gi|1024156    39 ELDEALQAEIQAAFRTDEIRRSQPTPQDEMRYGMSYFHETIWKGVPKFLR 88

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALK iGinERlPY++P+ikFssWmGGDRDG nPRvtPEvtRDvCLL
  gi|1024156    89 RVDTALKSIGINERLPYNAPVIKFSSWMGGDRDG-NPRVTPEVTRDVCLL 137

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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                    aRm+AanlYisq+ED+mFElsmWRCndELR+ AE        +   K+Yi
  gi|1024156   138 ARMIAANLYISQIEDVMFELSMWRCNDELRALAEQHLASRETK---KHYI 184

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFW+ +P tEPYRv+LG vRDKLYntRERa  LL +G+s+i EeA    v
  gi|1024156   185 EFWRAIPATEPYRVLLGYVRDKLYNTRERALQLLTKGYSDIQEEATIGTV 234

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeF+EPLE+CYksL +CGDk iADG LLD++Rqv tFGLsL KLDiRqEs
  gi|1024156   235 EEFMEPLEVCYKSLVDCGDKTIADGVLLDFIRQVNTFGLSLAKLDIRQES 284

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+tD +DAittHL+iGsY+eW+EeKRqEWLl+EL+GKRPLl +D+P tE
  gi|1024156   285 ERHTDAIDAITTHLGIGSYKEWPEEKRQEWLLSELQGKRPLLVPDMPVTE 334

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+ vl+ frvLAELP DsFG+YiismataPsDvLAvELLqRECg++q+L
  gi|1024156   335 EVEAVLGCFRVLAELPRDSFGPYIISMATAPSDVLAVELLQRECGIRQPL 384

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPL
  gi|1024156   385 PVVPL---------------------------------------------- 389

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|1024156     - ------------------------------------------------- -

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

  gi|1024156     - ------------------------------------------------- -

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|1024156     - ------------------------------------------------- -

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|1024156     - ------------------------------------------------- -

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|1024156     - ------------------------------------------------- -

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|1024156     - ------------------------------------------------- -

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1024156     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|1024156     - -------------    -

gi|119964668|gb|ABM17097.1|: domain 1 of 1, from 1 to 878: score 181.5, E = 2.3e-51
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqD.LHGedLkEa
                        + Aq  +   G +s     ++    ++     +L D + Ged
  gi|1199646     1    -MQAQPLANRTGTIS-STGHVDLWRPMVNLLWSLLDDvVRGEDNPHL 45

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    v +      e        +  E G      d  +a  +A+ +   L L n
  gi|1199646    46 VDDAHGYFDE------VLQHRESGGFQPKPDVREAEALARYFTERLRLQN 89

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    LAE  +lA  + ++ ++     D ++    s     l +L  +l++  +E
  gi|1199646    90 LAE--DLARAKVVEMRR----KDGSEPPRGS-----LNQLAKLLDQRQAE 128

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                     F   +     +vlt HPt s RR +Lq   ++   L   s   v
  gi|1199646   129 PFG--RPLVGRMVLTFHPTESTRRTILQHIRKLGQLLDPASGVSVAHAQH 176
```

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                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                          L  Ei A +Rt   R  +Pt  DE+  G+ Y+   ++   P  L
  gi|1199646   177 DTQIFRLREEIRALWRTPSRRQDRPTVLDEVELGIFYLEHSLFSMLPDLL 226

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                       D  L    +  R+ + v      sW+GGDRDG +P vt  vt
  gi|1199646   227 LELDQVLARHRLG-RIDWAVD-----SWIGGDRDG-HPQVTAQVTEHTLR 269

                    LaRmmAanlYisqvEDLmFElsm........WRCndELRvRAEElyrtaa
                            lY   ++DL   l  +++  +++  C   +   AEE    a
  gi|1199646   270 RHQETILRLYQPLLDDLERTLTAsdryleksEQCRRWIALLAEEFPDVAD 319

                    rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                         + Y        P EP R ++G +R++L  t       L +
  gi|1199646   320 VL--ARRY--------PMEPLRQMVGLMRERLAAT-------LNH----- 347

                    sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                     +   y +  +F   +E   +      D+   +  L  lLRq+  FG  L
  gi|1199646   348 -DPRGYRQAHQFRQDVEQLGRFWDADPDRWPYE--LKRLLRQIDIFGFHL 394

                    vKLDiRqEseRqtD.vlDAittHLeiGsYReWsEeKRqEWLlaELkGKRP
                      LDiRq s  + ++v+D     L    YR  sE  ++  +la L    P
  gi|1199646   395 ASLDIRQHSRVHIEgVVD-----LAGEEYRTLSERDKMK-VLAQLIEHPP 438

                    LlgsDLPktEEvkDvldaf.rvLAELPiDsFGaYiismataPsDvLAvEL
                       +    t E+k+  + +++        +   Y++sma   sD LAv
  gi|1199646   439 AWIPSSSVTAELKETFQVIsQARRQYGPRAVSRYLVSMAHHASDLLAVLA 488

                    LqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...q
                    L R      +L ++PL E L DLe A   +++ F    ++ +++ ++  q
  gi|1199646   489 LGRAVDPELSLDIIPLVETLDDLENAVVILDQAFQEPVWRQHLQSRqfyQ 538

                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                    evm+GYsDs KDAG + A W++Y+Aq  ++  A ++Gv L  FHGRGG
  gi|1199646   539 EVMLGYSDSTKDAGTFTASWKIYQAQNQLMLWAEQHGVTLGFFHGRGGAL 588

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                    GRGGGPt  AiL qPP t    lR+t qGEv+ + F    L +rsL   t
  gi|1199646   589 GRGGGPTSYAILGQPPKTRLSPLRMTQQGEVLSQKFLLPSLAWRSLELMT 638

                    AAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlA
                     A + H  +P   P  +    m+++   A   YR +v   P F EYF
  gi|1199646   639 VAHVQHAADPGWEPDADTVGWMDHLGDLAVKTYRELV-HAPGFWEYFLAV 687

                    tPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvG
                    tP  E   +n GsRP+ R      + LRAiPW+FaWtq R  +P W G G
  gi|1199646   688 TPIREMSALNWGSRPSWRE-QFCWDDLRAIPWVFAWTQNRMGIPAWYGAG 736

                    AAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyD
                     A   A+ +    l +++ + ++WPF    l  lE+   K D  +A  y
  gi|1199646   737 TALDQALSQ-PEGLSRIQMLRRQWPFLNTMLHNLELALVKSDDMVAEAYQ 785

                    kLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRd
                     L   E    F   + ++     + L  i G    L G P LK  +  R+
  gi|1199646   786 SLATPELKDRFWPLIQEERRRLTNALQAISGGPP-LSGQPRLKTAVTWRN 834

                    sYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnp
                    + +  Ln +q   LK  R               A E+
  gi|1199646   835 PQVDALNYLQIELLKTYR----------------ATED------------ 856

                    tervaPGLEDtLiLtmKGiAAGmqntG<-*
                         P L   L  tm GiA G+ ntG
  gi|1199646   857 -----PKLLPILSQTMEGIALGLRNTG    878

gi|229815948|ref|ZP_04446271.1|: domain 1 of 1, from 46 to 941: score 178.7, E = 1.7e-50
                    *->siDAqLR.lLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEa
                        i A LR+ L+     e   L eYDA +lD F +++  +   +  +
  gi|2298159    46    DIPAELRdNLALFLRLERRVLREYDAKVLDVFDELMMNVIRANAGDP 92

                    vqECYElsAeYEGK..kDt...kKLeELGakLtsLdPaDailvAkailHm
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                  E    + +  G +  Dt++     +  a + +L    a ++ +a+
gi|2298159    93 GAEADGEAVDEQGMpaSDTpsaCAFRDAVALIDALPVDQAQVIVRAFTAF 142

                  LnLAnLAEE....velAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLv
                    LAnL EE+ +  +l  R R+      D  D a+A t +     + +L
gi|2298159   143 FHLANLSEEnyrvAQLRERERNVSTE--DAVDPANALTVA-----FHQLN 185

                  lklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLs
                         +   e L       v+tAHPt + R+++  K  Ri   L
gi|2298159   186 EEV--GGAKATELLSRLEFHPVFTAHPTEARRKAVEGKIRRIARLLEE-- 231

                  AKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEt
                     +   D  E +  +  Ei A  Rt  i   +PtP +E    +  +  t
gi|2298159   232 RPYMGGSDLVENERHMLQEIDALVRTSPIALKKPTPVEEADTIIDIFDST 281

                  vWkGvPKFLRRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRv
                  +++ +P   RR D  +    +   +P   P   +  sW+G DRDG nP v
gi|2298159   282 LFDTIPVIYRRFDDWVLG-EVAGTVPPVCPaFFHPGSWIGSDRDG-NPNV 329

                  tPEvtRDvCL.LaRmmAanlY..isqv.EDLmFElsmWRCndELRvRAEE
                  t  v R v  + a  m + l ++   v+  L  E +     dEL
gi|2298159   330 TAKVSRQVAAkYATHMISKLAdkCRRVgRNLTLEAAYTQPSDELL----N 375

                  lyrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLA
                  l +            E  + +   EP R ++  +  +L  t  R
gi|2298159   376 LWSHQVEM--SEVLTERAREISNSEPHRAVMLVMAARLDATVAR------ 417

                  tGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvs
                          + +y   EeFLE L +  +sL   G +  A G +  l+ qv
gi|2298159   418 ------NADTMYRTAEEFLENLRVVQRSLAAAGARRAAYGPVQTLIWQVE 461

                  tFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaEL
                  tFG  +v ++ Rq s  +   l  i +H   G               EL
gi|2298159   462 TFGFHMVEMEFRQHSVVHSRALADIREHGIHG----------------EL 495

                  kGKRPLlgsDLPktEEvkDvldaf.rvLAELPiDsFGaYiismataPsDv
                             P+t Ev D   a++ +           Yiis + + s v
gi|2298159   496 A----------PMTREVLDTFRAIgSIQKRFGQKMARRYIISFTKSASHV 535

                  LAvELLqRECgvkq....tLrvvPLFEkLADLeAAPAavekLFsiDWYin
                    v  L      + ++ +tL v+PLFE+L DLe     +e + +i    n
gi|2298159   536 ADVYELANLAFAHAedvpTLDVIPLFEQLEDLEGCVDVLEEMLAIPAVQN 585

                  ridG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                  r+  ++++ e+m+GYsDs KDAG   A   L  A E i+  A k+ + Lv
gi|2298159   586 RLAEsgrRMEIMLGYSDSSKDAGPTTATLALHSAEERIVAWAEKHDIDLV 635

                  lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                  l HGRGG vGRGGGP   A+L+qP   +n   +vt qGEvi   +G   L
gi|2298159   636 LMHGRGGAVGRGGGPANRAVLAQPAGSVNCFFKVTEQGEVIFARYGNPAL 685

                  CFrsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvv...AtEEYRsvvv
                    r +   +AAtL            E      emA   ++A  E     +
gi|2298159   686 AQRHVESVAAATLLNSAPSVERTNTEMTARYAEMAAAlneASHERYLDLL 735

                  KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWt
                      F  +F   tP +E G + iGsRPaKR  + + ++ LR iPW+F+W
gi|2298159   736 NTEEFTPWFSCVTPLTEVGLLPIGSRPAKRGLGAkSLDDLRTIPWVFSWS 785

                  qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                  q R  L  W G+G A           l  L+  Y+eWP F   +D +Em
gi|2298159   786 QARINLAAWYGLGTACEK-----LGDLELLQRAYREWPLFNTFIDNIEMS 830

                  FAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE
                   AK D  iA +y  L    +L    +++ d+   t+ ++L+i G    LE
gi|2298159   831 IAKTDNRIAKMYLALGDRADLA---DKVFDEMMLTRSWVLRIVGDAWPLE 877

                  GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                      L q +R+R++++  L   q   L+ +R        + +ls E  +E
gi|2298159   878 HRRVLGQAVRVRNPFVDALSLAQVRALREVR------ANQDELSEEAKAE 921
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                   nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                           + L         LE     t+ G+ AG+qntG
  gi|2298159   922 F-------MSLV--------LE-----TVTGVSAGLQNTG    941

gi|20196798|emb|CAC86371.1|: domain 1 of 1, from 1 to 386: score 178.4, E = 2e-50
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2019679     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2019679     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2019679     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                              vltAHPtqs RRsLLqK+++iRnCL+qL+AKD+t ++Kk
  gi|2019679     1 ----------VLTAHPTQSLRRSLLQKHTKIRNCLTQLYAKDITEDEKK 39

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDEAL  EiqAAFRtDEiRRaqPtPqDEmR+GmsY+HEt+WkGvPKFLR
  gi|2019679    40 ELDEALQAEIQAAFRTDEIRRAQPTPQDEMRYGMSYFHETIWKGVPKFLR 89

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   RvDtALK iGinERlPY++PLikFssWmGGDRDG nPRvtP+vtRDvC+L
  gi|2019679    90 RVDTALKSIGINERLPYNAPLIKFSSWMGGDRDG-NPRVTPDVTRDVCML 138

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   aRm+AanlY+ q+ED+mFElsmWRCndELR+ AE    t   +   K+Yi
  gi|2019679   139 ARMIAANLYVAQIEDVMFELSMWRCNDELRAEAEKHLATRETK---KHYI 185

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                   EFW+q+P tEPYRv+LG vRDKLYntRERa H+L +G+sei+ +     v
  gi|2019679   186 EFWRQIPATEPYRVLLGHVRDKLYNTRERALHMLTKGFSEIPLDTTIRSV 235

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   EeF+ PLELCYksLC+CGDk iADG LLD++RqvstFGLsL KLDiRqEs
  gi|2019679   236 EEFMAPLELCYKSLCDCGDKTIADGVLLDFMRQVSTFGLSLAKLDIRQES 285

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                   eR+tD +DAittHL+iGsY+eW+EeKRqEWLl+EL+GKRPL+ +D+P  +
  gi|2019679   286 ERHTDAIDAITTHLGIGSYKEWPEEKRQEWLLSELQGKRPLMVPDMPVSD 335

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   Ev+Dvl+ f+vLAELP+DsFG+YiismataPsDvLAvELLqREC+v+++L
  gi|2019679   336 EVADVLGCFKVLAELPSDSFGPYIISMATAPSDVLAVELLQRECKVRNPL 385

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +
  gi|2019679   386 P---------------------------------------------- 386

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|2019679     - ---------------------------------------------- -

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

  gi|2019679     - ---------------------------------------------- -

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|2019679     - ---------------------------------------------- -

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|2019679     - ---------------------------------------------- -

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
```

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  gi|2019679     - ------------------------------------------------ -

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|2019679     - ------------------------------------------------ -

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|2019679     - ------------------------------------------------ -

                   tmKGiAAGmqntG<-*

  gi|2019679     - -------------    -

gi|157273487|gb|ABV27386.1|: domain 1 of 1, from 1 to 915: score 177.3, E = 4.5e-50
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                             + vP   s                 Di       d +  v
  gi|1572734     1    -------MTVPTASS--------------PLADIARA--ERDYRFLV 24

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       E+ Ae      ++ L   G+   s+      + A +i     L n+
  gi|1572734    25 ACFREVLAETGASDLAQALPVEGTFPNSVTSHRRFVQACSIT--FQLLNM 72

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEE   A  RR            + A         l +L  ++    +++
  gi|1572734    73 AEENAAAQNRRALESS------AGCAAEPGLWGAVLHRLRQQG-WPSADI 115

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     AL+   v+ vltAHPt + R  +L  + R+   L +L     t+++++
  gi|1572734   116 AAALRHLHVEPVLTAHPTEAKRATVLEHHRRLYLLLVKLENSVWTPNERR 165

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    + + + RE+   +Rt Ei   +Pt  DE+R  + Y+  t+ + +    R
  gi|1572734   166 AIRDEIKRELERLWRTGEIYLEKPTVADELRNVLHYLTTTLPEAIGWLDR 215

                   RvDtALKniGinERl....PYdvPLikFssWmGGDRDGknPRvtPEvtRD
                   R   A   + +   +++++P   P i F  W+GGDRDG +P vtPE tR+
  gi|1572734   216 RLLDAWDELQLDAEVrptdPARLPRITFGTWVGGDRDG-HPLVTPETTRE 264

                   vCLLaRmmAanlYisqvEDLmFElsmW.RCndELRvRAEElyrtaardkv
                     L  R  A  l  s + +L   +s+ + C +   v A  l +ta++
  gi|1572734   265 ALLTLRRSALQLLHSRLKELAARISLSdHCQSPPAVLATYL-STARSA-- 311

                   vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                           +      PY     +v   L      aR L  + +
  gi|1572734   312 ---HDPVLQAALERNPYESWRQAVNVML------AR-LPGQELGWTTARR 351

                   vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                    y    e    L L   sL   G k + D  +  lLR v tFG  L  LD
  gi|1572734   352 TYASAAELAADLRLLGESLQMVGAKRLCDLEVWPLLRLVETFGFHLAALD 401

                   iRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaELkGKRPLlgs
                   iRq s  +   +  + +  +++G Y  W E +R  +  aEL   RPL+ s
  gi|1572734   402 IRQNSAVHEQAVVELLQAAGVdGRYDTWDETRRCTFWEAELTQARPLVSS 451

                   DLPktEEvkDvldafrvLAELPiD....sFGaYiismataPsDvLAvELL
                   ++P  +  + v++a+rv AE     + +  Ga i+sm+ + sD LAv  L
  gi|1572734   452 EMPLGDAAERVVGALRVAAEYGRQygwsGLGALIVSMTRTTSDLLAVYGL 501

                   qRECgvkq........tLrvvPLFEkLADLeAAPAavekLF.......si
                    RE g+  +++++   +L+vvPLFE L DL+  P  +    +++ +++s+
  gi|1572734   502 AREAGLTIstsdglvcPLPVVPLFETLDDLKHSPDVLSAFLdhpmtrrSL 551

                   DWYinrid.GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGv
                    W     ++  q+vm+GYsDs KDAG ++  W LY+Aq  +  vA+  Gv
  gi|1572734   552 AWMQRPGQpPVQQVMIGYSDSNKDAGPVASLWGLYRAQQALSAVAQARGV 601

                   KLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGE
                   +L  FHGRGGt  RG GPtH  + + PP+ + G lR t qGE i + +
  gi|1572734   602 RLRFFHGRGGTPSRGAGPTHRFLNALPPESVSGDLRLTEQGETISQKYAN 651
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                    EnLCFrsLqRFtAAtLEHGmnPPvsPk.PEWRk.LmeemAvvAtEEYRsv
                           L   +A  LE  +      k+P   +++m+ +A      YR++
  gi|1572734   652 LITATYELELLAAGVLETYLLAQSTKKtPHPIEpIMDFLAEQSYRAYRAL 701

                    vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaW
                     +  P F E+F  AtP        iGsRPa+R     +  LRAiPW+F+W
  gi|1572734   702 -LDLPGFLEFFAHATPIDAIEASRIGSRPARRTGKRTLADLRAIPWVFSW 750

                    tqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEm
                     q RF LP W G+G A           l +L+     W   R  l  +
  gi|1572734   751 SQARFFLPGWYGLGTALERLATHHPEWLAQLRQDAMRWYPTRLLLMNVGS 800

                    vFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtkdlLLkiAGHkDl
                         D      y +L+    +++    s+ ++++ t+  + ++ G   l
  gi|1572734   801 QLLLADTTWMEAYAELVPDVAIrRTVLASILAEFERTRRGVEQVFG-VPL 849

                    LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                     E        + LR + +  L   q   LK  R            s E
  gi|1572734   850 TERRQRTALTMQLRRAGLSALHQRQIELLKAWRAAR-------AASDEVQ 892

                    dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     E       Lv L               +t+  i  G++ tG
  gi|1572734   893 SES-----LLVDLL--------------MTVNAISSGLKSTG    915

gi|241771836|ref|ZP_04769202.1|: domain 1 of 1, from 1 to 890: score 177.2, E = 4.6e-50
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDL.HGedLkEa
                         DA +           +++ +  A+L     D +   + G  L  +
  gi|2417718     1    MTDAMI-----------DHVKQNTAMLEGFLTDAVNSFgRGTVLSKI 36

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                                    + L    a +  L  ++a   A+ +  +  L
  gi|2417718    37 -----------------EALRADNADVDDLSESEAAHAARVLTCLSTLTV 69

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    L E+v         +k+   F    +A t   +   +++   k+  s +E
  gi|2417718    70 LSEDV-------ANLKRVETFPGTQEAIT---LANAVQQARAKG-HSQAE 108

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + e L        v+tAHPt   R s++ ++  i   L+  + +     ++
  gi|2417718   109 IEETLNGILASPVFTAHPTEMRRASVVEREYDITQFLSA-YERTTRASER 157

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    k L+E L R +   F t   R  + t  DE+   +  +   +    P  +
  gi|2417718   158 KALEEDLFRAVALLFNTRLNRPERITVADEIQNSLGAVRRAI---LPALV 204

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                           + i +   lP    ++k  sW+GGDRDG +P v
  gi|2417718   205 ELYGDWNREIELEGELP---NVLKLGSWIGGDRDG-HPHVDDTTMNYAFH 250

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                        +   +Y++q++ L  El +    +EL    + l   a++   +
  gi|2417718   251 NQAKLVLDFYFQQLDKLDIELTL---SEELAPVTDALLELARKSSDTNVH 297

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                              EPYR  L  ++ +L  t   a   L + ++  +    y
  gi|2417718   298 -------RVDEPYRRALTFIKTRLASTW-QAILKLPHPLAS-PLAGAYET 338

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     E+F+  L +   sL e G k +    L   +      G  L  LD+Rq
  gi|2417718   339 SENFVRDLLIIRDSLIEYGGKRLVGRTLKSTIQIARSCGFHLLSLDMRQN 388

                    seRqtDvl.DAittHLeiGsYReWsEeKRqEWLlaELkGKRPllgsDLPk
                    s  +  v+ +   +  e+  Y + sE+ R   L+aEL   R L  +
  gi|2417718   389 SAVHERVIaELFAQSSELLDYSSLSENERVSALVAELTNDRLLRWPFAKY 438

                    tEEvkDvldafrvLAELPi....DsFGaYiismataPsDvLAvELLqREC
                     +E +  l  +   AE+  + ++D+ GaY++sma + sD+L   +L +
  gi|2417718   439 SDETRRELRIIDAAAEVIRtfgpDAIGAYVVSMAKSVSDILEPLVLLKQA 488

                    gv.......kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid..GK
                    g+  ++++++  +rv PLFE + DLeAAP  +++   +   +  + ++
```

```
  gi|2417718   489 GLvyggpspHTMIRVSPLFETIEDLEAAPDIMKRWLGLPAMRSLMGrpAV 538

                   qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                   qevm+GYsDs KD G  +  W L kA   i  v  + Gv L lFHGRGG
  gi|2417718   539 QEVMLGYSDSNKDGGYTASRWSLHKASSAIKAVCNQKGVALRLFHGRGGS 588

                   vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                   vGRGGGP   Ai++qP  t+ G +Rvt qGE+i   FG      ++L  F
  gi|2417718   589 VGRGGGPSFNAIMAQPEGTVGGQIRVTEQGEMIARKFGNKTTAGKTLDSF 638

                   tAAtL.......EHGmnPPvsPkPEWRk..LmeemAvvAtEEYRsvvvKE
                    AA    + + +E   +       E + ++Lm+++     + YR++v+ +
  gi|2417718   639 SAAVFlaslpvkERDAHHIKESEAEAKYgpLMNQLCKASFDAYRALVYDD 688

                   PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtR
                   P F ++FR+ tP  E   + iGsRPa R  sG ie LRAiPW+F+W q R
  gi|2417718   689 PHFLDFFRSVTPISEISDLKIGSRPASRTKSGKIEDLRAIPWVFSWSQSR 738

                   FHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAK
                     LP + G+ AA K A+  D    q L +m +eW FF v l  +Em  AK
  gi|2417718   739 MVLPGFYGFNAAVK-ALGVDD---QTLIDMCNEWDFFEVFLANMEMALAK 784

                   GDPGiAaLyDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                    D  +A+Ly  +   + e +     +R++ +E   l  +i     lL
  gi|2417718   785 SDMEMASLYAGMASDpVEAQRIFATIRQEHEEMTALAKRIRKAGTLLSTH 834

                   PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                     L+  +    + + tLn +q   LK+ R+ + +
  gi|2417718   835 EQLRGSIERSHALLQTLNRMQVKLLKKRREGNKH---------------- 868

                   kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        LvkL             + Lt+ GiA  + ntG
  gi|2417718   869 ----KLVKLA-----------MQLTVNGIASALRNTG    890

gi|196228554|ref|ZP_03127421.1|: domain 1 of 1, from 1 to 926: score 174.8, E = 2.5e-49
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                             +  G+ + d   i ++   +++ L    +  Ge L+E
  gi|1962285     1    --------MTKGQPASDYVTIGFEK--IERDLRFFIECLGEVLRELG 37

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                            + G  D+ K e      t   P+   lv +    +L   n+
  gi|1962285    38 HSDLASHLPWFG-SDPTKFE------TEQVPGQIGLVYSIAFQIL---NM 77

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    EE   Ay R i+ +  G  a+ +         E + kL   +   Pe v
  gi|1962285    78 VEENAAAYVRTIRERESGLIAERGL------WGERFAKLKAEG--VPESV 119

                   F.eALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +e L    v+ vltAHPt + R ++L ++   R   a Ls  D
  gi|1962285   120 IgEMLARVRVEPVLTAHPTEAKRLAVLDQH---RSLFALLSGPDRETLPN 166

                   kELDEALHREiqAA....FRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGv
                    EL   L    +AA ++ +Rt Ei   +Pt  DE R    Y+ +
  gi|1962285   167 SEL-HSLRAKTKAAlerlWRTGEILLEKPTLTDERRNVFHYLRDVFPSVL 215

                   PKFLRRvDtALKniGinE...RlPYdvPLikFssWmGGDRDGknPRvtPE
                   P    R + A    G   ++ R     P ++F  W+GGDRDG +P vt E
  gi|1962285   216 PALDERLEEAWVAAGFDAshlRDESKLPQVRFGTWVGGDRDG-HPGVTAE 264

                   vtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaar
                   vt +     R  A  +  +q+  L   ls+    + L +        aar
  gi|1962285   265 VTAETLERLRANAFVVLRQQLVMLAEKLSLSQWMQPLPA-----SLVAAR 309

                   dkvvKyYiEFWKqvPPt...EPYRviLGdvRDKLYntRERaRHLLAtGis
                   dk+     E  + v  t+++EP+R  +  + D+L         ++ + is
  gi|1962285   310 DKLAESLGEKARAVLSTntsEPWRQYVELMIDRL------PIEIVPHRIS 353

                   eisEe.AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFG
                   ++  ++  y + E+    L +   sL e G + +AD  +  +LR v   G
  gi|1962285   354 QLRADpGSYERAEQLAADLGILRDSLVEVGAQRLADSDVRPVLRAVQLVG 403
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                    LsLvKLDiRqEseRqtDvlDAittHLei.Gs.YReWsEeKRqEWLlaELk
                      L +LDiRq s  +   l  +    +++Gs++ eW E+ R  +L  EL+
  gi|1962285   404 FHLAQLDIRQNSVFHVKALSQLMDASGLdGSqWEEWTENERLRFLEKELR 453

                    GKRPLlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPs
                      RP l +      E   vl+ fr LA +  +   D  Ga i+sm+   s
  gi|1962285   454 SPRPFLHASASAGPEADAVLGCFRTLAAhiarYGADGIGALIVSMTRRLS 503

                    DvLAvELLqRECgvkq........tLrvvPLFEkLADLeAAPAa......
                    D L v +L RE g+ ++ +++    L+vvPLFE L DLeAAP   +   +
  gi|1962285   504 DLLIVYVLAREAGLTRslpeglvcVLPVVPLFETLDDLEAAPSIlgafld 553

                    ..vek....LFsiDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAq
                    +++ +++ +  +  W + ++   q+vmvGYsDs KD G ++  W L kAq
  gi|1962285   554 epMTRrslnFLAWNWGREKLSLTQQVMVGYSDSNKDSGIFASQWGLQKAQ 603

                    EEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvt
                      +++  ++ G+++  FHGRGGtv RG GPtH  + + P   + G +R t
  gi|1962285   604 ARLAQLGRDTGIRIRFFHGRGGTVSRGAGPTHRFLEALPNNSLSGDIRLT 653

                    vqGEviEfsFGEEnLCFrsLqRF....tAAtLEHGmnPPvsPkPEWRkLm
                     qGE i + FG        L     + +A t++H    Pv   P    ++
  gi|1962285   654 EQGETIAQKFGHFVTATYNLELLlagvAATTIDHERSAPVT--PPLAPVL 701

                    eemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG
                    e++       YR +   E  F+ ++R AtP     +  iGsRP++R
  gi|1962285   702 ERLSRASQQSYRRLLDAED-FITFYRQATPIDALEHSRIGSRPSRRTGNP 750

                    GiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYk
                     +  LRAiPW+F+W q RF +P W G G   K   + +   l  +k+  +
  gi|1962285   751 SLADLRAIPWVFSWNQSRFYVPGWFGAGSGLKALTETE---LADIKDQLR 797

                    eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvE
                    +WPF    l  +E   A  D  +   y +L+    L+ +F k + d++
  gi|1962285   798 TWPFLYYVLTNIEASIASTDLELMQAYADLVEDTSLRDrFMKIIIDEWNL 847

                    tkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPs
                    t+++L k+ G   + E  P +   l+LR   +  L       LK+ R
  gi|1962285   848 TREMLEKLRG-ASMAERRPRMLRTLKLRADALRVLHLQEIHLLKKWR--G 894

                    ykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAA
                    y+     +   E A+E    +d L+ +n                   iA
  gi|1962285   895 YR-----KAGDEAAAEK-MLPDLLLSIN-----------------AIAS 920

                    GmqntG<-*
                    G+  tG
  gi|1962285   921 GLRTTG    926

gi|18076761|emb|CAC84924.1|: domain 1 of 1, from 1 to 364: score 172.2, E = 1.5e-48
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807676     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807676     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807676     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807676     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807676     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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  gi|1807676     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807676     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807676     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807676     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807676     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807676     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807676     1 -----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqE++iKvAKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807676     9 RLSAAWQLYKAQEDLIKVAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|1807676    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L++emAvvAt EYRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|1807676   109 KPEWRTLLDEMAVVATNEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++KDiKnl
  gi|1807676   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGTAFKHVVQKDIKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+EmY+eWPFFRvt+DL+EmvFAKG PGiA+LyDkLLv+E+L+ F ++
  gi|1807676   209 RILQEMYNEWPFFRVTIDLVEMVFAKGNPGIASLYDKLLVSEDLWSFAER 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+EtkdlLL++AGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|1807676   259 LRANYQETKDLLLQVAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+++v +rPh+sKE  d   k+a+eLvkLnpt+++aPGLEDtLiL
  gi|1807676   309 KRIRDPNFHVKVRPHISKEISDAS-KPAAELVKLNPTSEYAPGLEDTLIL 357

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807676   358 TMKGIAA------    364

gi|7768121|emb|CAB90621.1|: domain 1 of 1, from 1 to 365: score 170.3, E = 5.7e-48
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768121     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768121     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768121     - ------------------------------------------------ -
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                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768121     - ------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768121     - ------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768121     - ------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768121     - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768121     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768121     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768121     - ------------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768121     - ------------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768121     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqE++iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768121     9 RLSAAWQLYKAQEDLIKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|7768121    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++emAvvAtEEYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|7768121   109 KPEWRALLDEMAVVATEEYRSIVLQEPRFVEYFRLATPEMEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKhAi+KDiKnl
  gi|7768121   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGTAFKHAIEKDIKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+EmY+eWPFFRvt+DL+EmvFAKG PGiAaL+DkLLv+++L+ FG++
  gi|7768121   209 HMLQEMYNEWPFFRVTIDLIEMVFAKGNPGIAALHDKLLVSDDLWSFGER 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR +Y+Etk+lLL++AGH+DlLEGDP LKqrlRLRdsYittLnv+qA tL
  gi|7768121   259 LRTNYEETKNLLLQVAGHRDLLEGDPHLKQRLRLRDSYITTLNVCQACTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDP+++vt+rPh+sK+  d   k+a+eLvkLnpt+++aPGLEDtLiL
  gi|7768121   309 KRIRDPNFHVTVRPHISKDIIDSSNKRAAELVKLNPTSEYAPGLEDTLIL 358

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|7768121   359 TMKGIAA------    365

gi|7768376|emb|CAB90716.1|: domain 1 of 1, from 1 to 364: score 169.4, E = 1e-47
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
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gi|7768376     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|7768376     - ---------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|7768376     - ---------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|7768376     - ---------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|7768376     - ---------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|7768376     - ---------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|7768376     - ---------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|7768376     - ---------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|7768376     - ---------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|7768376     - ---------------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|7768376     - ---------------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
gi|7768376     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqE++iKvAKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|7768376     9 RLSAAWQLYKAQEDLIKVAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
gi|7768376    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++emAvvAt EYRs+v++EPRFvEYFRlAtPElEYG+mniGsR
gi|7768376   109 KPEWRTLLDEMAVVATNEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++ DiKnl
gi|7768376   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGTAFKHVVQEDIKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+EmY+eWPFFRvt+DL+EmvFAKG PGiA+LyDkLLv+E+L PFG++
gi|7768376   209 RILQEMYNEWPFFRVTIDLVEMVFAKGNPGIASLYDKLLVSEDLLPFGER 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y+EtkdlLL++AGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
gi|7768376   259 LRANYQETKDLLLQVAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
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                  KRiRDPs++v +rPh+sKE  d   k+a+eLvkLnp +++aPGLEDtLiL
  gi|7768376   309 KRIRDPSFHVKVRPHISKEISDAS-KPAAELVKLNPMSEYAPGLEDTLIL 357

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|7768376   358 TMKGIAA------    364

gi|7768374|emb|CAB90715.1|: domain 1 of 1, from 1 to 364: score 168.8, E = 1.6e-47
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768374     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768374     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768374     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768374     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768374     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768374     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768374     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768374     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768374     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768374     - ---------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768374     - ---------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|7768374     1 -----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqE++iKvAKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768374     9 RLSAAWQLYKAQEDLIKVAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEvi +sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|7768374    59 PPDTIHGSLRVTVQGEVIKQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++emAvvAt EYRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|7768374   109 KPEWRTLLDEMAVVATNEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++KDiKnl
  gi|7768374   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGTAFKHVVQKDIKNL 208
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                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvt+DL+EmvFAKG PGiA+LyDkLLv+E+L+ F ++
  gi|7768374   209 RILQEMYNEWPFFRVTIDLVEMVFAKGNPGIASLYDKLLVSEDLWSFAER 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+EtkdlLL++AGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|7768374   259 LRANYQETKDLLLQVAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+++v +rPh+sKE  d   k+a+eLvkLnpt+++aPGLEDtLiL
  gi|7768374   309 KRIRDPNFHVKVRPHISKEISDAS-KPAAELVKLNPTSEYAPGLEDTLIL 357

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|7768374   358 TMKGIAA------    364

gi|217977880|ref|YP_002362027.1|: domain 1 of 1, from 3 to 919: score 168.8, E = 1.6e-47
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        + A  Rl     v      +   A   ++   iL  L    L E+v
  gi|2179778     3    ELQAERRLEQALSVV----DVSDGAPSGERIAAILYQL----LLEVV 41

                    qECY.ElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                    q   +E++    G           ++L   +P     v +a      L
  gi|2179778    42 QRHHpEIAPVLSGE----------TVLQNAAPEVLSRVFQAHGIWFQLLS 81

                    LAE.EvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    + E++  +  RRR ++       + a   t + +     kL +      +
  gi|2179778    82 IVEqDAAMGERRRTEREL----GEQAVPGTFANVIAKAAKLGVPA----A 123

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    ++ e L    v  v+tAHPt + R  +L K+ Ri   L  L     t  +
  gi|2179778   124 DIAEKLGRTRVRPVITAHPTEAKRVTVLEKHRRIYRLLVELEQPRWTGRE 173

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    +  + + L  Ei   + t E+R  +P    E+  G+ ++HEt+++GvP
  gi|2179778   174 RSGIIDQLRDEIELLWMTGELRLEKPSVEQEIAWGLHFFHETLFEGVPEL 223

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    L++ D ALK     E         +F sW+GGDRDG nP vt  vtR
  gi|2179778   224 LKKFDRALKRFYPSENFAL-TQFFQFGSWIGGDRDG-NPFVTNKVTRRAL 271

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                             +Y + +  Lm  ls+            E    a +d
  gi|2179778   272 RENAKASLRFYEQRLFNLMKSLSISERALPPPSGFREALNRALSDSGDGA 321

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                     i       P EPYR         LY    + +  LA    e      y
  gi|2179778   322 GIALRN---PGEPYRQF-------LYCAHAKVKATLALYEGERTPGPHYI 361

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                      ++ +  L +  ++L e G   +A   +  +   v  F     +LD+R
  gi|2179778   362 SADDLISDLAVTEQALAESGSVGLAQDLVRPVRFAVEAFRFRTQRLDLRE 411

                    EseRqtDvlDAi..ttHLei.GsYReWsEeKRqEWLlaELkGKRPLlgsD
                       + t  l A+ +  H e +G       +  + W+laEL   RP +g+
  gi|2179778   412 NTTKLTSTLQALwrAMHTEAdGEPPAVESDEWKAWILAELA--RPRIGPP 459

                    LPktE..EvkDvldafrvL....AELPiDsFGaYiismataPsDvLAvEL
                    + +  ++E ++ l+ f+  ++++ E   ++FG++++sm+ + +DvL   L
  gi|2179778   460 VYRALppEAEETLGMFKLArdrdEEFDREAFGSFVLSMTRSAADVLGAYL 509

                    LqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsiDWYi..
                    L +E  + ++ ++ +  tL + PLFE + DL+AAP  +  L s+   +++
  gi|2179778   510 LAKEADLYHdatrveacTLSITPLFETITDLRAAPQIMRELLSLPLVRrs 559

                    nrid.GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                     r+++G qevm+GYsDs KD G ls  W L kAq+ ++K+  + G+ +
  gi|2179778   560 ARMQgGVQEVMIGYSDSNKDGGFLSSNWELAKAQDKLAKIGAEAGIPISF 609

                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
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                    FHGRGG v RGG Pt  Ai +qP   i+G lRvt qGEv+ f +
  gi|2179778   610 FHGRGGSVSRGGAPTAQAIAAQPAGSIQGRLRVTEQGEVVSFKYANRGTA 659

                    FrsLqRFtAAtLEHGm...nPPvsPkPEWRkLmeemAvvAtEEYRsvvvK
                       +        EH ++ +    + + E+ + me +       Y   +
  gi|2179778   660 AFQMEMLGSSVFEHTLtleRAAPALRAEFEEAMEALSGASHAAYANFI-N 708

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                     P    YF +A P  E   +niGsRPa+R  +  +  LRAiPW+FaW q
  gi|2179778   709 HPDLLTYFQSASPLDEISMLNIGSRPARRFGARTLSDLRAIPWVFAWAQN 758

                    RFHLPvWLGvGAAFKhAid.KDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                    R  +  W GvG      +d +  + l  Lk m+ e   FR+ +  +E
  gi|2179778   759 RHVITGWYGVGSGIASFLDvRKERGLTLLKRMFAESDLFRMIVGEVEKTL 808

                    AKGDPGiAaLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLkiAGHkDlL
                       D  iA  y  L+  ++++ + FG  + ++Y  t+  +Lki G  ++
  gi|2179778   809 GMVDLDIAREYAGLVYDDDVREtiFG-MIEAEYRLTRANILKITGEEEIA 857

                    EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                       P  + rl  R   i  +n  q   L+  R          +lsKE
  gi|2179778   858 QRFPAYRSRLETRLKTINKVNREQVELLRNFR------ASTNELSKEAFK 901

                    EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     n                       L+L +  i  G+  tG
  gi|2179778   902 SN----------------------LLLSINCISSGLGATG    919

gi|119356395|ref|YP_911039.1|: domain 1 of 1, from 1 to 922: score 168.5, E = 1.9e-47
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                              +     v + ek  +    Ll  F ++L DL  ++L E
  gi|1193563     1    ------MITTTSSVINFEKAERDFTFLLQCFQEMLHDLGEKELAEHL 41

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                                K+ + +L+         d  D     +a++    L n+
  gi|1193563    42 ----------PWKRASMRLD---------DYPDIERAIQAYSIFFQLLNM 72

                    AEEvelA.yRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    AEE   A+yRR i+  k       +           l +L   +  + eE
  gi|1193563    73 AEENSGAqYRRTIETEK-------GLSELKGLWGKNLHRLKKNG-ITEEE 114

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +   L   +vD+ ltAHPt + R+ +L ++  +   L +   +  t+ ++
  gi|1193563   115 ILSELSRVTVDVALTAHPTEAKRKTVLEQHRQLYILLVKRENQMWTPLEQ 164

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +++   +   +   +Rt E+   +P    E R  + Y+     +  P
  gi|1193563   165 EDIRKEIKVVMERLWRTGELLYDKPAVSAERRNIVHYLYNIFPEVLPMLD 214

                    RRvDtALKniGin.ERl..PYdvPLikFssWmGGDRDGknPRvtPEvtRD
                    +R   A +  G  +E+l +P   PL++F sW+GGDRDG +P vt  vtR+
  gi|1193563   215 KRLLHAWQECGFApEKLadPQTLPLLRFGSWVGGDRDG-HPLVTAKVTRE 263

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                      L  R  A  l    +  L   ls+    +      EE  rt a +
  gi|1193563   264 TLLEMRRKALALIAFHLTRLASKLSLSEKHQLPPDALEERIRTLANH--L 311

                    KyYiEFWKqvPPtEPYRviLGdvRDKL.YntRERaRHLLAtGiseisEeA
                        E        EP+R  +  +   L+ n R        +   +  +
  gi|1193563   312 GEDGEVALIRNRHEPWRQFINLMIASLpKNPRNE------HDTGNQNDIF 355

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                     y    e L+ LEL  +sL + G + iAD  +  + R v tFG  L  LD
  gi|1193563   356 SYGSSRELLDDLELLRQSLLNVGARHIADSDVAPVYRIVQTFGFHLASLD 405

                    iRqEseRqtDvlDAittHLei.Gs.YReWsEeKRqEWLlaELkGKRPLlg
                    iRq se +   l  +    +++Gs +  W Ee R  +L  EL+  RP
  gi|1193563   406 IRQNSEFHDLALSQLMSAAGLnGSaFLTWNEEERTAFLDRELQSPRPFTH 455

                    sDLPktEEvkDvldafrvLA....ELPiDsFGaYiismataPsDvLAvEL
                    +D+    E + vld +rvL ++ +E  ++  G+ i+sm+   sD L v L
  gi|1193563   456 PDMKAGPEAEAVLDCYRVLLdhckEYGSEGIGSLIVSMTRNASDLLVVYL 505
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                    LqRECgvkqt........LrvvPLFEkLADLeAAPAavekLFs......i
                      RE g+  + ++++   L+vvPLFE + DLe  P  +    s++ ++++
  gi|1193563   506 FMREVGLMTPfkehdacmLPVVPLFETIEDLEKSPDIMRTFLShpltrrT 555

                    DWYinridG....KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKk
                          ++G +++ q+vm+GYsDs KD G ++  W LY+AqE +    Kk
  gi|1193563   556 LGMQQEMNGwekpAQQVMIGYSDSNKDGGIFASIWNLYRAQESLLEAGKK 605

                    yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                        +  FHGRGG + RG GPtH  + +qP    +  +R t qGE i +
  gi|1193563   606 SETEILFFHGRGGSISRGAGPTHRFLRAQPHGSFQAGIRFTEQGETIAQK 655

                    FGEEnLCFrsLqRFtAAt....LEHGmnPPvsPkPEWRkLmeemAvvAtE
                    +         L  F A  +++ L H  +   s   E   Lm+ +
  gi|1193563   656 YANRISALYNLELFMAGVtgelLKHRNKEKTS--HELEPLMDMLSRTSNL 703

                    EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                     YR ++  E  F+++FR AtP        iGsRP++R     +  LRAiP
  gi|1193563   704 AYRRLIEAEG-FIDFFREATPIDIIEATRIGSRPSRRSGKKSLADLRAIP 752

                    WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                    W+F+W q RF L  W G+G A     +        ++     W   R  +
  gi|1193563   753 WVFSWNQARFSLSGWFGIGSALEQLQHEHPEACDNIRRQDASWAPLRYII 802

                    DLlEmvFAKGDPGiAaLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLki
                       +   A  D  i   y  L+   eL+ + FG  + ++Y  t+ ++  +
  gi|1193563   803 SNADASLATVDTEIMREYAALVENSELRSriFG-IIENEYHKTRTMIESL 851

                    AGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPh
                     G + l E    +   + LR+  +  L   q   LK+ R    + t +
  gi|1193563   852 YGAH-LEEQRLNVSRFISLRQEGLRELHRQQIRLLKKWR--KLHQTGQ-- 896

                    lsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-
                            n kkad+L  L            L Lt+  i  G+  tG
  gi|1193563   897 --------N-KKADNL--LA-----------ELFLTVNAISGGLRTTG   922

                    *

  gi|1193563     -   -

gi|194335801|ref|YP_002017595.1|: domain 1 of 1, from 1 to 922: score 168.3, E = 2.3e-47
                    *->siDAqLRlLvPGKvsedekLieYDAL.LlDkFLDiLqDLHGedLkEa
                              +     v  d +  e D L Ll  F ++L DL Ged
  gi|1943358     1    ------MITTTSSVI-DFEKAERDFLfLLLCFQEVLRDL-GED---- 35

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                         El+        +  Le       +L         +a++    L n
  gi|1943358    36 -----ELAEHLPSENRSIPLERYPNSERAL---------QAFSIFFQLLN 71

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AEE   A  RR+           + A        tl +   ++  + +E
  gi|1943358    72 MAEENSAAQNRRMLEAE------QGLAHLTGLWGRTLLRFRERG-ITEKE 114

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + + L   s+D vltAHPt + R+ +L ++  +   L q   +  t+ +K
  gi|1943358   115 IGNLLPEVSIDAVLTAHPTEAKRKTVLEQHRQLYLLLVQRENQMWTPLEK 164

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     ++   +   i   +Rt Ei   +P   DE R  + Y+H    +  P
  gi|1943358   165 LDIRNEIKVVIERLWRTGEILFEKPEVSDERRNVIHYLHNIFPEVLPMLD 214

                    RRvDtALKniGinERl...PYdvPLikFssWmGGDRDGknPRvtPEvtRD
                    +R   A +  G      ++P + P + F sW+GGDRDG +P vt Evt +
  gi|1943358   215 KRLLQAWRDTGFHTASlsdPRNLPRLSFGSWVGGDRDG-HPLVTAEVTEE 263

                    vCLLaRmmAanlYisqvEDLmFElsm.WRCn...dELRvRAEElyrtaar
                         R  A  l +  +  L   ls + R  +++ EL  R E l +
  gi|1943358   264 TLGDMRQNALALVLRHLRQLASKLSFsERLQppgKELLLRIETLCQKLGD 313

                    dkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseis
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                    + +         q    EP+R  L  +   L    +R+  L     s+
  gi|1943358   314 KSIAAM------QRNRHEPWRQFLNLMIASLPLEADRSGALHIAVESD-- 355

                    EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                        y   +e LE L L  +sL + G + iAD  ++ + R v tFG  L
  gi|1943358   356 ---RYGSSDELLEDLSLLRQSLLDVGAQHIADTEVVPVYRIVQTFGFHLG 402

                    KLDiRqEseRqtDvlDAittH..LeiGsYReWsEeKRqEWLlaELkGKRP
                    KLDiRq s  +   l  + t ++L+   + eW E  R+ +L  EL+  RP
  gi|1943358   403 KLDIRQNSHFHDLALSQLMTAsgLNGNDFLEWDEPARRAFLDRELQSPRP 452

                    LlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLA
                       +D+    E +  l  ++vL  + +    D  G+ i+sm+   sD L
  gi|1943358   453 FTHPDMSVGAEAETLLACYKVLLNhckmYGTDGIGSLIVSMTRNASDLLV 502

                    vELLqRECgvkqt........LrvvPLFEkLADLeAAPAavekLFsiDW.
                    + L  RE g+  + ++++   L+vvPLFE + DL+  PA ++       +
  gi|1943358   503 IYLFAREVGLMTPfgdgdaciLPVVPLFETIEDLQKSPAILQEFLHHPVt 552

                    .....YinridGK....qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKv
                    +++ +Y     GK++  q+vm+GYsDs KD G ++  W LY+AqE +
  gi|1943358   553 qrslqYQKTKAGKtkavQKVMIGYSDSNKDGGIFASTWALYRAQEALLEA 602

                    AKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEvi
                    A k    +  FHGRGG + RG GPtH  i +qP    +  +  t qGE i
  gi|1943358   603 AEKSNTDILFFHGRGGSISRGAGPTHRFIKAQPHGSFHAGICFTEQGETI 652

                    EfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE..WRkLmeemAvvAt
                     + +         L  F A      +      k  ++   +m+ +
  gi|1943358   653 AQKYANRISAVYNLELFMAGVASAMIRQRKNEKRAhpLEAVMDMLSEKSN 702

                    EEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAi
                      YR ++  E  F  +FR AtP        iGsRP++R     ++ LRAi
  gi|1943358   703 QAYRKLIEAEG-FLAFFREATPIDIIESSRIGSRPSRRSGQTSLKDLRAI 751

                    PWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvt
                    PW+F+W q RF L  W GvG A  h        +  ++   + WP  R
  gi|1943358   752 PWVFSWNQARFSLSGWYGVGSALEHLHTTNPDTFDEIRVRSHAWPPLRYI 801

                    lDLlEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLki
                    +   +   A  D  i   y +L+    ++ +    + ++Y  tk+++
  gi|1943358   802 ISNADTSMASADLQIMHQYAELVGDSTIREhILGMIEAEYHRTKKYI--- 848

                    AGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPh
                        +lL  +P   qr+ + + +i            R    +     + +
  gi|1943358   849 ----ELLFAEPLEIQRMNV-NKFIAP----------RREGLEILHRQQIK 883

                    lsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-
                    l KE+            +     + a  +   L Lt+  i  G+  tG
  gi|1943358   884 LLKEWRKLK--------ESD-RAEEAESILHELFLTINAISGGLRTTG   922

                    *

  gi|1943358     -   -

gi|18073888|emb|CAC84967.1|: domain 1 of 1, from 1 to 364: score 167.9, E = 3e-47
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807388     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807388     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807388     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807388     - ---------------------------------------------- -
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                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807388    - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807388    - ------------------------------------------------ -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807388    - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807388    - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807388    - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807388    - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807388    - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807388    1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqE++iK AK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807388    9 RLSAAWQLYKAQEDLIKAAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PP+sP
  gi|1807388   59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPISP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++emAvvAtEEYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|1807388  109 KPEWRALLDEMAVVATEEYRSIVFQEPRFVEYFRLATPEMEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtR HLPvWLG+G AFK+Ai+KDiKnl
  gi|1807388  159 PSKRKPSGGIESLRAIPWIFAWTQTRVHLPVWLGFGTAFKYAIEKDIKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+EmY+ WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+++L+ FG++
  gi|1807388  209 HMLQEMYNAWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSDDLWSFGER 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR+ Y+Etk+lLL++AGH+DlLEGDPYLKqrl LRdsYittLnv+qAYtL
  gi|1807388  259 LRASYEETKNLLLQVAGHRDLLEGDPYLKQRLCLRDSYITTLNVCQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDP+++v lrPh+sKE  d n k a+eLvkLnpt+++aPGLEDtLiL
  gi|1807388  309 KRIRDPNFHVNLRPHISKEIMDSN-KTAAELVKLNPTSEYAPGLEDTLIL 357

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807388  358 TMKGIAA------    364

gi|32473418|ref|NP_866412.1|: domain 1 of 1, from 1 to 937: score 167.8, E = 3.2e-47
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      +    R   P        ++    L lD  +D L       L  a
  gi|3247341    1    -MQLDCRRSLPFSTQRTVTMVSANILALD--VDQLNRDWQWMLS-AL 43

                  qECYElsAeYEGKkDtkKLeEL....GakLt.sLdPaDailvAkailHmL
```

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                q       +       +KL EL + +G kL ++ +PaD++ + +a++
gi|3247341     44 QSVLQRGGD-------EKLAELlpvpGCKLDpAKAPADSVQLTQAYSIAF 86

                nLAnLAEEvelA.yRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkln
                 L  +AE    A++R Ri+          + A   +   E l++L+ ++
gi|3247341     87 QLLSMAEQSSAAqFRDRIESES-------GMADLPALWGESLQQLIDRG- 128

                KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                 + + +   L    v+LvltAHPt + R  +L  + R+          D+
gi|3247341    129 WTADMIAAELPSMRVELVLTAHPTEAKRATVLAHHRRLFRRFQLRHQTDL 178

                tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                 +  + E +EA+   +   +Rt Ei   +P  q E R  m Y+     k
gi|3247341    179 PPWRRSENEEAIESVLSILWRTGEIYLDKPDLQSERRNVMDYLTVVFPKA 228

                vPKFLRRvDtALKniGinERl...PYdvPLikFssWmGGDRDGknPRvtP
                      R   A + +G+ E+   +P   P + F  W+GGDRDG +P vtP
gi|3247341    229 LQPLDQRLRQAWREVGLSEKAiadPLALPRLTFGTWVGGDRDG-HPLVTP 277

                EvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaa
                Evt +  +  R  A  l  + +  L    s+      L    + l r a
gi|3247341    278 EVTEETLMQLRRGAVELMREELIQLARLTSV--SAYWLPPTSDFLTRIAE 325

                rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                r + +           P+EP+R  +      L      +   +  G
gi|3247341    326 RAHAMGPAGAAAIARNPNEPWRQFI-----NLMLASLPSEKTMMSG---- 366

                sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                 E+  y +  e L  L     sL       +A  ++   +R   tFG  L
gi|3247341    367 KEQHTYQRSRELLADLRCLHESLVAVDLGDVATSAVAPTMRIAQTFGFHL 416

                vKLDiRqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKR
                  LDiRq s ++   ++ + +  ++  ++  +W E+KR+ +L  EL   R
gi|3247341    417 AVLDIRQNSAKHDTAIEQLLRAAGMADWKfaSWDEDKRMKFLNEELANSR 466

                PLlgsDLPktEEvkDvldafrvLAELPi....DsFGaYiismataPsDvL
                PL  +D    EE   vl+a+rv+    ++++ D  Ga i+sm+   sD L
gi|3247341    467 PLTHPDSSAGEEADAVLGALRVVTQYRSkhgaDGLGALIVSMTRKTSDLL 516

                AvELLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsiDW
                Av LL RE g+ q+++++   +L+vvPLFE + DLe  P   +
gi|3247341    517 AVYLLAREVGLLQrtesgavcPLPVVPLFETIDDLERSPEIYDGFLQHPI 566

                YinridGKq.........evmvGYsDsGKDAGRlsAAWqLYkAqEEiiK
                 +n +    ++++ + + ++vm+GYsDs KD G l+    L  Aq  + +
gi|3247341    567 TRNSLTAIAqregatapvgQVMIGYSDSNKDGGILASLVGLRHAQRKLTQ 616

                vAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEv
                vA+ +Gv+   FHGRGGt+ RG GPtH  i s P  ti G +R t qGE
gi|3247341    617 VARSHGVRARFFHGRGGTISRGAGPTHRFIKSLPDHTIAGDMRLTEQGET 666

                iEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPE..WRkLmeemAvvA
                i + +  E      L  F A      +    s  P+++    + ++A  A
gi|3247341    667 IAQKYAHEPTAIYNLELFLAGVTRKSLADSRSEEPDhpLEPTLVKLAAWA 716

                tEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRA
                   Y  +   +  FvE+FR AtP     +  iGsRPa+R     ++ LRA
gi|3247341    717 RTTYHELLHSDG-FVEFFREATPIDAIEQSRIGSRPARRTGQQTLDDLRA 765

                iPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRv
                iPW+F+W q R  L  W GvG A K          +  +kE  ++W
gi|3247341    766 IPWVFSWGQARCYLSGWYGVGTALKKLQTECPDEFDAVKEALRDWAPLHY 815

                tlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLk
                 +  +       D  +   y  L+    L+ +F  ++  +++   +++
gi|3247341    816 LISNVATSVTAVDIEVMKQYAALVENPALRErFVTDIETQWKLACEMVEA 865

                iAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrP
                + G   +    P ++  + LR   +  L   q   L+R R
gi|3247341    866 VYGG-PMESQRPNVQRMIALRSEGLRLLHRQQISLLQRWR---------- 904
```

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                  hlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<
                    s     E   +ad L  L             L+L +  iA G+  tG
  gi|3247341   905 --SYNKMGEH-TQADAL--LP-----------ALLLSVNAIASGLGTTG  937

                  -*

  gi|3247341     -    -

gi|7768132|emb|CAB90627.1|: domain 1 of 1, from 1 to 370: score 167.7, E = 3.3e-47
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768132     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768132     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768132     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768132     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768132     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768132     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768132     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768132     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768132     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768132     - ---------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768132     - ---------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|7768132     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWq+Yk qEE++Kv K++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768132     9 RLSAAWQMYKVQEELVKVSKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP+ti+GslRvtvqGEviE+sFGE nLCFr+LqR+tAAtLEHGmnPP sP
  gi|7768132    59 PPETIHGSLRVTVQGEVIEQSFGEQNLCFRTLQRYTAATLEHGMNPPKSP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L+++mAvvAtEEYRs+v+KEPRFvEYFRlAtPE+EYG+mniGsR
  gi|7768132   109 KPEWRALLDQMAVVATEEYRSIVFKEPRFVEYFRLATPETEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAF+h ++KDi+n
```

```
  gi|7768132   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGVGAAFRHVLEKDIRNH 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L++mY+++PFFRvt+DLlEmvFAKGDP iAaLyDkLLv+E+L+PFG +
  gi|7768132   209 NMLRDMYNNFPFFRVTIDLLEMVFAKGDPEIAALYDKLLVSEDLQPFGAR 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y++tk  LL++AGH+DlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|7768132   259 LRANYEDTKRRLLEVAGHRDLLEGDPYLKQRLRLRDPYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+++vt rPhlsKE  d n k a+eLvkLnpt+++aPGLEDtLiL
  gi|7768132   309 KRIRDPDFQVTERPHLSKEIMDMN-KAAAELVKLNPTSEYAPGLEDTLIL 357

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|7768132   358 TMKGIAAGMQNTG    370

gi|7768364|emb|CAB90712.1|: domain 1 of 1, from 1 to 370: score 167.5, E = 3.9e-47
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768364     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768364     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768364     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768364     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768364     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768364     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768364     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768364     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768364     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768364     - ---------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768364     - ---------------------------------------------- -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768364     1 -----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768364     9 RLSAAWQLYKAQEELIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58
```

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                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEHGm+PP+sP
  gi|7768364     59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHGMHPPISP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emAvv t EYRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|7768364    109 KPEWRTLLDEMAVVSTKEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkP GGiesLRAiPWiFa tqtRFHLPvWLG+GAAFKh i+KDi+nl
  gi|7768364    159 PAKRKPTGGIESLRAIPWIFAMTQTRFHLPVWLGFGAAFKHVIEKDIRNL 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+ WPFFRvt+DL+EmvFAKGDP iAaLyDkLLv+EeL+ FG+
  gi|7768364    209 NMLREMYNMWPFFRVTIDLIEMVFAKGDPEIAALYDKLLVSEELQSFGEL 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Et  lLL++A HkDlLEGDPYLKqrlRLRd+YittLnv qAYtL
  gi|7768364    259 LRKNYEETSRLLLEVAEHKDLLEGDPYLKQRLRLRDPYITTLNVSQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP++kvt rPhlsK+  + n  +a+eLvkLnpt++++PGLEDtL+L
  gi|7768364    309 KRIRDPDFKVTERPHLSKDIMESN-NPAAELVKLNPTSEFPPGLEDTLVL 357

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|7768364    358 TMKGIAAGMQNTG    370

gi|189499547|ref|YP_001959017.1|: domain 1 of 1, from 1 to 922: score 165.7, E = 1.3e-46
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                               ++    s    +++YD  L+D     L D   + L+E+
  gi|1894995      1    --------MITSATS----VVDYDKALVD--FRFLLDCFRKVLQEFG 33

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        El+A     +         ++  sL P     v +a+  +  L n+
  gi|1894995     34 ET--ELAAHLPWDE--------ASVPISLIPNRGRAV-QAYTIVFQLLNM 72

                    AEEvelA.yRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    AEE   A++RR  +  k       +      D    lKk+
  gi|1894995     73 AEENSGAqFRRTLEATK----EPSSLSGLWGDAFSHLKKIGISE----SR 114

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + e L   sv+ vltAHPt + RR +L ++  +   L +L  +  t+ ++
  gi|1894995    115 IVEELSHISVEPVLTAHPTEAKRRTVLEQHRELYLLLVKLENQMWTPAER 164

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +++   +   +   +Rt Ei   +Pt   E    + Y+
  gi|1894995    165 EDIRTEITVVLERLWRTGEIFFEKPTVDAERQNVIHYLYNIFPSVLSMLD 214

                    RRvDtALKniGinERl...PYdvPLikFssWmGGDRDGknPRvtPEvtRD
                    +R   A    G      ++P + P + F sW+GGDRDG +P vtPEvt +
  gi|1894995    215 KRLIQAWTDAGFDRASiedPKNFPKLSFGSWVGGDRDG-HPFVTPEVTQE 263

                    vCLLaRmmAanlYisqvEDLmFElsm.WRCndELRvRAEElyrtaardkv
                      +  R     l  + + +L   ls++ R  +   +  E +  t  r+ +
  gi|1894995    264 TLMEMRQYSLRLVQNHLRELASKLSLsERFQSPTPAISERI--TRLRE-L 310

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                    +    +      P EP+R  +      L         +L     e
  gi|1894995    311 TDTRGDNAISRNPKEPWRQFI-----NLMIAALPPEPVLHEFHDEEHYPD 355

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                     y + +e L  L++   sL   G   iA   +  + R v tFG  L KLD
  gi|1894995    356 RYRHHDELLSDLDILRDSLLTIGAENIAKNDVNPVYRIVQTFGFHLGKLD 405

                    iRqEseRqtDvlDAittHLei..GsYReWsEeKRqEWLlaElkGKRPLlg
                    iRq s  +   +  + +  + ++  + +W E  R+ +L +EL   RP
  gi|1894995    406 IRQNSRIHDLAMSQLMRAAGFknCDFPDWNEKERMAFLNSELLSPRPFTH 455

                    sDLPktEEvkDvldafrvLA....ELPiDsFGaYiismataPsDvLAvEL
                    +D+    E +  l  +r L ++ +       G+ i+sm+   sD LA+ L
```

```
  gi|1894995   456 PDMEVGPEAETLLRCYRALGkhlkQFGPHGIGSLIVSMTRNVSDLLAIYL 505

                   LqRECgvkqt........LrvvPLFEkLADLeAAPAavekLF.......s
                     RE g+  t+++++   ++vvPLFE + DL   P  +    +++ +++s
  gi|1894995   506 FAREVGLMTThdggdacmIPVVPLFETIDDLTKSPEILREFLdnpltrrS 555

                   iDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKk
                   i + +   +G +++q+vmvGYsDs KD G  s  W LY+A E +  v ++
  gi|1894995   556 IAYHRQIRNGTrpsQQVMVGYSDSNKDGGITSSLWNLYRAEEKMLEVGRE 605

                   yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                     + +  FHGRGG + RG GPtH  i +qP   ++  lRvt qGE i +
  gi|1894995   606 QDIDILFFHGRGGSISRGAGPTHRFIRAQPHCSLETGLRVTEQGETISQK 655

                   FGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPEW..RkLmeemAvvAtEEY
                   +         L  F A   E  +   v Pk   +   +m+ +Av     Y
  gi|1894995   656 YANKINATYNLELFMAGVTEARLAHRVNPKSKMsiEPVMDLLAVESNRAY 705

                   RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWi
                   Rs++  E    E+F  AtP        iGsRP++R     ++ LRAiPW+
  gi|1894995   706 RSLIESEG-LLEFFHQATPIDIIESSRIGSRPSRRSGKESLDDLRAIPWV 754

                   FaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDL
                   F+W q RF +  W G+G A  h  +     +  ++E    WP  R
  gi|1894995   755 FSWNQARFAISGWYGFGSALEHLRKTQPEAFDLIREKDFSWPPLRYIASN 804

                   lEmvFAKGDPGiAaLyDkLLvaEeLkPFG.ksLRdkYvEtkdlLLkiAGH
                   +    A  DP i   y  L+   + +      + ++Y  t++lL
  gi|1894995   805 VSTSIATVDPEIMQKYAMLVENPDTRHRNlTMITAEYRRTRELL------ 848

                   kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                    D+  G         L d +    nvf   t++     + +  l+  l +
  gi|1894995   849 -DIFYGGS-------LQDKF---FNVFRFITMRQEGLSELH-HLQIDLLR 886

                   EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +             L   e  a  +   L+Lt+  iA G+  tG
  gi|1894995   887 TWRKHK---------LSGKEDTADAMLPELLLTVNAIASGLRSTG    922

gi|8247239|emb|CAB92916.1|: domain 1 of 1, from 1 to 370: score 165.4, E = 1.7e-46
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|8247239     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|8247239     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|8247239     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|8247239     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|8247239     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|8247239     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|8247239     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|8247239     - ---------------------------------------------- -
```

```
                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|8247239     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|8247239     - ------------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|8247239     - ------------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|8247239     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYk qEE++KvAK+yGvKL++FHGRGGtvGRGGGPtH+AiLsq
  gi|8247239     9 RLSAAWQLYKTQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHIAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEEnLCF++LqR+tAAtLEHGm+ P sP
  gi|8247239    59 PPDTIHGSLRVTVQGEVIEQSFGEENLCFKTLQRYTAATLEHGMQVPFSP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+emA+vAt+EYRs+v++EPR vEYFRlAtPElEYG+mniGsR
  gi|8247239   109 KPEWRALMDEMAIVATDEYRSIVFQEPRLVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD Knl
  gi|8247239   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIQKDLKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q L+EmY+eWPFFRvt+DL+EmvF KG PGiAaLyDkLLv+ eL  FG++
  gi|8247239   209 QILREMYNEWPFFRVTIDLIEMVFTKGSPGIAALYDKLLVSPELLSFGEQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR+kY+Etk lLLk+AGHk+lLEGDPYLKqrlRLR++YittLnv+qAYtL
  gi|8247239   259 LRAKYEETKRLLLKVAGHKELLEGDPYLKQRLRLRNPYITTLNVCQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDPsy+ t +Ph s E  + n  +a+eLvkLnpt+++aPGLEDtLiL
  gi|8247239   309 KRIRDPSYHLTGKPHPSTEMMNSN-NQAAELVKLNPTSEYAPGLEDTLIL 357

                  tmKGiAAGmqntG<-*
                  tmKGiAAGmqntG
  gi|8247239   358 TMKGIAAGMQNTG    370

gi|18073874|emb|CAC84957.1|: domain 1 of 1, from 1 to 364: score 165.0, E = 2.3e-46
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807387     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807387     - ------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807387     - ------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807387     - ------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807387     - ------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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  gi|1807387     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807387     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807387     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807387     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807387     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807387     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807387     1 -----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYk qEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807387     9 RLSAAWQLYKTQEELVKVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1807387    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emA++At EYRs+v++E  F+EYFR AtPElEYG+mniGsR
  gi|1807387   109 KPEWRTLMDEMAIIATKEYRSIVFQETCFIEYFRRATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD+Knl
  gi|1807387   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIIEKDVKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L++mY++WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv EeL+PFG++
  gi|1807387   209 HMLQDMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVPEELRPFGEQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR +Y+Etk lLL+iAGHkDlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|1807387   259 LRHNYEETKHLLLQIAGHKDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   K iRDP+y+vt+rPhlsKEy  E sk+a+eLvkLnpt+++aPGLEDtLiL
  gi|1807387   309 KQIRDPDYHVTVRPHLSKEYI-ESSKPAAELVKLNPTSEYAPGLEDTLIL 357

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807387   358 TMKGIAA------    364

gi|257784777|ref|YP_003179994.1|: domain 1 of 1, from 61 to 955: score 164.7, E = 2.8e-46
                   *->siDAqLRlLvPGKvsed...ekLieYDALLlDkFL...DiLqDLHGe
                       +   LRl+   Kv  + +++ L  +D LL++    ++D L     +
  gi|2577847    61    NLTFFLRLVR--KVLAEynpDLLTSFDTLLVEAIKagpDDLSTTRAP 105

                   dLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHm
                    L Ea+     +  e   K+         + + sL   D++l+ +a++
  gi|2577847   106 LLLEAINAVLKVDSE---KESLNAFLRFASTIDSLSMEDSVLLMRAFVTF 152

                   LnLAnLAEEvelAyRRRikkkkhGDFaDEasAtt.EsDiEEtlKkLvlkl
                     LAnL EE    yR    + +     D +sA  +  +i   +++L+
  gi|2577847   153 FHLANLCEE---NYRVTSLRSR-EASVDSSSAEDpINEITVAYRQLIDEC 198
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                    nKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKD
                        eE    L       v+tAHPt  +RR  + +  Ri   L     +
  gi|2577847   199 --GEEEAKARLNRLEFHPVFTAHPTE-ARRKNVERRIRIISELLD-ERQR 244

                    vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWk
                    +    + E +  +  Ei   FRt  i   +PtP +E    +  +  t+++
  gi|2577847   245 LGGPARVENERRMLQEIDGLFRTSPIGHKKPTPLEEADTVLNIFDTTLFE 294

                    GvPKFLRRvDt.AL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtP
                     vP   RR D  AL+ n G     P   P  +  sW+G DRDG nP vt
  gi|2577847   295 MVPSVYRRFDNwALgENAGCVP--PVCPPFFRPGSWIGSDRDG-NPNVTA 341

                    EvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaa
                     v R v    R+      ++ + +   E+s        R    +  +t+a
  gi|2577847   342 LVSRQVAEKYRVHV----LQALAEATKEVS--------RGLTLDGISTPA 379

                    rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtG.ise
                    +          W q    E    +     DK      Ra   +  G++s
  gi|2577847   380 SP----ALANLWAQ--QVEMSQALTSRAVDKAGSELHRAAMRVISGrLSA 423

                    isE...eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstF
                      E++ + +y + EeF+  L +   sL + G + iA G +  l+ q  tF
  gi|2577847   424 TIErnaDLMYQNAEEFIADLRVIQDSLVQAGARRIAYGPIQRLIWQAQTF 473

                    GLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkG
                    G  Lv ++ Rq s  +   l  +  H    s  e +         a L
  gi|2577847   474 GFHLVEMEFRQHSLVHKRALADLEAH---PSTAEKP---------AKLDA 511

                    KRPLlgsDLPktEEvkDvldaf.rvLAELPiDsFGaYiismataPsDvLA
                              +t Ev D   +++ +     i +   Yiis + +  Dv
  gi|2577847   512 ----------MTQEVLDTFRSIgSIQKKNGINAARRYIISFTQSAQDVEN 551

                    vELLqRECgvkq....tLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                    v  L R     +++ + L v+PLFE++ DLe A  +++++  i     r+
  gi|2577847   552 VYKLARLAFANEedvpVLDVIPLFEQIEDLENAVTTLDQVIQIPEVQERL 601

                    ...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                    +++d K evm+GYsDs KD G   A   L k q  ++  A k  + L+l
  gi|2577847   602 tqtDRKLEVMLGYSDSSKDEGPTTATLVLHKTQAALAEWAEKNSIDLILM 651

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGG vGRGGGP   A+LsqP   +nG  + t qGEvi   +G+  L
  gi|2577847   652 HGRGGAVGRGGGPANRAVLSQPKGSVNGRFKLTEQGEVIFARYGDPTLAR 701

                    rsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtE.....EYRsv.v
                    r +   + AtL   m P +  k    ++  + A  A E ++ +  R ++
  gi|2577847   702 RHVESVAGATLLQ-MAPSLEQKNTHADV--KFASLASEldkasKQRFLeL 748

                    vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaW
                    +    F E+F + tP +E G + iGsRPaKR  + + ++ LRAiPWiF+W
  gi|2577847   749 IHSDGFAEWFSVVTPLTEIGLLPIGSRPAKRGLGAkSLDDLRAIPWIFSW 798

                    tqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEm
                     q R  L  W G+G A        +  + +L+E YkeWP F   +D +Em
  gi|2577847   799 SQARINLAAWYGLGSACEA-----VGDIERLREAYKEWPLFTTFIDNIEM 843

                    vFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlL
                       K D  iA Ly  L    eL    + +  +   t++++L i G k  L
  gi|2577847   844 SISKVDARIARLYLALGDRPELS---EMVLSEMSLTRKWVLAITGNKWPL 890

                    EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                    E    L   +RLR +++  L v q   L  +R  +   t+         +
  gi|2577847   891 ENRRVLGPVIRLRLPFVNILSVTQVHALSELRTRDDMLTP---------E 931

                    EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    E     +++  L              + t+ G+AAG+qntG
  gi|2577847   932 ER----ANITYLI-------------LCTVSGVAAGLQNTG    955

gi|145637525|ref|ZP_01793183.1|: domain 1 of 1, from 3 to 588: score 163.6, E = 5.8e-46
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                  K s                D   D  Ge L
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gi|1456375     3    ------------KCS-----------------DEFRDKYGEHL---- 16

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E Y
gi|1456375    17 -EPY---------------------------------------------- 19

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                                                       + v+k
gi|1456375    20 -----------------------------------RFVVKN------- 25

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       L+nq     ltA
gi|1456375    26 ---LRNQ-----LTA---------------------------------- 32

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                                                     ++Y+
gi|1456375    33 -------------------------------TLAYF------------- 37

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                      D  L n                          + PRv
gi|1456375    38 --DDHLSN--------------------------RTPRV----------- 48

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                                                         + ++
gi|1456375    49 ---------------------------------------SESE------- 52

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                                +iL d
gi|1456375    53 -------------IILED------------------------------- 57

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                     +  EPL  CY+sL +CG ++iA GsLL +L  +s FG+ L ++DiRqEs
gi|1456375    58 NQLWEPLYDCYQSLIQCGMRIIANGSLLNILHRISCFGVTLSQMDIRQES 107

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                     R+tD +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
gi|1456375   108 TRHTDAIAEITRYIGLGDYSQWMEDDKQAFLIRELSSRRPLIPQNWTPSP 157

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E k++ld+ +v+A         Y+isma + sDvLAv LL +E gv   +
gi|1456375   158 ETKEILDTCKVIAQQKQGVIACYVISMARSASDVLAVHLLLKEAGVPYHI 207

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    +vvPLFE L DL+AA   + +LF + WY+  i+ +q vm+GYsDs KDAG
gi|1456375   208 PVVPLFETLEDLDAAEKVMTQLFNVGWYRGVINNRQMVMIGYSDSAKDAG 257

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                     ++A W  Y+AqE ++    k G+ L+lFHGRGGt+GRGG P H A+Lsq
gi|1456375   258 MMAASWAQYRAQEALVNLTEKLGIELTLFHGRGGTIGRGGAPAHAALLSQ 307

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP  ++  lRvt qGE+i f  G   +   +   ++ A LE  + PP  P
gi|1456375   308 PPRSLKNGLRVTEQGEMIRFKLGLPAVAVETFDLYASAILEANLLPPPEP 357

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR +m+e+  +  + YR vv  +  Fv YFR+AtPE E  k+ +GsR
gi|1456375   358 KPEWRTIMDELSTISCDIYRGVVRGDKDFVPYFRSATPEQELSKLPLGSR 407

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKR P GG+esLRAiPWiFaW q R  LP WLG GAA +  i++    +
gi|1456375   408 PAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGAAIRQVIEQGKGDI 457

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      ++ m ++WPFF   + +lEmvF K D  +   yD+ Lv  eL+  G++
gi|1456375   458 --IHKMCENWPFFSTRIGMLEMVFSKSDTWLSQQYDQRLVKKELWYLGEN 505

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR + ++  + +L +    +l+   P++   + LR+ Y   Ln +q   L
gi|1456375   506 LRKQLEDDIQTVLSLSHQSELMSDLPWIADSIALRNIYTDPLNLLQVELL 555

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
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                   R R                  En             e+v P +E  L++
  gi|1456375   556 HRFR------------------EN------------PEQVNPDVEQALMI 575

                   tmKGiAAGmqntG<-*
                   t+ GiAAGm ntG
  gi|1456375   576 TITGIAAGMRNTG    588

gi|193214511|ref|YP_001995710.1|: domain 1 of 1, from 2 to 922: score 163.1, E = 8.4e-46
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       i   L +  P Kv +d +       L+  F D+L +    +L
  gi|1932145     2    QISSSL-IFDPEKVQQDFE------FLMHCFHDVLEEAGEAELARLL 41

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       E                    L + d   +  +A+a++    L  +
  gi|1932145    42 PWHRE-------------------ALLGTDINMTERLAQAYSIAFQLLGM 72

                   AEE.velAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   AE +  + yRR  +          +     +   E l +L  ++  + e
  gi|1932145    73 AEQnAAIQYRRQLETEL-------GLTKLTALWGESLAHLKARG-LTSEQ 114

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   + e L    v+LvltAHPt + R  +L  + R+   L +   +  t+ ++
  gi|1932145   115 IAETLPQIYVELVLTAHPTEAKRSTVLGHHRRLYLLLVKRENQMWTPSER 164

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   + + + +   +   +Rt Ei   +P    E R  + Y+     +  P
  gi|1932145   165 EAIRDEIKETLALLWRTGEIFLEKPGIALERRNILHYLKTVFPEVLPVLD 214

                   RRvDtALKniGinERl..PY.dvPLikFssWmGGDRDGknPRvtPEvtRD
                    R   A K +G   +  + Y++ P +kF  W+GGDRDG +P vt EvtR+
  gi|1932145   215 ARLKQAWKSVGFDPKAisSYkNLPHLKFGTWVGGDRDG-HPLVTDEVTRE 263

                   vCLLaRmmAanlYisqvEDLmFElsmW.RCn...dELRvRAEElyrtaar
                        R+ A  l  +q+ ++   ls+ +R  ++++ L  R  El     +
  gi|1932145   264 TFAELRLSALLLLHEQLSEMAKNLSISdRLQpppEKLSNRIHELVAQLGK 313

                   dkvvKyYiEFWKqvPPtEPYRviLGdvRDKL.YntRERaRHLLAtGisei
                           E      P EP+R  L  + D L+       + +L +
  gi|1932145   314 S------GEDALLRNPGEPWRQFLNLMQDSLpLEVNYYGKGVLLH----- 352

                   sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                    +   y k  e L  L L   sL e G   iA  s+  + R  s FG  L
  gi|1932145   353 -DKFHYKKAAELLADLQLLHDSLYEIGAGRIAAQSVQPVFRSLSHFGFHL 401

                   vKLDiRqEseRqtDvlDAittHLeiG..sYReWsEeKRqEWLlaELkGKR
                     LDiRq s  +   +  +    +i ++ + +W EeKR  +L  EL+  R
  gi|1932145   402 AVLDIRQNSGFHDRAISQLLAAAGIEdnDFGNWREEKRLQFLRDELRSPR 451

                   PLlgsDLPktEEvkDvldafrvLAELPi....DsFGaYiismataPsDvL
                   P         +E   v+  +rvL E   ++++D  Ga i+sm+ + sD L
  gi|1932145   452 PFTHCHAALGDEASAVISCYRVLVEEMQkngeDGIGALIVSMTRSASDLL 501

                   AvELLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLF....
                    v LL RE g+ ++++ +   +L++vPLFE + DL+  P  +    + +
  gi|1932145   502 SVYLLAREVGLLRqdeagmycPLPIVPLFETIDDLNKSPNILRAFLdfpm 551

                   ...siDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiK
                   + +s+ + + r++  ++ q+vmvGYsDs KD G ++  W LY Aq E++K
  gi|1932145   552 tarSLAYQKMRMNREkpvQQVMVGYSDSNKDGGIFASLWSLYNAQAELAK 601

                   vAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEv
                   +  + G+ +  FHGRGGt+ RG GPtH  i + P   ++G lR+t qGE
  gi|1932145   602 IGEDNGIGICFFHGRGGTISRGAGPTHRFIKALPHLSLQGRLRMTEQGES 651

                   iEfsFGEEnLCFrsLqRFtA....AtLEHGmnP.PvsP.kPEWRkLmeem
                   i + +         L  F A+ ++ tL     P+P+ P +    kL e+
  gi|1932145   652 IAQKYANRITAAYNLELFLAnvtrSTLLDKYFPePIHPlHGTMNKLAEKS 701

                   AvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGie
                     v tE      +    F+++FR AtP     +  iGsRP++R     +
  gi|1932145   702 LSVYTE-----LLNTDGFIDFFREATPIDAIEQSKIGSRPSRRSGKKSLS 746
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                    sLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWP
                     LRAiPW+F+W q R+ L  W GvG A           +  +     +W
  gi|1932145   747 DLRAIPWVFSWGQARYYLSGWFGVGSALESLYSESPADFATVASHLYTWA 796

                    FFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtk
                         l       A  D  + + y  L+  E +++k FG  ++ ++  tk
  gi|1932145   797 PLHYVLSNAATSIALADLDMMSRYAALVENECVreKIFG-MIKGEFIRTK 845

                    dlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsyk
                     +L ki G   l E  P +   + LR   +  L   q   L   R
  gi|1932145   846 TMLEKIYGGA-LEEKRPNIYRMIALRKEGLDVLHSQQLALLTEWR----- 889

                    vtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGm
                       r    +E  +E                    L   L+Lt+  iA Gm
  gi|1932145   890 --KRRNTGREQDAEK------------------LIPHLLLTINAIANGM 918

                    qntG<-*
                      tG
  gi|1932145   919 GSTG    922

gi|7768372|emb|CAB90714.1|: domain 1 of 1, from 1 to 364: score 163.1, E = 8.4e-46
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768372     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768372     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768372     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768372     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768372     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768372     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768372     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768372     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768372     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768372     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768372     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768372     1 -----------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
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                    RlsAAWqLYkAqE++iKvAKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768372      9 RLSAAWQLYKAQEDLIKVAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|7768372     59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emAvvAt EYRs+v++ PRFvEYFRlAt ElEYG+mniGsR
  gi|7768372    109 KPEWRTLLDEMAVVATNEYRSIVFQXPRFVEYFRLATLELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++KDiKnl
  gi|7768372    159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGTAFKHVVQKDIKNL 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvt+DL+EmvFAKG PGiA+LyDkLLv+E+L PFG++
  gi|7768372    209 RILQEMYNEWPFFRVTIDLVEMVFAKGNPGIASLYDKLLVSEDLLPFGER 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+EtkdlLL++AGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|7768372    259 LRANYQETKDLLLQVAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPs++v +rPh+sKE  d   k+a+eLvkLnp +++aPGLEDtLiL
  gi|7768372    309 KRIRDPSFHVKVRPHISKEISDAS-KPAAELVKLNPMSEYAPGLEDTLIL 357

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|7768372    358 TMKGIAA------    364

gi|18073872|emb|CAC84956.1|: domain 1 of 1, from 1 to 364: score 162.6, E = 1.2e-45
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807387      -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807387      - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807387      - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807387      - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807387      - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807387      - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807387      - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807387      - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807387      - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807387      - ---------------------------------------------- -
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                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807387     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807387     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYk qEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807387     9 RLSAAWQLYKTQEELVKVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1807387    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+emA++At EYRs+v++E  F+EYFR AtPElEYG+mniGsR
  gi|1807387   109 KPEWRTLMDEMAIIATKEYRSIVFQETCFIEYFRRATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD+Knl
  gi|1807387   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIEKDVKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L++mY++WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv EeL+PFG++
  gi|1807387   209 HMLQDMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVPEELRPFGEQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR +Y+Etk+lLL+iAGHkDlLEGDPYLKqrlRLRd+YittLnv+qA tL
  gi|1807387   259 LRHNYEETKQLLLQIAGHKDLLEGDPYLKQRLRLRDAYITTLNVCQACTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  K iRDP+y+vt+rPhlsKEy  E sk+a+eLvkLnpt+++aPGLEDtLiL
  gi|1807387   309 KQIRDPDYHVTVRPHLSKEYI-ESSKPAAELVKLNPTSEYAPGLEDTLIL 357

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807387   358 TMKGIAA------    364

gi|171911854|ref|ZP_02927324.1|: domain 1 of 1, from 4 to 929: score 162.2, E = 1.5e-45
                  *->siDAqL..RlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                        A L+++ L     s    Lie    LlDk L  L +     L+
  gi|1719118     4    ---AWLgdKTLETKPAS---TLIEHGFKLLDKELSFLMEAFAAALRR 44

                  avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                  +          + G+  ++            + +    + +a++    L
  gi|1719118    45 IGEPELADRMPWTGQPLPE------------QSGPNRPLCQAYSTAFQLL 82

                  nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                  nL EE      RR + k  G  a+ +      D    ++ L l
  gi|1719118    83 NLVEERVALQVRRLREKELGPLAERG---LWPDKLAAMRELDLDA----R 125

                  EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                   + e +K   v+ vltAHPt + R s+  ++  i   L        t+ +
  gi|1719118   126 AMVEIMKSVRVEPVLTAHPTEAKRDSVRERHREIYDLLERRENPAFTPRE 175

                  KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                  ++ +   L   +   +Rt Ei  ++P   +E+   + ++ E   + v +
  gi|1719118   176 QERVRGFLEAQLESLWRTGEIHVTRPSIAEELENALFFLREVFPEAVTRT 225

                  LRRvDtALKniGinERlPYdv.PLikFssWmGGDRDGknPRvtPEvtRDv
                        A    G+      + +PLi+F  W+GGDRDG +P vt Evt+
  gi|1719118   226 RTHLREAWIAAGLDPVALKELpPLIRFGTWIGGDRDG-HPFVTAEVTKSS 274

                  CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      R  A  l+  ++  L + l + +  +E+ +   El     ++
  gi|1719118   275 LQSLRNNALRLFARKLNRLAYNLPLSKHFQEVPASLGELVTRLVKELEGY 324

                  yYiEFWKqv..PPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
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                     ++    +++  +EP+R     +R KL  tR            + ++ A
  gi|1719118   325 EVVDVPALLdhHDEEPWRLAASLMRGKLLLTR------------DHPDAA 362

                   .vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                   ++y         L L    L   G   +    +  l  q   FG     L
  gi|1719118   363 tIYAAPAALDADLLLLAECLSAVGAEHLVQDYVDPLRHQLAAFGFHSAIL 412

                   DiRqEseRqtDvlDAittHLei...GsYReWsEeKRqEWLlaELkGKRPL
                   D+Rq s  +   l  +    ++++  s+ +WsE  ++  L  EL   RP
  gi|1719118   413 DVRQNSAFHEKALTQLLVKAGVpnaASFPSWSEGEKRTLLDHELASPRPF 462

                   lgsDLPktEEvkDvldafrvLAELPi....DsFGaYiismataPsDvLAv
                   l + L    E   vl+ +rvLAE   ++++   G+ i+sm+    D L v
  gi|1719118   463 LSPGLSAGPEADAVLECYRVLAEYRArhggAGLGSLIVSMTRGVNDLLTV 512

                   ELLqREC........gvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYi
                    +L RE +  + + +g++ +L+vvPLFE + DL  AP  v+   s    +
  gi|1719118   513 YVLAREAglieltaqGLRSPLPVVPLFETMDDLAHAPSVVDDFLSHPVTR 562

                   nridGK.......qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKky
                     + G +++++++ ++m+GYsDs KD G ++  W L +AqE +  v +++
  gi|1719118   563 ISLTGEggsntpdFQMMLGYSDSNKDCGIFASQWGLHRAQEALFEVTRRH 612

                   GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF
                   Gv+ v FHGRGGtvGRG GPtH  + + P   + Gs R+t qGE i + +
  gi|1719118   613 GVRPVFFHGRGGTVGRGAGPTHWFMEALPHGSLGGSFRMTEQGETISQKY 662

                   ...GEEnLCFrsLqR.FtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEE
                   ++ G       +L  +  AAt  H       P    R++++++A    E
  gi|1719118   663 shlGSATYQVETLTAsVSAATAKH--RHASKPADPCREILDRLAGWSIEA 710

                   YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPW
                   YR + +  P F+ ++R AtP        iGsRP++R     +e LRAiPW
  gi|1719118   711 YRGL-LHAPDFITFYREATPIDALENSRIGSRPSRRTGRASLEDLRAIPW 759

                   iFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlD
                   +F+Wtq RF LP W GvG AF          +  L+    e  F R  l
  gi|1719118   760 VFSWTQSRFYLPGWFGVGSAFERLKVEAPDDYAALEGSISESSFLRYVLT 809

                   LlEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAG
                    ++         i   y  L+  E ++ +F + + +++  t++ L  i
  gi|1719118   810 NMDGSIVSANEEIMLAYGSLVTDEAVRTrFMELIIAEFHRTREHLGTILH 859

                   HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                           P +   l +R++ +  L   q   LK  R    + t     +
  gi|1719118   860 GGGFGSRRPRMARTLQVREAPLKVLHHQQVALLKEWR----RLTAAGDTA 905

                   KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      A+E    +d L+ +n                   iA G+  tG
  gi|1719118   906 ---AAEA-MIPDLLISIN-----------------AIASGLRTTG    929

gi|193212217|ref|YP_001998170.1|: domain 1 of 1, from 1 to 919: score 162.0, E = 1.7e-45
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       i   + ++   K +     i++   LlD F+++Lq+L    L
  gi|1932122     1    MITTTMSVVDFDKAA-----IDFQ-FLLDCFIEVLQELGQTKL---- 37

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         +    G +        Ga      P  a+   +a++ +  L n+
  gi|1932122    38 ------ATHLRGEHS-------GAITECEHPERAV---QALSVVFQLLNM 71

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEE   A  RR           E+         E l++L  ++  + +E+
  gi|1932122    72 AEENSAAQYRRQLESN------EGVESLSGLWGEALRHLQKLG-ITEAEI 114

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      L n  v+  ltAHPt + RR +L ++  +   L +   +  t+ +++
  gi|1932122   115 AAELPNIEVEPTLTAHPTEAKRRTVLEQHRELYLLLVKRENRMWTPAERE 164

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    +   +   +   +Rt Ei   +P    E    + Y+H    +  P
  gi|1932122   165 KIRTDIKVVLERLWRTGEILFEKPDVGTERQNVLHYLHTIFPDVLPMIDQ 214
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                    RvDtALKniGinERl...PYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                    R + A    G   +++ +P + P + F sW+GGDRDG +P vt + tR+
  gi|1932122   215 RLEKAWSVAGFDPKItadPRNLPRLSFGSWVGGDRDG-HPLVTADTTRET 263

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                        R  A  l    +E L   ls+    +      EE     + +
  gi|1932122   264 LQEMRRHAIRLVRHHLEQLASKLSISGRFQSPTGAMEERMEIMRHK---- 309

                    yYiEFWKqvPPt..EPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                       E  + +  +++EP+R  L  +   L          L   + e +
  gi|1932122   310 LGEEGQRALDRNrhEPWRQFLNLMIASLPDES------LQEHFDE-PAHY 352

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                     y +  e L  +EL   sL   G   i  G +  + R   tFG  L +LD
  gi|1932122   353 QYKRHTELLSDIELFMSSLSAIGGANISLGDVAPVFRIAQTFGFHLGRLD 402

                    iRqEseRqtDvlDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLlg
                    iRq s  +   l  + t  ++++  + eWsEeKR+E+L  EL   RP
  gi|1932122   403 IRQNSRFHDLALSQLMTAAGLdgAGFPEWSEEKRMEFLERELLSPRPFTH 452

                    sDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAvEL
                    +D+    E + vl  +rvL E+ ++   D  G+ i+sm+   sD L v L
  gi|1932122   453 PDMQVGPEAETVLACYRVLFEharqYGYDGIGSLIVSMTRNVSDLLVVYL 502

                    LqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                      RE g+ +++++++  +++vvPLFE + DLe     +++  +    +
  gi|1932122   503 FAREVGLMEphgdgdacPIPVVPLFETIDDLERSHDILDRFLAHPVTRRS 552

                    idGKqev..........mvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKk
                    i  +qe ++++++ ++ mvGYsDs KD G +   W LY+A E +i   +k
  gi|1932122   553 IALQQELhgrskpvqqaMVGYSDSNKDGGIITSLWGLYRAEERLIEAGRK 602

                    yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                    +G+ +  FHGRGG + RG GPtH  i +qP   ++  lRvt qGE i +
  gi|1932122   603 HGIDVLFFHGRGGSISRGAGPTHRFIRAQPHGSLDAGLRVTEQGETIAQK 652

                    FGEEnLCFrsLqRFtA....AtLEHGmnPPvsPkPEWRkLmeemAvvAtE
                    +         L  F A+ ++A LEH  +    P+P   k m+ +A
  gi|1932122   653 YANRISAAYNLELFLAgiteARLEH-RKDGYRPHP-LEKAMDLLARSSNQ 700

                    EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                     YR ++  +    ++FR AtP        iGsRPa+R     ++ LRAiP
  gi|1932122   701 AYRQLIEADG-LLDFFRQATPIDIIESSRIGSRPARRTGKQSLDDLRAIP 749

                    WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                    W+F+W q RF +  W G G A       D   +  ++     W  F   +
  gi|1932122   750 WVFSWNQARFGISGWYGAGTALEELRTTDPDSFDIMRQTDFSWAPFHYII 799

                    DLlEmvFAKGDPGi....AaLyDkLLvaEeLkPFGksLRdkYvEtkdlLL
                      +       DP + ++ A+L ++  + E+L      + ++Y  t  lL
  gi|1932122   800 NNVATSVLSADPWVmekyASLVEDRTIRENLLGM---IQAEYLRTMRLLE 846

                    kiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlr
                     i G   l E    +   +  R   +  L  +q   LKR R
  gi|1932122   847 LIYGGS-LKEKYFNVYRFIENRKEGLGKLHSLQIDLLKRWR--------- 886

                    PhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG
                              n +ka +    n  ++ a  L   L+Lt+  i  G+  tG
  gi|1932122   887 ----------N-HKATG----N--QEQAESLLPELLLTVNAISGGLRTTG 919

                    <-*

  gi|1932122     -     -

gi|18076765|emb|CAC84926.1|: domain 1 of 1, from 1 to 364: score 161.9, E = 1.9e-45
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807676     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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gi|1807676     - ------------------------------------------------- -

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1807676     - ------------------------------------------------- -

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1807676     - ------------------------------------------------- -

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1807676     - ------------------------------------------------- -

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1807676     - ------------------------------------------------- -

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1807676     - ------------------------------------------------- -

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1807676     - ------------------------------------------------- -

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1807676     - ------------------------------------------------- -

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|1807676     - ------------------------------------------------- -

                 EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|1807676     - ------------------------------------------------- -

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                       sDsGKDAG
gi|1807676     1 -------------------------------------------SDSGKDAG 8

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 RlsAAWqLYkAqE++iKvAKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1807676     9 RLSAAWQLYKAQEDLIKVAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                 PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
gi|1807676    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 108

                 kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                 kPEWR L++emAvvAt EYRs+v++EPR vEYFRlAtPElEYG+mniGsR
gi|1807676   109 KPEWRTLLDEMAVVATNEYRSIVFQEPRLVEYFRLATPELEYGRMNIGSR 158

                 PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                 P++ kPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++KDiKnl
gi|1807676   159 PSQQKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGTAFKHVVQKDIKNL 208

                 qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   L+EmY+eWPFFRvt+DL+EmvFAKG PGiA+LyDkLLv+E+L+ F ++
gi|1807676   209 RILQEMYNEWPFFRVTIDLVEMVFAKGNPGIASLYDKLLVSEDLWSFAER 258

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                 LR++Y+EtkdlLL++AGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
gi|1807676   259 LRANYQETKDLLLQVAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 308

                 KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                 KRiRDP+++v +rPh+sKE  d   k+a+eLvkLnpt+++aPGLEDtLiL
gi|1807676   309 KRIRDPNFHVKVRPHISKEISDAS-KPAAELVKLNPTSEYAPGLEDTLIL 357
```

```
                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807676   358 TMKGIAA------    364

gi|18073868|emb|CAC84951.1|: domain 1 of 1, from 1 to 373: score 161.9, E = 1.9e-45
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807386     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807386     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807386     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807386     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807386     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807386     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807386     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807386     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807386     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807386     - ---------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807386     - ---------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|1807386     1 -----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807386     9 RLSAAWQLYKAQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDt++GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGmnPPv+P
  gi|1807386    59 PPDTVHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMNPPVAP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++emAvvAtE YRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|1807386   109 KPEWRALLDEMAVVATEKYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhAi+KD++nl
  gi|1807386   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAIEKDVRNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+ mY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+ FG++
```

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  gi|1807386   209 HMLQAMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWSFGER 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR +Y +tk +LL+iAGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|1807386   259 LRTHYDDTKSYLLQIAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEn........skkadeLvkLnptervaP
                   KRiRDPsy+vt+rPh+sKE  +  ++++++++s +a eLvkLn t+++aP
  gi|1807386   309 KRIRDPSYRVTVRPHISKEIMESSssssssstSNPAYELVKLNTTSEYAP 358

                   GLEDtLiLtmKGiAAGmqntG<-*
                   GLEDtLiLtmKGiAA
  gi|1807386   359 GLEDTLILTMKGIAA------    373

gi|197116626|ref|YP_002137053.1|: domain 1 of 1, from 1 to 911: score 161.5, E = 2.5e-45
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          q     P K   d          lD  +D L ++    L+E
  gi|1971166     1    ---MQDTKETPDKLQRD----------LDYLMDCLAEMF-SGLQEK- 32

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       ElsA               +  sL+P+      +a +    L  +
  gi|1971166    33 ----ELSACL-------------PRADSLAPGADCRFVRAWSIAFQLLSM 65

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEE + A   R  +        E     E  +   +   +     + eE
  gi|1971166    66 AEE-NFAVQSRRALEA------EQGLVAEPGLWGRVLEQIKESGVTAEEL 108

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      L    v+ vltAHPt + R s+L     +   L +      t+ +K
  gi|1971166   109 AAKLGQIRVEPVLTAHPTEAKRASVLRHLRELYLLLVKRENTVWTPAEKD 158

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ++ + +   +   +Rt Ei   +P    E+   +  + E   k +P
  gi|1971166   159 DIRDDIVAMLERLWRTGEIHLEKPHVLNELASMIYHLREIFPKAIPILDQ 208

                   RvDtALKniGinERl.PYdvPL..ikFssWmGGDRDGknPRvtPEvtRDv
                   R+  A    G+   ++P    L++i Fs W+GGDRDG +P vtPEvt
  gi|1971166   209 RICRAWSEAGLAGAIsPLTTALprISFSTWVGGDRDG-HPLVTPEVTEAT 257

                   CLLaRmmAanlYisqvEDLmFElsmWRC....ndELRvRAEEl..yrtaa
                       R+ A  l   q+  L   ls+ R   ++   L  R + l  ++ +a
  gi|1971166   258 LKELRLNALMLIHGQLTTLGSRLSLSRRlihpSAGLQRRLDQLaaHSGPA 307

                   rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                            E  +   P+EP+R ++  ++ +L         +L   +
  gi|1971166   308 GS-------EALRR-NPEEPWRQMVNLIKARLPVDVTGEEEILCGDLG-- 347

                   sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                        y + +e    L L   sL   G   +A   ++ +LR v  FG  L
  gi|1971166   348 ---TRYCHSDELAHDLRLLRDSLVAAGASRLALADVVPVLRTVEVFGFHL 394

                   vKLDiRqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKR
                     LDiRq s  +   +D +    +i   R ++WsEeKR  +L  EL   R
  gi|1971166   395 ASLDIRQNSSYHDKAVDQLLAAAGISDHRfsQWSEEKRLAFLDQELASPR 444

                   PLlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvL
                   P + +D     E + vl+ frvLA +      D+ G+ i+sm+ + sD L
  gi|1971166   445 PFVRADAKPGPEAEGVLGCFRVLAAhialYGTDAIGPLIVSMTRSVSDLL 494

                   AvELLqRECgvkqt........LrvvPLFEkLADLeAAPAavekLF...s
                    v LL RE g+  +++++    L+vvPLFE + DL+   A +e    +++
  gi|1971166   495 VVYLLAREAGLTAAgeggavclLPVVPLFETIDDLRGSSAILEAFLvhpA 544

                   iDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKk
                   +     ++ G ++ q+vmvGYsDs KD G l+  W LY+ qE +   A++
  gi|1971166   545 TRRTLAHLHGDqpvQQVMVGYSDSNKDGGILASLWSLYRGQEAMLETARR 594

                   yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                    Gv+L  FHGRGGt+ RG GPt   +   P     G lR t qGEvi +
  gi|1971166   595 LGVRLRFFHGRGGTISRGAGPTSRFLRGLPEGSTGGDLRLTEQGEVISQK 644
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                    FGEEnLCFrsLqRFtAAtLEHGmnP..PvsPkPEWRkLmeemAvvAtEEY
                    +         L    A t    + P++P  Pk     Lm+++A      Y
  gi|1971166   645 YSNPLNAAYNLELLLAGTAVVTLPPrqPAIPKERLESLMDRLAQRSRFAY 694

                    RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWi
                      + + EP F+ +FR AtP        iGsRPa+R  s  +  LRAiPW+
  gi|1971166   695 EQL-LAEPGFIKFFRQATPIDVIECSSIGSRPARRSRSATLSDLRAIPWV 743

                    FaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDL
                    F+W q R+ L  W GvG A    ++ D + +  L    + W      +
  gi|1971166   744 FSWSQARYFLSGWYGVGSALEELLNEDERSFRELAGHSQSWTALHYIISN 793

                    lEmvFAKGDPGiAaLyDkLLvaEeLk.PFGksLRdkYvEtkdlLLkiAGH
                         A  D  i   y  L+    +++P    L+ +Y  t  +L +i G
  gi|1971166   794 TATSIATADLQIMQAYAGLVLDQTVRdPIFALLKGEYLRTTRILEEIYGG 843

                    kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                      l E    +   l  R+  +  L   q   L+  R P+
  gi|1971166   844 A-LAERRASVYTSLARREGALKVLHDRQIDLLRQWRRPE----------- 881

                    EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       + n  + +eL+           LE     t+  iAAG+  tG
  gi|1971166   882 --TQQNRAQCEELLFWL--------LE-----TVNAIAAGLGTTG    911

gi|18073870|emb|CAC84955.1|: domain 1 of 1, from 1 to 364: score 161.5, E = 2.5e-45
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807387     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807387     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807387     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807387     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807387     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807387     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807387     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807387     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807387     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807387     - ------------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807387     - ------------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
```

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  gi|1807387     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYk qEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807387     9 RLSAAWQLYKTQEELVKVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1807387    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emA++At EYRs+v++E  F+EYFR AtPElEYG+mniGsR
  gi|1807387   109 KPEWRTLMDEMAIMATKEYRSIVFQETCFIEYFRRATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD+Knl
  gi|1807387   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIEKDVKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L++mY++WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv EeL+PFG++
  gi|1807387   209 HMLQDMYNQWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVPEELRPFGEQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR +Y+Etk+lLL+iAGHkDlLEGDPYLKqrlRLRd+YittLnv+qA tL
  gi|1807387   259 LRHNYEETKQLLLQIAGHKDLLEGDPYLKQRLRLRDAYITTLNVCQACTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   K iRDP+y+vt+rPhlsKEy  E sk+a+eLvkLnpt+++aPGLEDtLiL
  gi|1807387   309 KQIRDPDYHVTVRPHLSKEYI-ESSKPAAELVKLNPTSEYAPGLEDTLIL 357

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807387   358 TMKGIAA------    364

gi|21674458|ref|NP_662523.1|: domain 1 of 1, from 1 to 914: score 161.3, E = 2.8e-45
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           +       v  d  L+++  LL D F+++L  L  e L
  gi|2167445     1    -----MITSTTSVVDFDKALLDFRYLL-DCFIEVLENLGQEAL---- 37

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                          A   G      + E        d a+  + A +i  +  L n+
  gi|2167445    38 -------ARHIGGDSKTPIRE-------FDCAERAIQAWSI--VFQLLNM 71

                   AEEvelA.yRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   AEE   A+yRRRi+       + E+         E l++L  ++  + +E
  gi|2167445    72 AEENSAAqYRRRIE-------SSEGVESLSGLWGEALRHLKNLG-VTEAE 113

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   +   L    v+  ltAHPt + RR +L ++  +   L +   +  t+ ++
  gi|2167445   114 IAAELPQIEVEPTLTAHPTEAKRRTVLEQHRELYLLLVKRENRMWTPAER 163

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     +   +   +   +Rt Ei   +P    E    + Y+H    +  P
  gi|2167445   164 DKIRTDIKVVLERLWRTGEILLQKPEVSAERQNVLHYLHTIFPDILPILD 213

                   RRvDtALKniGinERl...PYdvPLikFssWmGGDRDGknPRvtPEvtRD
                    R + A    G    ++ +P + P + F sW+GGDRDG +P vt E t +
  gi|2167445   214 NRLEKAWAVAGFDPAItadPRNLPRLSFGSWVGGDRDG-HPLVTAETTQE 262

                   vCLLaRmmAanlYisqvEDLmFElsm.WRCndELRvRAEElyrtaardkv
                        R  A  l   q+E L   ls++ R  +  R+  EE   t + +
  gi|2167445   263 TLQEMRRHAIELVHRQLERLASMLSLsGRLQSPSRA-MEERMETLRHKLG 311

                   vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                       + F + +   EP+R        +  n    a   L  G  e  E
  gi|2167445   312 KAGALAFERNL--HEPWR--------QFVNLMIAA---LPAGTTE-NEHY 347

                   vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                    y +  e L  LEL   sL       iA G +  + R v tFG  L +LD
  gi|2167445   348 CYRRHTELLKDLELLMSSLTAINASTIARGDVAPVYRIVQTFGFHLGRLD 397
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                    iRqEseRqtDvlDAittHLeiG..sYReWsEeKRqEWLlaELkGKRPLlg
                    iRq s  +   l  +    ++ ++ + eWsEe R E+L  EL   RP
  gi|2167445   398 IRQNSRFHDLALSQLMMAAGLDgkGFPEWSEEARLEFLERELLSPRPFTH 447

                    sDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAvEL
                    +D+    E + v+  +rvL ++ ++   D  G+ i+sm+   sD L + L
  gi|2167445   448 PDMHAGPEAETVIACYRVLFDhyrqFGPDGIGSLIVSMTRNLSDLLVIYL 497

                    LqRECg..vkq......tLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                      RE g  v++++++  +++vvPLFE + DLe     +++  +    +
  gi|2167445   498 FAREVGlmVRHgdgdacPIPVVPLFETIDDLERSHDILDRFLAHPVTRRS 547

                    i......dGK....qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKk
                    i  +++  G++++ q+vmvGYsDs KD G +   W LY+  E +i   +k
  gi|2167445   548 IalqqelHGRqkpvQQVMVGYSDSNKDGGIVTSLWSLYRSEERLIETGRK 597

                    yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                    +Gv +  FHGRGG + RG GPtH  i +qP   ++  lRvt qGE i +
  gi|2167445   598 HGVDILFFHGRGGSISRGAGPTHRFIRAQPHGSLDAGLRVTEQGETISQK 647

                    FGEEnLCFrsLqRFtAAtLEHGm.nPPvsPkPE.WRkLmeemAvvAtEEY
                    +         L  F A   E  + +     +P +  k+m+ +A      Y
  gi|2167445   648 YANRISAAYNLELFLAGVTEARLvHRKEGYRPHpLEKVMDTLARSSNKAY 697

                    RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWi
                    R ++  +    E+FR AtP        iGsRPa+R  s  +e LRAiPW+
  gi|2167445   698 RQLIEADG-LLEFFRQATPIDIIESSRIGSRPARRTGSQSLEDLRAIPWV 746

                    FaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDL
                    F+W q RF +  W G G A       D   +  ++     W  F   +
  gi|2167445   747 FSWNQARFGISGWYGAGSALEELRATDPETFEVMRKSDFSWAPFHYIINN 796

                    lEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGH
                    +       DP i   y  L+   +++ +    + ++Y  t  lL
  gi|2167445   797 IATSILSVDPWIMEQYASLVENKNIREnLLGMIQAEYLRTMRLL------ 840

                    kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                     DlL G P       LR+      nv   +   R    s    l+  l K
  gi|2167445   841 -DLLYGGP-------LREKH---FNVAR-FIETRQEGLSKLHRLQIDLLK 878

                    EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     +       a +    n  e+ a  L   L Lt+  i  G+  tG
  gi|2167445   879 SWRSAK---ASG----N--EQQADALLPELFLTVNAISSGLRTTG    914

gi|284029411|ref|YP_003379342.1|: domain 1 of 1, from 7 to 879: score 161.3, E = 2.9e-45
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          A  R  +   v   e+L     LL +    +L +  G+ L + v
  gi|2840294     7    QASARTRTRARFEVP--EELRADVRLLGEILGRVLVEYAGQPLLDDV 51

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        El    +G       e L a        D   vA+a+     L nL
  gi|2840294    52 EKLRELTIAGDGEAA----EQLVASWPHERAED---VARAFTCYFHLTNL 94

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     EE    +R R+ + +  D + +a A   s++   + ++        e
  gi|2840294    95 SEEL---HRARVLRER--DRSGDAPAV--SELAQAVERISADA---GEQQ 134

                    FeALKn.qsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                      AL n+     vltAHPt + RR++L    Ri   L           +
  gi|2840294   135 ARALLNgLEFRPVLTAHPTEARRRAVLATIRRISSLLEERNDPRAGDSEL 184

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     E    L   +   +Rt  +R ++PtP DE+R  m+ + Et+++ v
  gi|2840294   185 AENRRRLVEQVDILWRTSQLRTSRPTPLDEVRSAMAVFEETLFDVVGNVY 234

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    RR D AL       R P  +P ++  sW+GGDRDG nP vt  +tR+
  gi|2840294   235 RRLDDALAGDAAGTRPPVVAPFVRLGSWIGGDRDG-NPNVTAAITREAMQ 283

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                    +          +  ++L   l +        +    +   a+
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  gi|2840294   284 IQADHVLRALEQATDELGRALTLDAATTPPSAPVRRILEDARAA--NPAL 331

                   iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                   i       P EP R +L     +L  tR R              +  y +
  gi|2840294   332 IADIETRSPSEPHRQLLLLAARRLAATRSR------------DADFGYPR 369

                   vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                     +FL  L +   sL   G    A G L  l+ qvs FG  L  L++Rq
  gi|2840294   370 AADFLHELKVLQDSLVSAGAPRQAYGQLQQLIWQVSSFGFHLAELEVRQH 419

                   seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                   s  +   l+ +   L+ G                EL+           +t
  gi|2840294   420 SSVHAKALEEV---LGGG----------------ELSD----------QT 440

                   EEvkDvldafrvLAELPiDsFGa.....YiismataPsDvLAv.ELLqRE
                   EE   vl ++rv+  +    FG++  ++Y++s + + +D  Av EL
  gi|2840294   441 EE---VLATLRVIGQI-QQRFGPeacrrYVVSFTRSAADLAAVyELADAA 486

                   Cgvk.qtLrvvPLFEkLADLeAAPAavekLFsiDWYinri...dGKqevm
                      ++  L vvPLFE   DL+     ++    +   + r++ +d + evm
  gi|2840294   487 MDGRpIELDVVPLFETGEDLQNSVEVLDNAIQLTRVRHRLtanDRRFEVM 536

                   vGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRG
                   +GYsDs KD G +sA   LY Aq  i   A++  ++L+lFHGRGG  GRG
  gi|2840294   537 LGYSDSAKDVGPVSATLALYDAQARITAWAQRNAIRLTLFHGRGGALGRG 586

                   GGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAt
                   GGP   A+L+q P  + G  + t qGE i   +G   +  r +   tAAt
  gi|2840294   587 GGPANRAVLAQAPGSVGGRFKLTEQGEAIPARYGNAPIAQRHIEQVTAAT 636

                   LEHGmnPPvsPkPEWRkLmeemAvv.......AtEEYRsvvvKEPRFvEY
                   L     P v  +       ++ Avv+++ ++ A   Y  +v K   F E+
  gi|2840294   637 L-LASTPAVEDRAA--AAANRFAVVektldeaARTAYHRLV-KADGFAEW 682

                   FRlAtPElEYGkmniGsRPaKR.kPsGGiesLRAiPWiFaWtqtRFHLPv
                   F   tP  E G++ +GsRPa+R+     +e LRAiPW+FaW q R   P
  gi|2840294   683 FGRVTPLEELGQLPLGSRPARRgVAVSSLEDLRAIPWVFAWSQARVNAPG 732

                   WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                   W G+G A        +  +  L++  k+WP F v l+  Em  AK D  i
  gi|2840294   733 WYGLGSALAA-----VGDVAVLQDANKNWPLFQVMLENAEMSLAKTDRRI 777

                   AaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                    + y +L    +L    + + d+   t +++Lk+     lL G   L
  gi|2840294   778 LGRYLELGDRPDLS---QLMLDEHALTTEWVLKVLDGDRLLAGRRVLGRA 824

                   lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                   + LR++Y+  L  +q   L+ +R              +  dE+     ++
  gi|2840294   825 VELRNPYVDALSYLQLRALRDLR------------TDDSLDEQ-----QI 857

                   vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   v+              L+Lt+ G+AAG+qntG
  gi|2840294   858 VRTR----------RLLLLTVSGVAAGLQNTG    879

gi|20196790|emb|CAC86367.1|: domain 1 of 1, from 1 to 382: score 160.8, E = 4e-45
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2019679     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2019679     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2019679     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                                 HPtqsvRRsLLqKna+iRn L qL+AKD+t ++K+
  gi|2019679     1 --------------HPTQSVRRSLLQKNAKIRNSLKQLYAKDITADEKQ 35
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                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEAL R iqAAFRtDEiRR+qPtPqDEmR+GmsY+HEt+WkGvP+FLR
  gi|2019679     36 ELDEALQRQIQAAFRTDEIRRTQPTPQDEMRYGMSYFHETIWKGVPRFLR 85

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALK iGinERlPY++PLi+FssWmGGDRDG nPRvtPEvtRDv LL
  gi|2019679     86 RVDTALKSIGINERLPYNAPLIRFSSWMGGDRDG-NPRVTPEVTRDVVLL 134

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlYisq+EDLmFElsmWRC dELR+RAEE y  + +    K+Yi
  gi|2019679    135 ARMMAANLYISQIEDLMFELSMWRCTDELRARAEEWYHVSSKI--EKHYI 182

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+P  EPYRviLG vRDKLY tRER+R LL  G+s+i+E   +t+v
  gi|2019679    183 EFWKQIPLDEPYRVILGYVRDKLYATRERSRQLLIDGFSNIPESSAFTNV 232

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    EeFLEPLELCY+sLC  GDk+i DGsLLD+LRqvstFGLsL KLDiRq s
  gi|2019679    233 EEFLEPLELCYRSLCASGDKAITDGSLLDFLRQVSTFGLSLGKLDIRQKS 282

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    eR+tDv+DAittHL+iGsYReW E+KR EWLl+EL+GKRPLl +D+P+t+
  gi|2019679    283 ERHTDVIDAITTHLGIGSYREWDEDKRIEWLLSELRGKRPLLAPDMPQTD 332

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    E++Dvl+a+rv+AELP+DsFG+Yiismata sDvL v LLqREC v
  gi|2019679    333 EIADVLGALRVIAELPSDSFGPYIISMATATSDVLTVHLLQRECRV---- 378

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG

  gi|2019679      - ------------------------------------------------- -

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|2019679      - ------------------------------------------------- -

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                                                                    P
  gi|2019679    379 -------------------------------------------------P 379

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kP+
  gi|2019679    380 KPD---------------------------------------------- 382

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|2019679      - ------------------------------------------------- -

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|2019679      - ------------------------------------------------- -

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|2019679      - ------------------------------------------------- -

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|2019679      - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|2019679      - -------------    -

gi|18073864|emb|CAC84949.1|: domain 1 of 1, from 1 to 373: score 160.6, E = 4.6e-45
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807386      -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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gi|1807386     - ------------------------------------------------ -

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1807386     - ------------------------------------------------ -

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1807386     - ------------------------------------------------ -

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1807386     - ------------------------------------------------ -

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1807386     - ------------------------------------------------ -

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1807386     - ------------------------------------------------ -

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1807386     - ------------------------------------------------ -

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1807386     - ------------------------------------------------ -

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|1807386     - ------------------------------------------------ -

                 EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|1807386     - ------------------------------------------------ -

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                       sDsGKDAG
gi|1807386     1 ------------------------------------------SDSGKDAG 8

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1807386     9 RLSAAWQLYKAQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                 PPDt++GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGmnPPv+P
gi|1807386    59 PPDTVHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMNPPVAP 108

                 kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                 kPEWR L++emAvvAtE YRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
gi|1807386   109 KPEWRALLDEMAVVATEKYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                 PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                 P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhAi+KD++nl
gi|1807386   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAIEKDVRNL 208

                 qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  +L+ mY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+ FG++
gi|1807386   209 HMLQAMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWSFGER 258

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                 LR +Y +tk +LL+iAGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
gi|1807386   259 LRTHYDDTKSYLLQIAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 308

                 KRiRDPsykvtlrPhlsKEyAdEn........skkadeLvkLnptervaP
                 KRiRDPsy vt+rPh+sKE  +  ++++++++s +a eLvkLn t+++aP
gi|1807386   309 KRIRDPSYSVTVRPHISKEIMESSssssssstSNPAYELVKLNTTSEYAP 358

                 GLEDtLiLtmKGiAAGmqntG<-*
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                 GLEDtLiLtmKGiAA
  gi|1807386   359 GLEDTLILTMKGIAA------    373

gi|253698863|ref|YP_003020052.1|: domain 1 of 1, from 2 to 912: score 160.5, E = 5.1e-45
                 *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          R   P K   d          lD  +D L ++    L E
  gi|2536988     2    ---QDNREQTPEKLQRD----------LDYLMDCLAEMF-SGLGEK- 33

                 qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     ElsA          L   G    sL+P+      +a +    L  +
  gi|2536988    34 ----ELSA---------CLPRAG----SLAPGVDCRFVRAWSIAFQLISM 66

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                 AEE      RR     hG  a+ +           l ++   +  + e+
  gi|2536988    67 AEENFAVQSRRSLESSHGLVAEPGL------WGRVLEQIKESG-VTAEDL 109

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   AL    v+ vltAHPt + R s+L     +   L +      t+ +K
  gi|2536988   110 AAALGKIRVEPVLTAHPTEAKRASVLRHLRELYLLLVKRENTVWTPAEKD 159

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                 ++   +   +   +Rt Ei   +P    E+   +  + E   k +P   +
  gi|2536988   160 DIRNDIVAMLERLWRTGEIHLEKPHVLNELSSMIYHLREIFPKAIPILDK 209

                 RvDtALKniGinERl.PYdvPL..ikFssWmGGDRDGknPRvtPEvtRDv
                 R+  A    G+   ++P    L++i Fs W+GGDRDG +P vtPEvt
  gi|2536988   210 RICRAWTEAGLAGAIsPLTTALprISFSTWVGGDRDG-HPLVTPEVTEAT 258

                 CLLaRmmAanlYisqvEDLmFElsmWRC....ndELRvRAEEl..yrtaa
                     R+ A  l   q+  L   ls  R    +  EL  R + l   + +a
  gi|2536988   259 LKELRLNALMLIHGQLTTLGSRLSFSRRlmlpSAELQKRLDQLaaRSGPA 308

                 rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                      +          P+EP+R ++  +R +L         +L   +
  gi|2536988   309 GSDALRR--------NPEEPWRQMVNLIRARLPVDVTGEEEILCGDLG-- 348

                 sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                      y + +e    L L   sL   G   +A   ++ +LR v  FG  L
  gi|2536988   349 ---TRYCHSDELAGDLRLLRDSLMAAGASRLALADVVPVLRTVEVFGFHL 395

                 vKLDiRqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKR
                   LDiRq s  +   +D +    ++   R ++WsEeKR  +L  EL   R
  gi|2536988   396 ASLDIRQNSSYHDKAVDQLLAAAGVSDHRfsQWSEEKRLAFLDQELASPR 445

                 PLlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvL
                 P + +D     E + vl+ frvLA +      D+ G+ i+sm+ + sD L
  gi|2536988   446 PFVRADAKPGPEAEGVLGCFRVLAAhialYGTDAIGPLIVSMTRSVSDLL 495

                 AvELLqRECgvkqt........LrvvPLFEkLADLeAAPAavekLF...s
                  v LL RE g+  ++ +++   L+vvPLFE + DL+   A +e    +++
  gi|2536988   496 VVYLLAREAGLTAAgaggqvclLPVVPLFETIDDLQGSSAILEAFLvhpA 545

                 iDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKk
                 +     ++ G ++ q+vmvGYsDs KD G l+  W LY+ qE +   A++
  gi|2536988   546 TRRTLAHLHGDkpvQQVMVGYSDSNKDGGILASLWSLYRGQEAMLATARR 595

                 yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                  Gv+L  FHGRGGt+ RG GPt   +   P     G lR t qGEvi +
  gi|2536988   596 LGVRLRFFHGRGGTISRGAGPTSRFLRGLPEGSAGGDLRLTEQGEVISQK 645

                 FGEEnLCFrsLqRFtAAtLEHGmnP..PvsPkPEWRkLmeemAvvAtEEY
                 +         L    A      + P++P  Pk     Lm+++A      Y
  gi|2536988   646 YSNPLNAAYNLELLLAGAAVVTLAPrrPAVPKERLESLMDRLAQRSRFAY 695

                 RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWi
                   + + EP F+++FR AtP        iGsRPa+R  s  +  LRAiPW+
  gi|2536988   696 EQL-LAEPGFIDFFRQATPIDVIECSSIGSRPARRSRSATLSDLRAIPWV 744

                 FaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDL
                 F+W q R+ L  W GvG A    ++ D + +  L    + W      +
  gi|2536988   745 FSWSQARYFLSGWYGVGFALEELLNEDERSFRELAGHSQSWTALHYIISN 794
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                   lEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGH
                        A     i   y  L+    ++ +    L+ +Y  t  +L +i G
  gi|2536988   795 TATSVATANLQIMQAYAGLVLDQGVRDrIFALLKGEYLRTTRILEEIYGG 844

                   kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                     l E    +   l  R+  +  L   q   L+  R P+
  gi|2536988   845 A-LAERRASVYSSLARREEALKVLHDRQIDLLRQWRRPE----------- 882

                   EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     A+ n  + +eL  L             L+ t+  iAAG+  tG
  gi|2536988   883 --AQQNRAQCEEL--LF----------RLLETINAIAAGLGTTG    912

gi|83779598|gb|ABC47615.1|: domain 1 of 1, from 1 to 364: score 160.2, E = 6e-45
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|8377959     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|8377959     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|8377959     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|8377959     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|8377959     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|8377959     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|8377959     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|8377959     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|8377959     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|8377959     - ---------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|8377959     - ---------------------------------------------- -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|8377959     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqE++iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|8377959     9 RLSAAWQLYKAQEDLIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP+ti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PPvsP
  gi|8377959    59 PPETIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPVSP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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                    kPEWR L++emA vAt+EYRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|8377959   109 KPEWRALLDEMALVATDEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KDi nl
  gi|8377959   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIKKDIWNL 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L++mY+ WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+EeL+PFG++
  gi|8377959   209 NMLQDMYNSWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEELWPFGEK 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Etk++LL+iAGH+DlLEGDP LKqrlRLRdsYittLnv+qAYtL
  gi|8377959   259 LRTNYEETKKFLLQIAGHRDLLEGDPHLKQRLRLRDSYITTLNVCQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPsy v +rPh+sKE  + n k a eL+ Lnpt+++aPGLEDtLiL
  gi|8377959   309 KRIRDPSYSVNVRPHISKEIMETN-KSASELLILNPTSEYAPGLEDTLIL 357

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|8377959   358 TMKGIAA------    364

gi|210632317|ref|ZP_03297284.1|: domain 1 of 1, from 46 to 941: score 159.5, E = 9.7e-45
                    *->siDAqLR.lLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEa
                        i A LR+ L+     e   L eYD  +lD F +++  +   +  +
  gi|2106323    46    DIPAELRdNLALFLRLERRVLREYDPAVLDTFDELMMNVIRANAGDP 92

                    vqECYElsAeYEGK.....kDtkKLeELGakLtsLdPaDailvAkailHm
                      E      +  G + +++  ++   +  a + +L    a ++ +a+
  gi|2106323    93 GAEADGEDVDEQGMpasstSSAEAFRDAIALIDALPVDRAQVIVRAFTAF 142

                    LnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkln
                      LAnL EE    yR  i + +    + E        +   + +L
  gi|2106323   143 FHLANLSEE---SYRVGILRERERNVSTEDAVDPANALTVAFHQLTEEV- 188

                    KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                       +   e L       v+tAHPt + R+++  K  Ri   L   s   +
  gi|2106323   189 -GGAKATELLSRLEFHPVFTAHPTEARRKAVEGKIRRIADLLEERSR--L 235

                    tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                       D  E +  +  Ei A  Rt  i   +PtP +E    +  +  t+++
  gi|2106323   236 GGSDLVENERHMLQEIDALVRTSPIALKKPTPVEEADTIIDIFDSTLFDT 285

                    vPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                    +P   RR D  +         P      +  sW+G DRDG nP vt  v
  gi|2106323   286 IPVVYRRFDDWVLGEYAGTVPPVCPAFFHPGSWIGSDRDG-NPNVTAKVS 334

                    RDvCL.LaRmmAanlY..isqv.EDLmFElsmWRCndELRvRAEElyrta
                    R v  + a  m a l ++   v+  L  E +  +  dEL      l +
  gi|2106323   335 RQVAAkYATHMIAKLAdkCRRVgRNLTLEAAYTKPSDELL----NLWSHQ 380

                    ardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGise
                              E  + +   EP R ++  +  +L  t  R
  gi|2106323   381 VEM--SEVLTERAREISNSEPHRAVMLVMAARLDATVTR----------- 417

                    isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                       + +y   ++FL  L +  +sL   G    A G +  ++ q  tFG
  gi|2106323   418 -NADTMYRSCDDFLADLRVVQRSLAGAGAVRAAYGPVQTIIWQAETFGFH 466

                    LvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRP
                    +v ++ Rq s  +   l  i +H   G                EL
  gi|2106323   467 MVEMEFRQHSVVHSRALADIREHGIHG----------------ELA---- 496

                    LlgsDLPktEEvkDvldaf.rvLAELPiDsFGaYiismataPsDvLAvEL
                          P+t Ev D   a++ +           Yiis + +   v  v
  gi|2106323   497 ------PMTREVLDTFRAIgSIQKRYGQKMAHRYIISFTKSAQHVADVYE 540

                    LqRECgvkq....tLrvvPLFEkLADLeAAPAa...vekLFsiDWYinri
                    L      + ++ ++L v+PLFE+L DLe      +++ kL ++     +
  gi|2106323   541 LANLAFAHAedvpALDVIPLFEQLEDLEGSVDVldeMLKLPAVQARLAQT 590
```

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                    dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                      + evm+GYsDs KDAG   A   L  AqE i+  A+k  + Lvl HGR
  gi|2106323   591 GRRMEVMLGYSDSSKDAGPTTATLALHSAQERIAAWAQKNDIDLVLMHGR 640

                    GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                    GG vGRGGGP   A+L+qP   +n   +vt qGEvi   +G   L  r +
  gi|2106323   641 GGAVGRGGGPANRAVLAQPAGSVNCFFKVTEQGEVIFARYGNSTLAQRHV 690

                    qRFtAAtLEHGmnPPvsPkPEWRkLmeemAvv...AtEEYRsvvvKEPRF
                       +AAtL            E  +   +mA v ++A  E     +    F
  gi|2106323   691 ESVAAATLLNSAPSVERTNTETTERYADMASVlnrASHERYLDLLNTEDF 740

                    vEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWtqtRFH
                      +F   tP +E G + iGsRPaKR  + + ++ LR iPW+F+W q R
  gi|2106323   741 TPWFSTVTPLTEVGLLPIGSRPAKRGLGAkSLDDLRTIPWVFSWSQARIN 790

                    LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                    L  W G+G A           l  L+  Y+eWP F   +D +Em  AK D
  gi|2106323   791 LAAWYGLGTACEA-----LGDLELLQRAYREWPLFSTFIDNIEMSIAKTD 835

                    PGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                      iA +y  L    +L    +++ d+   t+ ++L+i G k  LE    L
  gi|2106323   836 NRIAKMYLALGDRSDLA---NKVFDEMMLTRSWVLRIVGDKWPLEHRRVL 882

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                     q +R+R++++  L   q   L+ +R        + +ls E  +E
  gi|2106323   883 GQAVRVRNPFVDALSLAQVRALREVR------ANQDELSEEAKAEY---- 922

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       + L         LE     t+ G+ AG+qntG
  gi|2106323   923 ---MSLV--------LE-----TVTGVSAGLQNTG    941

gi|18072430|emb|CAC84922.1|: domain 1 of 1, from 1 to 362: score 159.3, E = 1.1e-44
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807243     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807243     - ------------------------------------------------ -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807243     - ------------------------------------------------ -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807243     - ------------------------------------------------ -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807243     - ------------------------------------------------ -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807243     - ------------------------------------------------ -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807243     - ------------------------------------------------ -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807243     - ------------------------------------------------ -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807243     - ------------------------------------------------ -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
```

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  gi|1807243     - ------------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807243     - ------------------------------------------------- -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807243     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqE++iKvAK++G+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807243     9 RLSAAWQLYKAQEDLIKVAKEFGIKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRF+AAtLEHGm+PPvsP
  gi|1807243    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFAAATLEHGMHPPVSP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR+Lm+em vvAtEEYRs+v+KE RFvEYFR+AtPElEYG+mniGsR
  gi|1807243   109 KPEWRELMDEMGVVATEEYRSIVFKEERFVEYFRSATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD+Knl
  gi|1807243   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIEKDSKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+ mY+eWPFFRvt+DL+EmvFAKGDPGi aLyDkLLv+E+L+ FG++
  gi|1807243   209 HTLRQMYNEWPFFRVTIDLVEMVFAKGDPGITALYDKLLVSEDLWSFGEK 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR+++ Et+dlLLk+AGH+DlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|1807243   259 LRANFLETRDLLLKVAGHRDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+++v lrPhlsKE        a+eL+kLn t+++aPGLEDtLiL
  gi|1807243   309 KRIRDPNFHVQLRPHLSKESSTNS---AAELLKLNTTSEYAPGLEDTLIL 355

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807243   356 TMKGIAA------    362

gi|70950271|ref|XP_744473.1|: domain 1 of 1, from 1 to 726: score 157.9, E = 3.1e-44
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                  s
  gi|7095027     1    --------------S------------------------------- 1

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7095027     - ------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                                                          k
  gi|7095027     2 ----------------------------------------KI------- 3

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                                                 CL
  gi|7095027     4 ---------------------------------CL-------------- 5

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7095027     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                                      Fs W GGDRDG nP v P  t  vC +
  gi|7095027     6 ----------------------FSLWAGGDRDG-NPFVLPKTTQYVCYM 31

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEEly...rtaardk...
                     ++   l+i  +E L+  l +  C    +     l+++ +    dk++
  gi|7095027    32 NNIIWCELFIPMIEKLIINLTIHQCTVHFKNYVKNLQhniSDIIFDKdqy 81
```

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                    .vvKyYiEF..WKqvPPtEPYRviLGdvRDKLYntRERaRHLLA.tGise
                     + K +  F+++ +    E YR +L  v  KL       + L+ +  +
  gi|7095027    82 cLRKKFQWFspFSKYNKKEIYRRVLLIVLTKLKSVVYVYKALISgEPVDP 131

                    isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                      E+ ++   EeF E L  CYksL e G   iA+G L D++R v  FGL
  gi|7095027   132 DFENLMFKSTEEFEEILLECYKSLIESGNALIAEGYLKDVIRNVNIFGLH 181

                    LvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRP
                    L+KLDiRqEse++t  +  i + L+i  Y    Ee R  +L   L+  RP
  gi|7095027   182 LMKLDIRQESEKHTQAMNYICQKLNIKKYELLNEEERIAFLTDILESNRP 231

                    LlgsDLPktEEv....kDvldafrvLAELPiDsFGaYiismataPsDvLA
                    +++  + +  +v+++   ++++f +   L   + GaY+ism+   sD+L
  gi|7095027   232 IIPNNIEQEPDVpsdfLNIINTFDMCSRLEESALGAYVISMCQNASDILL 281

                    vELLq...RECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri.
                    vE+ q++ +    ++t rvvPL E +  L+     +e L    WY+n+++
  gi|7095027   282 VEVFQesfKKSLHRKTQRVVPLLETIQSLQMSSTILENLIKNPWYKNHLk 331

                    ...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                    ++ d  qe+m+GYsDsGKD GRl  AW L+kAqE +++v  ky v +  F
  gi|7095027   332 nnfDNIQEIMIGYSDSGKDGGRLTSAWELFKAQEKLVQVGAKYSVDVRFF 381

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                    HGRGG v RGGGP HLAiLsqP  ti+  +Rvt+qGEvi + FG   +
  gi|7095027   382 HGRGGSVSRGGGPQHLAILSQPINTIKNYIRVTIQGEVITQDFGLKGMAL 431

                    rsLqRFtAAtLEHG.mnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPR
                    rs+  +  A L    ++  vs k EWR+Lm+++    t EYR +v+  P
  gi|7095027   432 RSIETYISALLKCSlLKNRVSIKKEWRDLMDDISELTTKEYRKIVYENPD 481

                    FvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFH
                    Fv YFR AtPE+E Gk+n+GsRP+KRk  G +esLRAiPW+F+Wtq R H
  gi|7095027   482 FVKYFRYATPEIEIGKLNLGSRPSKRK-KGNVESLRAIPWVFSWTQNRMH 530

                    LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                    L vWLG+   + + ++     l  L++mYk+WPF      L+ mv AK
  gi|7095027   531 LSVWLGIEEVYEYIMNNN--KLEILQDMYKNWPFCTSFFNLISMVMAKAS 578

                    PGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                      iA  yD +Lv  +Lk  G +LR+k +   +l L +   +   + D
  gi|7095027   579 IQIAEEYD-ILVPNNLKYIGVELREKLKKSMKLTLLVTNEHNFCDNDQIT 627

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPh.............l
                    K  +  R  ++t  n +q   LKR+R  +    l P++ + ++++++ ++
  gi|7095027   628 KRSIEARTKWVTVCNLIQIQALKRLRNKETNTHLDPKnvnfsqddnnmtV 677

                    sKE..yAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<
                    sKE+++ +  s   +e+ k n   +      Dt  + +   A   +n
  gi|7095027   678 SKEksFLNNTSINDEEINKENTITNSDTKKYDTEYIFLTKSASYDKNEH  726

                    -*

  gi|7095027     -    -

gi|170750063|ref|YP_001756323.1|: domain 1 of 1, from 12 to 916: score 157.7, E = 3.4e-44
                    *->siDAqLRl..LvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkE
                        +DA   +++++ G  se+   i + AL     LD+    H +dL
  gi|1707500    12    -VDATAFAppVIVGTSSEQALDILFQAL-----LDVARR-HDPDLEA 51

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    +     ++s     +  ++ L            a a+ v      ++ +A
  gi|1707500    52 VLHGTADIS-----RFSPQML------------ARALQVQGIWFQLISIA 84

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                        E + A RRR +  +      E+ A         +     ++   Pe
  gi|1707500    85 ----EQNAAMRRRRHVER-----TEGRAALSGSFAKVFADARKQG-VPPE 124

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
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                    +   L    +   ltAHPt   R  +L K  Ri   L  L     t  +
  gi|1707500   125 KIQALLTDLRIRPTLTAHPTEGKRVTVLEKFRRIYLVLRELEMPRWTDRE 174

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    +  L   L   i   + t E+   + t   E+  G+ ++ Et+++  P
  gi|1707500   175 RNGLMNELRDQIELVWMTGELHLEKATVEREVAWGLHFFDETLFEMLPET 224

                    LRRvDtALKni..GinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                    L     AL    +G   R+P   P  +F sW+GGDRDG nP vt  vtR
  gi|1707500   225 LEALHEALAETypGTEFRVP---PFFQFGSWIGGDRDG-NPYVTAAVTRQ 270

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndEL..RvRAEElyrtaardk
                          +     Y + v +L   ls+      L++  RAE   + a +
  gi|1707500   271 TLHRNALASLTRYRDRVRELGRTLSLTERSLPLpeGFRAELDRQLAESG- 319

                    vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                                 P EPYR  L  v  K+  t       +A    e +
  gi|1707500   320 ----QARAITRRNPGEPYRQYLSCVLRKIEAT-------IARNEGEHPSG 358

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                      y   +  +E L    + L e    ++A   +  + R v  F  s v+L
  gi|1707500   359 PDYASADGLIEDLRTLERGLTEAKCGALARDLVRPVRRMVEIFRFSTVRL 408

                    DiRqEseRqtDvlDAi.ttHLeiGsYReWsEeKRqEWLlaELkGKRPLlg
                    D+R    R tD l A+  +  + G          + WL aEL   R
  gi|1707500   409 DLRENTTRTTDTLHALwRQRNGDGEPPALGSAAWRQWLDAELARPRDPER 458

                    s..DLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAv
                    s +DLP  +  ++ l +f  +AE ++ L  ++FGa+++sm+ +  DvL
  gi|1707500   459 SfeDLP--DAARETLATFALVAEmreaLDREAFGAFVLSMTRSVEDVLGA 506

                    ELLqRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYi
                     LL +E gv  +  +++  +L++vPLFE + DL+AAPA +  L  +   +
  gi|1707500   507 YLLAKEAGVfldaagteICPLPIVPLFETIDDLRAAPAIMRALLGTPVVR 556

                    nrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                         ++G qevm+GYsDs KD G ++A W LYkAq  + +   + Gv +
  gi|1707500   557 RSTRwqgGVQEVMIGYSDSNKDGGFVAANWELYKAQSKLTRLGEELGVGI 606

                    vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                      FHGRGG v RGG PtH  i++qPP  i G  R t qGEv+ f +
  gi|1707500   607 AFFHGRGGSVSRGGVPTHRGIMAQPPGSIRGRFRTTEQGEVVSFKYANRG 656

                    LCFrsLqRFtAAtLEHGmnPPvsPk.PEWRkLmeemAvvAtEEYRsvvvK
                         +   +A   EH +       +P   + +e +A      Y  + ++
  gi|1707500   657 TAAYQMELLAASVFEHALAGDGERVgPGHDDALEALAGASRAAYVQL-LQ 705

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                        v+YF  A P  E   +niGsRPa+R  +  +  LRAiPW+FaW q
  gi|1707500   706 TDGLVDYFQAASPLDEIALLNIGSRPARRFGARALSDLRAIPWVFAWSQN 755

                    RFHLPvWLGvGAAFKhAidKDiKn.lqkLkEmYkeWPFFRvtlDLlEmvF
                    R  +  W GvG      id   + +   Lk ++ e     R  lD +E
  gi|1707500   756 RHVITGWYGVGSGLASFIDVRGRDgEAALKRLFTESRILRLVLDEVEKTL 805

                    AKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLE
                       D  iA  y  L+     + +    + ++Y  t++++L++ G  +l E
  gi|1707500   806 MMVDLDIARAYAGLVPDPGPRDrIFSMIEAEYALTREMVLRVSGGTELAE 855

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                      P  + rl+ R + i  +   q   L R R                +E
  gi|1707500   856 RFPLFRDRLKGRLPTINQVSREQVELLARYR----------------AE 888

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                          e vk              L+L +  iA G   tG
  gi|1707500   889 TDEDRREAVKSA-----------LLLSINCIAVGFGATG    916

gi|18073866|emb|CAC84950.1|: domain 1 of 1, from 1 to 373: score 157.6, E = 3.7e-44
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807386     -    ---------------------------------------------- -
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|1807386    - ------------------------------------------------ -

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1807386    - ------------------------------------------------ -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1807386    - ------------------------------------------------ -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1807386    - ------------------------------------------------ -

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1807386    - ------------------------------------------------ -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1807386    - ------------------------------------------------ -

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1807386    - ------------------------------------------------ -

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1807386    - ------------------------------------------------ -

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|1807386    - ------------------------------------------------ -

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|1807386    - ------------------------------------------------ -

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
gi|1807386    1 -------------------------------------------SDSGKDAG 8

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGG PtHLAiLsq
gi|1807386    9 RLSAAWQLYKAQEELVKVAKEYGVKLTMFHGRGGTVGRGGCPTHLAILSQ 58

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PPDt++GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGmnPPv+P
gi|1807386   59 PPDTVHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMNPPVAP 108

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                kPEWR L++emAvvAtE YRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
gi|1807386  109 KPEWRALLDEMAVVATEKYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKhAi+KD++nl
gi|1807386  159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHAIEKDVRNL 208

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                 +L+ mY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+ FG++
gi|1807386  209 HMLQAMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWSFGER 258

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR +Y +tk +LL+iAGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
gi|1807386  259 LRTHYDDTKSYLLQIAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 308

                KRiRDPsykvtlrPhlsKEyAdEn........skkadeLvkLnptervaP
                KRiRDPsy+vt+rPh+sKE  +  ++++++++s +a eLvkLn t+++aP
```

```
  gi|1807386   309 KRIRDPSYRVTVRPHISKEIMESSssssssstSNPAYELVKLNTTSEYAP 358

                   GLEDtLiLtmKGiAAGmqntG<-*
                   GLEDtLiLtmKGiAA
  gi|1807386   359 GLEDTLILTMKGIAA------    373

gi|7768244|emb|CAB90659.1|: domain 1 of 1, from 1 to 364: score 157.3, E = 4.6e-44
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768244     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768244     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768244     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768244     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768244     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768244     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768244     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768244     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768244     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768244     - ---------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768244     - ---------------------------------------------- -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768244     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqE+++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768244     9 RLSAAWQLYKAQEDLVKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEH m PP sP
  gi|7768244    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHSMCPPASP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    PEWR+L++emAv At EYRs+v+ EPRFvEYFRlAtPElEYG+mniGsR
  gi|7768244   109 EPEWRELLDEMAVAATKEYRSIVFHEPRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh idKDiKnl
  gi|7768244   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIDKDIKNL 208
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                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY  WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+PFG++
  gi|7768244   209 LMLQEMYTRWPFFRVTIDLIEMVFAKGDPGIAALYDKLLVSEDLWPFGEQ 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y Etk+lLL++AGHkDlLEG PYL+qrlRLRdsYittLn +qAYtL
  gi|7768244   259 LRNNYNETKNLLLQVAGHKDLLEGNPYLRQRLRLRDSYITTLNACQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+vt+rPhlsKE  +   k a+eLvkLnpt+++aPGLEDtLiL
  gi|7768244   309 KRIRDPNYHVTVRPHLSKEIMESH-KAAAELVKLNPTSEYAPGLEDTLIL 357

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|7768244   358 TMKGIAA------    364

gi|18073652|emb|CAC83643.1|: domain 1 of 1, from 1 to 362: score 156.6, E = 7.7e-44
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807365     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807365     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807365     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807365     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807365     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807365     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807365     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807365     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807365     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807365     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807365     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807365     1 ----------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807365     9 RLSAAWQLYKAQEELIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+ FGEE+LCFr+LqRFtAAtLEHGm+PP++P
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  gi|1807365    59 PPDTIHGSLRVTVQGEVIEQCFGEEHLCFRTLQRFTAATLEHGMHPPIAP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR+Lm+emAv+At EYRs v+ E RFvEYFR+AtPElEYG+mniGsR
  gi|1807365   109 KPEWRQLMDEMAVIATQEYRSYVFHEKRFVEYFRSATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KDi+nl
  gi|1807365   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIEKDIRNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+ mY+eWPFFRvtlDL+EmvFAK DPGiAaLyDkLLv+E+L+ FG++
  gi|1807365   209 HTLQQMYNEWPFFRVTLDLVEMVFAKHDPGIAALYDKLLVSEDLWSFGEQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR +YvEtkdlLL++AGHk++LEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|1807365   259 LRKNYVETKDLLLQVAGHKEVLEGDPYLKQRLRLRDSYITTLNVLQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPsy+vtlrPhlsKE    +   a+eLvkLnpt+++aPGLEDtLiL
  gi|1807365   309 KRIRDPSYHVTLRPHLSKESSTKP---AAELVKLNPTSEYAPGLEDTLIL 355

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807365   356 TMKGIAA------    362

gi|83779594|gb|ABC47613.1|: domain 1 of 1, from 1 to 364: score 155.9, E = 1.2e-43
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|8377959     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|8377959     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|8377959     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|8377959     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|8377959     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|8377959     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|8377959     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|8377959     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|8377959     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|8377959     - ---------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|8377959     - ---------------------------------------------- -
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                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|8377959     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqE++iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|8377959     9 RLSAAWQLYKAQEDLIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP sP
  gi|8377959    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPDSP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++emAvvAtEEYRsvv+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|8377959   109 KPEWRALLDEMAVVATEEYRSVVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KDi+nl
  gi|8377959   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIIKKDIRNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+EmY+ WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+ FG++
  gi|8377959   209 HVLQEMYNAWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWAFGED 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR +Y+Etk+lLL+iAGHkDlLEGD YLKqrlRLRdsYittLnv+qAYtL
  gi|8377959   259 LRTNYEETKKLLLQIAGHKDLLEGDLYLKQRLRLRDSYITTLNVCQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDPsy v  rPh+s+E   E sk a+eL+ Lnp++++aPGLEDtLiL
  gi|8377959   309 KRIRDPSYNVKFRPHISREIM-ETSKSANELLILNPSSEYAPGLEDTLIL 357

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|8377959   358 TMKGIAA------    364

gi|18073860|emb|CAC84947.1|: domain 1 of 1, from 1 to 364: score 153.6, E = 5.8e-43
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807386     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807386     - ---------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807386     - ---------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807386     - ---------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807386     - ---------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807386     - ---------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807386     - ---------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807386     - ---------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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  gi|1807386     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807386     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807386     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807386     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqE+++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807386     9 RLSAAWQLYKAQEDLVKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEH m PP sP
  gi|1807386    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHSMCPPASP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    PEWR+L++emAv At EYRs+v+ EPRFvEYFRlAtPElEYG+mniGsR
  gi|1807386   109 EPEWRELLDEMAVAATKEYRSIVFHEPRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh idKDiKnl
  gi|1807386   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIDKDIKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY  WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+ FG++
  gi|1807386   209 LMLQEMYTRWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWLFGEQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y Etk+lLL++AGHkDlLEG PYL+qrlRLRdsYittLn +qAYtL
  gi|1807386   259 LRNNYNETKNLLLQVAGHKDLLEGNPYLRQRLRLRDSYITTLNACQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y+vt+rP+lsKE  + n k a+eLvkLnpt+++aPGLEDtLiL
  gi|1807386   309 KRIRDPNYHVTVRPPLSKEIMESN-KAAAELVKLNPTSEYAPGLEDTLIL 357

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807386   358 TMKGIAA------    364

gi|83779602|gb|ABC47617.1|: domain 1 of 1, from 1 to 364: score 153.3, E = 7.4e-43
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|8377960     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|8377960     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|8377960     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|8377960     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|8377960     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|8377960     - ------------------------------------------------ -
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                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|8377960     - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|8377960     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|8377960     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|8377960     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|8377960     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|8377960     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqE++iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|8377960     9 RLSAAWQLYKAQEDLIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP sP
  gi|8377960    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPDSP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++emAvvAtEEYRsvv+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|8377960   109 KPEWRALLDEMAVVATEEYRSVVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KDi+nl
  gi|8377960   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIIKKDIRNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+EmY+ WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+ FG++
  gi|8377960   209 HVLQEMYNAWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWAFGEN 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR + +Etk+lLL+iAGHkDlLEGD YLKqrlRLRdsYittLnv+qAYtL
  gi|8377960   259 LRTNCEETKKLLLQIAGHKDLLEGDLYLKQRLRLRDSYITTLNVCQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDPsy v  rPh+sKE   E sk a+eL+ Lnp++++aPGLEDtLiL
  gi|8377960   309 KRIRDPSYNVKFRPHISKEIM-ETSKSANELLILNPSSEYAPGLEDTLIL 357

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|8377960   358 TMKGIAA------    364

gi|18073830|emb|CAC84932.1|: domain 1 of 1, from 1 to 364: score 152.7, E = 1.1e-42
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807383     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807383     - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807383     - ------------------------------------------------ -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|1807383     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807383     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807383     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807383     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807383     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807383     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807383     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807383     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807383     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqE+++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807383     9 RLSAAWQLYKAQEDLVKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEH m PP sP
  gi|1807383    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHSMCPPASP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    PEWR+L++emAv At EYRs+v+ EPRFvEYFRlAtPElEYG+mniGsR
  gi|1807383   109 EPEWRELLDEMAVAATKEYRSIVFHEPRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh idKDiKnl
  gi|1807383   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIDKDIKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY  WPFFRvt+DL+Em FAKGDPGiAaLyDkLLv+E+L+PFG++
  gi|1807383   209 LMLQEMYTRWPFFRVTIDLVEMGFAKGDPGIAALYDKLLVSEDLWPFGEQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y Etk+lLL++AGHkDlLEG PYL+qrlRLRdsYittLn +qAYtL
  gi|1807383   259 LRNNYNETKNLLLQVAGHKDLLEGNPYLRQRLRLRDSYITTLNACQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y+vt+rP lsKE  + n k a+eLvkLnpt+++aPGLEDtLiL
  gi|1807383   309 KRIRDPNYHVTVRPRLSKEIMESN-KAAAELVKLNPTSEYAPGLEDTLIL 357

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807383   358 TMKGIAA------    364

gi|18073828|emb|CAC84931.1|: domain 1 of 1, from 1 to 364: score 152.2, E = 1.5e-42
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807382     -    ------------------------------------------- -
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                 qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|1807382     - ------------------------------------------------ -

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1807382     - ------------------------------------------------ -

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1807382     - ------------------------------------------------ -

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1807382     - ------------------------------------------------ -

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1807382     - ------------------------------------------------ -

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1807382     - ------------------------------------------------ -

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1807382     - ------------------------------------------------ -

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1807382     - ------------------------------------------------ -

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|1807382     - ------------------------------------------------ -

                 EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|1807382     - ------------------------------------------------ -

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                       sDsGKDAG
gi|1807382     1 -----------------------------------------SDSGKDAG 8

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 RlsAAWqLYkAqE+++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1807382     9 RLSAAWQLYKAQEDLVKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                 PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEH m PP sP
gi|1807382    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHSMCPPASP 108

                 kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  PEWR+L++emAv At EY s+v+ EPRFvEYFRlAtPE+EYG+mniGsR
gi|1807382   109 EPEWRELLDEMAVAATKEYASIVFHEPRFVEYFRLATPEVEYGRMNIGSR 158

                 PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                 P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh idKDiKnl
gi|1807382   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIDKDIKNL 208

                 qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  +L+EmY  WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+PFG++
gi|1807382   209 LMLQEMYTRWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWPFGEQ 258

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                 LR++Y Etk+lLL++AGHkDlLEG PYL+qrlRLRdsYittLn +qAYtL
gi|1807382   259 LRNNYNETKNLLLQVAGHKDLLEGNPYLRQRLRLRDSYITTLNACQAYTL 308

                 KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                 KRiRDP+y+vt+rP lsKE  + n k a+eLvkLnpt+++aPGLEDtLiL
gi|1807382   309 KRIRDPNYHVTVRPRLSKEIMESN-KAAAELVKLNPTSEYAPGLEDTLIL 357
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                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|1807382   358 TMKGIAA------    364

gi|220926859|ref|YP_002502161.1|: domain 1 of 1, from 1 to 920: score 152.2, E = 1.6e-42
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            L l vP     d+                    + G + +Ea
  gi|2209268     1    ---MTLALSVPAGAT-DQSFAP-------------PVITGTSSREAT 30

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDai...lvAkail...Hm
                       +    +   ++++    EL ++L + +     +++l+A+a+  ++
  gi|2209268    31 DILFHSLLDVCRRHEP----ELESVLHGNANISDFspeLMARALQvqgIW 76

                    LnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkln
                      L  +AE      RRR   +  G  a  +s      + E ++  +
  gi|2209268    77 FQLISIAEQNTAMRRRRHVERTSGRHALRGSFSAV--LAEAVQNRIPAR- 123

                    KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                        E+   LK   +   ltAHPt   R  +L K  Ri   L  L
  gi|2209268   124 ----EIHALLKDLRIRPTLTAHPTEGKRVTVLEKFRRIYLLLRELELPRW 169

                    tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                    t  ++  L   L   i   + t E+   +Pt   E+  G+ ++ Et+++
  gi|2209268   170 TERERNGLMADLRDQIELVWMTGELHLEKPTVEQEVAWGLHFFDETLFEM 219

                    vPKFLRRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEv
                     P  +   +  L+     E   ++vP   +F sW+GGDRDG nP vt  v
  gi|2209268   220 LPEVMVSLEESLREYFPDET--FEVPaFFQFGSWIGGDRDG-NPFVTASV 266

                    tRDvCLLaRmmAanlYisqvEDL..mFElsmWRCndELRvRAEElyrtaa
                    tR       +     Y + v  L++m  +s          +AE   + aa
  gi|2209268   267 TRATLRRNALASMRRYRDGVVHLgrMLSISERSLPAPASFKAELARQLAA 316

                    rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                    +       iE      P E YR  L  +  KL  t  R      tG  +
  gi|2209268   317 SG--DARGIE---RRNPGELYRQYLTCILRKLEATIARNEGDAITGAPD- 360

                    sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                         y + ++ +  L +  + L e     +A   +  + R v  F  s
  gi|2209268   361 -----YSDADDLINDLRVLEQGLIEAKCPSLAVDLVRPVRRMVEIFRFST 405

                    vKLDiRqEseRqtDvlDAittHLeiGsYReWsEe...KRqEWLlaELkGK
                    v+LDiR    R t  l A+    + G     +E +++  +EWLl EL
  gi|2209268   406 VRLDIRENTTRTTRALHALWAQ-GRGDDAAPPEVdspAWKEWLLEELA-- 452

                    RPLlg..sDLPktEEvkDvldafrvLAELPi....DsFGaYiismataPs
                    RPL g++s     +E ++ l++fr + E+ ++ ++++FG++++sm+ +
  gi|2209268   453 RPLEGqrSFQSLPDEARETLETFRLVGEMRSqldrEAFGSFVLSMTHSVP 502

                    DvLAvELLqRECgv........kqtLrvvPLFEkLADLeAAPAavekLFs
                    D+L v LL +E g+  +  + +  +L++vPLFE + DL+AAP  ++ L
  gi|2209268   503 DILGVYLLAKEAGLfldaagieICPLPIVPLFETIDDLRAAPTIMKELLQ 552

                    iDWYinrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKk
                    i   +     ++G qevm+GYsDs KD G +s  W L kAq  +  + K
  gi|2209268   553 IPVVRRSTRwqgGVQEVMIGYSDSNKDGGFVSSNWELAKAQAKLTEIGKA 602

                    yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                     Gv +  FHGRGG v RGG Pt  Ai +qPP  i G  R t qGEv+ f
  gi|2209268   603 AGVPIAFFHGRGGSVSRGGAPTGRAIAAQPPGSIRGRFRTTEQGEVVSFK 652

                    FGEEnLCFrsLqRFtAAtLEHGmn....PPvsPkPEWRkLmeemAvvAtE
                    +         +   +     H +n++++P  +PkPE+ + me +
  gi|2209268   653 YANRGTAAYQMELLASSVFAHALNserdPSFAPKPEFDDAMEALSGASRA 702

                    EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                     Y  +v   P  v YF  A P  E   +niGsRPa+R  +  +  LRAiP
  gi|2209268   703 AYVKLV-SHPDLVTYFGAASPLDEIALLNIGSRPARRFGARSLADLRAIP 751

                    WiFaWtqtRFHLPvWLGvGAAFKhAid.KDiKnlqkLkEmYkeWPFFRvt
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                  W+FaW q R  +  W GvG   K  +d +       L+ m+ e   FR
  gi|2209268   752 WVFAWSQNRHVITGWYGVGSGLKSFLDvRGEAGGALLRRMFAESRLFRLV 801

                  lDLlEmvFAKGDPGiAaLyDkLL..vaEeLkPFGksLRdkYvEtkdlLLk
                  lD +E      D  iA  +  L+++va     F   + ++Y  t++++++
  gi|2209268   802 LDEVEKTLLTVDLDIARDFASLVpdVAVRDEIF-SMIAAEYRLTREMVVR 850

                  iAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrP
                  + G  ++ E  P  + rl  R + i  +   q   L+R R
  gi|2209268   851 VSGDAEVAERFPQFRGRLAERLPVINQVSREQVELLRRFR---------- 890

                  hlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<
                         E     de+ +              L+L +  iA G   tG
  gi|2209268   891 -------GET----DEVRRET--------FKSALLLSINCIAVGFGATG  920

                  -*

  gi|2209268     -    -

gi|18076769|emb|CAC84952.1|: domain 1 of 1, from 1 to 363: score 151.6, E = 2.4e-42
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807676     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807676     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807676     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807676     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807676     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807676     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807676     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807676     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807676     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807676     - ---------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807676     - ---------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|1807676     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE++KvAKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807676     9 RLSAAWQLYKAQEELVKVAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58
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                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP+tinGs RvtvqGEviE+sFGEE LCFr+LqRFtAAtLEHGm PP+sP
  gi|1807676     59 PPETINGSFRVTVQGEVIEQSFGEERLCFRTLQRFTAATLEHGMLPPISP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR +++e+AvvAtEEYRsvv+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|1807676    109 KPEWRAILDEIAVVATEEYRSVVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|1807676    159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHILQKDIRNL 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLv++eLk FG++
  gi|1807676    209 QVLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVSDELKSFGEQ 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Et++lLL++AGHkDlLEGDPYLKqrlRLR+sYittL v+qAYtL
  gi|1807676    259 LRANYEETEQLLLQVAGHKDLLEGDPYLKQRLRLRESYITTLSVCQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+++v +r +lsKE  d n  k++eLvkLnp++++aPGLEDtLiL
  gi|1807676    309 KRIRDPNFQVHMRAPLSKEILDSN--KPAELVKLNPSSEYAPGLEDTLIL 356

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|1807676    357 TMKGIAA------    363

gi|10303369|emb|CAA65116.1|: domain 1 of 1, from 1 to 369: score 151.4, E = 2.7e-42
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1030336     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1030336     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1030336     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1030336     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1030336     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1030336     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1030336     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1030336     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1030336     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1030336     - ------------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
```

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  gi|1030336     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1030336     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1030336     9 RLSAAWQLYKAQEELIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEHGm+PP sP
  gi|1030336    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHGMHPPTSP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L++emAvv t EYRs+v++EPRFv+YFRlAtPElEYG+mniGsR
  gi|1030336   109 KPEWRALLDEMAVVSTKEYRSIVFQEPRFVDYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFK Ai+KDi+nl
  gi|1030336   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKNAIEKDIRNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY+ WPFFRvtlDL+EmvFAKGDP iAaLyDkLLv+EeL+ FG++
  gi|1030336   209 HMLREMYNMWPFFRVTLDLVEMVFAKGDPEIAALYDKLLVSEELQSFGER 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR +Y+Et  lLL++AG + lLEGDPYL qrlRLRd+YittLnv qAYtL
  gi|1030336   259 LRKEYEETSRLLLEVAGAR-LLEGDPYLTQRLRLRDPYITTLNVSQAYTL 307

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP++kvt rPhlsK+  + n  +a+eLvkLnpt++++PGLEDtL+L
  gi|1030336   308 KRIRDPNFKVTERPHLSKDIMESN-NPAAELVKLNPTSEFPPGLEDTLVL 356

                   tmKGiAAGmqntG<-*
                   tmKGi AGmqntG
  gi|1030336   357 TMKGIRAGMQNTG    369

gi|83779596|gb|ABC47614.1|: domain 1 of 1, from 1 to 364: score 150.5, E = 5.3e-42
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|8377959     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|8377959     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|8377959     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|8377959     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|8377959     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|8377959     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|8377959     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|8377959     - ------------------------------------------------ -
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```
                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|8377959     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|8377959     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|8377959     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|8377959     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqE++iKvAK++GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|8377959     9 RLSAAWQLYKAQEDLIKVAKQFGVKLTMFHGRGGTVGRGGGPSHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|8377959    59 PPDTIRGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++emAv+AtEEYRs+v+KEP FvEYFRlAtPElEYG+mniGsR
  gi|8377959   109 KPEWRALLDEMAVIATEEYRSIVFKEPQFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KDi+nl
  gi|8377959   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIIKKDIRNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+Em + WPFFRvt+DLlEmvFAKGDPGiAaLyDkLLv+E+L+ FG++
  gi|8377959   209 HVLQEMHNAWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVSEDLWTFGEK 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR +Y+Etk +LL+iAGHkDlLEGDPYLKqrlRLR+sYittLnv+q YtL
  gi|8377959   259 LRTNYEETKTFLLQIAGHKDLLEGDPYLKQRLRLRNSYITTLNVCQSYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDPsy v +rPh+sKE   E sk a+eL+ Lnp++++aPGLEDtLiL
  gi|8377959   309 KRIRDPSYNVKVRPHISKEIM-ETSKSANELLILNPSSEYAPGLEDTLIL 357

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|8377959   358 TMKGIAA------    364

gi|18073838|emb|CAC84936.1|: domain 1 of 1, from 1 to 364: score 150.2, E = 6.5e-42
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807383     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807383     - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807383     - ------------------------------------------------ -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807383     - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807383     - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
```

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  gi|1807383     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807383     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807383     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807383     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807383     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807383     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807383     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqE++iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807383     9 RLSAAWQLYKAQEDLIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP sP
  gi|1807383    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPDSP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L++emAvvAtEEYRsvv+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|1807383   109 KPEWRALLDEMAVVATEEYRSVVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KDi+nl
  gi|1807383   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIIKKDIRNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY+ WPFFRvt+DL+EmvFAKGDPGi aLyDkLLv+E+L+ FG++
  gi|1807383   209 HMLQEMYNAWPFFRVTIDLVEMVFAKGDPGITALYDKLLVSEDLWAFGEN 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR + +Etk+lLL+iAGHkDlLEGD YLKqrlRLRdsYittLnv+qA+tL
  gi|1807383   259 LRTNCEETKKLLLQIAGHKDLLEGDLYLKQRLRLRDSYITTLNVCQAFTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPsy v  rPh+sKE   E sk a+eL+ Lnp++++aPGLEDtLiL
  gi|1807383   309 KRIRDPSYNVKFRPHISKEIM-ETSKSANELLILNPSSEYAPGLEDTLIL 357

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807383   358 TMKGIAA------    364

gi|18073844|emb|CAC84939.1|: domain 1 of 1, from 1 to 363: score 149.9, E = 7.6e-42
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807384     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807384     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807384     - ------------------------------------------------ -
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                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807384     - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807384     - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807384     - ------------------------------------------------ -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807384     - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807384     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807384     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807384     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807384     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|1807384     1 -----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE++KvAKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807384     9 RLSAAWQLYKAQEELVKVAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP+tinGs RvtvqGEviE+sFGEE LCFr+LqRFtAAtLEHGm PP+sP
  gi|1807384    59 PPETINGSFRVTVQGEVIEQSFGEERLCFRTLQRFTAATLEHGMLPPISP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR +++e+AvvAtEEYRsvv+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|1807384   109 KPEWRAILDEIAVVATEEYRSVVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkP GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|1807384   159 PSKRKPRGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHILQKDIRNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLv++eLk FG++
  gi|1807384   209 QVLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVSDELKSFGEQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y+Et++lLL++AGHkDlLEGDPYLKqrlRLR+sYittL v+qAYtL
  gi|1807384   259 LRANYEETEQLLLQVAGHKDLLEGDPYLKQRLRLRESYITTLSVCQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDP+++v +r +lsKE  d n  k++eLvkLnpt+++aPGLEDtLiL
  gi|1807384   309 KRIRDPNFQVHMRAPLSKEILDSN--KPAELVKLNPTSEYAPGLEDTLIL 356

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807384   357 TMKGIAA------    363

gi|221195730|ref|ZP_03568784.1|: domain 1 of 1, from 63 to 970: score 149.9, E = 8e-42
                  *->siDAqLRlLvPGKvsedekLie.YDALLlDkFLDiLqDLHGedLkEa
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                  +   LRl+       de+L +++D LL+        D
gi|2211957    63    NLALFLRLVRKVLSEYDEDLRRsFDTLLVNAIAAGPDDASARIEELR 109

                  vqE.......CYElsAeYEGKk..DtkK.....LeELGakLtsLdPaDai
                  v E++++ +    ++A  +  ++ D++K++ ++     +k+  L    +
gi|2211957   110 VSEkgspagfVASIAAAIDSARtaDAEKrslnsFLQFVSKIDDLSVEKST 159

                  lvAkailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEt
                  l+ +a++    LAnL EE    yR    + +       a      Di
gi|2211957   160 LLMRAFVTYFHLANLCEE---NYRVQSLRAREAAVPTTAAENPINDITVA 206

                  lKkLvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnC
                  +++L+       e     LK      v+tAHPt  +RR  + K  RiR
gi|2211957   207 YRQLIEEC--GEETARLCLKRLEFHPVFTAHPTE-ARRKTIEK--RIRTI 251

                  LaqLsAK.DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGm
                     L  ++ +    + E +  +  Ei A FRt  i   +PtP +E    +
gi|2211957   252 SELLDERsQLGGIARLENERRMLEEIDALFRTSPIAHKKPTPIEEADTIL 301

                  sYiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDG
                    +  t+++ +P   RR D            P   P  +  sW+G DRDG
gi|2211957   302 NLFDTTLFEMIPSVYRRFDDWELGDAAGTVPPVCPPFFHPGSWIGSDRDG 351

                  knPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAE
                   nP vt  v R v    R+           D+   l +
gi|2211957   352 -NPNVTARVSRKVAEKYRVHVLDALARATHDISRSLTLDGISTPPSDELA 400

                  Elyrtaardkvv KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLL
                   l +       +     F K     E  R  +  + D+L  t  R   L+
gi|2211957   401 QLWSHQTEMSETLSSHAFDKA--GSELHRATMRVISDRLNATIKRNSDLM 448

                  AtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqv
                              y + Ee++  L +   sL   G    A G +  ++ q
gi|2211957   449 ------------YQNAEEYIADLRIVQDSLAKAGAVRAAYGPMQKIIWQA 486

                  stFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaE
                   tFG  Lv ++ Rq s  +t  l+ i +H   G   e  E  R+
gi|2211957   487 QTFGFHLVEMEFRQHSLVHTRALEDILEHGRAG---EKGELDRM------ 527

                  LkGKRPLlgsDLPktEEvkDvldaf.rvLAELPiDsFGaYiismataPsD
                                t Ev D   a++ +     i +   Yiis + +  D
gi|2211957   528 --------------THEVMDTFRAIgSIQRKNGINAARRYIISFTRSAED 563

                  vLAvELLqRECgvkq....tLrvvPLFEkLADLeAAPAavekLFsiDWYi
                  v  v  L R    ++++ + L v+PLFE++ DLe A   +ek+  +
gi|2211957   564 VENVYKLARLSFSHEedapVLDVIPLFEQIEDLENAVTIMEKVIQLPDVQ 613

                  nridG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                   r+  ++++ evm+GYsDs KDAG  sA   L  Aq  ++  A k  + L
gi|2211957   614 RRLAQtgrRLEVMLGYSDSSKDAGPTSATLVLHAAQAALAEWAEKNDIDL 663

                  vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                  vl HGRGG vGRGGGP   A+LsqP   +n   + t qGEvi   +G+
gi|2211957   664 VLMHGRGGAVGRGGGPANRAVLSQPKGSVNCRFKLTEQGEVIFARYGDPT 713

                  LCFrsLqRFtAAtLEHGm....nPPvsPkPEWRkLmeemAvvAtEEYRsv
                  L  r +   + AtL    ++ ++        +  L  e+     E +  +
gi|2211957   714 LACRHVESVAGATLLQSApsveHVNTDMTIKYASLAKELDHASQERFHTL 763

                  vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFa
                   +    F E+F + tP +E G + iGsRPaKR  + + ++ LRAiPWiF+
gi|2211957   764 -LDTKGFAEWFSVVTPLTEIGLLPIGSRPAKRGLGAkSLDDLRAIPWIFS 812

                  WtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlE
                  W q R  L  W G+G A        i  l +L+  YkeWP F   +D +E
gi|2211957   813 WSQARINLAAWYGLGTACEA-----IGDLGRLRAAYKEWPLFTTFIDNIE 857

                  mvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDl
                  m  AK D  iA Ly  L    eL    + +  +   t++++L i G k
gi|2211957   858 MSLAKVDTRIARLYLSLGDQAELS---EMVLSEMALTRKWVLAITGNKWP 904
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                    LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                    LE    L   +RLR +++  L v q   L  +R           + KE
  gi|2211957   905 LENRRVLGPVIRLRLPFVNVLSVTQVHALSELR-----------IHKESL 943

                    dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      +  + +  + L              + t+ G+AAG+qntG
  gi|2211957   944 TPE--ERERFIYLI-------------LCTVSGVAAGLQNTG    970

gi|78187483|ref|YP_375526.1|: domain 1 of 1, from 1 to 923: score 149.5, E = 1e-41
                    *->siDAqLRlLvPGKvsedekLieYDA.LLlDkFLDiLqDLHGedLkEa
                              ++       d +  e DA+ L+  F ++L  L  e L
  gi|7818748     1    -------MISTTSTIIDFEKAERDAgFLISCFQEMLCCLGEEAL--- 37

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                                    + +L   G  +      D+    +a++    L n
  gi|7818748    38 ----------------AARLPRGGRGIDLGHYPDTERALQAYSIFFQLLN 71

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    +AEE   A  RR     hG       A  E     tl  +  ++  s eE
  gi|7818748    72 MAEENSAAQNRRTLEAEHG------AASLEGLWGRTLLPVQQQG-LSEEE 114

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                        L    v  vltAHPt + R+ +L  +  i   L +   +  t+ ++
  gi|7818748   115 ARIVLSRVQVHPVLTAHPTEAKRKTVLELHRNIYLLLVKRENQMWTPAEQ 164

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     ++   +   +   +Rt Ei   +P   DE      Y+     + +
  gi|7818748   165 LDIRREITSAMETLWRTGEILFQKPSIADERANVAHYLENIFPDAITMMD 214

                    RRvDtALKniGinER...lPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                    RR   A    G   R+ ++P d P i+FssW+GGDRDG +P vt +vt +
  gi|7818748   215 RRLMKAWEAAGFSARsfkVPDDLPSIRFSSWVGGDRDG-HPLVTADVTAE 263

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEEl..yrtaardk
                         R+    l    +  L   ls+    d L    EEl +     r+k
  gi|7818748   264 TLGDMRLKSVGLIDAALRNLGSKLSL---SDRLQDPGEELigRMDTLRKK 310

                    vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                      K  ++  +     EP+R  +  +R  L             G    s
  gi|7818748   311 HGKRGMDAVRR-NEREPWRQFINLMRVSLPPA--------IRGSGSGSGS 351

                    Av.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                    A +y    e L  L +  +sL e G   iA   +  l R v  FG  L
  gi|7818748   352 AFrYHSARELLGDLAILTRSLEEIGAENIARELVFPLSRTVQSFGFHLAS 401

                    LDiRqEseRqtDvlDAittHLeiGs.....YReWsEeKRqEWLlaELkGK
                    LDiRq s  +   l A+ +  + G +++++Y + sEeK++E L  EL+
  gi|7818748   402 LDIRQNSRIHDLALTALIRAAGNGEqdetpYIDMSEEKKRELLDRELRSP 451

                    RPLlgsDLPktEEvkDvldafrvLA....ELPiDsFGaYiismataPsDv
                    RP   +D+    E + vl+ frvL ++ +    +  G+ i+sm+ + sD
  gi|7818748   452 RPFTRPDMQAGPEAESVLGCFRVLSghirSFGTEGIGSLIVSMTRSVSDL 501

                    LAvELLqRECgvkqtL........rvvPLFEkLADLeAAPAavekLFsiD
                    L v L  RE g+  ++++++    +vvPLFE + DLe  P  ++   s
  gi|7818748   502 LSVYLFARETGLMTSIkgksacivPVVPLFETIGDLEKSPGILDAFLSHP 551

                    W......YinridGKq....evmvGYsDsGKDAGRlsAAWqLYkAqEEii
                     ++++ +Y  r dG +++  evm+GYsDs KD G l  AW LY+A E +
  gi|7818748   552 VtessleYQRRRDGAKrrvmEVMIGYSDSNKDGGLLTSAWALYRAEEAML 601

                    KvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGE
                     v +++   +  FHGRGG + RG GPtH  i +qP    nG +R t qGE
  gi|7818748   602 EVGRRHNTCIRFFHGRGGSISRGAGPTHRFIRAQPYGACNGGMRFTEQGE 651

                    viEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPEWRk..LmeemAvv
                     i + +         L  F A      +      k     +++m+++
  gi|7818748   652 TIAQKYANRISAVYNLELFMAGVAGSLIRESRHEKAAHHLepVMDRLSSA 701

                    AtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLR
                        YR ++  E  Fv +FR A P        iGsRP++R  +  ++ LR
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  gi|7818748   702 SYSAYRTLIETEG-FVTFFRQAAPVDIIEANRIGSRPSRRTGGDSLDDLR 750

                   AiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFR
                   AiPW+F+W q RF L  W GvG A     + D   +  ++   ++WP  R
  gi|7818748   751 AIPWVFSWNQARFSLSGWYGVGSALEALNESDPEAFEDIRIRSHQWPPLR 800

                   vtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLL
                     +   +   A  D  +  Ly  L+    L+ +    + d+Y  tk ++
  gi|7818748   801 YIISNADTGLAAADLSVMRLYAGLVTEAGLRDkIMGMIEDEYRKTKRFI- 849

                   kiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlr
                         D+L   P   qr          Lnv     L+R      +
  gi|7818748   850 ------DILYSKPLATQR----------LNVNRFIELRREGLGLLHRWQV 883

                   PhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG
                     +     +E       L+     ++ a  +   L Lt+  i  G+  tG
  gi|7818748   884 QRI-----AEW----RKLLDDG-RKEEADAMLPELFLTVNAISGGLRTTG 923

                   <-*

  gi|7818748     -     -

gi|124268439|ref|YP_001022443.1|: domain 1 of 1, from 5 to 920: score 149.4, E = 1.1e-41
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                             l  P   +      + DAL     L     L G      v
  gi|1242684     5    ---SRPDLADPDESA--AGAERADALARSELLR--AALIG------V 38

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDai...lvAkai...lHm
                    E YE               E+  +L + +P + ++++l+A++i+ +
  gi|1242684    39 IERYE--------------PEVARVLRGEAPLERMstrLLARTIqaqAIW 74

                   LnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkln
                     L  +AE  +   RRR   ++       + A         +   v  +
  gi|1242684    75 FQLLAIAEQNRDMRRRREVERQ------RGHAQVRGTFAHVFHTAVEAG- 117

                   KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                      + + eAL    +  v+tAHPt + R  +L ++ Ri   L  L
  gi|1242684   118 LDAKQIREALCSLRIRPVITAHPTEAKRVTVLERHRRIYLRLFDLESPRW 167

                   tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                   t  ++++L  A+  E+   + t E++  +Pt   E+  G+ ++ E +++
  gi|1242684   168 TDREREDLTRAISDEVELLWLTGELKLDKPTVDQEVAWGLYFFDENLFDV 217

                   vPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                   vP+   R++ A       E l   v +  F sW+GGDRDG nP vt  vt
  gi|1242684   218 VPQLYGRIEAAFAKQFPGETLELPV-VFGFGSWIGGDRDG-NPFVTSTVT 265

                   RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk
                   R      R+     Y s + DL   ls+    +E  +   E +r a
  gi|1242684   266 RHTLWQMRLASLRRYRSRLADLARNLSI----SERAAALPEDFRAAVAA- 310

                   vvKyYiEFWKqvP...PtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                        +     v  ++P E +R  +  +  +L  t   aR       ++
  gi|1242684   311 -ALAALPDGAGVAarnPGELFRQFIAGMLARLDAT--IARNGEQPEPADA 357

                   sEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                   + +A +y + ++ +  +EL  ++L e G + +A   L  lLR v tF  +
  gi|1242684   358 ARDAApYEHADQLIGDIELMHRALVETGAQPLAKTFLAPLLREVRTFRFA 407

                   LvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaEL.....
                    v+LDiR    R    l  + + +             ++WLl+EL  +++
  gi|1242684   408 TVRLDIRENTIRINATLGELYRAVRGSEPPASDSAEWKDWLLTELaaprr 457

                   kGKRPLlgsDLPktEEvkDvldafrvLAEL....PiDsFGaYiismataP
                    G  PL  + L  t E ++ l +fr +AE++++   ++FG  i+sm+ +
  gi|1242684   458 AGEAPLATAGL--TPEAQETLATFRTVAEMrdrvDREAFGTLILSMTHSA 505

                   sDvLAvELLqRECgv........kqtLrvvPLFEkLADLeAAPAavekLF
                    DvL v LL +  g+ ++ +  ++ tL+vvPL E + DL+ APA ++ L
  gi|1242684   506 TDVLGVYLLAKHAGLfndaqaveRCTLPVVPLLETIPDLRRAPAILKELL 555
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                    siDWYin..ridGK.qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                    ++     + r+ G  qevm+GYsDs KD G + A W L kAq  + +
  gi|1242684   556 AVPLVQRslRLHGNvQEVMIGYSDSNKDGGYFTANWELSKAQATMTRLGE 605

                    kyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf
                    + GvK+  FHGRGG v RGG Pt  Ai + P   i G  R t qGEv+ +
  gi|1242684   606 DLGVKIAFFHGRGGSVSRGGAPTGRAIAALPAGSIRGGFRSTEQGEVVSY 655

                    sFGEEnLCFrsLqRFtAAtLEHGm....nPPvsPkPEWRkLmeemAvvAt
                     +         +   +   L H + ++++  + Pk E+ + me +  v
  gi|1242684   656 KYANRGTAHYQVELLASSVLQHVLlserESALVPKHEFDEAMEAISGVSW 705

                    EEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAi
                      YR ++  E     Y     P  E   +niGsRPa+R  +  +  LRAi
  gi|1242684   706 TAYRQLMESE-HLLAYLQGSSPLEELALLNIGSRPARRTQARTLADLRAI 754

                    PWiFaWtqtRFHLPvWLGvGAAFKhAid.KDiKnlqkLkEmYkeWPFFRv
                    PW+FaWtq R  L  W G+G      ++ +  + l  L+ m++e   FR
  gi|1242684   755 PWVFAWTQNRHMLTGWYGLGSGLAAFVEvRKARGLDLLQRMFHEGRLFRT 804

                    tlDLlEmvFAKGDPGiAaLyDkLLvaEeLk.PFGksLRdkYvEtkdlLLk
                     +D +E      D  iA  +  L+    +++P  + +  +Y  t +++Lk
  gi|1242684   805 VIDEVEKTLLTVDLDIAREFAGLVADPAVRePIFQAIEREYRLTCEMVLK 854

                    iAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrP
                    + G + + E  P L+ rl  R   +  +   q   L+ +RD
  gi|1242684   855 VSGGRQVAERFPQLRRRLARRLQTMNQVSREQVQLLRALRDG-------- 896

                    hlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<
                           d++  + + L+ +n                   AAG+  tG
  gi|1242684   897 ------GDDD-VRTAFLLSIN-----------------CAAAGLGATG  920

                    -*

  gi|1242684     -    -

gi|18076771|emb|CAC84953.1|: domain 1 of 1, from 1 to 363: score 149.3, E = 1.2e-41
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807677     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807677     - ---------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807677     - ---------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807677     - ---------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807677     - ---------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807677     - ---------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807677     - ---------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807677     - ---------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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  gi|1807677     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807677     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807677     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807677     1 -----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE++KvAKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807677     9 RLSAAWQLYKAQEELVKVAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP+tinGs RvtvqGEviE+sFGEE LCFr+LqRFtAAtLEHGm PP+sP
  gi|1807677    59 PPETINGSFRVTVQGEVIEQSFGEERLCFRTLQRFTAATLEHGMLPPISP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR +++e+AvvAtEEYRsvv+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|1807677   109 KPEWRAILDEIAVVATEEYRSVVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|1807677   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHILQKDIRNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLv++eLk FG++
  gi|1807677   209 QVLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVSDELKSFGEQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Et++lLL++AGHkDlLEGDPYLKqrlRLR+sYittL v+qAYtL
  gi|1807677   259 LRANYEETEQLLLQVAGHKDLLEGDPYLKQRLRLRESYITTLSVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+ +v +r +lsKE  d n  k++eLvkLnpt+++aPGLEDtLiL
  gi|1807677   309 KRIRDPNIQVHMRAPLSKEILDSN--KPAELVKLNPTSEYAPGLEDTLIL 356

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807677   357 TMKGIAA------    363

gi|18072424|emb|CAC84919.1|: domain 1 of 1, from 1 to 362: score 149.1, E = 1.3e-41
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807242     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807242     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807242     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807242     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807242     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807242     - ------------------------------------------------ -
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                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807242     - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807242     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807242     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807242     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807242     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|1807242     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqE++iKvAK++G+KL++FHGRGGtvGRGG PtHLAiLsq
  gi|1807242     9 RLSAAWQLYKAQEDLIKVAKEFGIKLTMFHGRGGTVGRGGCPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRF+AAtLEHGm+PPvsP
  gi|1807242    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFAAATLEHGMHPPVSP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR+Lm+em vvAtE YRs+v+KE RFvEYFR+AtPElEYG+mniGsR
  gi|1807242   109 KPEWRELMDEMGVVATEKYRSIVFKEERFVEYFRSATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD+Knl
  gi|1807242   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIEKDSKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+ mY+eWPFFRvt+DL+EmvFA+GDPGi aLyDkLLv+E+L+ FG++
  gi|1807242   209 HILRQMYNEWPFFRVTIDLVEMVFARGDPGITALYDKLLVSEDLWSFGEK 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR+++ Et+dlLLk+AGH+DlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|1807242   259 LRANFLETRDLLLKVAGHRDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDP+++v lrPhlsKE        a+eL+kLn t+++aPGLEDtLiL
  gi|1807242   309 KRIRDPNFHVQLRPHLSKESSTNS---AAELLKLNTTSEYAPGLEDTLIL 355

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807242   356 TMKGIAA------    362

gi|83779600|gb|ABC47616.1|: domain 1 of 1, from 1 to 364: score 148.8, E = 1.6e-41
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|8377960     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|8377960     - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|8377960     - ------------------------------------------------ -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|8377960     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|8377960     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|8377960     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|8377960     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|8377960     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|8377960     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|8377960     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|8377960     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|8377960     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqE++iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|8377960     9 RLSAAWQLYKAQEDLIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP sP
  gi|8377960    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPDSP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L++emA+vAtEEYRsvv+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|8377960   109 KPEWRALLDEMAIVATEEYRSVVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KDi+nl
  gi|8377960   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIIKKDIRNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY+ WPFFRvt+DL+EmvFAKGDPGi aLyDkLLv+E+L+ FG++
  gi|8377960   209 HMLQEMYNAWPFFRVTIDLVEMVFAKGDPGITALYDKLLVSEDLWAFGEN 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR + +Etk+lLL+iAGHkDlLEGD YLKqrlRLRdsYittLnv+qAYtL
  gi|8377960   259 LRTNCEETKKLLLQIAGHKDLLEGDLYLKQRLRLRDSYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPsy v  rPh+sKE   E sk a+eL+ Lnp++++ PGLEDtLiL
  gi|8377960   309 KRIRDPSYNVKFRPHISKEIM-ETSKSANELLILNPSSEYGPGLEDTLIL 357

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|8377960   358 TMKGIAA------    364

gi|18073858|emb|CAC84946.1|: domain 1 of 1, from 1 to 364: score 148.2, E = 2.6e-41
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807385     -    ------------------------------------------- -
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|1807385    - ------------------------------------------------- -

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1807385    - ------------------------------------------------- -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1807385    - ------------------------------------------------- -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1807385    - ------------------------------------------------- -

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1807385    - ------------------------------------------------- -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1807385    - ------------------------------------------------- -

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1807385    - ------------------------------------------------- -

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1807385    - ------------------------------------------------- -

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|1807385    - ------------------------------------------------- -

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|1807385    - ------------------------------------------------- -

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                      sDsGKDAG
gi|1807385    1 -------------------------------------------SDSGKDAG 8

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLYkAqE+++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1807385    9 RLSAAWQLYKAQEDLVKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEH m PP sP
gi|1807385   59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHSMCPPASP 108

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                 PEWR+L++emAv At EYR  v  EPRFvEYFRlAtPElEYG+mniGsR
gi|1807385  109 EPEWRELLDEMAVAATKEYRLFVSHEPRFVEYFRLATPELEYGRMNIGSR 158

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh idKDiKnl
gi|1807385  159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIDKDIKNL 208

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                 +L+EmY  WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+PFG++
gi|1807385  209 LMLQEMYTRWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWPFGEQ 258

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR++Y Etk+lLL++AGHkDlLEG PYL+qrlRLRdsYittLn +qAYtL
gi|1807385  259 LRNNYNETKNLLLQVAGHKDLLEGNPYLRQRLRLRDSYITTLNACQAYTL 308

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                KRiRDP+y+vt+rP+lsKE  + n k a+eLvkLnpt+++aPGLEDtLiL
gi|1807385  309 KRIRDPNYHVTVRPPLSKEIMESN-KAAAELVKLNPTSEYAPGLEDTLIL 357
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                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807385   358 TMKGIAA------    364

gi|18076774|emb|CAC84954.1|: domain 1 of 1, from 1 to 363: score 148.2, E = 2.6e-41
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807677     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807677     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807677     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807677     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807677     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807677     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807677     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807677     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807677     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807677     - ---------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807677     - ---------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|1807677     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE++KvAKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807677     9 RLSAAWQLYKAQEELVKVAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP+tinGs RvtvqGEviE+sFGEE LCFr+LqRFtAAtLEHGm PP+sP
  gi|1807677    59 PPETINGSFRVTVQGEVIEQSFGEERLCFRTLQRFTAATLEHGMLPPISP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR +++e+AvvAtEEYRsvv+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|1807677   109 KPEWRAILDEIAVVATEEYRSVVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|1807677   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHILQKDIRNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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                    q LkEmY+eWPFFRvtlDLlEmvFAKGDP iAaLyDkLLv++eLk FG++
  gi|1807677   209 QVLKEMYNEWPFFRVTLDLLEMVFAKGDPRIAALYDKLLVSDELKSFGEQ 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Et++lLL++AGHkDlLEGDPYLKqrlRLR+sYittL v+qAYtL
  gi|1807677   259 LRANYEETEQLLLQVAGHKDLLEGDPYLKQRLRLRESYITTLSVCQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+++v +r +lsKE  d n  k++eLvkLnpt+++aPGLEDtLiL
  gi|1807677   309 KRIRDPNFQVHMRAPLSKEILDSN--KPAELVKLNPTSEYAPGLEDTLIL 356

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|1807677   357 TMKGIAA------    363

gi|18073834|emb|CAC84934.1|: domain 1 of 1, from 1 to 364: score 148.1, E = 2.7e-41
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807383     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807383     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807383     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807383     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807383     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807383     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807383     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807383     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807383     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807383     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807383     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807383     1 ----------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqE+++KvAK++GvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|1807383     9 RLSAAWQLYKAQEDLVKVAKEFGVKLTMFHGRGGTVGRGGGPAHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti GslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEH m PP sP
  gi|1807383    59 PPDTILGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHSMCPPASP 108
```

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                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                     PEWR L++emAv At EYRsvv++EPRFvEYFRlAtPElEYG+mniGsR
  gi|1807383   109 EPEWRALLDEMAVTATKEYRSVVFQEPRFVEYFRLATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkP GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh idKDiKnl
  gi|1807383   159 PSKRKPNGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIDKDIKNL 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmYk WPFFRvt+DL+EmvFAKGDPGiAaLyDk Lv+E+L+PFG++
  gi|1807383   209 LTLQEMYKRWPFFRVTIDLVEMVFAKGDPGIAALYDKALVSEDLWPFGEQ 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y Etk lLL++AGHkDlLEGDPYL+qrlRLRdsYittLnv+qAYtL
  gi|1807383   259 LRNNYNETKTLLLQVAGHKDLLEGDPYLRQRLRLRDSYITTLNVCQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP y vt+rPhlsKE  + n k+a+eLvkLnpt+++aPGLEDtLiL
  gi|1807383   309 KRIRDPHYNVTVRPHLSKEITESN-KPAAELVKLNPTSEYAPGLEDTLIL 357

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|1807383   358 TMKGIAA------    364

gi|18073822|emb|CAC84916.1|: domain 1 of 1, from 1 to 364: score 148.0, E = 2.9e-41
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807382     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807382     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807382     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807382     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807382     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807382     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807382     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807382     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807382     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807382     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807382     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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                                                        sDsGKDAG
  gi|1807382     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqL+kAqE++iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807382     9 RLSAAWQLFKAQEDLIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAt EHGm+PPvsP
  gi|1807382    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATPEHGMHPPVSP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR+Lm+emAvvAt EYRs+v+++ RFvEYFRlAtPElEYG+mniGsR
  gi|1807382   109 KPEWRELMDEMAVVATNEYRSIVFQDKRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh ++KDi+nl
  gi|1807382   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVLEKDIRNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+ mY+eWPFFRvt+DL+EmvFA+GDPGiAaLyDkLLv+E+ +P G +
  gi|1807382   209 HILQQMYNEWPFFRVTIDLVEMVFARGDPGIAALYDKLLVSEDXWPVGAQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR  YvEtk+lLL++AGH+DlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|1807382   259 LRSIYVETKNLLLQVAGHRDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+++  lrPhlsKE      k+a+eLvkLnpt+++aPGLEDtLiL
  gi|1807382   309 KRIRDPNFHCNLRPHLSKETMSST-KPAAELVKLNPTSEYAPGLEDTLIL 357

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807382   358 TMKGIAA------    364

gi|18073846|emb|CAC84940.1|: domain 1 of 1, from 1 to 366: score 147.2, E = 5.1e-41
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807384     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807384     - ---------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807384     - ---------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807384     - ---------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807384     - ---------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807384     - ---------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807384     - ---------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807384     - ---------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807384     - ---------------------------------------------------- -
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                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807384     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807384     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807384     1 -----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAW LYkAqEE+++vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807384     9 RLSAAWALYKAQEELVQVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP+t+nGslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|1807384    59 PPETVNGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++e+AvvAtE YRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|1807384   109 KPEWRALLDEIAVVATEKYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF +Ai+KD+Knl
  gi|1807384   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFGYAIQKDVKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+ mY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+EeL+PFG++
  gi|1807384   209 SVLQKMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEELWPFGER 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++++Etk l+LkiAGHkDlLEGDPY +qrlRLRdsYittLn +qAYtL
  gi|1807384   259 LRADFEETKGLILKIAGHKDLLEGDPYSRQRLRLRDSYITTLNALQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEns.kkadeLvkLnptervaPGLEDtLi
                  KRiRDP+y v lrPh+sKEy d  s+k+a+eLvkLnp++++aPGLEDtLi
  gi|1807384   309 KRIRDPNYNVQLRPHISKEYMDSTSnKPAAELVKLNPSSEYAPGLEDTLI 358

                  LtmKGiAAGmqntG<-*
                  LtmKGiAA
  gi|1807384   359 LTMKGIAA------    366

gi|114326718|ref|YP_743875.1|: domain 1 of 1, from 1 to 926: score 147.2, E = 5.2e-41
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         q   +  G    d          l      L DL
  gi|1143267     1    MTNMQRSDIMTGTSRPDVSAAGRGTACL------LRDL--------- 32

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                      E++A       +   +E    L  + P       +a      L  +
  gi|1143267    33 --LLEVAARHHPDIVPALTGEGRWSLSTMTPQALGRALQAQGIWFQLLSI 80

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AE  e    RR   k+ G  aD    t ++ + E     ++
  gi|1143267    81 AEQKEAMRQRRAVEKQ-GSRAD-VRGTFDAVLAEAKAAGISAD-----TL 123

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   + L    +  v+tAHPt + R  +L K+  i   L  L     t  +
  gi|1143267   124 SDTLAGLRIRPVVTAHPTEAKRVTVLEKHREIYLLLLELDNPRWTEREHA 173

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   L   L   i   + t E+R  +   q E+  G+ ++ E +++ vP+
  gi|1143267   174 RLVRRLRDQIELLWLTGELRLEKVSVQQEVHWGLHFFRESLFEIVPQVAA 223

                  RvDtALKniGinERlP...Ydv.PLikFssWmGGDRDGknPRvtPEvtRD
                    + A+         P+++ d++  ++F sW+GGDRDG nP vt +vtR
  gi|1143267   224 SLEEAVAAQYPDAPAsprRDAgGFLQFGSWVGGDRDG-NPYVTNDVTRW 272

                  vCLLaRmmAanlYisqvEDLmFElsmWRCn........dELRvRAEElyr
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                            Y  q+  L+  ls+     + ++     +R R E +
  gi|1143267   273 TLRENAQASLEHYRKQIARLIKSLSVTEHAltipqwflALVRERVEAMTD 322

                    taardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi
                     +              q  P EP+R  L  +  +L    E +  L   G
  gi|1143267   323 APSLA-----------QRNPGEPFRQFLTVMDVRL----EDTLRLQTGGD 357

                    sei.sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstF
                    ++ ++    y   +  ++ L    k+L + G   iA   +  l      F
  gi|1143267   358 ADFgATSHAYPSADALIDDLRAMEKALEDAGSPEIAADLIRPLRCSAEIF 407

                    GLsLvKLDiRqEseRqtDvlDAittHL.eiGsYReWsEeKRqEW...Lla
                      s v+LD+Rq s R t  l A  + +++ G   e + +   EW++ Ll
  gi|1143267   408 RFSTVRLDLRQNSTRLTNALHAYWRDVtGQGLQSEPPSDDSAEWeefLLD 457

                    ELkGKR..PLlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiism
                     L+  R   L + D P  E+ ++vl+ f+ +AE +++L  ++FG++i+sm
  gi|1143267   458 ALQQPRlaRLTPQDWP--EDAREVLEMFQLVAEmrgrLDREAFGSFILSM 505

                    ataPsDvLAvELLqRECgv........kqtLrvvPLFEkLADLeAAPAav
                    + + +D+L   ++ +  g+  ++ + +   L++vPLFE + DL+AAP  +
  gi|1143267   506 TRSVADILGAYVMAKQAGLfldsvgmeLCELPIVPLFETIDDLRAAPLIM 555

                    ekLFsiDWYi..nridGK.qevmvGYsDsGKDAGRlsAAWqLYkAqEEii
                     +L  i   +++ r +G  qevm+GYsDs KD G +sA W L++Aq  ++
  gi|1143267   556 RRLLNIPVIRrsARRQGNvQEVMIGYSDSNKDGGFISANWELFRAQSRLA 605

                    KvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGE
                    +v ++ G+ +  FHGRGG v RGG Pt  Ai +qPP  i G  Rvt qGE
  gi|1143267   606 QVGQDAGIAIAFFHGRGGSVSRGGAPTRRAIAAQPPGSIRGRFRVTEQGE 655

                    viEfsFGEEnLCFrsLqRFtAAtLEHGm......nPPvsPkPEWRkLmee
                    v+   +             +A  L+H +++++  +   s +PE+ + me
  gi|1143267   656 VVSAKYANKGTASYQAELLAASVLDHALrserlaDSIASVRPEYEDAMEA 705

                    mAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi
                    +   A   YRs++   P  v YF +A P  E+  +niGsRPa+R  +  +
  gi|1143267   706 LSGAANAAYRSLI-GNPHMVGYFQSASPLEEFALLNIGSRPARRFGARSL 754

                    esLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAid.KDiKnlqkLkEmYke
                      LRAiP++FaWtq R  +  W GvG A    +d +  +    L+ m+ +
  gi|1143267   755 SDLRAIPFVFAWTQNRHLITSWYGVGSAISTFLDvRGERGEEVLRRMFAD 804

                    WPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksL.RdkYvEt
                    +P FR   D +E      D  iA Ly  L+  Ee +     L  ++Y+ t
  gi|1143267   805 YPLFRLIADEVEKALLFVDLEIARLYAGLVPEEEARQAILPLvEAEYQLT 854

                    kdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsy
                      ++ +i G   + E     + rl  R + i   n  q   L+R RD
  gi|1143267   855 CAMITRISGDAQVGERFHRYRTRLTERLPVINAANREQVELLRRFRD--- 901

                    kvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAG
                                      +d+ vk              L+L +  iA G
  gi|1143267   902 ------------------APDDAVKSA------------LLLSINCIAGG 921

                    mqntG<-*
                       tG
  gi|1143267   922 FGTTG    926

gi|163851228|ref|YP_001639271.1|: domain 1 of 1, from 12 to 922: score 146.2, E = 9.9e-41
                    *->siDAqLR.lLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEa
                       + D    + ++ G   ed   i + AL     LD+    H ++L ++
  gi|1638512    12    ATDTTFApPVITGTATEDALEILFHAL-----LDVARR-HDPELEDV 52

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                                G+ D        +  t    a a+ v      ++ +A
  gi|1638512    53 LH----------GRADI-------SSFTPEMLARALQVQGIWFQLVSIA- 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                       E + A RRR +  +     D +           l     ++   P+
  gi|1638512    85 ---EQNAAMRRRRHVER-----DQGREALNGSFAKVLAEASARG-IGPQQ 125
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                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                +   LK   +   +tAHPt   R  +L K  Ri   L  L     t  ++
gi|1638512   126 IHALLKDLRIRPTITAHPTEGKRVTVLEKLRRIYLVLRELELPRWTERER 175

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                  L   L   i   + t E+   + t   E+  G+ ++ Et+++  P  L
gi|1638512   176 NGLMNELRDQIELIWMTGELHLEKATVEREVAWGLHFFDETLFEMLPEML 225

                RRvDtALKniGinERlPYdv.PLikFssWmGGDRDGknPRvtPEvtRDvC
                   +  L      E   ++v+P  +F sW+GGDRDG nP vt  vtR+
gi|1638512   226 LSLEESLAQYYPDET--FEVpPFFQFGSWIGGDRDG-NPYVTASVTRETL 272

                LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    +     Y + +  L   ls       +  R   +  t +++ +
gi|1638512   273 QRNALASLRRYRDGITHLGRVLS-------ITERSLPVPETFRSE-LAHM 314

                YiEF..WKqvP...PtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                  E ++ + + +++P E YR  L  v  KL  t  R +     G   +
gi|1638512   315 LAESgdARAIAnrnPGEAYRQFLSCVLRKLKATIARNK-----GARSVGP 359

                eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                +  y   +  +  L    k L +    ++A   +  + R v  F  s v+
gi|1638512   360 D--YPSADGLINDLRTLEKGLADAKCGALATDIVRPVRRMVEIFRFSTVR 407

                LDiRqEseRqtDvlDAittHLeiGsYReWsEe..KRqEWLlaELkGKRP.
                LD+R  s R t  l A+ + L  G     + +++  ++WLl+EL   R +
gi|1638512   408 LDLRENSTRTTKTLHALWK-LRNGDREPPALDspAWKDWLLTELARPRTp 456

                .....LlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataP
                +++ + +   LP  ++ ++ l +f  + E +++L  ++FGa+i+sm+ +
gi|1638512   457 etsfeDFADRLP--DDARETLATFALVGEmrdtLDREAFGAFILSMTRST 504

                sDvLAvELLqRECgv........kqtLrvvPLFEkLADLeAAPAavekLF
                 DvL   LL +E g+  ++++++  +L++vPLFE + DL+AAPA ++ L
gi|1638512   505 VDVLGAYLLAKEAGIfldttgteICPLPIVPLFETIDDLRAAPAIMKELL 554

                siDWYinrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                 i   +     ++G qevm+GYsDs KD G ++  W LYkAq  +
gi|1638512   555 GIPVVRRSTRwqgGVQEVMIGYSDSNKDGGFIASNWELYKAQVRLTTLGN 604

                kyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf
                + Gv +  FHGRGG v RGG PtH  i +qPP  i+G  R+t qGEv+ f
gi|1638512   605 HLGVPIAFFHGRGGSVSRGGVPTHRGIAAQPPGSIQGRFRITEQGEVVSF 654

                sFGEEnLCFrsLqRFtAAtLEHGmnPP...vsPkPEWRkLmeemAvvAtE
                 +         +   +A   EH +   +++   + E+ + +e +
gi|1638512   655 KYANRGTAAYQMELLAASVFEHALLSEgngNGSRAEFDDALEALSGASRA 704

                EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                 Y  +   E   v+YF  A P  E   +niGsRPa+R  +  +  LRAiP
gi|1638512   705 AYVNLLQAEG-LVDYFQAASPLDEISLLNIGSRPARRFGAKSLSDLRAIP 753

                WiFaWtqtRFHLPvWLGvGAAFKhAid.KDiKnlqkLkEmYkeWPFFRvt
                W+FaW q R  +  W GvG   K  id +       L+ ++++   FR
gi|1638512   754 WVFAWSQNRHVITGWYGVGSGLKSFIDvRGEAGEALLRRLFRDCRVFRLV 803

                lDLlEmvFAKGDPGiAaLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLk
                lD +E      D  iA  y  L+  E ++ + FG  + ++Y  t++++L+
gi|1638512   804 LDEVEKTLLMVDLEIARDYAGLVEDEGIRAriFG-MIEAEYALTREMVLR 852

                iAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrP
                + G  +l    P    rlR R + i  +   q   L+R R
gi|1638512   853 VSGDSELAQRFPQFSERLRGRLPTINQVSREQVELLRRYRSET------- 895

                hlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<
                       dE+     e vk              L+L +  iA G   tG
gi|1638512   896 -------DED---KREAVKSA------------LLLSINCIAVGFGATG  922

                -*
```

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  gi|1638512     -    -

gi|1166442|emb|CAA61086.1|: domain 1 of 1, from 1 to 364: score 146.1, E = 1.1e-40
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1166442     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1166442     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1166442     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1166442     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1166442     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1166442     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1166442     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1166442     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1166442     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1166442     - ---------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1166442     - ---------------------------------------------- -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1166442     1 -----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqE+++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1166442     9 RLSAAWQLYKAQEDLVKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEH m PP sP
  gi|1166442    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHSMCPPASP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    PEWR+L++emAv AtEEYR +v+ EPRFvEY  +AtPElEYG+mniGsR
  gi|1166442   109 EPEWRELLDEMAVAATEEYRTIVFHEPRFVEYSASATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh idKDiKnl
  gi|1166442   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIDKDIKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY+ WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+PFG++
  gi|1166442   209 LMLQEMYNRWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWPFGEQ 258
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                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y Etk+lLL++AGHkDlLEG PYL+qrlRLRdsYittLn +qAYtL
  gi|1166442   259 LRNNYNETKNLLLQVAGHKDLLEGNPYLRQRLRLRDSYITTLNACQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiR+P+y+vt+rP lsKE  + n k a eLvkLnpt+++aPGLEDtLiL
  gi|1166442   309 KRIREPNYHVTVRPRLSKEIMESN-KAASELVKLNPTSEYAPGLEDTLIL 357

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|1166442   358 TMKGIAA------    364

gi|18076757|emb|CAC84915.1|: domain 1 of 1, from 1 to 364: score 146.0, E = 1.1e-40
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807675     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807675     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807675     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807675     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807675     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807675     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807675     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807675     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807675     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807675     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807675     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                            sDsGKDAG
  gi|1807675     1 ----------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807675     9 RLSAAWQLYKAQEELIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1807675    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    k EWR+Lm+emAvvAt EYRs+v++  RFvEYFRlAtPE+EYG+mniGsR
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  gi|1807675   109 KQEWRELMDEMAVVATKEYRSIVFQNKRFVEYFRLATPETEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+h ++KDi+nl
  gi|1807675   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHVLEKDIRNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+ mY+eWP FRvt+DL+EmvFA GDPGiAaLyDkLLv+E+L+  G +
  gi|1807675   209 HMLQQMYNEWPVFRVTIDLVEMVFAEGDPGIAALYDKLLVSEDLWLLGSQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR ++ EtkdlLLk+AGH+DlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|1807675   259 LRSNFAETKDLLLKVAGHRDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+++  lrPhlsKE      k+a++LvkLnpt+++aPGLEDtLiL
  gi|1807675   309 KRIRDPNFHCNLRPHLSKETMSSS-KPAADLVKLNPTSEYAPGLEDTLIL 357

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807675   358 TMKGIAA------    364

gi|18073842|emb|CAC84938.1|: domain 1 of 1, from 1 to 364: score 145.7, E = 1.4e-40
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807384     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807384     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807384     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807384     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807384     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807384     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807384     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807384     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807384     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807384     - ---------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807384     - ---------------------------------------------- -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807384     1 -----------------------------------------SDSGKDAG 8
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                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqE++iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807384      9 RLSAAWQLYKAQEDLIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP sP
  gi|1807384     59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPDSP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emAvvAtEEYRsvv+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|1807384    109 KPEWRALLDEMAVVATEEYRSVVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFH PvWLG+GAAFKh i+KDi+nl
  gi|1807384    159 PSKRKPSGGIESLRAIPWIFAWTQTRFHSPVWLGFGAAFKHIIKKDIRNL 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+ WPFFRvt+DL+EmvFAKGDPGi aLyDkLLv+E+L+ FG++
  gi|1807384    209 HMLQEMYNAWPFFRVTIDLVEMVFAKGDPGITALYDKLLVSEDLWAFGEN 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR + +Etk+lLL+iAGHkDlLEGD YLKqrlRLRdsYittLnv+qA+tL
  gi|1807384    259 LRTNCEETKKLLLQIAGHKDLLEGDLYLKQRLRLRDSYITTLNVCQAFTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPsy v  rPh+sKE   E sk a+eL+ Lnp++++aPGLEDtLiL
  gi|1807384    309 KRIRDPSYNVKFRPHISKEIM-ETSKSANELLILNPSSEYAPGLEDTLIL 357

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|1807384    358 TMKGIAA------    364

gi|7320917|emb|CAB81955.1|: domain 1 of 1, from 1 to 372: score 145.7, E = 1.5e-40
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7320917      -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7320917      - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7320917      - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7320917      - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                                      iRR++PtPqDEmRaGmsY+HEt+WkGvPKFLR
  gi|7320917      1 ------------------IRRTPPTPQDEMRAGMSYFHETIWKGVPKFLR 32

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    R+DtALK iGinER+PY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|7320917     33 RIDTALKSIGINERMPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 81

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq+EDLmFElsmWRC dELR+RA  l++ +++d   K+Yi
  gi|7320917     82 ARMMAANLYYSQIEDLMFELSMWRCSDELRARALQLHSASKKD--AKHYI 129

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    EFWKq+PP+EP+RviLGdvRDKLYntRER+R LL  Gis+i+Ee  +t+v
  gi|7320917    130 EFWKQIPPNEPFRVILGDVRDKLYNTRERTRQLLSNGISDIPEEVTFTNV 179

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    + FLEPLELCY+sLC  GD+ iADGsLLD++RqvstFGLsLv+LDiR Es
  gi|7320917    180 DGFLEPLELCYRSLCSTGDQPIADGSLLDFMRQVSTFGLSLVRLDIRRES 229

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    +R+tDv+DAit+HL+iGsY eWsEe+Rq WLl+EL+GKRPL+g+DLPkt+
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  gi|7320917   230 DRHTDVVDAITKHLGIGSYEEWSEERRQAWLLSELQGKRPLFGPDLPKTD 279

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                    Ev+Dvld+f+v+ ELP D FGaYiismata sDvL vELLqREC+vk++L
  gi|7320917   280 EVRDVLDTFHVISELPADNFGAYIISMATAASDVLVVELLQRECHVKKPL 329

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    rvvPLFEkLADLeAAPAa+++LFsi WY+nridGKqevm+GYs
  gi|7320917   330 RVVPLFEKLADLEAAPAALARLFSINWYRNRIDGKQEVMIGYS------- 372

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|7320917     - ------------------------------------------------- -

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

  gi|7320917     - ------------------------------------------------- -

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|7320917     - ------------------------------------------------- -

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|7320917     - ------------------------------------------------- -

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|7320917     - ------------------------------------------------- -

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|7320917     - ------------------------------------------------- -

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|7320917     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|7320917     - -------------    -

gi|18073836|emb|CAC84935.1|: domain 1 of 1, from 1 to 364: score 145.5, E = 1.6e-40
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807383     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807383     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807383     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807383     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807383     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807383     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807383     - ------------------------------------------------- -
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                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807383     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807383     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807383     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807383     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807383     1 -----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqE++iKvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807383     9 RLSAAWQLYKAQEDLIKVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+Gs RvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP sP
  gi|1807383    59 PPDTIHGSPRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPDSP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++emAvvAtEEYRsvv+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|1807383   109 KPEWRALLDEMAVVATEEYRSVVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KDi+nl
  gi|1807383   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIIKKDIRNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+EmY+ WPFFRvt+DL+EmvFAKGDPGi aLyDkLLv+E+L+ FG++
  gi|1807383   209 HMLQEMYNAWPFFRVTIDLVEMVFAKGDPGITALYDKLLVSEDLWAFGEN 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR + +Etk+lLL+iAGHkDlLEGD YLKqrlRLRdsYittLnv+qA+tL
  gi|1807383   259 LRTNCEETKKLLLQIAGHKDLLEGDLYLKQRLRLRDSYITTLNVCQAFTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDPsy v  rPh+sKE   E sk a+eL+ Lnp++++aPGLEDtLiL
  gi|1807383   309 KRIRDPSYNVKFRPHISKEIM-ETSKSANELLILNPSSEYAPGLEDTLIL 357

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807383   358 TMKGIAA------    364

gi|254467180|ref|ZP_05080591.1|: domain 1 of 1, from 1 to 886: score 144.5, E = 3.3e-40
                  *->siDAqLRlLvPGKvsed.ekLieYDALLlDkFLDiLqDLHGedLkEa
                            +  P     d+ +   Y A L         +LH   L
  gi|2544671     1    -------MGDPAETTCDgVEDTGYAAGLRG-------ELHTLWLDVL 33

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   q   E++A        k + E    L + +Pa a +  +a+     L
  gi|2544671    34 RQRAPEVAA--------KAVSETAWDLSGGQPATAYM--QAFNIWFQLLK 73

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                  + EE      RR+   + G    E+s     D       L   l  +Pe
  gi|2544671    74 IVEENAAMRDRRMAETQDGPEVVEGSFARALD-------LAGEL-ATPER 115

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    e     s+   ltAHPt + R  +L  + Ri   L  L AK  t+ ++
  gi|2544671   116 LQEVASQFSIGPTLTAHPTEAKRVTILEIHRRIYRGLVSLEAKRWTPRER 165

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK.F
                    L   L  Ei   + t E+RR +P  qDE+  G+ ++ + +++ vP+ F
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  gi|2544671   166 AGLLADLRSEIDLLWMTGELRRDRPSLQDEIQWGLQFFRDSLYEAVPQlF 215

                   LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R +  A   +G       d+P +kF sW+GGDRDG nP vt E t
  gi|2544671   216 ERYIAAAEPRLGDTA----DAPCLKFHSWIGGDRDG-NPNVTVEAT---- 256

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                         Aa l  +    L       R    L   AE +   aa   +
  gi|2544671   257 ------AAALTANRAAILD------RYQTALTTAAERISISAAVFALPEG 294

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vy
                         +v    P    L + R      R     +LA   +  +E A+ y
  gi|2544671   295 TSARLAKVIAAAPGAAALSA-RNPGEVFRQALTAILARIKATAAEGAgAY 343

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                    ++ +F+  L     +L e G   +A   +  +  q   FG   v LD+R
  gi|2544671   344 KHLGDFVAGLTEVEAALEEIGANRLAARYVRPIRWQADVFGFRTVTLDVR 393

                   qEseRqtDvlDAittHLe....iGsYReWsEeKRqEWLlaELkGKRPLlg
                   q s   t+ l  i    ++ ++ Gs  eWs   R+E   a L     +++
  gi|2544671   394 QNSTVTTETLTEIWARSGnvpdFGS-PEWSARLRRELGSASLP---YMMP 439

                   sDL.PktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELLq
                    +L+P+  E+   l  +r+  A     + G++++sm+ +  D LAv LL
  gi|2544671   440 DELsPQSGELLKLLRLMRdAGAGEDPQAMGPFLLSMTRSTDDLLAVYLLA 489

                   RECgv...kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri...dGK
                   R  g + +k +L+vvPLFE + DL+AAP  ++ L  + + +  ++++d +
  gi|2544671   490 RYAGFgaeKAALKVVPLFETIGDLRAAPGILDGLLDVPFARRSLksgDSR 539

                   qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                    evm+GYsDs KD G l   W L kAq  i +    + +K v FHGRGG
  gi|2544671   540 IEVMLGYSDSNKDGGFLCSTWELEKAQRLITRTLAAHRMKPVFFHGRGGS 589

                   vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                   v RGG P   Ai +qP  ti G +R+t qGEv+   +       + L
  gi|2544671   590 VSRGGAPAERAIAAQPAGTIAGRMRITEQGEVVSSKYANRGTALHQLELM 639

                   tAAtLEHGmnPPvsP.kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                   +   L H ++  v P  PE  +  e +A +    Y s  +  P F +YF
  gi|2544671   640 ASSVLRHSLQDDVPPvNPEHDDAFEALAGMSQAAY-SNLLNAPGFLDYFQ 688

                   lAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG
                    A P  E   + iGsRPa+R  +G ++ LRAiPW+FaW q R  +  W G
  gi|2544671   689 QASPVEELAMLKIGSRPARRFGAGSLDDLRAIPWVFAWSQNRHMITGWYG 738

                   vGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                   +G A  ++   +  +    L++m+   P FR  +D +E    + D  iAa
  gi|2544671   739 FGSAVAsFRRFRGARGEAVLQDMFAGSPLFRLVVDEVEKTLLQSDMEIAA 788

                   LyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                    y  L+   e++++ FG s+R +Y+   + +L        L GD     r
  gi|2544671   789 DYATLVQDGEIrdRIFG-SIRKEYQLACEAIL-------FLTGD----SR 826

                   lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                   l LR + +            R R    +  lr         E  k    L
  gi|2544671   827 LALRFPRL------------RARFGRVETMLR---------EIHKTQVRL 855

                   vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   ++ n   + +  +   L+  m  +AAG+  tG
  gi|2544671   856 LQEN-RAEKPSTVPVPLMQSMNCVAAGLGWTG    886

gi|1166448|emb|CAA61085.1|: domain 1 of 1, from 1 to 364: score 143.8, E = 5.2e-40
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1166448     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1166448     - ---------------------------------------------- -
```

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                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1166448    - ------------------------------------------------- -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1166448    - ------------------------------------------------- -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1166448    - ------------------------------------------------- -

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1166448    - ------------------------------------------------- -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1166448    - ------------------------------------------------- -

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1166448    - ------------------------------------------------- -

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1166448    - ------------------------------------------------- -

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|1166448    - ------------------------------------------------- -

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|1166448    - ------------------------------------------------- -

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                      sDsGKDAG
gi|1166448    1 ------------------------------------------SDSGKDAG 8

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLYkAqE+++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1166448    9 RLSAAWQLYKAQEDLVKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEH m PP sP
gi|1166448   59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHSMCPPASP 108

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                 PEWR+L++emAv AtEEYR +v+ EPRFvEY  +AtPElEYG+mn+GsR
gi|1166448  109 EPEWRELLDEMAVAATEEYRTIVFHEPRFVEYSASATPELEYGRMNVGSR 158

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh idKDiKnl
gi|1166448  159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIDKDIKNL 208

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                 +L+EmY+ WPFFRvt+DL+Emv AKGDPGiAaLyDkLLv+E+L+PFG++
gi|1166448  209 LMLQEMYNRWPFFRVTIDLVEMVLAKGDPGIAALYDKLLVSEDLWPFGEQ 258

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR++Y Etk+lLL++AGHkDlLEG PYL+qrlRLRdsYittLn +qAYtL
gi|1166448  259 LRNNYNETKNLLLQVAGHKDLLEGNPYLRQRLRLRDSYITTLNGCQAYTL 308

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                KRiRDP+y+vt+rP lsKE  + n k a+eLvkLnpt+++aPGLEDtLiL
gi|1166448  309 KRIRDPNYHVTVRPRLSKEIMESN-KAAAELVKLNPTSEYAPGLEDTLIL 357

                tmKGiAAGmqntG<-*
                tmKGiAA
gi|1166448  358 TMKGIAA------    364
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gi|18073904|emb|CAC84980.1|: domain 1 of 1, from 1 to 364: score 143.6, E = 6.1e-40
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807390     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807390     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807390     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807390     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807390     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807390     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807390     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807390     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807390     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807390     - ---------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807390     - ---------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                         sDsGKDAG
  gi|1807390     1 -----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqE ++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807390     9 RLSAAWQLYKAQEGLVKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGE iE+sFGEE+LCFr+LqR+tAAtLEH m PP sP
  gi|1807390    59 PPDTIHGSLRVTVQGEAIEQSFGEEHLCFRTLQRYTAATLEHSMCPPASP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   PEWR+L++emAv At EYRs+v+ EPRFvEYFRlAtPElEYG+mniGsR
  gi|1807390   109 EPEWRELLDEMAVAATKEYRSIVFHEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh idKDiKnl
  gi|1807390   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIDKDIKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+EmY  WPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+E+L+PFG++
  gi|1807390   209 LTLQEMYTRWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEDLWPFGEQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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                    LR++Y Etk+lLL++AGHkDlLEG PYL+qrlRLRdsYittLn +qAYtL
  gi|1807390   259 LRNNYNETKNLLLQVAGHKDLLEGNPYLRQRLRLRDSYITTLNACQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+vt+rP lsKE  + n   a+eLvkLnpt+++aPGLEDtLiL
  gi|1807390   309 KRIRDPNYHVTVRPRLSKEIMESN-NAAAELVKLNPTSEYAPGLEDTLIL 357

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|1807390   358 TMKGIAA------    364

gi|18073878|emb|CAC84958.1|: domain 1 of 1, from 1 to 365: score 143.2, E = 8e-40
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807387     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807387     - ---------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807387     - ---------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807387     - ---------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807387     - ---------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807387     - ---------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807387     - ---------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807387     - ---------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807387     - ---------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807387     - ---------------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807387     - ---------------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807387     1 ------------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqE+++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807387     9 RLSAAWQLYKAQEDLVKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEH m PP sP
  gi|1807387    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHSMCPPASP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                     PEWR+L++emAv At EYRs+v+ EPRFvEYFRlAtPElEYG+mniGsR
  gi|1807387   109 EPEWRELLDEMAVAATKEYRSIVFHEPRFVEYFRLATPELEYGRMNIGSR 158
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                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh idKDiKnl
  gi|1807387   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIDKDIKNL 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY  WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+PFG++
  gi|1807387   209 LMLQEMYTRWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWPFGEQ 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y Etk+lLL++AGHkDlLEG PYL+qrlRLRdsYittLn +qAYtL
  gi|1807387   259 LRNNYNETKNLLLQVAGHKDLLEGNPYLRQRLRLRDSYITTLNACQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|1807387   309 KRIRDPSYQVPVRPPIAKEIMEGSVSSANQLVKLNPTSEYAPGLEDTLIL 358

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|1807387   359 TMKGIAA------    365

gi|1552964|gb|AAB08697.1|: domain 1 of 1, from 1 to 364: score 142.2, E = 1.6e-39
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1552964     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1552964     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1552964     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1552964     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1552964     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1552964     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1552964     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1552964     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1552964     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1552964     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1552964     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                           sDsGKDAG
  gi|1552964     1 ----------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
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                    RlsAAWqLYkAqEE+iKvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1552964      9 RLSAAWQLYKAQEELIKVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGs+RvtvqGEviE+sFGEE LCFr+LqRFtAAtLEHGm+PP+sP
  gi|1552964     59 PPDTINGSIRVTVQGEVIEQSFGEERLCFRTLQRFTAATLEHGMHPPLSP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAvvAt+EYRs+v+K+PRFvEYFR+AtPElEYG+mniGsR
  gi|1552964    109 KPEWRALMDEMAVVATDEYRSIVFKDPRFVEYFRSATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KR+PsGGiesLRAiPWiFaWtqt+FHLPvWLG+G AFKh i KD Knl
  gi|1552964    159 PSKRRPSGGIESLRAIPWIFAWTQTKFHLPVWLGFGSAFKHVIGKDPKNL 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+L+EmY+eWPFFRvt+DL+EmvFAKGDP iAa+yDkLLv+ +L+PFG+
  gi|1552964    209 QMLQEMYNEWPFFRVTIDLVEMVFAKGDPVIAAIYDKLLVSKDLQPFGEC 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR+kY EtkdlLLk+AGHkDlLEGDPYLKqrl LRdsYit Ln +qAYtL
  gi|1552964    259 LREKYTETKDLLLKVAGHKDLLEGDPYLKQRLQLRDSYITALNACQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP y v  rPhlsK+  +   k a+eLvkLnp++++aPGLEDtLiL
  gi|1552964    309 KRIRDPGYNVQARPHLSKDMVNNG-KSAAELVKLNPGSEYAPGLEDTLIL 357

                    tmKGiAAGmqntG<-*
                    tmKG+ A
  gi|1552964    358 TMKGVRA------    364

gi|7768123|emb|CAB90622.1|: domain 1 of 1, from 1 to 364: score 142.2, E = 1.6e-39
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768123      -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768123      - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768123      - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768123      - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768123      - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768123      - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768123      - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768123      - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768123      - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768123      - ---------------------------------------------- -
```

```
                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768123     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768123     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYk qEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768123     9 RLSAAWQLYKTQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+ P+sP
  gi|7768123    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMQLPISP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+emAvvAt EYRs+v+ E RFvEYFRlAtPElEYG+mniGsR
  gi|7768123   109 KPEWRALMNEMAVVATNEYRSIVFEESRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD Knl
  gi|7768123   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIEKDKKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+EmY+eWPFFRvt+DL+EmvF KG PGiAaLyDkLLv+ +L PFG++
  gi|7768123   209 NILREMYNEWPFFRVTIDLIEMVFTKGSPGIAALYDKLLVSTDLLPFGEQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y+Etk lLL++AGHkDlLEGDPYLKqrlRLR +YittLnv qAYtL
  gi|7768123   259 LRANYEETKRLLLQVAGHKDLLEGDPYLKQRLRLRYPYITTLNVWQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDPsy+ t +P ls E  + n k+a+eLvkLnpt+++aPGLEDtLiL
  gi|7768123   309 KRIRDPSYHLTAKPNLSNEIMNSN-KPAAELVKLNPTSEYAPGLEDTLIL 357

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|7768123   358 TMKGIAA------    364

gi|218530096|ref|YP_002420912.1|: domain 1 of 1, from 12 to 922: score 141.9, E = 2e-39
                  *->siDAqLR.lLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEa
                     + D    + ++ G   ed   i + AL     LD+    H ++L ++
  gi|2185300    12   ATDTTFApPVITGTATEDALEILFHAL-----LDVARR-HDPELEDV 52

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                              G+ D        +  t    a a+ v      ++ +A
  gi|2185300    53 LH----------GRADI-------SSFTPEMLARALQVQGIWFQLVSIA- 84

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     E + A RRR +  +     D +           l     ++   P+
  gi|2185300    85 ---EQNAAMRRRRHVER-----DQGREALNGSFAKVLAEASARG-IGPQQ 125

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  +   LK   +   +tAHPt   R  +L K  Ri   L  L     t  ++
  gi|2185300   126 IHALLKDLRIRPTITAHPTEGKRVTVLEKLRRIYLVLRELELPRWTERER 175

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    L   L   i   + t E+   + t   E+  G+ ++ Et+++  P  L
  gi|2185300   176 NGLMNELRDQIELIWMTGELHLEKATVEREVAWGLHFFDETLFEMLPEML 225

                  RRvDtALKniGinERlPYdv.PLikFssWmGGDRDGknPRvtPEvtRDvC
                     +  L      E   ++v+P  +F sW+GGDRDG nP vt  vtR+
  gi|2185300   226 LSLEESLAQYYPDET--FEVpPFFQFGSWIGGDRDG-NPYVTASVTRETL 272

                  LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                      +     Y + +  L   ls       +  R   +  t +++ +
  gi|2185300   273 QRNALASLRRYRDGITHLGRVLS-------ITERSLPVPETFRSE-LAHM 314

                  YiEF..WKqvP...PtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
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                     E ++ + + +++P E YR  L  v  KL  t  R +     G   +
  gi|2185300   315 LAESgdARAIAnrnPGEAYRQFLSCVLRKLEATIARNK-----GARSVGP 359

                   eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                   +  y   +  +  L    k L +    ++A   +  + R v  F  s v+
  gi|2185300   360 D--YPSADGLINDLRTLEKGLADAKCGALATDIVRPVRRMVEIFRFSTVR 407

                   LDiRqEseRqtDvlDAittHLeiGsYReWsEe..KRqEWLlaELkGKRP.
                   LD+R  s R t  l A+ + L  G     + +++  ++WLl+EL   R +
  gi|2185300   408 LDLRENSTRTTKTLHALWK-LRNGDREPPALDspAWKDWLLTELARPRTp 456

                   .....LlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataP
                   +++ + +   LP  ++ ++ l +f  + E +++L  ++FGa+i+sm+ +
  gi|2185300   457 etsfeDFADRLP--DDARETLATFALVGEmrdtLDREAFGAFILSMTRST 504

                   sDvLAvELLqRECgv........kqtLrvvPLFEkLADLeAAPAavekLF
                    DvL   LL +E g+  ++++++  +L++vPLFE + DL+AAPA ++ L
  gi|2185300   505 VDVLGAYLLAKEAGIfldttgteICPLPIVPLFETIDDLRAAPAIMKELL 554

                   siDWYinrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                    i   +     ++G qevm+GYsDs KD G ++  W LYkAq  +
  gi|2185300   555 GIPVVRRSTRwqgGVQEVMIGYSDSNKDGGFIASNWELYKAQVRLTTLGN 604

                   kyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf
                   + Gv +  FHGRGG v RGG PtH  i +qPP  i+G  R+t qGEv+ f
  gi|2185300   605 HLGVPIAFFHGRGGSVSRGGVPTHRGIAAQPPGSIQGRFRITEQGEVVSF 654

                   sFGEEnLCFrsLqRFtAAtLEHGmnPP...vsPkPEWRkLmeemAvvAtE
                    +         +   +A   EH +   +++   + E+ + +e +
  gi|2185300   655 KYANRGTAAYQMELLAASVFEHALLSEgngNGSRAEFDDALEALSGASRA 704

                   EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                    Y  +   E   v+YF  A P  E   +niGsRPa+R  +  +  LRAiP
  gi|2185300   705 AYVNLLQAEG-LVDYFQAASPLDEISLLNIGSRPARRFGAKSLSDLRAIP 753

                   WiFaWtqtRFHLPvWLGvGAAFKhAid.KDiKnlqkLkEmYkeWPFFRvt
                   W+FaW q R  +  W GvG   K  id +       L+ ++++   FR
  gi|2185300   754 WVFAWSQNRHVITGWYGVGSGLKSFIDvRGEAGEALLRRLFRDCRVFRLV 803

                   lDLlEmvFAKGDPGiAaLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLk
                   lD +E      D  iA  y  L+    ++ + FG  + ++Y  t++++L+
  gi|2185300   804 LDEVEKTLLMVDLEIARDYAGLVEDAGIRAriFG-MIEAEYALTREMVLR 852

                   iAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrP
                   + G  +l    P    rlR R + i  +   q   L+R R
  gi|2185300   853 VSGDSELAQRFPQFSERLRGRLPTINQVSREQVELLRRYRSET------- 895

                   hlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<
                          dE+     e vk              L+L +  iA G   tG
  gi|2185300   896 -------DED---KREAVKSA-----------LLLSINCIAVGFGATG  922

                   -*

  gi|2185300     -    -

gi|7768238|emb|CAB90653.1|: domain 1 of 1, from 1 to 365: score 141.5, E = 2.7e-39
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768238     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768238     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768238     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768238     - ---------------------------------------------- -
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                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768238    - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768238    - ------------------------------------------------ -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768238    - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768238    - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768238    - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768238    - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768238    - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768238    1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqE+++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768238    9 RLSAAWQLYKAQEDLVKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEH m PP sP
  gi|7768238   59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHSMCPPASP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   PEWR+L++emAv At EYRs+v+ EPRFvEYFRlAtPElEYG+mniGsR
  gi|7768238  109 EPEWRELLNEMAVAATKEYRSIVFHEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh idKDiKnl
  gi|7768238  159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIDKDIKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+EmY  WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+PFG++
  gi|7768238  209 LMLQEMYTRWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWPFGEQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y Etk+lLL++AGHkDlLEG PYL+qrlRLRdsYittLn +qAYtL
  gi|7768238  259 LRNNYNETKNLLLQVAGHKDLLEGNPYLRQRLRLRDSYITTLNACQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|7768238  309 KRIRDPSYQVPVRPPIAKEIMEGSVSSANQLVKLNPTSEYAPGLEDTLIL 358

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|7768238  359 TMKGIAA------    365

gi|18072436|emb|CAC84929.1|: domain 1 of 1, from 1 to 363: score 141.0, E = 3.7e-39
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807243    -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
```

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gi|1807243     - ------------------------------------------------- -

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1807243     - ------------------------------------------------- -

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1807243     - ------------------------------------------------- -

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1807243     - ------------------------------------------------- -

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1807243     - ------------------------------------------------- -

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1807243     - ------------------------------------------------- -

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1807243     - ------------------------------------------------- -

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1807243     - ------------------------------------------------- -

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|1807243     - ------------------------------------------------- -

                 EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|1807243     - ------------------------------------------------- -

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                       sDsGKDAG
gi|1807243     1 -------------------------------------------SDSGKDAG 8

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 RlsAAWqLYkAqEE+++vAK+yGvKL++FHG+GGtvGRGGGPtHLAiLsq
gi|1807243     9 RLSAAWQLYKAQEELVQVAKQYGVKLTMFHGKGGTVGRGGGPTHLAILSQ 58

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                 PP+tinGslRvtvqGEviE+sFGEE LCF++LqR+tAAtLEHGm PP sP
gi|1807243    59 PPETINGSLRVTVQGEVIEQSFGEERLCFKTLQRYTAATLEHGMRPPTSP 108

                 kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                 kPEWR +++e+AvvAtEEYRsvv+KEPRFvEYFRlAtPElEYG+mniGsR
gi|1807243   109 KPEWRAILDEIAVVATEEYRSVVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                 PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                 P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh + KD +nl
gi|1807243   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHILRKDRRNL 208

                 qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLv++eLkPFG++
gi|1807243   209 RILKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVSDELKPFGEQ 258

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                 LR++Y+Etk+lLLk AGH DlLEGDPYLKqr+RLR++YittLnv+qAYtL
gi|1807243   259 LRANYEETKQLLLKAAGHTDLLEGDPYLKQRIRLREAYITTLNVCQAYTL 308

                 KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                 KRiRDP++kv +rP+lsKE  d n  k +eLvkLnp++++aPGLEDtLiL
gi|1807243   309 KRIRDPNFKVDVRPPLSKEILDSN--KQAELVKLNPASEYAPGLEDTLIL 356
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                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|1807243   357 TMKGIAA------    363

gi|188581006|ref|YP_001924451.1|: domain 1 of 1, from 12 to 922: score 139.9, E = 8.1e-39
                    *->siDAqLR.lLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEa
                       + D    + ++ G   ed   i + AL     LD+    H ++L ++
  gi|1885810    12    ATDSTFApPVITGTATEDALEILFHAL-----LDVARR-HDPELEDV 52

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                                G+ D        +  t    a a+ v      ++ +A
  gi|1885810    53 LH----------GRADI-------SSFTPEMLARALQVQGIWFQLVSIA- 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                       E + A RRR +  +     D +           l     ++   P+
  gi|1885810    85 ---EQNAAMRRRRHVER-----DQGREALNGSFAKVLAEASARG-IGPQQ 125

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +   LK   +   +tAHPt   R  +L K  Ri   L  L     t  ++
  gi|1885810   126 IHALLKDLRIRPTITAHPTEGKRVTVLEKLRRIYLVLRELELPRWTERER 175

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      L   L   i   + t E+   + t   E+  G+ ++ Et+++  P  +
  gi|1885810   176 NGLMNELRDQIELIWMTGELHLEKATVEREVAWGLHFFDETLFEMLPEVM 225

                    RRvDtALKniGinERlPYdv.PLikFssWmGGDRDGknPRvtPEvtRDvC
                       +  L      E   ++v+P  +F sW+GGDRDG nP vt  vtR+
  gi|1885810   226 VSLEESLAQYYPDET--FEVpPFFQFGSWIGGDRDG-NPYVTASVTRETL 272

                    LLaRmmAanlYisqvEDLmFElsmW.RCndELRvRAEElyrtaardkvvK
                        +     Y + +  L   ls+ +R      +   El    a
  gi|1885810   273 QRNALASLRRYRDGITHLGRVLSITeRSLPVPEAFRQELAHMLAES---- 318

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                              P E YR  L  v  KL  t  R +     G   +  +  y
  gi|1885810   319 GDGRAIANRNPGEAYRQFLTCVLRKLEATIARNK-----GARSVGPD--Y 361

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                       +  +  L    k L +    ++A   +  + R v  F  s v+LD+R
  gi|1885810   362 PSADGLINDLRTLEKGLADAKCGALATDIVRPVRRMVEIFRFSTVRLDLR 411

                    qEseRqtDvlDAittHLeiGsYReWsEe..KRqEWLlaELkGKRP.....
                      s R t  l A+ + L  G     + + +  +EWLl+EL   R ++++
  gi|1885810   412 ENSTRTTKTLHALWK-LRNGDREPPALDapAWKEWLLTELARPRTpetsf 460

                    .LlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvL
                    + +   LP  ++ ++ l +f  + E +++L  ++FGa+i+sm+ +  DvL
  gi|1885810   461 eDFADRLP--DDARETLATFALVGEmrdtLDREAFGAFILSMTRSTVDVL 508

                    AvELLqRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiDW
                       LL +E g+  + ++++  +L++vPLFE + DL+AAP  ++ L  i
  gi|1885810   509 GAYLLAKEAGIfldatgteICPLPIVPLFETIDDLRAAPTIMKELLGIPV 558

                    Yinrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGv
                     +     ++G qevm+GYsDs KD G ++  W LYkAq  +     + Gv
  gi|1885810   559 VRRSTRwqgGVQEVMIGYSDSNKDGGFIASNWELYKAQVRLTVLGNHVGV 608

                    KLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGE
                     +  FHGRGG v RGG PtH  i +qPP  i+G  R+t qGEv+ f +
  gi|1885810   609 PIAFFHGRGGSVSRGGVPTHRGIAAQPPGSIQGRFRITEQGEVVSFKYAN 658

                    EnLCFrsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvv.
                           +   +A   EH +           +L + +         + v+
  gi|1885810   659 RGTASYQMELLAASVFEHALLSEGNGNGSRAELDDALEALSGASRAAYVn 708

                    .vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaW
                     ++    v+YF  A P  E   +niGsRPa+R  +  +  LRAiPW+FaW
  gi|1885810   709 lLQADGLVDYFQAASPLDEIALLNIGSRPARRFGAKSLSDLRAIPWVFAW 758

                    tqtRFHLPvWLGvGAAFKhAid.KDiKnlqkLkEmYkeWPFFRvtlDLlE
                     q R  +  W GvG   K  id +  +    Lk m++e   FR  lD +E
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  gi|1885810   759 SQNRHVITGWYGVGSGLKSFIDvRGAQGEALLKRMFRECRVFRLVLDEVE 808

                   mvFAKGDPGiAaLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLkiAGHk
                         D  iA  y  L+  E ++ + FG   R+ Y  t++++L++ G
  gi|1885810   809 KTLMMVDLEIARDYAGLVEDEGIRAriFGMIERE-YALTREMVLRVSGDG 857

                   DlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKE
                   +l    P    rlR R + i  +   q   L+R R
  gi|1885810   858 ELAQRFPQFSERLRGRLPTINQVSREQVELLRRYRSET------------ 895

                   yAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     dE+     e vk              L+L +  iA G   tG
  gi|1885810   896 --DED---KREAVKSA-----------LLLSINCIAVGFGATG    922

gi|254560927|ref|YP_003068022.1|: domain 1 of 1, from 12 to 922: score 139.8, E = 8.6e-39
                   *->siDAqLR.lLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEa
                      + D    + ++ G   ed   i + AL     LD+    H ++L ++
  gi|2545609    12    ATDTTFApPVITGTATEDALEILFHAL-----LDVARR-HDPELEDV 52

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                               G+ D        +  t    a a+ v      ++ +A
  gi|2545609    53 LH----------GRADI-------SSFTPEMLARALQVQGIWFQLVSIA- 84

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                      E + A RRR +  +     D +           l     ++   P+
  gi|2545609    85 ---EQNAAMRRRRHVER-----DQGREALNGSFAKVLAEASARG-IGPQQ 125

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   +   LK   +   +tAHPt   R  +L K  Ri   L  L     t  ++
  gi|2545609   126 IHALLKDLRIRPTITAHPTEGKRVTVLEKLRRIYLVLRELELPRWTERER 175

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                     L   L   i   + t E+   + t   E+  G+ ++ Et+++  P  L
  gi|2545609   176 NGLMNELRDQIELIWMTGELHLEKATVEREVAWGLHFFDETLFEMLPEML 225

                   RRvDtALKniGinERlPYdv.PLikFssWmGGDRDGknPRvtPEvtRDvC
                      +  L      E   ++v+P  +F sW+GGDRDG nP vt  vtR+
  gi|2545609   226 LSLEESLAQYYPDET--FEVpPFFQFGSWIGGDRDG-NPYVTASVTRETL 272

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                       +     Y + +  L   ls       +  R   +  t +++ +
  gi|2545609   273 QRNALASLRRYRDGITHLGRVLS-------ITERSLPVPETFRSE-LAHM 314

                   YiEF..WKqvP...PtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                     E ++ + + +++P E YR  L  v  KL  t  R +     G   +
  gi|2545609   315 LAESgeARAIAnrnPGEAYRQFLSCVLRKLEATIARNK-----GARSVGP 359

                   eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                   +  y   +  +  L    k L +    ++A   +  + R v  F  s v+
  gi|2545609   360 D--YPSADGLINDLRTLEKGLADAKCGALATDIVRPVRRMVEIFRFSTVR 407

                   LDiRqEseRqtDvlDAittHLeiGsYReWsEe..KRqEWLlaELkGKRP.
                   LD+R  s R t  l A+ + L  G     + +++  ++WLl+EL   R +
  gi|2545609   408 LDLRENSTRTTKTLHALWK-LRNGDREPPALDspAWKDWLLTELARPRTp 456

                   .....LlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataP
                   +++ + +   LP  ++ ++ l +f  + E +++L  ++FGa+i+sm+ +
  gi|2545609   457 etsfeDFADRLP--DDARETLATFALVGEmrdtLDREAFGAFILSMTRST 504

                   sDvLAvELLqRECgv........kqtLrvvPLFEkLADLeAAPAavekLF
                    DvL   LL +E g+  ++++++  +L++vPLFE + DL+AAPA ++ L
  gi|2545609   505 VDVLGAYLLAKEAGIfldttgteICPLPIVPLFETIDDLRAAPAIMKELL 554

                   siDWYinrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                    i   +     ++G qevm+GYsDs KD G ++  W LYkAq  +
  gi|2545609   555 GIPVVRRSTRwqgGVQEVMIGYSDSNKDGGFIASNWELYKAQVRLTTLGN 604

                   kyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf
                   + Gv +  FHGRGG v RGG PtH  i +qPP  i+G  R+t qGEv+ f
  gi|2545609   605 HLGVPIAFFHGRGGSVSRGGVPTHRGIAAQPPGSIQGRFRITEQGEVVSF 654
```

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                    sFGEEnLCFrsLqRFtAAtLEHGmnPP...vsPkPEWRkLmeemAvvAtE
                     +         +   +A   EH +   +++   + E+ + +e +
  gi|2545609   655 KYANRGTAAYQMELLAASVFEHALLSEgngNGSRAEFDDALEALSGASRA 704

                    EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                     Y  + ++    v+YF  A P  E   +niGsRPa+R  +  +  LRAiP
  gi|2545609   705 AYVNL-LQAQGLVDYFQAASPLDEISLLNIGSRPARRFGAKSLSDLRAIP 753

                    WiFaWtqtRFHLPvWLGvGAAFKhAid.KDiKnlqkLkEmYkeWPFFRvt
                    W+FaW q R  +  W GvG   K  id +       L+ ++++   FR
  gi|2545609   754 WVFAWSQNRHVITGWYGVGSGLKSFIDvRGEAGEALLRRLFRDCRVFRLV 803

                    lDLlEmvFAKGDPGiAaLyDkLL..vaEeLkPFGksLRdkYvEtkdlLLk
                    lD +E      D  iA  y  L+++ +   + FG  + ++Y  t++++L+
  gi|2545609   804 LDEVEKTLLMVDLEIARDYAGLVedASIRARIFG-MIEAEYALTREMVLR 852

                    iAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrP
                    + G  +l    P    rlR R + i  +   q   L+R R
  gi|2545609   853 VSGDSELAQRFPQFSERLRGRLPTINQVSREQVELLRRYRSET------- 895

                    hlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<
                           dE+     e vk              L+L +  iA G   tG
  gi|2545609   896 -------DED---KREAVKSA------------LLLSINCIAVGFGATG  922

                    -*

  gi|2545609     -    -

gi|26554388|ref|NP_758322.1|: domain 1 of 1, from 6 to 911: score 139.4, E = 1.2e-38
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         D  L       + e ++ i++   Ll k   + +    e L  +
  gi|2655438     6    --DKRLIENKSFSINEMNETINFILSLLTK---VFKKHTSEKLYKIA 47

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     E      e   K   + ++ +  kL  L   D   + + +     L nL
  gi|2655438    48 LEVKNKIKEKNNKNLFEYVQKISKKLSNL---DFTYLCRYFAYHELLTNL 94

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     E++  A        k              D+++ l +      K    v
  gi|2655438    95 VEDIYQANYENKWEDK------------YLDVDDYLVRFFKDIKKNKINV 132

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK....Dvtv
                       LK   + +vltAHPtq vR  +L    +i   L + s  ++   +
  gi|2655438   133 -SKLKDIDISIVLTAHPTQVVRETILRLTRKIMEYLDKQSNYnslfNIHL 181

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                     DK+   E L   i   +    +R  + t   E++  + Y+  t +   P
  gi|2655438   182 LDKEQNIEVL---IDILWQVAILRDEKITVNNEIKNILNYFDTTFFSILP 228

                    KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                    K   +    LKn         +v  ik  sW+GGDRDG n  v  E   +
  gi|2655438   229 KINYKFNK-LKNENYVLDESDNV-CIKIGSWIGGDRDG-NSFVN-ESSLE 274

                    vCLLaRm.mAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                    +     ++   n+Y+s++  L  +l               l   + ++ +
  gi|2655438   275 IAFEGQVkKVFNFYFSKLNNLYNDL---------------LLHDSVSK-I 308

                    vKyYiEFWKqv....PPtEPYRviLGdvRDKLYntRERaRHLLA..tGis
                     K   EF K v  ++   EPY   +  +  KL+nt       + +   +
  gi|2655438   309 SKSIYEFTKDVylknREREPYSKAVVKIISKLWNTLQSFGYDISsfSNFK 358

                    eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                     +  +  y    +FL  L L   sL       iA   L+Dl+  v  F
  gi|2655438   359 IVDIDGKYNSTKDFLNDLYLILNSLKKNNSYEIAKRNLVDLIYSVKSFEF 408

                    sLvKLDiRqEseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaELkGK
                     L+ +DiRq s ++ + +D i    +i+  Y   s eK+ E Ll   + K
  gi|2655438   409 HLMSIDIRQNSKKHKELIDEIFSTNNIhQNYIYLSNEKKEELLLNIFE-K 457

                    RPLlg....sDLPktE.EvkDvldafrvLAELPiDsFGaYiismataPsD
                      +   ++  D  k E  +   ++ ++ L  L   s  +Yiis + +  D
```

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  gi|2655438   458 EMIWDfdklNDFNKSEiNIFKKINQIKSL--LGNNSISSYIISNTESFVD 505

                   vLAvELLqRECgvkq..tLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                   +L    L +     ++  L +vPLFE + D+  AP  vek+      +
  gi|2655438   506 ILETLFLYKIVNNTNdfNLNIVPLFETIEDISNAPLIVEKMITSPITRPI 555

                   i....dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                   i++  + K ev++GYsDs KD G +   W+LY  q E+  + Kk+ +K+
  gi|2655438   556 IenfwNNKIEVLLGYSDSCKDGGNFTSSWKLYTIQNELTAIVKKHNIKIS 605

                   lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                    FHGRGGt+GRGGGP   Ai sqP D in  lR t qGE+i   +
  gi|2655438   606 FFHGRGGTIGRGGGPSYYAINSQPKDSINDKLRFTEQGEIIWAKYSNPRK 655

                   CFrsLqRFtAAtLEHGmnPPvsPkP..EWRkLmeemAvvAtEEYRsvvvK
                    +  L     At    ++       ++E+++ me +  v  + Y  +v+K
  gi|2655438   656 GWFNLETILTATAQAIVDKTKNKYEddEFKNNMEYLSKVSFDKYQNLVYK 705

                   EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                      F   F   tP     k+niGsRP  R     +  LR iPW+F+W q
  gi|2655438   706 NQSFESVFFDITPINQISKLNIGSRPISRLNNKKLSDLRSIPWVFSWSQV 755

                   RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                   R  +P W G+G A    i++  Knl  Lk  Yk+  FF   l  +Em  A
  gi|2655438   756 RAMIPGWYGIGTALEQFINQNKKNLSILKKWYKNISFFNSLLSNIEMLLA 805

                   KGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                   K    i   y +     +      ++  +Y  t +++L i   k+lLE
  gi|2655438   806 KVNLDITKHYFDSSNNKDADAIYLDILSEYNKTLKMILLISDKKELLEDF 855

                   PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                     LK  l  R +Y+  Ln fq   L  iR                   n
  gi|2655438   856 RDLKISLEDRIPYLNILNYFQ---LELIR------------------KN- 883

                   kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                          kLn   +    + + +++ + GiA G+ n G
  gi|2655438   884 -------KLN---KKNKWIQEAILISINGIATGLRNSG    911

gi|18072432|emb|CAC84383.1|: domain 1 of 1, from 1 to 363: score 138.7, E = 1.8e-38
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807243     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807243     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807243     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807243     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807243     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807243     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807243     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807243     - ---------------------------------------------- -
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                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807243     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807243     - ------------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807243     - ------------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807243     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+++vAK+yGvKL++FHG+GGtvGRGGGPtHLAiLsq
  gi|1807243     9 RLSAAWQLYKAQEELVQVAKQYGVKLTMFHGKGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP+tinGslRvtvqGEviE+sFGEE LCF++LqR+tAAtLEHGm PP sP
  gi|1807243    59 PPETINGSLRVTVQGEVIEQSFGEERLCFKTLQRYTAATLEHGMRPPTSP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR +++e+AvvAtEEYRsvv+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|1807243   109 KPEWRAILDEIAVVATEEYRSVVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh + KD +nl
  gi|1807243   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHILRKDRRNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLv++eLkPFG++
  gi|1807243   209 RILKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVSDELKPFGEQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y+Etk+lLLk+AGH DlLEGDPYLKqr+RLR++YittLnv+qAYt
  gi|1807243   259 LRANYEETKQLLLKVAGHTDLLEGDPYLKQRIRLREAYITTLNVCQAYTK 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDP++kv +rP+lsKE  d n  k +eLvkLnp++++aPGLEDtLiL
  gi|1807243   309 KRIRDPNFKVDVRPPLSKEILDSN--KQAELVKLNPASEYAPGLEDTLIL 356

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807243   357 TMKGIAA------    363

gi|28572162|gb|AAB58883.2|: domain 1 of 1, from 12 to 922: score 138.7, E = 1.9e-38
                  *->siDAqLR.lLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEa
                     + D    + ++ G   ed   i + AL     LD+    H ++L ++
  gi|2857216    12    ATDTTFApPVITGTATEDALEILFHAL-----LDVARR-HDPELEDV 52

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                              G+ D        +  t    a a+ v      ++ +A
  gi|2857216    53 LH----------GRADI-------SSFTPEMLARALQVQGIWFQLVSIA- 84

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                     E + A RRR +  +     D +           l     ++   P+
  gi|2857216    85 ---EQNAAMRRRRHVER-----DQGREALNGSFAKVLAEASARG-IGPQQ 125

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  +   LK   +   +tAHPt   R  +L K  Ri   L  L     t  ++
  gi|2857216   126 IHALLKDLRIRPTITAHPTEGKRVTVLEKLRRIYLVLRELELPRWTERER 175

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    L   L   i   + t E+   + t   E+  G+ ++ Et+++  P  L
  gi|2857216   176 NGLMNELRDQIELIWMTGELHLEKATVEREVAWGLHFFDETLFEMLPEML 225

                  RRvDtALKniGinERlPYdv.PLikFssWmGGDRDGknPRvtPEvtRDvC
                     +  L      E   ++v+P  +F sW+GGDRDG nP vt  vtR+
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  gi|2857216   226 LSLEESLAQYYPDET--FEVpPFFQFGSWIGGDRDG-NPYVTASVTRETL 272

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                        +     Y + +  L   ls       +  R   +  t +++ +
  gi|2857216   273 QRNALASLRRYRDGITHLGRVLS-------ITERSLPVPETFRSE-LAHM 314

                    YiEF..WKqvP...PtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                      E ++ + + +++P E YR  L  v  KL  t  R +     G   +
  gi|2857216   315 LAESgdARAIAnrnPGEAYRQFLSCVLRKLEATIARNK-----GARSVGP 359

                    eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                    +  y   +  +  L    k L +    ++A   +  + R v  F  s v+
  gi|2857216   360 D--YPSADGLINDLRTLEKGLADAKCGALATDIVRPVRRMVEIFRFSTVR 407

                    LDiRqEseRqtDvlDAittHLeiGsYReWsEe..KRqEWLlaELkGKRP.
                    LD+R  s R t  l A+ + L  G     + +++  ++WLl+EL   R +
  gi|2857216   408 LDLRENSTRTTKTLHALWK-LRNGDREPPALDspAWKDWLLTELARPRTp 456

                    .....LlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataP
                    +++ + +   LP  ++ ++ l +f  + E +++L  ++FGa+i+sm+ +
  gi|2857216   457 etsfeDFADRLP--DDARETLATFALVGEmrdtLDREAFGAFILSMTRST 504

                    sDvLAvELLqRECgv........kqtLrvvPLFEkLADLeAAPAavekLF
                     +vL   LL +E g+  ++++++  +L++vPLFE + DL+AAPA ++ L
  gi|2857216   505 VEVLGAYLLAKEAGIfldttgteICPLPIVPLFETIDDLRAAPAIMKELL 554

                    siDWYinrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAK
                     i   +     ++G qevm+GYsDs KD G ++  W LYkAq  +
  gi|2857216   555 GIPVVRRSTRwqgGVQEVMIGYSDSNKDGGFIASNWELYKAQVRLTTLGN 604

                    kyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEf
                    + Gv +  FHGRGG v RGG PtH  i +qPP  i+G  R+t qGEv+ f
  gi|2857216   605 HLGVPIAFFHGRGGSVSRGGVPTHRGIAAQPPGSIQGRFRITEQGEVVSF 654

                    sFGEEnLCFrsLqRFtAAtLEHGmnPP...vsPkPEWRkLmeemAvvAtE
                     +         +   +A   EH +   +++   + E+ + +e +
  gi|2857216   655 KYANRGTAAYQMELLAASVFEHALLSEgngNGSRAEFDDALEALSGASRA 704

                    EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                     Y  +   E   v+YF  A P  E   +niGsRPa+R  +  +  LRAiP
  gi|2857216   705 AYVNLLQAEG-LVDYFQAASPLDEISLLNIGSRPARRFGAKSLSDLRAIP 753

                    WiFaWtqtRFHLPvWLGvGAAFKhAid.KDiKnlqkLkEmYkeWPFFRvt
                    W+FaW q R  +  W GvG   K  id +       L+ ++++   FR
  gi|2857216   754 WVFAWSQNRHVITGWYGVGSGLKSFIDvRGEAGEALLRRLFRDCRVFRLV 803

                    lDLlEmvFAKGDPGiAaLyDkLLvaEeLkP..FGksLRdkYvEtkdlLLk
                    lD +E      D  iA  y  L+    ++ + FG  + ++Y  t++++L+
  gi|2857216   804 LDEVEKTLLMVDLEIARDYAGLVEDAGIRAriFG-MIEAEYALTREMVLR 852

                    iAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrP
                    + G  +l    P    rlR R + i  +   q   L+R R
  gi|2857216   853 VSGDSELAQRFPQFSERLRGRLPTINQVSREQVELLRRYRSET------- 895

                    hlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<
                           dE+     e vk              L+L +  iA G   tG
  gi|2857216   896 -------DED---KREAVKSA------------LLLSINCIAVGFGATG  922

                    -*

  gi|2857216     -    -

gi|7768144|emb|CAB90626.1|: domain 1 of 1, from 1 to 364: score 138.6, E = 2e-38
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768144     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768144     - ---------------------------------------------- -
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                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|7768144    - ------------------------------------------------- -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|7768144    - ------------------------------------------------- -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|7768144    - ------------------------------------------------- -

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|7768144    - ------------------------------------------------- -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|7768144    - ------------------------------------------------- -

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|7768144    - ------------------------------------------------- -

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|7768144    - ------------------------------------------------- -

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|7768144    - ------------------------------------------------- -

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|7768144    - ------------------------------------------------- -

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                      sDsGKDAG
gi|7768144      1 ----------------------------------------SDSGKDAG 8

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLYkAqEE++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|7768144      9 RLSAAWQLYKAQEELVKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+ P+sP
gi|7768144     59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMQLPISP 108

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                kPEWR Lm+emAvvAt EYRs+v++E RFvEYFRlAtPElEYG+mniGsR
gi|7768144    109 KPEWRALMDEMAVVATNEYRSIVFQESRFVEYFRLATPELEYGRMNIGSR 158

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+KR+PsGGiesLRAiPWi aWtqtR HLPvWLG+GAAFKh i+KD Knl
gi|7768144    159 PSKRRPSGGIESLRAIPWILAWTQTRLHLPVWLGFGAAFKHVIEKDKKNL 208

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  L+EmY+eWPFFRvt+DL+EmvF KG PGiAaLyDkLLv+ +L PFG++
gi|7768144    209 NILREMYNEWPFFRVTIDLIEMVFTKGSPGIAALYDKLLVSSDLLPFGEQ 258

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR++Y+Etk lLL++AGHkDlLEGDPYLKqrlRLR +YittLnv qAYtL
gi|7768144    259 LRANYEETKRLLLQVAGHKDLLEGDPYLKQRLRLRYPYITTLNVWQAYTL 308

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                KRiRDPsy+ t +P ls E  + n k+a+eLvkLnpt+++aPGLEDtLiL
gi|7768144    309 KRIRDPSYHLTAKPNLSNEIMNYN-KPAAELVKLNPTSEYAPGLEDTLIL 357

                tmKGiAAGmqntG<-*
                tmKGiAA
gi|7768144    358 TMKGIAA------    364
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gi|194703414|gb|ACF85791.1|: domain 1 of 1, from 1 to 347: score 138.5, E = 2.1e-38
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1947034     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1947034     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1947034     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1947034     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1947034     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1947034     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1947034     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1947034     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1947034     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1947034     - ---------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1947034     - ---------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG

  gi|1947034     - ---------------------------------------------- -

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                                +++vAK+yGvKL+lFHGRGGtvGRGGGPtHLAiLsq
  gi|1947034     1 --------------MAQVAKRYGVKLTLFHGRGGTVGRGGGPTHLAILSQ 36

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGs+RvtvqGEviEf FGEE+LCF++LqRFtAAtLEHGm+PPvsP
  gi|1947034    37 PPDTINGSIRVTVQGEVIEFCFGEEHLCFQTLQRFTAATLEHGMHPPVSP 86

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWRkLm+emAvvAtEEYRsvvvKE RFvEYFR+AtPE+EYG+mniGsR
  gi|1947034    87 KPEWRKLMDEMAVVATEEYRSVVVKEARFVEYFRSATPETEYGRMNIGSR 136

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKR+P+GGi++LRAiPWiF+WtqtRFHLPvWLGvGAAFK+AidKD++n+
  gi|1947034   137 PAKRRPGGGITTLRAIPWIFSWTQTRFHLPVWLGVGAAFKFAIDKDVRNF 186

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q LkEmY+eWPFFRvtlDLlEmvFAKGDPGiA+LyD+LLvaEeLkPFGk+
  gi|1947034   187 QVLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAGLYDELLVAEELKPFGKQ 236

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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                    LRdkYvEt++lLL+iAGHkD+LEGDP+LKq+l LR++YittLnvfqAYtL
  gi|1947034   237 LRDKYVETQQLLLQIAGHKDILEGDPFLKQGLVLRNPYITTLNVFQAYTL 286

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP++kvt++P+lsKE+AdEn  k+++LvkLnp+++++PGLEDtLiL
  gi|1947034   287 KRIRDPNFKVTPQPPLSKEFADEN--KPAGLVKLNPASEYPPGLEDTLIL 334

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|1947034   335 TMKGIAAGMQNTG    347

gi|170744593|ref|YP_001773248.1|: domain 1 of 1, from 1 to 920: score 137.2, E = 5.3e-38
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            L l vP            D       +       G + +Ea
  gi|1707445     1    ---MTLALSVPAGAP--------DPSFAPPVIT------GTSSREAT 30

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDai...lvAkail...Hm
                       +    +   ++++    EL ++L + +     +++l+A+a+  ++
  gi|1707445    31 DILFHSLLDVCRRHEP----ELESVLHGNANISDFspdLMARALQvqgIW 76

                    LnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkln
                      L  +AE      RRR   +  G  a  +s      + E +   v
  gi|1707445    77 FQLISIAEQNTAMRRRRHVERTRGRHALRGSFSAV--LAEAVHNRVPAR- 123

                    KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
                        E+   LK   +   ltAHPt   R  +L K  Ri   L  L
  gi|1707445   124 ----EIHALLKDLRIRPTLTAHPTEGKRVTVLEKFRRIYLLLRELELPRW 169

                    tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                    t  ++  L   L   i   + t E+   +Pt   E+  G+ ++ Et+++
  gi|1707445   170 TERERTGLMADLRDQIELVWMTGELHLEKPTVEQEVAWGLHFFDETLFEM 219

                    vPKFLRRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEv
                     P  +   +  L+     E   ++vP   +F sW+GGDRDG nP vt  v
  gi|1707445   220 LPEVMVSLEESLREYYPDET--FEVPaFFQFGSWIGGDRDG-NPFVTAAV 266

                    tRDvCLLaRmmAanlYisqvEDL..mFElsmWRCndELRvRAEElyrtaa
                    tR       +     Y + v  L++m  +s          + E   + aa
  gi|1707445   267 TRSTLRRNALASMRRYRDGVIHLgrMLSISERSLPAPASFKTELARQLAA 316

                    rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                    +               P E YR  L  +  KL  t  R      tG  +
  gi|1707445   317 SG-----DARGIARRNPGELYRQYLTCILRKLEATIARNEGDAITGAPD- 360

                    sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                         y + ++ +  L +    L +     +A   +  + R v  F  s
  gi|1707445   361 -----YSDADDLINDLRVLEAGLTDAKCPSLAVDLVRPVRRMVEIFRFST 405

                    vKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKR...qEWLlaELkGK
                    v+LDiR    R t  l A+ +  + G     +E   +    WL aEL
  gi|1707445   406 VRLDIRENTTRTTRALQALWRQ-GRGDEAAPPEVDQpawTAWLTAELA-- 452

                    RPLlg..sDLPktEEvkDvldafrvLA....ELPiDsFGaYiismataPs
                    RPL g++s     EE ++ l++fr + + ++EL  ++FG++++sm+ +
  gi|1707445   453 RPLEGqrSFQSLPEEARETLETFRLVGemrkELDREAFGSFVLSMTHSVP 502

                    DvLAvELLqRECgv........kqtLrvvPLFEkLADLeAAPAavekLFs
                    D+L v LL +E g+  +  + +  +L++vPLFE + DL+AAPA +  L
  gi|1707445   503 DILGVYLLAKEAGLfldaagieICPLPIVPLFETIDDLRAAPAIMRELLQ 552

                    iDWYinrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKk
                    i   +     ++G qevm+GYsDs KD G +s  W L kAq  +  v K+
  gi|1707445   553 IPLVRRSTRwqgGVQEVMIGYSDSNKDGGFVSSNWELAKAQAKLTEVGKQ 602

                    yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                     Gv +  FHGRGG v RGG Pt  Ai +qPP  i G  R t qGEv+ f
  gi|1707445   603 AGVPIAFFHGRGGSVSRGGAPTGRAIAAQPPGSIRGRFRTTEQGEVVSFK 652

                    FGEEnLCFrsLqRFtAAtLEHGmn....PPvsPkPEWRkLmeemAvvAtE
                    +         +   +     H +n +++P  +P+P++ + me +
  gi|1707445   653 YANRGTAAYQMELLASSVFAHALNaerdPSFAPRPDFDDAMEALSGASRA 702
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                    EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                     Y  +v   P  v YF  A P  E   +niGsRPa+R  +  +  LRAiP
  gi|1707445   703 AYVKLV-SHPDLVTYFGAASPLDEIALLNIGSRPARRFGARSLADLRAIP 751

                    WiFaWtqtRFHLPvWLGvGAAFKhAid.KDiKnlqkLkEmYkeWPFFRvt
                    W+FaW q R  +  W GvG      +d +       L+ m+ e   FR
  gi|1707445   752 WVFAWSQNRHVITGWYGVGSGLMSFLDvRGEAGEALLRRMFAESRLFRLV 801

                    lDLlEmvFAKGDPGi....AaLyDkLLvaEeLkPFGksLRdkYvEtkdlL
                    lD +E      D  i ++ A+L  +  v Ee+      + ++Y  t+ ++
  gi|1707445   802 LDEVEKTLLTVDLDIardfAGLVPDARVREEIF---SMIAEEYHLTRRMV 848

                    LkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtl
                    +++ G  ++ E  P  + rl  R + i  +   q   L+R R
  gi|1707445   849 VRVSGDAEVAERFPQYRGRLTERLPVINQVSREQVELLRRFR-------- 890

                    rPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqnt
                              E     de+ +              L+L +  iA G   t
  gi|1707445   891 ---------GET----DEVRRET--------FKSALLLSINCIAVGFGAT 919

                    G<-*
                    G
  gi|1707445   920 G    920

gi|18072428|emb|CAC84921.1|: domain 1 of 1, from 1 to 362: score 136.9, E = 6.1e-38
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807242     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807242     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807242     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807242     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807242     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807242     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807242     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807242     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807242     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807242     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807242     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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                                                      sDsGKDAG
  gi|1807242     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+++vAK+yGvKL++FHG+GGtvGRGGGPtHLAiLsq
  gi|1807242     9 RLSAAWQLYKAQEELVQVAKQYGVKLTMFHGKGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP+tinGslRvtvqGEviE+sFGEE LCFr+LqR+tAAtLEHGm PP sP
  gi|1807242    59 PPETINGSLRVTVQGEVIEQSFGEERLCFRTLQRYTAATLEHGMRPPTSP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR +++e+AvvAtEEYRsvv+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|1807242   109 KPEWRAILDEIAVVATEEYRSVVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh + KD Knl
  gi|1807242   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHILRKDKKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q ++ mY+eWPFFRvtlDL+EmvFAKGDPGiAaLyDkLLv+E+L+ FG++
  gi|1807242   209 QHIRQMYNEWPFFRVTLDLIEMVFAKGDPGIAALYDKLLVSEDLWSFGEK 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR+++ Et+dlLLk+AGH+DlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|1807242   259 LRANFLETRDLLLKVAGHRDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+++v lrPhlsKE        a+eL+kLn t++++PGLEDtLiL
  gi|1807242   309 KRIRDPNFHVQLRPHLSKESSTNS---AAELLKLNTTSEYPPGLEDTLIL 355

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807242   356 TMKGIAA------    362

gi|18076763|emb|CAC84925.1|: domain 1 of 1, from 1 to 364: score 136.0, E = 1.2e-37
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807676     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807676     - ---------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807676     - ---------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807676     - ---------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807676     - ---------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807676     - ---------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807676     - ---------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807676     - ---------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807676     - ---------------------------------------------------- -
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                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807676     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807676     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807676     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWq+Yk qEE+++vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807676     9 RLSAAWQVYKTQEELVQVAKQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGslRvtvqGEviE+ FGEE LCFr+LqR+tAAtLEHGmnPP+sP
  gi|1807676    59 PPDTINGSLRVTVQGEVIEQCFGEERLCFRTLQRYTAATLEHGMNPPISP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++emAv+At EYRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|1807676   109 KPEWRSLLDEMAVIATNEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i KD Knl
  gi|1807676   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIAKDNKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+EmY+ WPFFRvt+DL+EmvFAKG PGiA+LyDkLLv+ eL PFG +
  gi|1807676   209 HTLREMYNGWPFFRVTIDLIEMVFAKGNPGIASLYDKLLVSSELLPFGVQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y+Etk lLL++AGHkDlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|1807676   259 LRENYEETKRLLLQVAGHKDLLEGDPYLKQRLRLRDPYITTLNVCQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDP y+vt rPhl+KE  +   k a+eLvkLnpt+++ PGLEDtLiL
  gi|1807676   309 KRIRDPGYHVTERPHLAKETTESI-KSAAELVKLNPTSEYGPGLEDTLIL 357

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807676   358 TMKGIAA------    364

gi|189346143|ref|YP_001942672.1|: domain 1 of 1, from 1 to 922: score 135.6, E = 1.5e-37
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            +     v + ek  +    Ll+ F ++L DL   +L
  gi|1893461     1    ------MITSTSSVIDFEKAERDTTFLLECFREVLRDLGEHEL---- 37

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                               D    e  G  L     ++  l  +a++    L n+
  gi|1893461    38 -------------ADHLPFENAGIPLERYPNTERAL--QAFSIFFQLLNM 72

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AEE   A  RR            +          tl +L   +  +  E+
  gi|1893461    73 AEENSGAQNRRALEAE------KGLEHLTGLWGRTLGRLRDTG-IAETEI 115

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     L   +v  vltAHPt + R+ +L ++  +   L +   +  t++++
  gi|1893461   116 LTLLPEIAVNAVLTAHPTEAKRKTVLEQHRQLYLLLVKRENQMWTPQEQL 165

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                  E+   +   +   +Rt Ei   +P    E R  + Y+     +  P   +
  gi|1893461   166 EIRNEIKVVMERLWRTGEILFDKPEVSAERRNVIHYLCNIFPEVLPLLDK 215

                  RvDtALKniGin.ERl..PYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                  R   A K  G  + +l++P   P + F sW+GGDRDG +P vt Evt +
  gi|1893461   216 RLLQAWKGTGFDpAKLsdPRSLPRLSFGSWVGGDRDG-HPLVTAEVTEET 264

                  CLLaRmmAanlYisqvEDLmFEls....mWRCndELRvRAEElyrtaard
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                      R  A  l +  + +L   ls ++++      L  R E l      +
  gi|1893461   265 LADMRSNALMLVLRHLRELASKLSlserLHAPGAPLARRIEHLAGSLGEK 314

                    kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei..
                           E  +     EP+R  +  +   L          L tG+s+  +
  gi|1893461   315 -----GREAMRR-NRHEPWRQFINLMIASLP---------LETGVSDAir 349

                    ..sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                    ++sE   y +  e LE L L   sL   G + iAD  +  + R v tFG
  gi|1893461   350 tpSEPCCYMDAAELLEDLTLLRESLTGIGAHCIADTDVAPVFRIVQTFGF 399

                    sLvKLDiRqEseRqtDvlDAittHLei.Gs.YReWsEeKRqEWLlaELkG
                     L  LDiRq s  +   l  + t  +++Gs++ eW E  R+ +L  EL+
  gi|1893461   400 HLGSLDIRQNSRFHDLALSQLMTAAGLdGSgFLEWDECERRAFLDRELHS 449

                    KRPLlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsD
                     RP   +D+    E +  l  +rvL +++++   D  G+ i+sm+   sD
  gi|1893461   450 PRPFTHPDMTAGPEAEALLACYRVLLDhgkqYGTDGLGSLIVSMTRNVSD 499

                    vLAvELLqRECgvkqt........LrvvPLFEkLADLeAAPAavekLF..
                     L v L  RE g+  ++++++   L+vvPLFE + DL+  P  ++    +
  gi|1893461   500 LLVVYLFAREVGLMTPsgdgdaclLPVVPLFETIDDLKKSPGILQEFLlh 549

                    .....siDWYinridGK....qevmvGYsDsGKDAGRlsAAWqLYkAqEE
                    + + +s++ Y+ +  GK ++ qevm+GYsDs KD G ++  W LY+AqE
  gi|1893461   550 pvtarSLE-YRRKKAGKarrvQEVMIGYSDSNKDGGIFASTWTLYRAQEA 598

                    iiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvq
                    +    +  G  +  FHGRGG + RG GPtH  i +qP       +  t q
  gi|1893461   599 LLEAGRLCGTDILFFHGRGGSISRGAGPTHRFIKAQPYGSFRAGMCFTEQ 648

                    GEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPEW..RkLmeemA
                    GE i + +         L  F A      +      k E++   +m+ +
  gi|1893461   649 GETIAQKYANRISAVYNLELFMAGIAGSVIRQQQRKKTEYplEPIMDLLS 698

                    vvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGies
                          YR ++  E  F  +FR AtP        iGsRP++R     +
  gi|1893461   699 EKSHSAYRQLIETEG-FLTFFREATPIDIIESNRIGSRPSRRSGKATLAD 747

                    LRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPF
                    LRAiPW+F+W q RF L  W GvG A       D   +  ++   + WP
  gi|1893461   748 LRAIPWVFSWNQARFALSGWYGVGSALEALHSIDPETFDEIRFRSHVWPP 797

                    FRvtlDLlEmvFAKGDPGi....AaLyDkLLvaEeLkPFGksLRdkYvEt
                     R  +   +   A  DP i ++ A+L  +  v E +      + ++Y+ t
  gi|1893461   798 LRNIVSNADAGIASADPEImqkyAGLVTDTTVRERILGM---IEAEYQRT 844

                    kdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsy
                    k ++       ++L  +P   qrl + + +i              R
  gi|1893461   845 KTYI-------EILFAEPLETQRLNV-NRFIAP-----------RREGL 874

                    kvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAG
                     +  + ++         k+  eL +    ++ a G+   L Lt+  i  G
  gi|1893461   875 AMLHQQQITL------LKRWRELRHTG-MDEEADGMLPELFLTVNAISGG 917

                    mqntG<-*
                    +  tG
  gi|1893461   918 LRTTG    922

gi|257792699|ref|YP_003183305.1|: domain 1 of 1, from 32 to 927: score 135.5, E = 1.7e-37
                    *->siDAqLR.lLvPGKvsedekLieYD...ALLlDk.FLDiLqDLHGed
                        i   LR+ Lv     e   L eYD+    L D+ F  ++    G+
  gi|2577926    32    EIPESLRdNLVLFLRMERKVLKEYDpavCALFDRlFNSMIRANEGNP 78

                    LkEavqECYEl....sAeYEGKkDtkKLeELGakLtsLdPaDailvAkai
                       a  E  + ++ + A+ EG +  +   EL   + +L    a +v +a+
  gi|2577926    79 GTVAADEPTDAqgipTADTEGARAFREAVEL---IDALPVDQAQVVVRAF 125

                    lHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvl
                         LAnL EE    yR    +      + E+   t  ++   + +L
  gi|2577926   126 TSFFHLANLSEE---NYRVETLRELERNVSMESAVDTSNELVVAYGHLLD 172
```

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                    klnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsA
                         Pe   e L       v+tAHPt + R+++   +++iR   a L
  gi|2577926   173 EV--GPERTAELLGRLEFHPVFTAHPTEARRKAV---EGKIRRIAALLDE 217

                    K.DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEt
                     + +      E +  +  Ei A  Rt      +PtP +E    +  +  t
  gi|2577926   218 HpYLGGSALLENERHMLQEIDALVRTSPTELKKPTPLEEADTVIDIFDNT 267

                    vWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvt
                    +++ vP+  RR D  +         P      +  sW+G DRDG nP vt
  gi|2577926   268 LFDTVPQVYRRFDDWVLGEDAGSVPPVCPAFFRPGSWIGSDRDG-NPNVT 316

                    PEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrta
                      v R v       Aa  +   v  L  E     C +  R    E   ta
  gi|2577926   317 AKVSRRV-------AAKYFAHMVAKLAQE-----CRNIGRNLTLESRYTA 354

                    ardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAt....
                     ++      +  W  +   E    + G v D L     Ra  L+   + +
  gi|2577926   355 PSE----ELMNLWSHL--VEMSETLTGRVADDLGFEPHRAVMLVMAarle 398

                    GiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvst
                    G      + +y   Ee L  L     sL   G    A G +  l+ qv t
  gi|2577926   399 GTVARNADIMYLSPEELLADLRTVQDSLARAGAARAAYGPVQTLIWQVAT 448

                    FGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELk
                    FG  +v ++ Rq s  +   l  i  H
  gi|2577926   449 FGFHMVEMEFRQHSLVHERALADIRSH---------------------- 475

                    GKRPLlgsDLPktEEvkDvldaf.rvLAELPiDsFGaYiismataP...s
                        +lg   P+t Ev D   a++ +           Yi+s + + ++ +
  gi|2577926   476 ---GVLGKLDPMTREVLDTFRAIgAIQKRYGQKMARRYIVSFTKSArhmA 522

                    DvLAv.ELLqRECgvkqtLrvvPLFEkLADLeAAPAa...vekLFsiDWY
                    Dv    EL     +    L v+PLFE+L DLe      +++ +L ++
  gi|2577926   523 DVYELaELAFSHAQDVPELDVIPLFEQLEDLENCVTVldgMLQLPAVQRR 572

                    inridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                      +   + evm+GYsDs KDAG + A   L  AqE i++ A + G+ +vl
  gi|2577926   573 LAQTGRRMEVMLGYSDSSKDAGPVTATLALHSAQERIARWAEERGIDVVL 622

                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                     HGRGG vGRGGGP   A+L+qP   +n   +vt qGEvi   +G   L
  gi|2577926   623 MHGRGGAVGRGGGPANRAVLAQPKGSVNCRFKVTEQGEVIFARYGNRSLA 672

                    FrsLqRFtAAtLEHGm..nPPvsPkPEWR..kLmeemAvvAtEEYRsvvv
                     r +   +AAtL    ++   v      R +++  ++   A E Y  +
  gi|2577926   673 LRHIESVAAATLMNSApsVERVNTEASVRfsDVAARLNEAAYERYLDLLH 722

                    KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFaWt
                     +  F  +F   tP  E G + iGsRPaKR  + + ++ LR iPW+F+W
  gi|2577926   723 TDG-FAPWFSTVTPLAEVGLLPIGSRPAKRGLGAqSLDDLRTIPWVFSWS 771

                    qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                    q R  L  W G+GAA        +  l  L+  Y+eWP F   +D +Em
  gi|2577926   772 QARINLAAWYGLGAACER-----VGDLELLQRAYREWPLFATFVDNVEMS 816

                    FAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE
                     AK D  iA +y  L   ++L     + + d+ + t+ + L i G    L
  gi|2577926   817 IAKTDARIAKMYLALGDRDDLA---QAVFDEMQLTRSWALAIVGDEWPLQ 863

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                        L   +R+R++Y+  L   q   L+ iR        + +ls E   E
  gi|2577926   864 HRRVLGCAIRVRNPYVDALSLAQVRALRVIRN------RQEELSDEVKTE 907

                    nskkadeLvkLnptervaPGLEDtLiL.tmKGiAAGmqntG<-*
                              L             LiL t+ G+ AG+qntG
  gi|2577926   908 Y---------LG------------LILaTVTGVSAGLQNTG    927

gi|18073880|emb|CAC84959.1|: domain 1 of 1, from 1 to 365: score 134.8, E = 2.7e-37
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
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gi|1807388     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|1807388     - ---------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1807388     - ---------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1807388     - ---------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1807388     - ---------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1807388     - ---------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1807388     - ---------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1807388     - ---------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1807388     - ---------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|1807388     - ---------------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|1807388     - ---------------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
gi|1807388     1 -------------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqE+++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|1807388     9 RLSAAWQLYKAQEDLVKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEH m PP sP
gi|1807388    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHSMCPPASP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   PEWR+L++emAv At EYRs+v+ EPRFvEYFRlAtPElEYG+mniGsR
gi|1807388   109 EPEWRELLDEMAVAATKEYRSIVFHEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh idKDiKnl
gi|1807388   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIDKDIKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+EmY  WPFFRvt+ L+EmvFA+GDPGiAaLyDkLLv+E+L+PFG++
gi|1807388   209 LMLQEMYTRWPFFRVTIYLVEMVFAQGDPGIAALYDKLLVSEDLWPFGEQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y Etk+lLL++AGHkDlLEG PYL+qrlRLRdsYittLn +qAYtL
gi|1807388   259 LRNNYNETKNLLLQVAGHKDLLEGNPYLRQRLRLRDSYITTLNACQAYTL 308
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                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|1807388   309 KRIRDPSYQVPVRPPIAKEIMEGSVSSANQLVKLNPTSEYAPGLEDTLIL 358

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807388   359 TMKGIAA------    365

gi|18076753|emb|CAC81349.1|: domain 1 of 1, from 1 to 362: score 133.8, E = 5.6e-37
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807675     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807675     - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807675     - ------------------------------------------------ -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807675     - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807675     - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807675     - ------------------------------------------------ -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807675     - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807675     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807675     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807675     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807675     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|1807675     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAW LYkAqE++iKvA ++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807675     9 RLSAAWALYKAQEDLIKVAFEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+Gs RvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PP++P
  gi|1807675    59 PPDTIHGSFRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPIAP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+emAvvAt EYRs+v++ PRFvEYFR+AtPElEYG+mniGsR
  gi|1807675   109 KPEWRALMDEMAVVATKEYRSIVFQNPRFVEYFRSATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++KDi+nl
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  gi|1807675   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHVMEKDIRNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+ mY+eWPFF  t+DL+EmvFAKGDPGiAaLyDkLLv+++L+  G +
  gi|1807675   209 HTLQQMYNEWPFFWGTIDLIEMVFAKGDPGIAALYDKLLVSDDLWAIGGQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++YvEtkdlLL++AGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|1807675   259 LRANYVETKDLLLQVAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y+v lrPhlsKE    +   a+eLvkLnpt+++aPGLEDtLiL
  gi|1807675   309 KRIRDPNYHVNLRPHLSKESSTKP---AAELVKLNPTSEYAPGLEDTLIL 355

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807675   356 TMKGIAA------    362

gi|7768119|emb|CAB90620.1|: domain 1 of 1, from 1 to 364: score 132.4, E = 1.4e-36
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768119     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768119     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768119     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768119     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768119     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768119     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768119     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768119     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768119     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768119     - ---------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768119     - ---------------------------------------------- -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768119     1 -----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYk qEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768119     9 RLSAAWQLYKTQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58
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                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFt AtLEHGm+ P+sP
  gi|7768119     59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTTATLEHGMQLPISP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAvvAt EYRs+v++E RFvEYFRlAtPElEYG+mniGsR
  gi|7768119    109 KPEWRALMDEMAVVATNEYRSIVFQESRFVEYFRLATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P KR PsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD Knl
  gi|7768119    159 PPKRNPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIEKDKKNL 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+EmY+eWPFFRvt+DL+EmvF KG PGiAaLyDkLLv+ +L PFG++
  gi|7768119    209 NMLREMYNEWPFFRVTIDLIEMVFTKGSPGIAALYDKLLVSTDLLPFGEQ 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Etk lLL++AGHkDlLEGDPYLKqrlRLR +YittLnv qAYtL
  gi|7768119    259 LRANYEETKRLLLQVAGHKDLLEGDPYLKQRLRLRYPYITTLNVWQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPsy+   +P ls E  + n k a+eLvkLnpt+++aPGLEDtLiL
  gi|7768119    309 KRIRDPSYHLPAKPNLSNEIMNSN-KSAAELVKLNPTSEYAPGLEDTLIL 357

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|7768119    358 TMKGIAA------    364

gi|34558172|ref|NP_907987.1|: domain 1 of 1, from 1 to 885: score 132.4, E = 1.4e-36
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                    s  ek+ +    + +k L++L ++    Lk
  gi|3455817      1    ------------MTS--EKMHQEVQFVFEKMLELLDEV-ASALKPQF 32

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        E+  +  GK D +++  L +     +    ++ A ++  m  L n+
  gi|3455817     33 LGLREVFTQ--GKLDKERVKSLLSSSPLKEQIPELVKAFSLYNM--LLNI 78

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     EE       R +                   iE  +K L   +    ++v
  gi|3455817     79 VEE-------RHSVDS----------DAMGLIEGMIKELKAEG-YERDDV 110

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     e L       v+tAHPt s RR  L  +  i   L  ++ +     D k
  gi|3455817    111 LEVLEELRFYPVFTAHPTESRRRTFLESHHEISTDLERIFHQ----GDAK 156

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    E  E L   +   ++   +R  +     E+   +  i   + k   K
  gi|3455817    157 EAHEHLRYRLMLLWKSHLVRNEKIEVLFELDNLLYIIESSMLKSAVKVCS 206

                    RvDtALKniGinERlPYdvPL....ikFssWmGGDRDGknPRvtPEvtRD
                     v          ERl  ++PL++++i+  sW+GGDRDG nP vt Ev
  gi|3455817    207 EV----------ERL-VEAPLkrspIRLGSWIGGDRDG-NPYVTNEVMTR 244

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                    v  +   m    Yi ++E L+ Els+    ++L      l     r+
  gi|3455817    245 VMKIQHEMIISHYIGKIERLIRELSI---ASDLCEPSLGLLESLERE--S 289

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                           ++  +EP+R  L  ++ KL n     R +     s++  e v
  gi|3455817    290 SELENSAAKLHKNEPFRAKLILMKKKLQN-----RLIFVNYASDM--EFV 332

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                    y    e +E ++L   sL     k      L ++   v   G  L+KLD
  gi|3455817    333 YKTPKELIEDIDLVLESLDSLSGKY-----LREFRNLVLLTGFHLMKLDF 377

                    RqEseRqtDvlDAittHLei..GsYReWsEeKRqEWLlaELkGKR....P
                    R   +   D +  i   L+ ++  + + +  KR E L   L+  R + +
  gi|3455817    378 REHRDAIRDAISEIFSLLGYsdSDFGQLPPSKRAEILDRALSLPRlnlnA 427

                    LlgsDLPktEEvkDvldafrv....LAELPiDsFGaYiismataPsDvLA
                    Llg    + EE+      ++  ++++ E  iDsF   iism+    D LA
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  gi|3455817   428 LLGRVSHQSEEIISAFLRIEWakgnISEEIIDSF---IISMTQDSTDLLA 474

                    vELLqRECgv.....kqtLrvvPLFEkLADLeAAPAavekLF...siDWY
                    v  L +  g+ +++++  + + PLFE + DL+ A   +e L +++    Y
  gi|3455817   475 VLWLAKQSGLwregqRTRISISPLFETIEDLQKAGMIMEELAknpHYALY 524

                    inridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                        +G qe+m+GYsDs KD G +   + L +A   +     k G+K  l
  gi|3455817   525 LRDHQGIQEIMIGYSDSSKDGGIFTSNFSLNRAVYHLTELEEKLGIKFRL 574

                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                    FHGRGG v RGGG    A+++ P   + G l+ t qGEvi   +    +C
  gi|3455817   575 FHGRGGSVSRGGGTLESALMASPAKSVAGVLKTTEQGEVISSKYLNPLIC 624

                    FrsLqRFtAAtLEHGmnPPvsPkPEWRk......LmeemAvvAtEEYRsv
                             AA L   +      + +  k+++ +++m+ +       YR +
  gi|3455817   625 DFNFSSTIAALLKKSVYDRFGKRIDCGKsdrftsVMQGVSEASYKAYRRL 674

                    vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaW
                    v+    F++YF+ AtP     k+niGsRP+KRk    +e LRAiPW+FaW
  gi|3455817   675 VYETEGFMDYFKEATPIGFIQKLNIGSRPSKRKETHRVEDLRAIPWVFAW 724

                    tqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEm
                    tq R  +P W GvG             +  LkE Y e PFF+ tlD +
  gi|3455817   725 TQNRSIIPAWFGVGSGLESVALAGGEEI--LKECYGECPFFKTTLDNIAQ 772

                    vFAKGDPGiAaLyDkLL....vaEeLkPFGksLRdkYvEtkdlLLkiAGH
                       K D  +A+Ly + +++++v E ++     + ++Y+ t  ++L + G
  gi|3455817   773 ALLKVDLDVASLYNEFVedgeVRERIWGM---IQEEYQKTLHWILYVRGE 819

                    kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                    ++lLE +  L+  + LR +Y+t Ln fq   +K+ R  sy
  gi|3455817   820 RELLENERVLRESILLRRPYLTALNLFQIELIKKYRASSY---------- 859

                    EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        E   + + +++                 t+ GiA G+ ntG
  gi|3455817   860 ----EK--QQERIIEQI-------------SSTIVGIAQGVRNTG    885

gi|18073882|emb|CAC84960.1|: domain 1 of 1, from 1 to 365: score 132.4, E = 1.5e-36
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807388     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807388     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807388     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807388     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807388     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807388     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807388     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807388     - ---------------------------------------------- -
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                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807388     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807388     - ------------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807388     - ------------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807388     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqE+++KvAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807388     9 RLSAAWQLYKAQEDLVKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqR+tAAtLEH m PP sP
  gi|1807388    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRYTAATLEHSMCPPASP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   PEWR+L++emAv At EYRs+v+ EPRFvEYFRlAtPElEYG+mniGsR
  gi|1807388   109 EPEWRELLNEMAVAATKEYRSIVFHEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtR HLPvWLG+GAAFKh idKDiKnl
  gi|1807388   159 PSKRKPSGGIESLRAIPWIFAWTQTRLHLPVWLGFGAAFKHVIDKDIKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+EmY  WPFFRvt+DL+EmvFAKGDPGiAaLyDkLLv+E+L+PF ++
  gi|1807388   209 LMLQEMYTRWPFFRVTIDLVEMVFAKGDPGIAALYDKLLVSEDLWPFVEQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y Etk+lLL++AGHkDlLEG PYL+qrlRLRdsYittLn +qAYtL
  gi|1807388   259 LRNNYNETKNLLLQVAGHKDLLEGNPYLRQRLRLRDSYITTLNACQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|1807388   309 KRIRDPSYQVPVRPPIAKEIMEGSVSSANQLVKLNPTSEYAPGLEDTLIL 358

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807388   359 TMKGIAA------    365

gi|224437040|ref|ZP_03658021.1|: domain 1 of 1, from 17 to 905: score 131.7, E = 2.4e-36
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                     +  A   +L P ++             +     iLq L   d kE
  gi|2244370    17    AHHAHSAALQPSQMD-----------FVSSM--ILQLLESVD-KELK 49

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       +    E   D   L    + + s d + +i+ A ++ Hm  L n+
  gi|2244370    50 DAFIAIKHSLE-NADNATLTQTLSHISSQDKTLSIIKAFTLYHM--LLNI 96

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   EE +l        +                  tl  L   +    +++
  gi|2244370    97 IEELNLSDSATLNALP-----------------QTLLDLKNEG-YDKQDI 128

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     L+n +   v+tAHPt s RR  L  + ++   +  ++      +D +
  gi|2244370   129 LKVLQNIAFYPVFTAHPTESRRRTFLEAHHKMSKNIRDIFS----SNDSQ 174

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     E L R +   + t  +R  +     E+   +  i   + +   + L
  gi|2244370   175 ARFELLYR-LNLLWHTHLVRSEKMEILFELDNLLYIIESSIVESATQVLS 223

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   + t    iG   +     P+i   sW+GGDRDG nP v  E+   v
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  gi|2244370   224 DIQTL---IGTSLK---HSPII-LGSWVGGDRDG-NPYVSNEIMTKVMKT 265

                    aRmmAanlYisqvEDLmFElsmWRCndELRv.RAEElyrtaardkvvKyY
                    a      +Yi + E L+ Els+    ++L+ + AE l++    +
  gi|2244370   266 AHRAIIEMYIKKCEKLIRELSL---SSDLKEpSAELLQSLQLEK------ 306

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytk
                         q+P tE         R KLY  + +    L       s +  y +
  gi|2244370   307 ----EQLPSTESTLYAKEPFRAKLYLIKKKLQNRLIAINTTDSVDFTYSN 352

                    vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                      e L  +++  +sL    D   A G L+++   v   G  L +LD R
  gi|2244370   353 SKELLGDIDMLIRSL----DSLSASG-LVEFYNLVLLGGFHLLRLDFREH 397

                    seRqtDvlDAittHLeiG..sYReWsEeKRqEWLlaELkGKRPLlgsDLP
                     +        i   +++ ++ +++ sE+K+ E L   L+ K+  l   L
  gi|2244370   398 RDVILSATSEIFCLIGLCdsDFKDMSEQKKYEILNLALSAKKLDLNTIL- 446

                    ktEEvkD....vldafrvLA....ELPiDsFGaYiismataPsDvLAvEL
                      EE+ D++++ ++af  +A  ++ +      ++iism+  PsD L v
  gi|2244370   447 --EELSDstrrFVGAFLRIAwakkHISESILQSFIISMSSEPSDLLCVLW 494

                    LqRECgv.............kqtLrvvPLFEkLADLeAAPAavekLFsiDW
                      +  g+ ++++++++++++  + + PLFE + DL+ A  +++ L++
  gi|2244370   495 FAKQSGLwkpgkkkeskkgRAKISIAPLFETIDDLQHAKHTIKTLYANAH 544

                    Yinri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGv
                    Y   + ++d  qe+mvGYsDs KD G ++  + LY A  ++iK   +
  gi|2244370   545 YQQYLldnDNIQEIMVGYSDSSKDGGIFASNYNLYFAIADLIKLQNELPL 594

                    KLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGE
                     +  FHGRGG v RGGG    A+Ls  P  + G l+ t qGE+i   +
  gi|2244370   595 TIAFFHGRGGSVSRGGGSLEEALLSATPQSVCGVLKTTEQGEMISAKYLN 644

                    EnLCFrsLqRFtAAtLEHGmnPPvs......PkPEWRkLmeemAvvAtEE
                     n+  + L     A L   mn     ++  +  P   kL+e +  v
  gi|2244370   645 KNIATKNLSSTISALLKKSMNDTFCiggaceIDPQMMKLLEPISQVSCVA 694

                    YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPW
                    YR +v+ +  F+ YF+ AtP      +n+GsRP+KRk    +e LRAiPW
  gi|2244370   695 YRKLVYEDKGFMTYFKHATPIEFIQNLNLGSRPSKRKDTQSVEDLRAIPW 744

                    iFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlD
                    +FaWtq R  LP W G+G     A+    Kn   Lk+ Y +  FF+ t+D
  gi|2244370   745 VFAWTQNRSILPAWYGLGS----ALASGDKN--ALKDCYANSLFFKTTID 788

                    LlEmvFAKGDPGiAaLyDkLL....vaEeLkPFGksLRdkYvEtkdlLLk
                     +   F K D  iA Ly + ++++++ + ++   + +  +Y+ t + LL
  gi|2244370   789 NISQAFLKVDVEIAKLYNEFVpdktIGDRIW---ELIYTQYQLTLEHLLY 835

                    iAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrP
                    + G   lL+ +  ++  + LR +Y+  Ln  q   +K+     y+    P
  gi|2244370   836 LRGENALLDSESEIRESILLRKPYLSVLNLTQIELIKK-----YQTCHYP 880

                    hlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<
                    +     A+E                    L + +  t+ GiA G+ ntG
  gi|2244370   881 Q-----AQER-------------------LMEQIHATIVGIAQGLRNTG  905

                    -*

  gi|2244370     -    -

gi|110597068|ref|ZP_01385357.1|: domain 1 of 1, from 1 to 918: score 131.5, E = 2.6e-36
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                              l     v + ek  +    Ll  F ++L DL Ge
  gi|1105970     1    ------MLTTTSNVIDFEKAERDFTFLLHCFQEVLCDL-GE------ 34

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                                Kk +  L   Ga L      D+    +a++ +  L n+
  gi|1105970    35 ------------KKLADHLPWQGASLPLEHYPDTERALQAFSIVFQLLNM 72
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                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                AEE   A  RR   +     aD +          tl +   +     eE+
gi|1105970    73 AEENSSAQNRRA--LE----ADKGLSHLTGLWGRTLLRFRERE-IPVEEI 115

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   L    +  vltAHPt + R+ +L ++  +   L +   +  t+ ++
gi|1105970   116 CSLLPEVVINTVLTAHPTEAKRKTVLEQHRQLYLLLVKRENQMWTPLEQL 165

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                E+   +   +   +Rt E+   +P   DE R  + Y+     +  P   +
gi|1105970   166 EIKSEIKSVLERLWRTGELLYEKPGIDDERRNVIHYLYNIFPEALPMLDK 215

                RvDtALKniGinERl...PYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                R   A +  G      ++P   P + F sW+GGDRDG +P vt Evt +
gi|1105970   216 RLQQAWRETGFDPAHlsdPRSLPRLNFGSWVGGDRDG-HPLVTAEVTEET 264

                CLLaRmmAanlYisqvEDLmFElsmW.RCn...dELRvRAEElyrtaard
                    R  A  l    + +L   ls+ +R  +++  L  R E l++  a +
gi|1105970   265 LAEMRRSALKLVRHHLYELASKLSLSdRLQtpgKPLVLRIETLKKKLAEK 314

                kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                          K     EP+R  L      L    E         i
gi|1105970   315 ----GSDALRKN--RHEPWRQFLNLLIAALPPDAE---------IPAACN 349

                eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                   y    e LE L L  +sL   G + +AD  +  + R v tFG  L
gi|1105970   350 HCGYNASVELLEDLSLLRHSLIAVGAQHLADMEVAPVYRIVQTFGFHLGT 399

                LDiRqEseRqtDvlDAittHLei.Gs.YReWsEeKRqEWLlaELkGKRPL
                LDiRq s  +   l  + t  +++Gs++ eW E  R+ +L  EL+  RP
gi|1105970   400 LDIRQNSHIHELALSQLMTAAGLdGSgFLEWDETARRVFLDLELQSPRPF 449

                lgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAv
                  +D+    E + vl  +rvL  ++++   D  G+ i+sm+   sD L v
gi|1105970   450 THPDMSAGAEAEAVLACYRVLLKhnksYGTDGLGSLIVSMTRNVSDLLIV 499

                ELLqRECgvkqt........LrvvPLFEkLADLeAAPAavekLFsiDW..
                 L  RE g+  ++++++   L+vvPLFE + DL+  PA +        ++
gi|1105970   500 YLFAREVGLMTPtgdgdaciLPVVPLFETIEDLRKSPAILSEFLHHPVtr 549

                ....YinridGK....qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvA
                ++ +Y+    GK+++ q+ m+GYsDs KD G +   W LY+AqE +i
gi|1105970   550 rsleYRREAAGKprkiQQAMIGYSDSNKDGGIFTSTWTLYRAQETLIAAG 599

                KkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviE
                K+ G  +  FHGRGG + RG GPtH  i +qP    +  +  t qGE i
gi|1105970   600 KESGTDILFFHGRGGSISRGAGPTHRFIKAQPYGSFKTGMCFTEQGETIA 649

                fsFGEEnLCFrsLqRFtAAtL.EHGmnPPvsPkPEWRk.LmeemAvvAtE
                + +         L  F A   +  G +     +    +++m+ +
gi|1105970   650 QKYANRISAVYNLELFMAGVAgALGKQQQSEHRAHPLEpMMDLLSEKSYQ 699

                EYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiP
                 YR ++     F  +FR AtP        iGsRP++R     +e LRAiP
gi|1105970   700 AYRELI-ETKGFLTFFRQATPIDIIESSRIGSRPSRRSGKNSLEDLRAIP 748

                WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                W+F+W q RF L  W GvG A  +  +     +  ++   + WP  R  +
gi|1105970   749 WVFSWNQARFSLSGWYGVGSALEYLHESNPEAFEEIRQRSHAWPPLRYII 798

                DLlEmvFAKGDPGiAaLyDkLLvaEe..LkPFGksLRdkYvEtkdlLLki
                   +   A  D  i   y  L+v++ +    F   + ++Y  tk ++
gi|1105970   799 SNADTSIASADLQIMRQY-ALMVSDRsvRERFLGMIEAEYHRTKTYI--- 844

                AGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPh
                    DlL       qr+          nv     L+R      +
gi|1105970   845 ----DLLYTAQLETQRI----------NVNRFISLRREGLDILHRQQITL 880

                lsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-
                l +     ns k +e      +e + P     L+Lt+  i  G+  tG
gi|1105970   881 LRQWRELKNSGKQEE------AESMLP----ELLLTVNAISGGLRTTG   918
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                  *

  gi|1105970     -   -

gi|7768200|emb|CAB90643.1|: domain 1 of 1, from 1 to 371: score 128.6, E = 2e-35
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768200     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768200     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768200     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768200     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768200     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768200     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768200     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768200     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768200     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768200     - ---------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768200     - ---------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768200     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768200     9 RLSAAWQLYKAQEELIEVAKQHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  P Dti GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEHGm PP+ P
  gi|7768200    59 PADTIRGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHGMIPPLTP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  k EWR Lm+emAvvAtE YRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|7768200   109 KQEWRALMDEMAVVATERYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh i+KD Knl
  gi|7768200   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFKHVINKDNKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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                    +L+ mY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL P G++
  gi|7768200   209 LMLQQMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELLPLGEQ 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR  Y +tk +LLki GH ++LEGDP+LKqrl+LR++YittLnv+qAYtL
  gi|7768200   259 LRTAYNDTKSYLLKITGHNEILEGDPFLKQRLKLRNAYITTLNVCQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPsy+v lrP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|7768200   309 KRIRDPSYQVPLRPPIAKEVMEGSISSANQLVKLNPTSEYAPGLEDTLIL 358

                    tmKGiAAGmqntG<-*
                    tmKG AAGmqntG
  gi|7768200   359 TMKGNAAGMQNTG    371

gi|18072442|emb|CAC84971.1|: domain 1 of 1, from 1 to 364: score 128.3, E = 2.5e-35
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807244     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807244     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807244     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807244     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807244     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807244     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807244     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807244     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807244     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807244     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807244     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807244     1 ----------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqE+++KvAKkyGvKL++FHGRGGtvGR GGPtHLAiLsq
  gi|1807244     9 RLSAAWQLYKAQEDMMKVAKKYGVKLTMFHGRGGTVGRRGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PP tinGs+Rvt+qGEviE+sFGEE LCF++LqR+tAAtLEHGmnP +sP
  gi|1807244    59 PPGTINGSIRVTIQGEVIEQSFGEERLCFKTLQRYTAATLEHGMNPAISP 108
```

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                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L++emAvvAt EYRs+v++EPRFvEYFRlAtPE+EYGkmniGsR
  gi|1807244   109 KPEWRALLDEMAVVATKEYRSIVFQEPRFVEYFRLATPETEYGKMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKh ++KD Kn+
  gi|1807244   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGVGAAFKHVMEKDKKNF 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q L+EmY+ WPFFRvt+DLlEmvFAKG P iAaLyDkLLv+E+L+PFG++
  gi|1807244   209 QTLREMYNVWPFFRVTIDLLEMVFAKGNPDIAALYDKLLVSEDLQPFGER 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++YvEtk lLL++AGHkDlLEGDPYLKqrlRLR++YittLnv+qAYtL
  gi|1807244   259 LRNNYVETKSLLLQVAGHKDLLEGDPYLKQRLRLRNAYITTLNVCQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP y v lrP lsK+  +   k+a+e + Lnpt+++aPGLEDtLiL
  gi|1807244   309 KRIRDPTYNVNLRPRLSKDVTERR-KPAAEFLTLNPTSEYAPGLEDTLIL 357

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|1807244   358 TMKGIAA------    364

gi|159897337|ref|YP_001543584.1|: domain 1 of 1, from 1 to 908: score 128.1, E = 2.7e-35
                    *->siDAqLRlLvPGKvsedekLieYDA.LLlDkFLDiLqDLHGedLkEa
                              +  P     d    + DA+ +l  F ++Lq+L   +L
  gi|1598973     1    ------MANLPSYDFADLIKADHDAeFVLTCFAEVLQELGEAEL--- 38

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                           A Y G      L    +    + P  ai  A+    +L   n
  gi|1598973    39 --------AAYLG------LPTTASINQTITPERAIQAASLSFQLL---N 71

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                    + EE   A  RRi+         E+          tl+ L   +  s e
  gi|1598973    72 MVEENAAAQQRRIREAA------EGFNAEVGLWGNTLQSLSQAG-FSAEQ 114

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    +  AL    v+ vltAHPt + R  +L    R+   L +      t+ ++
  gi|1598973   115 IGAALGQIYVEPVLTAHPTEAKRATMLEHYRRLYLLLVKRENPIWTPLEQ 164

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    + L + +  E+   +Rt Ei   +P   DE+R  + Y+
  gi|1598973   165 QALRDEIKVELERLWRTGEIFLEKPSVADELRNILHYLRHVFPASLVTLD 214

                    RRvDtALKniGinERl...PYdvPLikFssWmGGDRDGknPRvtPEvtRD
                     R   A +  G   Rl ++  + P ++F  W+GGDRDG +P vt  vtR
  gi|1598973   215 LRLQQAWQLQGFDRRLlptTEQLPHVQFGTWVGGDRDG-HPLVTAAVTRF 263

                    vCLLaRmmAanlYisqvEDLmFElsmW.RCndELRvRAEElyrtaardkv
                         R  A  +  +q+  L+  ls+ +R      +  E l   aa
  gi|1598973   264 ALQELRRNALEVLHEQLVQLVIKLSLSdRLQPPHAALLEALDASAAAL-G 312

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                     +  +   +   P+EP+R  +  +  +L               ++
  gi|1598973   313 QRGQMALARN--PEEPWRQWINLIIARLPES-----------GQLRQPW 348

                    vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                     y    e +  L      L   G + +    L  ++R v t G     LD
  gi|1598973   349 QYRSSSETVADLQFLAEQLHAVGAQRLVLNDLQPVIRSVQTLGFHSAVLD 398

                    iRqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKRPLlg
                    iRq s  +   ++ + +  +   Y  ++W+Ee+R E L  EL+  RP
  gi|1598973   399 IRQNSKFHDLAVEQLLQAAGFSDYQfsSWPEEQRLELLNRELQSARPFAH 448

                    sDLPktEEvkDvldafrvLA.ELP...iDsFGaYiismataPsDvLAvEL
                    + L    E   v d +rvLA+E+ +++    G+ iism+ + sD L v L
  gi|1598973   449 PSLELGNEASAVRDCYRVLAdEIAqhgTAGLGSLIISMTRSLSDLLVVYL 498

                    LqR........ECgvkqtLrvvPLFEkLADLeAAP....AavekLFsiDW
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                    L R+ +    +E g+   L+vvPLFE + DLe  P+  +A +++  s
  gi|1598973   499 LAReasllyvtEAGLACVLPVVPLFETIEDLEISPgildAFLAHPVSQAS 548

                    YinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                       r    q+vmvGYsDs KD G l+  W LY+ q  ++ v  k+ v++
  gi|1598973   549 RALRQTSVQQVMVGYSDSNKDGGILASLWSLYRSQGTLAAVGAKHHVRVR 598

                    lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                     FHGRGGt+ RG GPtH  + + P   + G lR+t qGE i + +
  gi|1598973   599 FFHGRGGTISRGAGPTHRFLNALPAAALAGDLRMTEQGETIAQKYANHIT 648

                    CFrsLqRFtAAtLEHGm......nPPvsPkPEWRkLmeemAvvAtEEYRs
                        L    A   E  + ++++++ P s  P    +m+ +       Y
  gi|1598973   649 AVYNLELMVAGVTEATLlgsqrdQTPHSLAP----IMDVLTAYSRQRYET 694

                    vvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFa
                    ++ + P F+ +F  AtP     +  iGsRPa+R     +  LRAiPW+F+
  gi|1598973   695 LI-QTPGFIQFFGQATPIDVIEQGKIGSRPARRTGQRTLGDLRAIPWVFS 743

                    WtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlE
                    W q RF L  W GvG    +  ++    + +Lk    eW   +  l  +
  gi|1598973   744 WSQARFFLSGWYGVGSSLAWLAEQHPEQFDQLKQAAFEWYPLKYLLTNVS 793

                    mvFAKGDPGiAaLyDkLLvaEeLk.PFGksLRdkYvEtkdlLLkiAGHkD
                          D      y +L+    +++P    + ++++ t++ L  i G
  gi|1598973   794 TSMLSADLATMQAYSQLVEDPSVRqPIMAAIEAEFKQTQQQLELIFGGS- 842

                    lLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEy
                    l E  P +   l  R+s +  L   q   L   R           l  E
  gi|1598973   843 LAERRPRIYRMLQGRQSRLSQLHQQQINLLHTWR----------SLPSEQ 882

                    AdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      E     + L  L             L+Lt+  iA G+  tG
  gi|1598973   883 IPER----ERL--LT-----------QLLLTVNAIASGLRTTG    908

gi|18073820|emb|CAC84914.1|: domain 1 of 1, from 1 to 363: score 127.4, E = 4.5e-35
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807382     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807382     - ---------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807382     - ---------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807382     - ---------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807382     - ---------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807382     - ---------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807382     - ---------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807382     - ---------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807382     - ---------------------------------------------------- -
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                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807382     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807382     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807382     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+iKvAK++G+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807382     9 RLSAAWQLYKAQEELIKVAKQFGIKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sF EE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|1807382    59 PPDTIHGSLRVTVQGEVIEQSFEEEHLCFRTLQRFTAATLEHGMHPPISP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  k EWR+Lm+emAvvAtEEYRs v+   RFvEYFRlAtPE+EYG+mniGsR
  gi|1807382   109 KQEWRELMDEMAVVATEEYRSYVFHNKRFVEYFRLATPETEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+h ++KDi+nl
  gi|1807382   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFRHVLEKDIRNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+ mY+eWP FRvt+DL+EmvFA  DPGiAaLyDkLLv+E+L+ FG +
  gi|1807382   209 HMLQQMYNEWPVFRVTIDLVEMVFAEEDPGIAALYDKLLVSEDLWLFGSQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR ++vEtkdlLLk+AGH++lLEGDPYLKqrlRLRdsYittLn +qAYtL
  gi|1807382   259 LRSNFVETKDLLLKVAGHRELLEGDPYLKQRLRLRDSYITTLNGCQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDP+++  lrPhlsKE       +a++LvkLnpt+++aPGLEDtLiL
  gi|1807382   309 KRIRDPNFHGNLRPHLSKETSSTK--PAADLVKLNPTSEYAPGLEDTLIL 356

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807382   357 TMKGIAA------    363

gi|7768220|emb|CAB90656.1|: domain 1 of 1, from 1 to 371: score 127.4, E = 4.5e-35
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768220     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768220     - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768220     - ------------------------------------------------ -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768220     - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768220     - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768220     - ------------------------------------------------ -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|7768220     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768220     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768220     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768220     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768220     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768220     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768220     9 RLSAAWQLYKAQEELIEVAKQHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEHGm PP+ P
  gi|7768220    59 PTDTIQGSLRVTIQGEVIERSFGEGQLCFKTLQRYTAATLEHGMIPPLTP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   k EWR Lm++mAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|7768220   109 KQEWRALMDDMAVVATERYRSIVFREPRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AF+h idKD+Knl
  gi|7768220   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFRHVIDKDSKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+ mY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL P G++
  gi|7768220   209 LMLQQMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELLPLGEE 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR  Y +tk +LLki GH ++LEGDP+LKqrl+LR++YittLnv+qAYtL
  gi|7768220   259 LRTGYNDTKSYLLKITGHNEILEGDPFLKQRLKLRNAYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|7768220   309 KRIRDPSYQVPVRPPIAKEIMEGSVSSANQLVKLNPTSEYAPGLEDTLIL 358

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|7768220   359 TMKGIAAGMQNTG    371

gi|7768117|emb|CAB90619.1|: domain 1 of 1, from 1 to 364: score 126.2, E = 1e-34
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768117     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768117     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768117     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768117     - ------------------------------------------------ -
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                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768117     - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768117     - ------------------------------------------------ -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768117     - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768117     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768117     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768117     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768117     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768117     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYk qEE++KvAK+yGv L++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768117     9 RLSAAWQLYKTQEELVKVAKEYGVELTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFt AtLEHGm+ P+sP
  gi|7768117    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTTATLEHGMQLPISP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+emAvvAt EYRs+v++E RFvEYFRlAtPElEYG+mniGsR
  gi|7768117   109 KPEWRALMDEMAVVATNEYRSIVFQESRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD Knl
  gi|7768117   159 PPKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIEKDKKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+EmY+eWPFFRvt+DL+Em F KG PGiAaLyDkLLv+ +L PFG++
  gi|7768117   209 NMLREMYNEWPFFRVTIDLIEMGFTKGSPGIAALYDKLLVSTDLLPFGEQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y+Etk lLL++AGHkDlLEGDPYLKqrlRLR +YittLnv qAYtL
  gi|7768117   259 LRANYEETKRLLLQVAGHKDLLEGDPYLKQRLRLRYPYITTLNVWQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDPsy+   +P ls E  + n k a+eLvkLnpt+++aPGLEDtLiL
  gi|7768117   309 KRIRDPSYHLPAKPNLSNEIMNSN-KSAAELVKLNPTSEYAPGLEDTLIL 357

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|7768117   358 TMKGIAA------    364

gi|1362025|pir||PC2168: domain 1 of 1, from 1 to 411: score 124.6, E = 3.3e-34
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1362025     -    ------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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gi|1362025     - ------------------------------------------------- -

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1362025     - ------------------------------------------------- -

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1362025     - ------------------------------------------------- -

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1362025     - ------------------------------------------------- -

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1362025     - ------------------------------------------------- -

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1362025     - ------------------------------------------------- -

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                  FWK +PPtEPYRviLGdvRDKLY tRER+R LL  Gis+i+EeA +t+v
gi|1362025     1 -FWKTIPPTEPYRVILGDVRDKLYHTRERSRQLLSNGISDIPEEATFTNV 49

                 EeF.........LEPLELCYksLC..............eCGDkviADG
                 E+ ++  ++   +L    LC    C+  +++ +  +  +      v A
gi|1362025    50 EQVkklydqlvlsLTCPALCLLLFCsllrsswsllsyvtaHYVHVVTAQX 99

                 ..sLLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWs
                    LLD+LRqvstFGLsLv+LDiRqEseR+tDvlDAit+HL+  sYR+Ws
gi|1362025   100 lmELLDFLRQVSTFGLSLVRLDIRQESERHTDVLDAITKHLDGSSYRDWS 149

                 EeKRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGaY
                 Ee+RqEWLl+EL+GKRPL+g+DLPktEE++Dvld+f+v+ ELP+D+FGaY
gi|1362025   150 EERRQEWLLSELSGKRPLFGPDLPKTEEIADVLDTFKVISELPSDCFGAY 199

                 iismataPsDvLAvELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLF
                 iismat+PsDvLAvELLqREC+vk +LrvvPLFEkLADLeAAPAav +LF
gi|1362025   200 IISMATSPSDVLAVELLQRECHVKTPLRVVPLFEKLADLEAAPAAVSRLF 249

                 siDWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyG
                 s+DWY+nri+GKqevm+GYsDsGKDAGRlsAAW LYkAqEE++KvAKkyG
gi|1362025   250 SLDWYKNRINGKQEVMIGYSDSGKDAGRLSAAWELYKAQEELVKVAKKYG 299

                 vKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFG
                 vKL++FHGRGGtvGRGGGPtHLAiLsqPPDt+nGslRvtvqGEviE+sFG
gi|1362025   300 VKLTMFHGRGGTVGRGGGPTHLAILSQPPDTVNGSLRVTVQGEVIEQSFG 349

                 EEnLCFrsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvv
                 EE+LCFr+LqRFtAAtLEHGmnPPvsPkPEWR L++ mAvvAtEEYRsvv
gi|1362025   350 EEHLCFRTLQRFTAATLEHGMNPPVSPKPEWRALLDAMAVVATEEYRSVV 399

                 vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWt
                 ++EPRFvEYFRl
gi|1362025   400 FQEPRFVEYFRL----------------------------------- 411

                 qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv

gi|1362025     - ------------------------------------------------- -

                 FAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE

gi|1362025     - ------------------------------------------------- -

                 GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE

gi|1362025     - ------------------------------------------------- -
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                  nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*

  gi|1362025     - ----------------------------------------    -

gi|18072438|emb|CAC84930.1|: domain 1 of 1, from 1 to 363: score 123.7, E = 6.1e-34
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807243     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807243     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807243     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807243     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807243     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807243     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807243     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807243     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807243     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807243     - ---------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807243     - ---------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|1807243     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+++vAK+yGvKL++FHG+GGtvGRGGGPtHLAiLsq
  gi|1807243     9 RLSAAWQLYKAQEELVQVAKQYGVKLTMFHGKGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP+tinGslRvtvqGEviE+sFGEE LCFr+LqR+tAAtLEHGm PP sP
  gi|1807243    59 PPETINGSLRVTVQGEVIEQSFGEERLCFRTLQRYTAATLEHGMRPPTSP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR +++e+AvvAtEEYRsvv+KEPRFvEYF  At ElEYG+mniGsR
  gi|1807243   109 KPEWRAILDEIAVVATEEYRSVVFKEPRFVEYFGRATLELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh + KD +nl
  gi|1807243   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHILRKDRRNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLv++eLkPFG++
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  gi|1807243   209 RILKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVSDELKPFGEQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Etk+lLLk+AGH DlLEGDPYLKqr+RLR++YittLnv+qAYt
  gi|1807243   259 LRANYEETKQLLLKVAGHTDLLEGDPYLKQRIRLREAYITTLNVCQAYTQ 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   +RiRDP++kv +rP+lsKE  d n  k +eLvkLnp++++aPGLEDtLiL
  gi|1807243   309 RRIRDPNFKVDVRPPLSKETLDSN--KQAELVKLNPASEYAPGLEDTLIL 356

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807243   357 TMKGIAA------    363

gi|7768218|emb|CAB90649.1|: domain 1 of 1, from 1 to 371: score 121.3, E = 3.1e-33
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768218     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768218     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768218     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768218     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768218     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768218     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768218     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768218     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768218     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768218     - ---------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768218     - ---------------------------------------------- -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768218     1 -----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768218     9 RLSAAWQLYKAQEELIEVAKQHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEH m PP+ P
  gi|7768218    59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHSMIPPLTP 108
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                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    k EWR Lm+emAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|7768218   109 KQEWRALMDEMAVVATERYRSIVFREPRFVEYFRLATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KR+PsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AF+h idKD Knl
  gi|7768218   159 PSKRRPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFRHVIDKDNKNL 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+ mY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL P G++
  gi|7768218   209 LMLQQMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELLPLGEQ 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR  Y +tk +LLki GH ++LEGDP+LKqrl+LR +YittLnv+qAYtL
  gi|7768218   259 LRTAYNDTKSYLLKITGHNEILEGDPFLKQRLKLRTAYITTLNVCQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|7768218   309 KRIRDPSYQVPVRPPIAKETMEGSISSANQLVKLNPTSEYAPGLEDTLIL 358

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|7768218   359 TMKGIAAGMQNTG    371

gi|18073648|emb|CAC83651.1|: domain 1 of 1, from 1 to 362: score 120.1, E = 7e-33
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807364     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807364     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807364     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807364     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807364     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807364     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807364     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807364     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807364     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807364     - ------------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807364     - ------------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
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  gi|1807364     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqE++iKvAK++GvKL++FHGRGGtvGRGGG tHLAiLsq
  gi|1807364     9 RLSAAWQLYKAQEDLIKVAKDFGVKLTMFHGRGGTVGRGGGLTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PP+sP
  gi|1807364    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPISP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   k EWRkLm+emAv+AtEEYRs+v+KE RFvEYFR+AtPElEYG+mniGsR
  gi|1807364   109 KLEWRKLMDEMAVIATEEYRSIVFKESRFVEYFRSATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P++RkPsGGiesLRAiPW+FaWtqtRFHLPvWLG+GAAFKh i  D   l
  gi|1807364   159 PSQRKPSGGIESLRAIPWLFAWTQTRFHLPVWLGFGAAFKHVIXXDXXXL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+ mY+e PFFRvt+DL+EmvFAKGDPGi ++yDkLLv+E+L+ FG++
  gi|1807364   209 HTLRQMYNELPFFRVTIDLVEMVFAKGDPGITSVYDKLLVSEDLWSFGEK 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR+ Y EtkdlLLk+AGHkDlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|1807364   259 LRAIYLETKDLLLKVAGHKDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+++   rPhlsKE    +   adeLvkLnpt+++aPGLEDtLiL
  gi|1807364   309 KRIRDPNFHCQQRPHLSKESSTKP---ADELVKLNPTSEYAPGLEDTLIL 355

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807364   356 TMKGIAA------    362

gi|118581379|ref|YP_902629.1|: domain 1 of 1, from 1 to 914: score 120.0, E = 7.9e-33
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            R L P   +   kL +   +L+D   ++L  L   +L
  gi|1185813     1    ---MEDRTL-PEETA---KLQRDVVVLMDFLAEVLDGLGEGSLA--- 37

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         s  + G++ t               +D   v +a++    L n+
  gi|1185813    38 -----ASLPFKGREATA--------------TDNDRVVHALSIAFQLLNM 68

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AEE      RR    +       + A         l +L  ++  + e +
  gi|1185813    69 AEENSAVQMRRKVESH------AGLAEEPGLWGQILSQLREQG-VAEETI 111

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      L    v++vltAHPt   R s L     +   + +L     t+ +++
  gi|1185813   112 HHELEKVVVEVVLTAHPTEVRRTSALYHLRELYQLIVKLENPVWTPMERR 161

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGv.PKFL
                   E+ E +   +   + t Ei   +P    E+ aG+ Y+   ++  v P
  gi|1185813   162 EIQEEIKAMLELLWQTGEIFIEKPHVLSEL-AGIIYYLRSIFPQVlPILE 210

                   RRvDtALKniGi...nERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                   +R   A + +G + +   +P   P ++F  W+GGDRDG +P vt  +tR
  gi|1185813   211 KRLRHAWQDVGFtcnAQEIPPRLPRLRFGTWVGGDRDG-HPLVTAAITRQ 259

                   vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                        R  A  l  +q+  +   ls+ R    + +   El    a
  gi|1185813   260 ALRELRNSAVSLVNEQLVTMAARLSLSRRLLPVPAPLAELIADVAAT--L 307

                   KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                       E      P EP+R ++      L   R           s  + +
  gi|1185813   308 GDRGEEALRRNPLEPWRQVI-----NLMIARLPVDSAGKESDSVQPGQGC 352

                   ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                   y    e    L L   sL   G   +A   +  + R v  FG  L  LDi
  gi|1185813   353 YQLAAELCNDLRLVQDSLTAAGALRLARDYVAPVRRTVEVFGFHLASLDI 402
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                    RqEseRqtDvlDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLlgs
                    Rq s  +   ++ + t  ++++  +  WsE +R E+L  EL   RP
  gi|1185813   403 RQNSAFHDLAVEQLMTAAGLqdTGFSGWSEVRRLEFLNRELASSRPFARH 452

                    DLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAvELL
                    D     E + v+d +r L ++ +    D  G+ i+sm+ a sD L v LL
  gi|1185813   453 DARPGHEAESVIDCYRELVDhirvWGRDGLGSLIVSMTRALSDLLVVYLL 502

                    qRECgvkqt........LrvvPLFEkLADLeAAPAavekLFsiDWYinri
                     RE g+  ++++++   L+vvPLFE + DL+     + +       +  +
  gi|1185813   503 AREAGLTVAgsnghvclLPVVPLFETIEDLQGSHLVLRQFLEHPMTRRTL 552

                    dG......KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                        ++ + q+vm+GYsDs KD G l+  W LY+AqE ++   ++ Gv +
  gi|1185813   553 SAlcgdapVQQVMIGYSDSNKDGGILASLWSLYRAQEAMAEAGRQCGVEV 602

                    vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                      FHGRGGt+ RG GPt   +   P   + G lR t qGEvi + +
  gi|1185813   603 RFFHGRGGTISRGAGPTSRFLRGLPQGSVVGNLRLTEQGEVIAQKYANPM 652

                    LCFrsLqRFtAAtLEHGmnPPvsPkPE..WRkLmeemAvvAtEEYRsvvv
                         L    A t    +     Pk  ++    m+++A      Y s+v
  gi|1185813   653 NAAYNLELLLAGTAGVSVTQNHCPKKAnpLEPAMDRLAETSRRAYESLVT 702

                    KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                     +  F+ +FR AtP        iGsRPa+R  +  i  LRAiPW+F+W q
  gi|1185813   703 GDG-FITFFRQATPIDVIESSRIGSRPARRSGGASIADLRAIPWVFSWSQ 751

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     R+ L  W GvG A    +  D + +  +      W      +  +
  gi|1185813   752 ARYSLSGWFGVGSALERFLREDERAFHEIAANAASWATLNYIVSNVATSI 801

                    AKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLE
                    A   P +   y  L+   eL+ +    + d+Y  t  +L  + G   lLE
  gi|1185813   802 ATANPEVMREYASLVEDGELRErIFTVIYDEYLRTTRMLELLFGG-PLLE 850

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                      P +   l  R+  +  L   q             + l P      A+
  gi|1185813   851 QHPRIHAVLARREESLLFLHRRQ-------------IELLPLWRHHRAAQ 887

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +  +a+eL+ L         LE     t+  iAAG+  tG
  gi|1185813   888 EHGQAEELLILL--------LE-----TVNAIAAGLRTTG    914

gi|18072426|emb|CAC84920.1|: domain 1 of 1, from 1 to 362: score 119.3, E = 1.2e-32
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807242     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807242     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807242     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807242     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807242     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807242     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|1807242     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807242     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807242     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807242     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807242     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807242     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+++vAK+yGvKL++FHG+GGtvGRGGGPtHLAiLsq
  gi|1807242     9 RLSAAWQLYKAQEELVQVAKQYGVKLTMFHGKGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP+tinGslRvtvqGEviE+sFGEE LCFr+LqR+tAAtLEHGm PP sP
  gi|1807242    59 PPETINGSLRVTVQGEVIEQSFGEERLCFRTLQRYTAATLEHGMRPPTSP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR +++e+AvvAtEEYRsvv+KEPRFvEYFRlAtP + YG+mniGsR
  gi|1807242   109 KPEWRAILDEIAVVATEEYRSVVFKEPRFVEYFRLATPLTRYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+ AAF h + KD Knl
  gi|1807242   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFVAAFNHILAKDKKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q ++ mY+eWPFFRvtlDL+EmvFAKGDPGiAaLyDkLLv+E+L+ FG++
  gi|1807242   209 QHIRQMYNEWPFFRVTLDLIEMVFAKGDPGIAALYDKLLVSEDLWSFGEK 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR+++ Et+dlLLk+AGH+DlLEGDPYLKqrlRLRdsYittLnv+qAYtL
  gi|1807242   259 LRANFLETRDLLLKVAGHRDLLEGDPYLKQRLRLRDSYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+++v lrPhlsKE        a+eL+kLn t++++PGLEDtLiL
  gi|1807242   309 KRIRDPNFHVQLRPHLSKESSTNS---AAELLKLNTTSEYPPGLEDTLIL 355

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807242   356 TMKGIAA------    362

gi|7768125|emb|CAB90618.1|: domain 1 of 1, from 1 to 364: score 117.9, E = 3.3e-32
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768125     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768125     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768125     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768125     - ------------------------------------------------ -
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                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768125    - ------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768125    - ------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768125    - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768125    - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768125    - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768125    - ------------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768125    - ------------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768125    1 -----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYk qEE +KvAK++GvKL++FHGRGGtvGRGGGPtHLAiL+q
  gi|7768125    9 RLSAAWQLYKTQEEPVKVAKEFGVKLTMFHGRGGTVGRGGGPTHLAILAQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+ FGEE+LCFr+LqRF+AAtLEHGm+ P+sP
  gi|7768125   59 PPDTIHGSLRVTVQGEVIEQLFGEEHLCFRTLQRFAAATLEHGMQLPISP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+emAvv t EYRs+v++EPRFvEYFRlAt E EYG+mniGsR
  gi|7768125  109 KPEWRALMDEMAVVPTKEYRSIVFQEPRFVEYFRLATXEXEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtR HLPvWLG+GAAFKh i+KD Knl
  gi|7768125  159 PSKRKPSGGIESLRAIPWIFAWTQTRLHLPVWLGFGAAFKHVIEKDKKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+EmY+eWPFFRvt+DL+EmvF KG PGiAaLyDkLLv+ +L PFG++
  gi|7768125  209 NILREMYNEWPFFRVTIDLIEMVFTKGSPGIAALYDKLLVSTDLVPFGEQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y+Etk lLL++AGHkDlLEGDPYLKqrlRLR +YittLnv+qAYtL
  gi|7768125  259 LRANYEETKRLLLQVAGHKDLLEGDPYLKQRLRLRYPYITTLNVCQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDPs + t +P ls E  +   k+a+eLv+Lnpt+++aPGLEDtLiL
  gi|7768125  309 KRIRDPSSHLTAKPSLSNEIMNSH-KPAAELVQLNPTSEYAPGLEDTLIL 357

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|7768125  358 TMKGIAA------    364

gi|260220723|emb|CBA28569.1|: domain 1 of 1, from 11 to 893: score 117.8, E = 3.5e-32
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      +     +    +  ++e+ +  D  Ll + L+D++ +  G d  E
  gi|2602207    11    PMNKAPAAETAKRAKDNERPLVEDIRLLGRILgDVIREQEGVDAYEL 57

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  +     ls  +    D +    L   L sL    ++ v +a+     LAn
```

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gi|2602207    58 IEKIRTLSVAFRRDADQEADKALKKLLKSLSGDQTVSVIRAFTYFSHLAN 107

                 LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                 LAE+ +   RR i+ +  GD       t E  iE  + +L   +  +P+
gi|2602207   108 LAEDRHHIRRRAIHERA-GD-------TQEGSIEVAMSRLRWAG-IAPKA 148

                 vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq...LsAKDvtv
                 + + L    v  vltAHPt   R+s+L  +  i   L+q++++  +   v
gi|2602207   149 ISNTLAQSFVSPVLTAHPTEVQRKSILDAERDIAQLLTQrdeIKQRASIV 198

                 eDK......kEL..DEALHRE.iqAAFRtDEiRRaqPtPqDEmRaGmsYi
                 + K++  ++kEL   EA  R ++   + t  +R ++ t  DE+   +sY+
gi|2602207   199 DSKkdaltpKELaaNEAQMRArVMQLWQTRLLRFSKLTVADEIENALSYY 248

                 HEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknP
                   t  + +PK     +  L n  +          ++   W+GGDRDG nP
gi|2602207   249 ESTFLREIPKLYADLEDMLGNQPVHS-------FLRMGQWIGGDRDG-NP 290

                 RvtPEvtRDvCLLaRmmAanlYisqvEDLmFEls....mWRCndELRvRA
                  v              +A   Y+  v  L  Els +  +  C  E+ + A
gi|2602207   291 NVSAQTLEYALRRQAEVALRHYLTEVHYLGGELSisamLADCTPEMQALA 340

                 EEl.yrtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYnt......
                 E  + + a r+                EPYR  L  +  +L  t ++ ++
gi|2602207   341 ESSpDQNAHRK---------------DEPYRRALTGMYARLAATlkeltg 375

                 RERaRHLLAtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGs
                  E aRH +A        +  y   E+F+  L +   sL      ++
gi|2602207   376 TEAARHAVAP-------QNPYVLAEDFVADLRVIEASLKANHGAALTAQR 418

                 LLDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEe
                 L  l+R v  FG  L  +D+Rq s+++ +v+  +     + ++Y + sEe
gi|2602207   419 LHPLIRAVEVFGFHLATVDLRQSSDKHEEVVAELLSTARVHAdYSSLSEE 468

                 KRqEWLlaELkGKRPLlgsDLPktEEvkDvldafrvLAELPiDsFG....
                  ++  Ll  L   RPL    +      +  l  f  +A +  + FG++
gi|2602207   469 EKRSLLLGLLNDARPLSVHGVAYSAHAQGELAIFA-MAKVMRERFGheai 517

                 .aYiismataPsDvLAvELLqRECg.........vkqtLrvvPLFEkLAD
                 + Yiis + + sD L v LLq+E g  +++ + +v   L vvPLFE + D
gi|2602207   518 rHYIISHTETVSDLLEVLLLQKEVGlmrgtldaeVTADLIVVPLFETIED 567

                 LeAAPAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWqL
                 L+ A   +   ++ +++   + r  G q++m+GYsDs KD G +   W L
gi|2602207   568 LRNAAPIMREFYAlpgVAELVKRSGGEQDIMLGYSDSNKDGGIFTSNWEL 617

                 YkAqEEiiK....vAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDt
                 Y+A   ++   +  A ++ ++L +FHGRGGtvGRGGGP   AiL+qPP t
gi|2602207   618 YRAEIALVElfdvLAAQHKIQLRMFHGRGGTVGRGGGPSYQAILAQPPGT 667

                 inGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHG.mnPPvsPkPE
                 + G +R t qGEvi   +   ++  r L    AAtLE   ++P  s
gi|2602207   668 VRGQIRLTEQGEVIGSKYANPEIGRRNLETLVAATLEATlLQPTKSATKA 717

                 WRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaK
                 + +   e+       YR++v+  P F EYF + tP  E   +niG
gi|2602207   718 FLEAAAELSQNSMSAYRALVYETPGFTEYFFSSTPLREIAELNIG----- 762

                 RkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkL

gi|2602207   763 ------------------------------------------------XX 764

                 kEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLR
                      +WPFFR  l  ++mv AK D  +A+ y +L+    L+k     +
gi|2602207   765 XXXXXQWPFFRTLLSNMDMVMAKSDLALASRYSELVGDARLrKKIFTAIE 814

                 dkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKR
                 +++  t + L  i G k  L     L+  +R R +Yi  L  +q   ++R
gi|2602207   815 AEWHGTAQALATITGEKNRLANNAALQRSIRHRFPYIDPLHHLQVELVRR 864

                 iRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtm
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                   R+               AdE     +  +++                 +
  gi|2602207   865 YREGK-------------ADER---VQRGIHIS----------------I 882

                  KGiAAGmqntG<-*
                   GiAAG+ ntG
  gi|2602207   883 NGIAAGLRNTG    893

gi|7768140|emb|CAB90630.1|: domain 1 of 1, from 1 to 364: score 117.7, E = 3.9e-32
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768140     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768140     - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768140     - ------------------------------------------------ -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768140     - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768140     - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768140     - ------------------------------------------------ -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768140     - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768140     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768140     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768140     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768140     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|7768140     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYk qEE++Kv K+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768140     9 RLSAAWQLYKTQEELVKVGKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti GslRvtvqGEviE+sFGEE+LCFr+LqRFt AtLEHGm+ P+sP
  gi|7768140    59 PPDTILGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTTATLEHGMQLPISP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+emAvvAt EYRs+v++E RFvEYFRlAtPElEYG+mniGsR
  gi|7768140   109 KPEWRALMDEMAVVATNEYRSIVFQESRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P K kPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD Knl
  gi|7768140   159 PPKGKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIEKDKKNL 208
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                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvt+DL+EmvF KG PGiAaLyDkLLv+ +L PFG++
  gi|7768140   209 NLLREMYNEWPFFRVTIDLIEMVFTKGSPGIAALYDKLLVSTDLLPFGEQ 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Etk lLL++AGHkDlLEGDPYLKqrlRLR +YittLnv qAYtL
  gi|7768140   259 LRANYEETKRLLLQVAGHKDLLEGDPYLKQRLRLRYPYITTLNVWQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPsy+   +P  s E  + n k+a+eLvkLnpt+++aPGLEDtLiL
  gi|7768140   309 KRIRDPSYHLNAKPNQSNEIMNSN-KPAAELVKLNPTSEYAPGLEDTLIL 357

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|7768140   358 TMKGIAA------    364

gi|110681362|ref|YP_684369.1|: domain 1 of 1, from 4 to 871: score 117.6, E = 4.1e-32
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       ++D q     PG  s+  +L +       + L    +   ++L +a
  gi|1106813     4    ALDTQ---AGPGPASDAGDLYQCLRAAWSRVL----ERRAPQLLDAT 43

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    q            +D       Ga+      +D +       H+  + n
  gi|1106813    44 Q------------QD-------GAQWHRDHYGDHLQASTIWFHLQQVLNE 74

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                        +         k hG Fa E  A    D    +K+L   +
  gi|1106813    75 VQTLRSLRQEATNGKLHG-FA-EVVADCPEDQRAAMKRLLQDG------- 115

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                          sv   +tAHPt + R  ++  + Ri       +A     +D
  gi|1106813   116 -----RLSVGPTITAHPTEAKRVTVMEIHRRI-------YALLCCADDTA 153

                    ELDEA...LHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     L E +++L  Ei   + t E+R  +P    E+  G+ ++   +++ vP+
  gi|1106813   154 RLAEVstsLEMEIDLLWLTGELRMERPSLAAEVEWGLQFYDASLFDAVPR 203

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                       R  tA++     E    d   ++F sW+GGDRDG nP vt EvtR
  gi|1106813   204 LFQRYRTAVRSAFGAEV--DDHCCLRFHSWIGGDRDG-NPNVTAEVTRQA 250

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                       +R m  n Y+  +E ++  ls+      +   A+ l+   +
  gi|1106813   251 LARSREMVLNAYVRALEKIVPRLSI--STKIVPLPADHLQALERIVDQRS 298

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                       E  Kq  P+E +R    ++RD +   R                   y
  gi|1106813   299 TDAESCKQRNPNEVFRQAGFAIRDAVAAGR------------------Y 329

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLR.qvstFGLsLvKLDi
                     ++ +FL  L +   +L   G  ++A G L+  LR q  tFG     LDi
  gi|1106813   330 AHISDFLADLSVLENALNAIGATALA-GQLIRPLRwQATTFGFRGHTLDI 378

                    RqEseRqtDvlDAittHLe.....iGsYReWsEeKRqEWLlaELkGKRPL
                    Rq s+  t  l A+   ++ +++++Gs   WsE   +E     L    P
  gi|1106813   379 RQNSDVVTRTLQAVWAAVDaspepLGS--AWSERLQREVRQETL----PT 422

                    lgsDLPktEEvkDvldafrvLAELPi....DsFGaYiismataPsDvLAv
                    l   L   EE  + l  +  + ++  ++++D+ G++++sm+ +  D LAv
  gi|1106813   423 LDG-LELSEEASELLALLALVRDVHEgsdpDAIGPFVLSMTRSADDLLAV 471

                    ELLqRECgv...kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid.
                     LL R  g + ++ +LrvvPLFE + DL+AAP  +  + ++      + +
  gi|1106813   472 LLLARYVGFdahQPSLRVVPLFETIEDLQAAPVILRDVLAVPIAARSMKs 521

                    ..GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                    ++G+ e+m+GYsDs KD G l   W L +Aq  i +   + G   v FHG
  gi|1106813   522 sgGRIEIMLGYSDSNKDGGFLCSSWSLDRAQRAITRTLAQQGATPVFFHG 571

                    RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
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                    RGG v RGG Pt  Ai +qP  t+nG+lR t qGEv+   +   +
  gi|1106813   572 RGGSVSRGGAPTDRAIAAQPCGTLNGALRLTEQGEVVTAKYANADTAVTQ 621

                    LqRFtAAtLEHGmnPPv.sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFv
                    L   +   L H   PP +   PE  ++me +       Y  + ++ P F
  gi|1106813   622 LELLASSVLRHSASPPFeTVDPEGEDVMETLSSLSQTAYQNL-LRHPGFL 670

                    EYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLP
                    +YF  A P  E   + iGsRPa+R  +  +  LRAiPW+FaW q R  +
  gi|1106813   671 DYFNQASPVNELALLKIGSRPARRFGAASLSDLRAIPWVFAWSQNRHMIS 720

                    vWLGvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                     W G+G A +++   + +     L+ + ++ P F   lD +E
  gi|1106813   721 SWYGFGQAIQdFRRVRGSVGDAALERISRKLPLFQLCLDEIEKSLMLVRL 770

                    GiAaLyDkLL....vaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                     iA Ly +L++++ +aE++  FG+ +Rd+Y    d +  + G   l
  gi|1106813   771 DIAELYARLVsdraMAEDV--FGR-IRDEYNRSVDAIETLTG-APLGTRF 816

                    PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                    P    r+   +  +      q   LK +R                A +
  gi|1106813   817 PNAADRIHRHEDTLRAAHHAQVALLKDVR----------------ASDA- 849

                    kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        +  ++             L+  m  i AG+  tG
  gi|1106813   850 ----QTARIR------------LMQSMNCISAGLGWTG    871

gi|212275001|ref|NP_001130365.1|: domain 1 of 1, from 1 to 354: score 117.4, E = 4.8e-32
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2122750     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2122750     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2122750     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2122750     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2122750     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2122750     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2122750     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2122750     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2122750     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|2122750     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|2122750     - ---------------------------------------------- -
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                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG

  gi|2122750     - ------------------------------------------------ -

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                           +YkAqEE+iKvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2122750     1 -------MYKAQEELIKVAKHYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 43

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE sFGEE+LCFr+LqR+tAAtLEHGm+PP+sP
  gi|2122750    44 PPDTIHGSLRVTVQGEVIEHSFGEEHLCFRTLQRYTAATLEHGMHPPISP 93

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAvvAt EYRs+v++EPRFvEYFR+AtPE+EYG+mniGs
  gi|2122750    94 KPEWRALMDEMAVVATKEYRSIVFQEPRFVEYFRSATPETEYGRMNIGSH 143

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAA Kh ++KDi+n+
  gi|2122750   144 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAIKHIMQKDIRNI 193

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      LkEmY+eWPFFRvtlDLlEmvFAKGDPGiAa+yDkLLva++L+ FG++
  gi|2122750   194 HILKEMYNEWPFFRVTLDLLEMVFAKGDPGIAAVYDKLLVADDLQSFGEQ 243

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Etk+lLL++AGHkD+LEGDPYLKqrlRLR+sYittLnv+qAYtL
  gi|2122750   244 LRKNYEETKELLLQVAGHKDVLEGDPYLKQRLRLRESYITTLNVCQAYTL 293

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPs++v ++P+lsKE+ dE   +++eLv+Ln  +++aPGLEDtLiL
  gi|2122750   294 KRIRDPSFQVSPQPPLSKEFTDES--QPAELVQLNEQSEYAPGLEDTLIL 341

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|2122750   342 TMKGIAAGMQNTG    354

gi|18073892|emb|CAC84969.1|: domain 1 of 1, from 1 to 362: score 117.3, E = 5.1e-32
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807389     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807389     - ------------------------------------------------ -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807389     - ------------------------------------------------ -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807389     - ------------------------------------------------ -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807389     - ------------------------------------------------ -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807389     - ------------------------------------------------ -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807389     - ------------------------------------------------ -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807389     - ------------------------------------------------ -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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  gi|1807389     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807389     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807389     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807389     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYk qEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807389     9 RLSAAWQLYKTQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti GslRvtvqGEviE+sFGEE LCF++LqR+tAAtLEHGm+ P sP
  gi|1807389    59 PPDTIMGSLRVTVQGEVIEQSFGEELLCFKTLQRYTAATLEHGMKLPFSP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emAvvAt EYRs+v++EPRFvEYFR+AtPElEYG+mniGsR
  gi|1807389   109 KPEWRALMDEMAVVATNEYRSIVFQEPRFVEYFRSATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD Knl
  gi|1807389   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIQKDLKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY+eWPFFRvt+DL+EmvF KG PGiA+LyDkLLv+ eL PFG++
  gi|1807389   209 NMLREMYNEWPFFRVTIDLIEMVFTKGSPGIATLYDKLLVSPELLPFGEQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR+kY+E k lLLk+AGHk+lLEGDPYLKqrlRLR +YittLnv+qAYtL
  gi|1807389   259 LRAKYEEAKRLLLKVAGHKELLEGDPYLKQRLRLRYPYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPsy+ t +Phl  E  + +   a+eLvkLnpt+++aPGLEDtLiL
  gi|1807389   309 KRIRDPSYHPTAKPHLPTEIMNYE---AAELVKLNPTSEYAPGLEDTLIL 355

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807389   356 TMKGIAA------    362

gi|18073840|emb|CAC84937.1|: domain 1 of 1, from 1 to 364: score 115.8, E = 1.4e-31
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807384     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807384     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807384     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807384     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807384     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807384     - ------------------------------------------------ -
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                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807384     - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807384     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807384     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807384     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807384     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|1807384     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqE++iKvAK++GvKL++FHG GGtvGRGGGPtHLAiLs
  gi|1807384     9 RLSAAWQLYKAQEDLIKVAKQFGVKLTMFHGFGGTVGRGGGPTHLAILSS 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    Dti+GslRvtvqGEviE+sFGEE+LCF +LqRFtAAtLEHGm+PP sP
  gi|1807384    59 SLDTIHGSLRVTVQGEVIEQSFGEEHLCFITLQRFTAATLEHGMHPPDSP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++emAvvAtEEYRsvv+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|1807384   109 KPEWRALLDEMAVVATEEYRSVVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KDi+nl
  gi|1807384   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIIKKDIRNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+EmY+ WPFFR t+DL+EmvFAKGDP i aLyDkLLv+E+L+ FG++
  gi|1807384   209 HMLQEMYNAWPFFRGTIDLVEMVFAKGDPRITALYDKLLVSEDLWAFGEN 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR + +Etk+lLL+iAGHkDlLEGD YLKqrlRLRdsYittLnv+qA+tL
  gi|1807384   259 LRTNCEETKKLLLQIAGHKDLLEGDLYLKQRLRLRDSYITTLNVCQAFTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDPsy v  rPh+sKE   E sk a+eL+ Lnp++++aPGLEDtLiL
  gi|1807384   309 KRIRDPSYNVKFRPHISKEIM-ETSKSANELLILNPSSEYAPGLEDTLIL 357

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807384   358 TMKGIAA------    364

gi|18073890|emb|CAC84968.1|: domain 1 of 1, from 1 to 362: score 115.6, E = 1.7e-31
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807389     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807389     - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807389     - ------------------------------------------------ -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|1807389     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807389     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807389     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807389     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807389     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807389     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807389     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807389     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807389     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYk qEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807389     9 RLSAAWQLYKTQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti GslRvtvqGEviE+sFGEE LCF++LqR+tAAtLEHGm+ P sP
  gi|1807389    59 PPDTIMGSLRVTVQGEVIEQSFGEELLCFKTLQRYTAATLEHGMKLPFSP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emAvvAt EYRs+v++EPRFvEYFR+AtPElEYG+mniGsR
  gi|1807389   109 KPEWRALMDEMAVVATNEYRSIVFQEPRFVEYFRSATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD Knl
  gi|1807389   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIQKDLKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY+eWPFFRvt+ L+EmvF KG PGiA+LyDkLLv+ eL PFG++
  gi|1807389   209 NMLREMYNEWPFFRVTIGLIEMVFTKGSPGIATLYDKLLVSPELLPFGEQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR+kY+Etk lLLk+AGHk+lLEGDPYLKqrlRLR +YittLnv+qAYtL
  gi|1807389   259 LRAKYEETKRLLLKVAGHKELLEGDPYLKQRLRLRYPYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPsy+ t +Phl  E  + +   a+eLvkLnpt+++aPGLEDtLiL
  gi|1807389   309 KRIRDPSYHPTAKPHLPTEIMNYE---AAELVKLNPTSEYAPGLEDTLIL 355

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807389   356 TMKGIAA------    362

gi|186470717|ref|YP_001862035.1|: domain 1 of 1, from 11 to 946: score 114.8, E = 2.8e-31
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      ++D  L  L+    s         AL  D +   + +L  e L+++
  gi|1864707    11    AVDG-LHKLAAASAS-------LPALSADEYEHAVIELLSELLRDIA 49
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                qECY.ElsAeYEGKkDtkKLeELGakLtsLdPaDail..vAkailHmLnL
                    +E+     G    + + EL          a  +l+++ +a      L
gi|1864707    50 RARQpEVERTLRGEAAHESMSELMRERMDDRTARVVLrrMLQAQGMWFQL 99

                AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                  +AE      RRR      G + D         i E  +  v
gi|1864707   100 LSIAEQSTAMRRRREIEIE-GGY-DRLPDSFARVIAEVAQAGVPAS---- 143

                eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                 Ev + L    v  vltAHPt + R  +L  + Ri   L  L     t+
gi|1864707   144 -EVRDVLGHMKVRPVLTAHPTEAKRVTVLEIHRRIYRRLMELESPRWTPR 192

                DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                +++ L  AL  +i   +   E+R  +Pt   E+  G+ ++ Et+++ vP
gi|1864707   193 ERHTLVLALRNDIELLWMSGELRLEKPTVAQEVAWGLHFFGETLFEAVPL 242

                FLRRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRD
                   + + AL      ER  +d P+  +F sW+GGDRDG nP v   vtR
gi|1864707   243 LFDKLESALERHYPGER--FDMPrFFQFGSWIGGDRDG-NPFVDDSVTRA 289

                vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                     R+     Y   + +L   ls+    +E     +  +   ar  +
gi|1864707   290 TLHENRLACLKRYRLRLVELAQTLSI---TSEALPVPDSFHEALARALMA 336

                KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                           P E +R  L  +  +L      a           + +
gi|1864707   337 SGEPASIASRNPGELFRQYLTCILRRLDASLANA----SRPGDGAPVQGG 382

                ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                yt  +e    L +  + L       +A   +  l   v tF  s v+LD+
gi|1864707   383 YTSADELAADLLVIEQTLLATESGQLARMLIRPLRHEVETFRFSTVQLDL 432

                RqEseRqtDvlDAi..ttHLeiGsYReWsEeKRqEWLlaELkG.......
                Rq        l  + + t    G+         + WLl EL  +++++ +
gi|1864707   433 RQNTTVIEQALHGLwrATCGTSGAPPASDSPEWKAWLLGELAQpsdseae 482

                .KRPL..lgsDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDv
                + R  ++l++D  +t  +   + a+r    +   +FGa+i+sm+   sDv
gi|1864707   483 rERRFqsLPPDEAQTLQIFRTVRAMR--QQVDRNAFGAFILSMTHRASDV 530

                LAvELLqRECgv........kqtLrvvPLFEkLADLeAAPAavekLFsiD
                L v LL +E g+ ++  +++  tL+vvPL E + DL+ AP  +  L ++
gi|1864707   531 LGVYLLAKEAGLfsdaagteSCTLPVVPLLETIDDLRRAPDILRELLAVP 580

                WYinrid...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyG
                  +  i  ++G qe+m+GYsDs KD G ++  W L kAq  i +   + G
gi|1864707   581 MVRRSIRaqgGVQEIMIGYSDSNKDGGFFASNWELSKAQTKIRRLGDELG 630

                vKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFG
                v +  FHGRGG v RGG     Ai + P   +nG  Rvt qGEv+ f +
gi|1864707   631 VAIAFFHGRGGSVSRGGIAAGRAIAALPAGSVNGRFRVTEQGEVVSFKYA 680

                EEnLCFrsLqRFtAAtLEHGm....nPPvsPkPEWRkLmeemAvvAtEEY
                        +   +   LEH ++++++  + Pk E+ + me +       Y
gi|1864707   681 NRGTAQYHVELLASSVLEHTLkserEDALQPKGEFDEAMEALSGASRAAY 730

                RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWi
                   +   P    YF  A P  E   +n+GsRPa+R  +  ++ LRAiPW+
gi|1864707   731 AKFI-EQPGMLAYFQAASPLEELSMLNMGSRPARRFGAKSLQDLRAIPWV 779

                FaWtqtRFHLPvWLGvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlD
                FaW q R  L  W GvG A  ++   +  + l  L+ m++e   FR  +D
gi|1864707   780 FAWAQNRHALTGWYGVGSAIDgFLCVRQERGLDLLRRMFQESRLFRLVID 829

                LlEmvFAKGDPGiAaLyDkLLvaEeLk.PFGksLRdkYvEtkdlLLkiAG
                 +E   A+    iA  y +L+  E++++    ++ ++Y  t +++  + G
gi|1864707   830 EVEKTLAQVNLEIAREYANLVPDEQIRdTIFTQIEAEYRLTLKMVQAVTG 879

                HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                        P    rl  R + i  +   q   L+  R  +
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  gi|1864707   880 SPGPGTRFPKFSARLQRRLPAIDLISRQQIELLRLYRSAQ---------- 919

                    KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                    ter        L+L +  iA G   tG
  gi|1864707   920 -------------------TERQRRAYQVPLLLSINCIASGFGATG    946

gi|110639236|ref|YP_679445.1|: domain 1 of 1, from 1 to 922: score 112.8, E = 1.2e-30
                    *->siDAqLRlLvPGKvsedekLieYDAL..LlDkFLDiLqDLHGedLkE
                            + +L    v +d     Y  L+ Ll  F ++L +   e+L
  gi|1106392     1    -----MSALT---VTQDKLGKTYHNLefLLNCFKEVLIENGEEELAR 39

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                         Y    +  GK  +  + E             i v +    +Ln+A
  gi|1106392    40 -----YIPWINKKGKASPDTITE-----------KHIQVYSIAFQLLNMA 73

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                         v+l  RR+ +  k       +           l  L  k   +Pe
  gi|1106392    74 EENGAVKL--RRKHESEK-------SLSSVNGLWGKSLLMLKQKK-ITPE 113

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                     + e L n  ++ vltAHPt + R  +L  +  +            t  +
  gi|1106392   114 QIAEELCNVRIEPVLTAHPTEAKRTIVLEHHRQLYLLFLRWEDSTYTELE 163

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                    K E+   +   +   +Rt Ei   +P    E    + Y+     + v
  gi|1106392   164 KSEIRREIKLTLDRLWRTGEIYLEKPDLSSERSNVLHYLTTVFPEVVSIL 213

                    LRRvDtALKniGinERlPY...dvPLikFssWmGGDRDGknPRvtPEvtR
                     RR   A   +G    l  + +  P i F  W+GGDRDG +P vt EvtR
  gi|1106392   214 DRRLGMAWEQMGFDPELIItytKLPKISFGNWVGGDRDG-HPLVTSEVTR 262

                    DvCLLaRmmAanlYisqvEDLmFElsmWRCndE....LRvRAEElyrtaa
                    +   L R+ A  l    +E L   ls      E+ ++L  R  El
  gi|1106392   263 ETLELFRLNAFILMHRHLEKLEKNLSFTCLFKEtikpLQKRINELVEETG 312

                    rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                     +      +E  K     E +R  +     KL     +       G+
  gi|1106392   313 TQ----ELLE--KESNNREIFRFYIELLIMKLPLEENKG-----DGLRLN 351

                    sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                         y +  + +E L +   +L   G ++iA   + D++R v tFG  L
  gi|1106392   352 EKTYSYNESQKLIEDLVILRDALLAFGARAIAYNDVRDMVRLVQTFGFHL 401

                    vKLDiRqEseRqtDvlDAittHLeiGsYR..eWsEeKRqEWLlaELkGKR
                      LDiRq s  +   +  +     +   R     Ee R  ++  EL   R
  gi|1106392   402 AHLDIRQNSKFHDNAISQLMNAASMDGDRflTLNEEERCKFINKELLSLR 451

                    PLlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvL
                    P   +      E + v   +rv+AE+ ++    + G+ i+sm+ + sD L
  gi|1106392   452 PFSYPNTTLGPEAEAVTSCLRVVAEhvekYGTKALGSLIVSMTRSTSDLL 501

                    AvELLqREC........gvkqtLrvvPLFEkLADLeAAPAavekLF....
                     v LL RE +   ++++g+   L+vvPLFE + DL+  P  + k  +++
  gi|1106392   502 LVYLLAREAglliktekGIVCKLPVVPLFETIEDLQGSPHILSKFLehpi 551

                    ...siDWYinridGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiK
                    +++s+++ +     K++ q+vm+GYsDs KD G l+    L   q  ++
  gi|1106392   552 tknSLEYHRTCTGEKekvQQVMIGYSDSNKDGGILASQSNLSNTQLKLVD 601

                    vAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEv
                    v KkyG ++  FHG+GG + RG GPt   i   P  ti+G +R t qGE
  gi|1106392   602 VGKKYGARIRFFHGKGGSISRGAGPTQWFIKTLPHNTIQGDMRLTEQGET 651

                    iEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPEWR..kLmeemAvvA
                    i + +         L    A t    +      +   R +k ++ +A
  gi|1106392   652 ISQKYANKINAAFNLELLEAGTAGYTILHKYTKHKKNRfdKHLDYLAEKS 701

                    tEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRA
                     E Y  ++  +  F+ +F  AtP     +  iGsRPa+R     +  LRA
  gi|1106392   702 KEFYTNLIT-DKNFITFFGQATPIDVIEQSKIGSRPARRSGKRTLADLRA 750
```

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                    iPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRv
                    iPW+F+W q RF +  W GvG A     +     +  Lk m       R
  gi|1106392   751 IPWVFSWAQSRFNITSWYGVGNALETFYKEQPEEFEYLKKMASSDTIIRY 800

                    tlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLk
                        ++   A  D  i   y  L+  Ee++ +  + +  +Y  tk++L
  gi|1106392   801 IFTNVDTSLAATDEKIFRSYATLVEDEEVRAeILDMIVKEYNKTKKML-- 848

                    iAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrP
                          lL   P+      +R s+    nv+ A  L    D  y    +
  gi|1106392   849 -----ALLFDNPF-----EVRRSFHHYSNVLRAEALN---DLHYD---QI 882

                    hlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<
                    +l + +   n           p ++ a  +   L+Lt+  iA  + ntG
  gi|1106392   883 ELLRKWRKMN---------TQPQSEKANKILTELLLTVNAIAGALRNTG  922

                    -*

  gi|1106392     -    -

gi|224417773|ref|ZP_03655779.1|: domain 1 of 1, from 3 to 883: score 112.6, E = 1.3e-30
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                s++ + ie+   L+   L+ +     ++++E+
  gi|2244177     3    --------------SNQTQEIEFIFSLMGELLEEV----APEIREIF 31

                    qECYE.lsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                        E+  A+Y  Kk+         +L  L+  D   + ka+     L n
  gi|2244177    32 IALKEdKTANYIAKKE---------VLKKLESKDISKLIKAFTLYYLLLN 72

                    LAEEvelAyRRRikkkkhGDFaDEasAtt..EsDiEEtlKkLvlklnKsP
                    + +E +l     ++kk+ G   DE  A   +E Di   lKk+
  gi|2244177    73 IVDERHLL--SFNSKKHIGSMIDELKAQKydEEDIKSVLKKIKFYP---- 116

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                              v+tAHPt s RR  L     +   L   +
  gi|2244177   117 --------------VFTAHPTESLRRTFLESYHEMYDDLNLWFG-----S 147

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                          E L   +   +    +R  +     E+   + ++   + +
  gi|2244177   148 GDNAAKEHLKYRLNLLWHSHIVRSEKIEVLFELDNLLYFMESSILQSGTN 197

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     L  v  AL+        P     i+  sW+GGDRDG nP vt  v  +v
  gi|2244177   198 ILEEVQNALQE-------PLKKSPIRLGSWIGGDRDG-NPYVTNGVMLEV 239

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                               Y+ q++ L  Els+    +E      El      +
  gi|2244177   240 MKRQHQTIIEHYLKQIDKLSRELSI---AQEYANPTQELLESLEEE--KE 284

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                    +  E  K++  +EP+R  L  +R KL n R  a  L    + e s   +y
  gi|2244177   285 HLDEMAKKLFLQEPFRAKLTCMRQKLQN-RIMALNLPQSALYE-SKPYIY 332

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq.vstFGLsLvKLDi
                        eF+  +++   sL    Dk    G  L  L+  v   G  L++LD
  gi|2244177   333 ESPKEFIKDIDMMLESL----DKR--SGIYLKKLKNlVLLAGFHLMQLDF 376

                    RqEseRqtDvlDAittHLei..GsYReWsEeKRqEW....LlaELkGKRP
                    Rq  +     l  i   L+  +G     +     E  ++ L a L
  gi|2244177   377 RQHRDVFWRALAEIFSLLGYvqGDLLLLPKKEQEEIlnnaLTAPLLDLNA 426

                    LlgsDLPktEEvkDvldafrvLAELPiD.sFGaYiismataPsDvLAvEL
                    L+g       E+      fr   +  +D+   + iism+    D L v
  gi|2244177   427 LYGKLSKESQELLMAFMNFRWAKDRISDnIIDSCIISMCQGANDLLCVLW 476

                    LqRECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG
                      +  g+ ++++k  + + PLFE + DLe AP  +  L +   Y   ++
  gi|2244177   477 FAKQSGLwrkgkKTRIGIAPLFETIGDLENAPVILRELCANPHYAEYLQS 526

                    ...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHG
                     ++ qe+m+GYsDs KD G +   + L kA   +i    +  +K  lFHG
```

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  gi|2244177   527 cknNQEIMIGYSDSSKDGGIFTSNYSLRKAINNLIVLEEELRIKFRLFHG 576

                   RGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                   RGG v RGGG    A+Ls P   + G l+ t qGEvi   +   +    s
  gi|2244177   577 RGGSVSRGGGALEDALLSAPDNSVAGFLKTTEQGEVISEKYLNPKKAEFS 626

                   LqRFtAAtL......EHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvK
                        A  L+++  +  G n  v  + ++  +m+++       YR +v+
  gi|2244177   627 FASALANLLkksvydKYGTNKQVCNR-DFESIMQKISEESFKTYRNLVYE 675

                   EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqt
                      F+EYF++AtP     ++niGsRP+KRk    +e LRAiPW+FaWtq
  gi|2244177   676 TEGFIEYFKSATPIEFIQQLNIGSRPSKRKNTQNVEDLRAIPWVFAWTQN 725

                   RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
                   R  +P W G+G     A  +  K +  L+  Yke  FF+ t+D +   F
  gi|2244177   726 RAIIPAWYGLGSGLELASARFDKEI--LRNCYKEDLFFKTTIDNISQAFL 773

                   KGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                   K D  iA  y + +  ++L+k   ++++ +Y  t ++LL + G   lLE
  gi|2244177   774 KVDLEIAKHYNEFVENDDLrKEIWQKIKSEYHLTLKWLLYVRGEETLLET 823

                   DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                      +++ + LR s++t Ln fq Y +   +   y +  +  ++K
  gi|2244177   824 QKHIQKSILLRKSFLTSLNFFQLYLMEQYKNATY-IEQKQRIAKQ----- 867

                   skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                          +i t+ GiA G+ ntG
  gi|2244177   868 ----------------------IITTIVGIAQGIRNTG    883

gi|7768115|emb|CAB90617.1|: domain 1 of 1, from 1 to 363: score 112.1, E = 1.8e-30
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768115     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768115     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768115     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768115     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768115     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768115     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768115     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768115     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768115     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768115     - ---------------------------------------------- -
```

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                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768115     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768115     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYk qEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768115     9 RLSAAWQLYKTQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti GslRvtvqGEviE+sFGEEnLCFr+LqR+t AtLEHGm+ P sP
  gi|7768115    59 PPDTILGSLRVTVQGEVIEQSFGEENLCFRTLQRYTTATLEHGMQLPFSP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+emAvvAt EYRs+v++E RFvEYFRlAtPElEYG+mniGsR
  gi|7768115   109 KPEWRALMDEMAVVATNEYRSIVFQESRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD Knl
  gi|7768115   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIEKDKKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+EmY+eWPFFRvt+DL+EmvF KG  GiAaLyDkLLv+ +L PFG++
  gi|7768115   209 NILQEMYNEWPFFRVTIDLIEMVFTKGSTGIAALYDKLLVSADLLPFGEQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y+Etk lLL++AGHkDlLEGDPYLKqrlRLR +YittLnv q YtL
  gi|7768115   259 LRANYEETKRLLLQVAGHKDLLEGDPYLKQRLRLRYPYITTLNV-QVYTL 307

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDP+y+ t +P  s E  + n k+a+eLvkLnpt++++PGLEDtLiL
  gi|7768115   308 KRIRDPNYHLTAKPNGSNEIRNSN-KPAAELVKLNPTSEYPPGLEDTLIL 356

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|7768115   357 TMKGIAA------    363

gi|7768138|emb|CAB90629.1|: domain 1 of 1, from 1 to 364: score 111.1, E = 3.8e-30
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768138     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768138     - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768138     - ------------------------------------------------ -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768138     - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768138     - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768138     - ------------------------------------------------ -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768138     - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
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  gi|7768138     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768138     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768138     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768138     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768138     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYk qEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768138     9 RLSAAWQLYKTQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti GslRvtvqGEviE+sFGEE+LCFr+LqRFt AtLEHGm+ P+sP
  gi|7768138    59 PPDTILGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTTATLEHGMQLPISP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emAvvAt EYRs+v++E RFvEYFRlAtPElEYG+mniGsR
  gi|7768138   109 KPEWRALMDEMAVVATNEYRSIVFQESRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD Knl
  gi|7768138   159 PPKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIEKDKKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+EmY+eWPFF+vt+DL+Em F KG PGiAaLyDkL+ + +L PFG++
  gi|7768138   209 NLLREMYNEWPFFKVTIDLIEMGFTKGSPGIAALYDKLVGSTDLLPFGEQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Etk lLL++AGHkDlLEGDPYLKqrlRLR +YittLnv qAYtL
  gi|7768138   259 LRANYEETKRLLLQVAGHKDLLEGDPYLKQRLRLRYPYITTLNVWQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPsy+   +P  s E  + n k+a+eLvkLnpt+++aPGLEDtLiL
  gi|7768138   309 KRIRDPSYHLNAKPNQSNEIMNSN-KPAAELVKLNPTSEYAPGLEDTLIL 357

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|7768138   358 TMKGIAA------    364

gi|156742915|ref|YP_001433044.1|: domain 1 of 1, from 7 to 910: score 110.3, E = 6.4e-30
                   *->siDAqLRlLvPGKvsedekLieYDA.LLlDkFLDiLqDLHGedLkEa
                       i Aq R             ie D + LlD+F + L      d++
  gi|1567429     7    DIPAQAR-------------IERDLrWLLDRFYEALDAAGAADIHAL 40

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                          s        + +L E        +P       +a+     L n
  gi|1567429    41 LPWTGNPSC-------PVRLPE-------RAP-------QAYAIAFQLLN 69

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   L EE   A  RR           ++ A         l +L   +  s +
  gi|1567429    70 LVEENAEAQTRRSAETI------DGPAALRGLWGQILVQLRDAG-LSAAQ 112

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   +  AL    v+LvltAHPt + R  +L     +   L +   +  t+ ++
  gi|1567429   113 IAAALPRIQVELVLTAHPTEAKRATVLAHYRELYLQLVKAENQMWTPLER 162

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   + + E +   +   +Rt +i   +P    E+R  + Y+     +
  gi|1567429   163 QGIAEDVRAILERLWRTGDIFLKRPDVSSELRNVIHYLRNVFPEALAYHD 212
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                    RRvDtALKniGinERl...PYdvPLikFssWmGGDRDGknPRvtPEvtRD
                     R       iG    l ++P   PLi F  W+GGDRDG +P vt +vtR
  gi|1567429   213 QRLRQIWEAIGNDPALlddPDSLPLITFGTWVGGDRDG-HPLVTADVTRM 261

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                      +  R  A  l  +q+  L+  ls+    + L     +    a  +
  gi|1567429   262 ALMELRSHALELLRDQLTTLVRRLSL----SNLLQTPPDFLTSALHH--- 304

                    KyYiEFWKqvPPtEPYRviLGdvRDKLY..ntRERaRHLLAtGiseisEe
                                  Y  +LGd   +  ++n  E  R ++   ++ ++E
  gi|1567429   305 --------------YADLLGDAGQQALdrNPHEPWRQMVNLMLARLPET 339

                    A......vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFG
                    A+ + ++ yt+  e +  L L   sL   G   +A   +  l+R v  FG
  gi|1567429   340 AgvpapgHYTRAAELIADLRLLDESLVAVGATRLARSDVRPLIRSVRVFG 389

                    LsLvKLDiRqEseRqtDvlDAittHLei.Gs.YReWsEeKRqEWLlaELk
                      L  LDiRq s  +   l  + t  +i+Gs+Y +W E +R+  + aEL+
  gi|1567429   390 FHLAVLDIRQNSAFHDRALAQLLTAAGIdGSdYPSWDEARRMALIEAELE 439

                    GKRPLlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPs
                      RP     +P   E + vl  +rvL E+ ++   D  Ga i+sm+   s
  gi|1567429   440 SPRPFTRMGMPVGPEAEAVLSCYRVLVEhihsYGADGLGALIVSMTRNLS 489

                    DvLAvELLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLF.
                    D L v L  RE g+  ++++++  +L++vPLFE + DLe  P  +
  gi|1567429   490 DLLVVFLFARETGLLVstpegpvcPLPIVPLFETIDDLERSPLVLRDYLa 539

                    ......siDWYinri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEE
                    ++  ++s++W +   + ++  q+vm+GYsDs KD G  +  W L kAq
  gi|1567429   540 hpivqrSLEWQRQTRgapERVQQVMIGYSDSNKDGGIGASLWALQKAQQA 589

                    iiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvq
                    ++   +  Gv++  FHGRGGt+ RG GPt   i + P + + G lR+t q
  gi|1567429   590 LAAEGRMAGVRIRFFHGRGGTMSRGAGPTGRFIRALPVEALAGDLRMTEQ 639

                    GEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPEWRkL.meemAv
                    GE i + +              A      +  P  P+P    + ++ +A
  gi|1567429   640 GETISQKYANRISAVYNFELLLAGVTGSTLR-PYTPRPQHLTMaLDLLAR 688

                    vAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesL
                         YR++v  E RF  +FR AtP        iGsRPa+R  +  ++ L
  gi|1567429   689 HSQRAYRALVEHE-RFLPFFREATPIDAIEASRIGSRPARRTGAQSLTDL 737

                    RAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFF
                    RAiPW+F+W q RF L  W G+G         +   +  L    +eW
  gi|1567429   738 RAIPWVFSWNQARFYLSGWYGIGSGLAMVQAEEPALFDTLCAEMREWAPL 787

                    RvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlL
                       l          D  i   y +L+     +    + + +++  t+ +L
  gi|1567429   788 HYLLGNAATSVMNADEHIMRAYAELVHDPVTRTvILDTILEEFARTRAML 837

                    LkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtl
                     ++ G   l E  PY+  +l LR + +  L   q   L+  R
  gi|1567429   838 ERVYGGS-LEEKRPYIARQLELRRAGLYSLHREQITSLRSWR-------- 878

                    rPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqnt
                           A  n  + ++  +L            L+L +  iAAG+  t
  gi|1567429   879 --------AVRNLDPEAGEAQLR----------LLLLLINAIAAGLRAT 909

                    G<-*
                    G
  gi|1567429   910 G    910

gi|18073850|emb|CAC84942.1|: domain 1 of 1, from 1 to 364: score 109.6, E = 1.1e-29
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807385     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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gi|1807385     - ------------------------------------------------ -

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1807385     - ------------------------------------------------ -

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1807385     - ------------------------------------------------ -

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1807385     - ------------------------------------------------ -

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1807385     - ------------------------------------------------ -

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1807385     - ------------------------------------------------ -

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1807385     - ------------------------------------------------ -

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1807385     - ------------------------------------------------ -

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|1807385     - ------------------------------------------------ -

                 EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|1807385     - ------------------------------------------------ -

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                       sDsGKDAG
gi|1807385     1 ------------------------------------------SDSGKDAG 8

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 RlsAAWqLYk qEE+ Kv Kk+GvKL++FHGRGGtvGRGGGPtHLAiL+q
gi|1807385     9 RLSAAWQLYKVQEELLKVSKKFGVKLTMFHGRGGTVGRGGGPTHLAILAQ 58

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                 P +ti GslRvt+qGEviE+sFGE +LCFr+LqR+tAAtLEHGmnPP sP
gi|1807385    59 PAETIGGSLRVTIQGEVIEQSFGEQHLCFRTLQRYTAATLEHGMNPPKSP 108

                 kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                 kPEWR L+++mAvvAtEEYRs+v+KEPRFvEYFRlAtPE+EYG+mniGsR
gi|1807385   109 KPEWRALLDQMAVVATEEYRSIVFKEPRFVEYFRLATPETEYGRMNIGSR 158

                 PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                 P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvG A Kh ++KDi+n
gi|1807385   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGVGGALKHVLEKDIRNH 208

                 qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  +L++mY+++PFFRvt+DLlEmvFAKGDP iAaLyDkLLv+EeL+ FG++
gi|1807385   209 NMLRDMYNNFPFFRVTIDLLEMVFAKGDPEIAALYDKLLVSEELQSFGER 258

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                 LR++Y++tk  LL++AGHkDlLEGDPYLKqrlRLRd+YittLnv+qAYtL
gi|1807385   259 LRANYEDTKRRLLEVAGHKDLLEGDPYLKQRLRLRDPYITTLNVCQAYTL 308

                 KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                 KRiRDP++kvt rPhlsKE  d   k a+eLvkLnpt+++aPGL DtLiL
gi|1807385   309 KRIRDPDFKVTERPHLSKEIMDAH-KAAAELVKLNPTSEYAPGLGDTLIL 357

                 tmKGiAAGmqntG<-*
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                  tmKGiAA
  gi|1807385   358 TMKGIAA------    364

gi|32266702|ref|NP_860734.1|: domain 1 of 1, from 12 to 899: score 109.2, E = 1.4e-29
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         +  lL P +v            + D  + +Lq +  e+Lk a
  gi|3226670    12    KKSPKSTLLQPIQVE----------FVSDTIIHLLQSVD-EELKNAF 47

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                           +    +D+  L  + a + + d +  i+ A ++ Hm  L n+
  gi|3226670    48 LNIKQSLQN----HDSTMLKRILADISAQDKTLFIIKAFTLYHM--LLNI 91

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   EE +l        +                  tlK L   +    ++
  gi|3226670    92 IEELNLSNNAMLNHLP-----------------KTLKELNQEG-YDKNDT 123

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   e L+      v+tAHPt s RR  L  +  +   +  ++A     + K
  gi|3226670   124 LEILQHLRFYPVFTAHPTESRRRTFLEAHHQMSENIKNIFAHN-DANAKS 172

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   L   LH      + t  +R  +     E+   +  i   + k   + L
  gi|3226670   173 QLLYRLH----LLWHTHLVRSEKMEILFELDNLLYIIESSILKSATQVLG 218

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   +   L       +     P+i   sW+GGDRDG nP v  Ev      +
  gi|3226670   219 DIKSTL------GKALESSPII-LGSWIGGDRDG-NPYVSNEVMTKTMKI 260

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                  a      +Yi   E L+ Elsm     +       l +  + d      +
  gi|3226670   261 AHKAIIEIYIRTSEKLIRELSM---SMDFIQPSKRLIQSLQND--SSELL 305

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                      ++   EP+R  L  ++ KL n       L+A    + s +  y +
  gi|3226670   306 NNEAKLFAKEPFRAKLYLIKKKLQN------RLIAINTTD-SIDFTYKDS 348

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   e LE +++   sL    D + A G L+++   v   G  L +LD R
  gi|3226670   349 NELLEDIDMMIESL----DDISARG-LVEFRHLVLLGGFHLLRLDFREHR 393

                  eRqtDvlDAittHLeiG..sYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                  +     +  i   ++  ++ +++  E+K+ E L   L+ K+  l   + +
  gi|3226670   394 DIILSTISEIFCLIGFCdsDFKDLNENKKIEILNYALSAKKYDLNTIIEQ 443

                  .tEEvkDvldafrvLA....ELPiDsFGaYiismataPsDvLAvELLqRE
                    E  k  ++af  +   ++ + +      ++iism+t  sD L v    +
  gi|3226670   444 lSESSKRLVGAFLRIQwakkHISKHILQSFIISMSTQASDLLCVLWFAKQ 493

                  Cgv............kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                   g+ ++++++++++k ++ + PLFE + DL+ A   ++ L++   Y
  gi|3226670   494 SGLwkpgkkkegkkgKASVSITPLFETIDDLQRAQSIIQTLYANTHYQQY 543

                  i...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                  + +++  qe+mvGYsDs KD G +   + LY A   + K   +  +++
  gi|3226670   544 LfdhNSTQEIMVGYSDSSKDGGIFTSNYNLYCAISNLTKLQTQLDIRISF 593

                  FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                  FHGRGG v RGGG    A+L   P  ++  l+ t qGE+i   +   ++
  gi|3226670   594 FHGRGGSVSRGGGSLEEALLCSAPQSVHSFLKTTEQGEMISAKYLNSHIA 643

                  FrsLqRFtAAtLEHGmnPPvsPk.....PEWRkLmeemAvvAtEEYRsvv
                   +       A L  G+       + +++P    L+e++       YR++v
  gi|3226670   644 TKNFSSTLSALLKKGVYDSYGTEkyknnPQTMALLENVSNASCATYRALV 693

                  vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWt
                  +    F EYF+ AtP      +n+GsRP+KRk    ie LRAiPW+FaWt
  gi|3226670   694 YENKGFLEYFKNATPIKFIQNLNLGSRPSKRKDTQKIEDLRAIPWVFAWT 743

                  qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                  q R  +  W G+G      +dK      +L++ Y++  FF+ t+D +
  gi|3226670   744 QNRAIISAWYGLGSGLA-NVDKN-----QLRDCYEQSLFFKTTIDNISQA 787
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                  FAKGDPGiAaLyDkLL....vaEeLkPFGksLRdkYvEtkdlLLkiAGHk
                    K D  iA+Ly + +++++v E+++   + +  +Y  t ++LL++ G
  gi|3226670   788 LLKVDLDIASLYNQFVkdkkVREDIW---EHIYTQYHLTMEYLLHLRGES 834

                  DlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKE
                   lL+ +  ++  + LR +Y+  Ln  q                 +l K
  gi|3226670   835 VLLDSEGAIRESILLRKPYLSVLNLTQI-----------------ELIKK 867

                  yAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                  y  E  k + +  +L           + +  t+ GiA G+ ntG
  gi|3226670   868 Y--ESCKYPKGQERLL----------EQIHATIVGIAQGIRNTG    899

gi|18073848|emb|CAC84941.1|: domain 1 of 1, from 1 to 364: score 108.5, E = 2.3e-29
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807384     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807384     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807384     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807384     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807384     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807384     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807384     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807384     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807384     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807384     - ---------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807384     - ---------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|1807384     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWq+Yk qEE+ Kv Kk+GvKL++FHGRGGtvGRGGGPtHLAiL+q
  gi|1807384     9 RLSAAWQMYKVQEELLKVSKKFGVKLTMFHGRGGTVGRGGGPTHLAILAQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  P +ti GslRvt+qGEviE+sFGE +LCFr+LqR+tAAtLEHGmnPP sP
  gi|1807384    59 PAETIGGSLRVTIQGEVIEQSFGEQHLCFRTLQRYTAATLEHGMNPPKSP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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                    kPEWR L+ +mAvvAtEEYRs+v+KEPRFvEYFRlAtPE+EYG+mniGsR
  gi|1807384   109 KPEWRALLGQMAVVATEEYRSIVFKEPRFVEYFRLATPETEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvG A Kh ++KDi+n
  gi|1807384   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGVGGALKHVLEKDIRNH 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L++mY+++PFFRvt+DLlEmvFAKGDP iAaLyDkLLv+EeL+ FG++
  gi|1807384   209 NMLRDMYNNFPFFRVTIDLLEMVFAKGDPEIAALYDKLLVSEELQSFGER 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y++tk  LL++AGHkDlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|1807384   259 LRANYEDTKRRLLEVAGHKDLLEGDPYLKQRLRLRDPYITTLNVCQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP++kvt rPhlsKE  d   k a+eLvkLnpt+++aPGLEDtLiL
  gi|1807384   309 KRIRDPDFKVTERPHLSKEIMDAH-KAAAELVKLNPTSEYAPGLEDTLIL 357

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|1807384   358 TMKGIAA------    364

gi|7768136|emb|CAB90625.1|: domain 1 of 1, from 1 to 364: score 107.8, E = 3.6e-29
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768136     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768136     - ---------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768136     - ---------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768136     - ---------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768136     - ---------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768136     - ---------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768136     - ---------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768136     - ---------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768136     - ---------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768136     - ---------------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768136     - ---------------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768136     1 ------------------------------------------SDSGKDAG 8
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                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYk qEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768136      9 RLSAAWQLYKTQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti GslRvtvqGEviE+sFGEEnLCFr+LqRFt AtLEHGm+ P+sP
  gi|7768136     59 PPDTILGSLRVTVQGEVIEQSFGEENLCFRTLQRFTTATLEHGMQLPISP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAvvAt EYRs+v++E RFvEYFRlAtPElEYG+mniGsR
  gi|7768136    109 KPEWRALMDEMAVVATNEYRSIVFQEKRFVEYFRLATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh i+KD  nl
  gi|7768136    159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGVAFKHVIEKDKNNL 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+eWPFFRvt+DL+EmvF KG  GiAaLyDkLLv+ +L PFG++
  gi|7768136    209 NILREMYNEWPFFRVTIDLIEMVFTKGSTGIAALYDKLLVSTDLLPFGEQ 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Etk lLL++AGHkDlLEGDP LKqrlRLR +YittLnv qAYtL
  gi|7768136    259 LRANYEETKRLLLQVAGHKDLLEGDPSLKQRLRLRYPYITTLNVWQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KR+RDPsy+ t +P ls    +   k+a+eLvkLnpt+++aPGLEDtLiL
  gi|7768136    309 KRMRDPSYHPTAKPNLSNKIMNSS-KPAAELVKLNPTSEYAPGLEDTLIL 357

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|7768136    358 TMKGIAA------    364

gi|164415616|gb|ABY53227.1|: domain 1 of 1, from 2 to 558: score 106.9, E = 6.7e-29
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                L  YD LL Dk L i
  gi|1644156      2    -----------------KTLAYYDELLQDKPLTI------------- 18

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1644156      - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1644156      - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1644156      - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1644156      - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                                                  RD
  gi|1644156     19 ------------------------------SRDE---------------- 22

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1644156      - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                                                             + t+
  gi|1644156     23 ---------------------------------------------ILTDD 27

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+  EPL  CY+sL +CG ++iA G LLD LR +  FGL L +LDiRqEs
  gi|1644156     28 EQLWEPLYDCYQSLHQCGMRIIANGGLLDCLRRIRCFGLGLSRLDIRQES 77

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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                     R+   +  it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|1644156    78 TRHEMAIAEITRYIGLGDYSQWTEDDKQAFLVRELSSRRPLVPTNWTPSP 127

                     EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                     E k++ld+ +v+AE P     aY+isma   sDvLAv LL +E g k t+
  gi|1644156   128 ETKEILDTCKVVAEQPEGVISAYVISMARGASDVLAVHLLLKEAGCKTTI 177

                     rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                     +v PLFE L DL+     +  LF i WY+  i+ Kq vm+GYsDs KDAG
  gi|1644156   178 PVSPLFETLDDLDHCEKVMTDLFNIGWYRGVINNKQMVMIGYSDSAKDAG 227

                     RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                      l+A W  Y+AqE ++    ky v L+lFHGRGGt+GRGG P H A+Lsq
  gi|1644156   228 MLAASWAQYRAQEALVNLSEKYNVELTLFHGRGGTIGRGGAPAHAALLSQ 277

                     PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                     PP  ++  lRvt qGE+i f  G   +   sL  ++ A LE  + PP  P
  gi|1644156   278 PPRSLKNGLRVTEQGEMIRFKLGLPAVAVSSLDLYASAILEANLCPPPEP 327

                     kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                     k EWR++m++   +  + YR +v  EP Fv YFR AtPE E  k+ +GsR
  gi|1644156   328 KQEWRDVMNKGSEISCDIYRGIVRGEPDFVPYFRAATPEQELSKLPLGSR 377

                     PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                     PaKR P GG+esLRAiPWiFaW q R  LP WLG G A +  i++    l
  gi|1644156   378 PAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGQALQQLIEQGNEAL 427

                     qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                       LkEm  eWP F   + +lEmvF K D  +A  yD+ Lv   L+  G+
  gi|1644156   428 --LKEMCTEWPLFSTRIGMLEMVFSKADLWLAEHYDQRLVPQHLHRLGNT 475

                     LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                     LR++     + +L +A    l+   P++   + LR+ Y   Ln +q   L
  gi|1644156   476 LRNQLAADINSVLSLAHEGQLMADLPWVAESIALRNVYTDPLNLLQVELL 525

                     KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                      R+R                 +E              e+  P LE  L++
  gi|1644156   526 HRLR-----------------AEG-------------ENPNPALEQALMI 545

                     tmKGiAAGmqntG<-*
                     t+ GiAAGm ntG
  gi|1644156   546 TITGIAAGMRNTG    558

gi|18076755|emb|CAC84274.1|: domain 1 of 1, from 1 to 362: score 106.4, E = 9.4e-29
                     *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807675     -    ---------------------------------------------- -

                     qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807675     - ---------------------------------------------- -

                     AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807675     - ---------------------------------------------- -

                     FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807675     - ---------------------------------------------- -

                     ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807675     - ---------------------------------------------- -

                     RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807675     - ---------------------------------------------- -

                     aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807675     - ---------------------------------------------- -
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                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807675     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807675     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807675     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807675     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|1807675     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAW LYkAqE+++KvA ++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807675     9 RLSAAWALYKAQEDLVKVAFQFGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+Gs Rvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PP++P
  gi|1807675    59 PPDTIHGSFRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPIAP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+e+AvvAt EYRs+v++ PRFvEYFR+AtPElEYG+mniGsR
  gi|1807675   109 KPEWRALMDEIAVVATKEYRSIVFQNPRFVEYFRSATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++KD +nl
  gi|1807675   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHVMEKDPRNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+ mY+eWPFF  t+DL+EmvFAKGDPGiAaLyDkLLv+++L+  G +
  gi|1807675   209 HTLQQMYNEWPFFWGTIDLIEMVFAKGDPGIAALYDKLLVSDDLWAIGGQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++YvEtkdlLL++AGH DlLEG PYLKqrl+LRdsYittLnv+qAYtL
  gi|1807675   259 LRANYVETKDLLLQVAGHSDLLEGNPYLKQRLKLRDSYITTLNVCQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDP  +v lrPhlsKE    +   a+eLvkLnpt+++aPGLEDtLiL
  gi|1807675   309 KRIRDPHVHVNLRPHLSKESSTKP---AAELVKLNPTSEYAPGLEDTLIL 355

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807675   356 TMKGIAA------    362

gi|7768113|emb|CAB90624.1|: domain 1 of 1, from 1 to 364: score 102.9, E = 1.1e-27
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768113     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768113     - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768113     - ------------------------------------------------ -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768113     - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|7768113     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768113     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768113     - ------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768113     - ------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768113     - ------------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768113     - ------------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768113     - ------------------------------------------------- -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768113     1 -----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYk qEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768113     9 RLSAAWQLYKTQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti GslRvtvqGEviE+sFGEEnLCFr+LqRFt AtLEHGm+ P+sP
  gi|7768113    59 PPDTILGSLRVTVQGEVIEQSFGEENLCFRTLQRFTTATLEHGMQLPISP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emAvvAt EYRs+v++E RFvEYFRlAtPElEYG+mniGsR
  gi|7768113   109 KPEWRALMDEMAVVATNEYRSIVFQEKRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh i+KD  nl
  gi|7768113   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGVAFKHVIEKDKNNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+EmY+eWPFFRvt+DL+Em F KG  GiAaLyDkLLv+ +L PFG++
  gi|7768113   209 NILREMYNEWPFFRVTIDLIEMGFTKGSTGIAALYDKLLVSTDLLPFGEQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Etk lLL++AGHkDlLEGDP LKqrlRLR +YittLnv qAYtL
  gi|7768113   259 LRANYEETKRLLLQVAGHKDLLEGDPSLKQRLRLRYPYITTLNVWQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KR+RDPsy+ t +P ls    +   k+a+eLvkLnpt+++aPGLEDtLiL
  gi|7768113   309 KRMRDPSYHPTAKPNLSNKIMNSS-KPAAELVKLNPTSEYAPGLEDTLIL 357

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|7768113   358 TMKGIAA------    364

gi|219847014|ref|YP_002461447.1|: domain 1 of 1, from 1 to 910: score 102.8, E = 1.2e-27
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           +  L   K        +    Ll  F  +L D+   ++  a
  gi|2198470     1    -----MQPLDHAKAE------QDFHFLLTCFQRMLRDIGAISVAAAL 36

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       E                G+   +++  +   +A+a+     L n+
  gi|2198470    37 PWLHE-----------------GTDQSAVAVRE---LAQAFGIAFQLLNI 66
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                AEEvelAyRRRikkkkhGDFaDEasAttEs.DiEEtlKkLvlklnKsPeE
                AEE      RR+  +         s   Es+   + l kL   +  + +E
gi|2198470    67 AEENAAVQQRRMTDRD-------PSLPPESgRWRDALLKLQRAG-FTADE 108

                vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                +  AL    v+ vltAHPt + R  +L     +   L     +   + ++
gi|2198470   109 IAAALPEIRVEPVLTAHPTEAKRTTVLDHYRELYLLLVRRESQRWSPAEQ 158

                kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                 E++  +   +   +Rt  i  ++P    E+R  + Y+     +  P
gi|2198470   159 AEIETDIIALLERLWRTGNIFLSKPDVASEVRNVLHYLVNVFPDVLPVLD 208

                RRvDtALKniGinERlPYd.vPLikFssWmGGDRDGknPRvtPEvtRDvC
                     A +  G    l  ++ P + F sW+GGDRDG +P vt E+t
gi|2198470   209 NQLRYAWQMSGFDPTLLTErWPKLTFGSWVGGDRDG-HPLVTAEITAQTL 257

                LLaRmmAanlYisqvEDLmFElsmWRCndELRv.....RAEElyrtaard
                   R+ A  l    +   +  ls+    ++L v+++++ AE + r
gi|2198470   258 HELRLQALRLLRRRIRQAVRHLSI----SDLLVptppgLAEQIRRMTNAL 303

                kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                      +       P+EP+R  L      L   R       A     + E
gi|2198470   304 --GMRGVQAVAR-NPNEPWRQAL-----HLMLARLPIDDAPAEAARLVDE 345

                eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                   y + +e L  L    + L e G   +AD  +  l+  v tFG  L
gi|2198470   346 PGRYRNADELLHDLQEFAQYLREVGCGRLADAEVRPLMYLVQTFGFHLAT 395

                LDiRqEseRqtDvlDAi..ttHLeiGsYReWsEeKRqEWLlaELkGKRPL
                LDiRq s+ +   l  + +   L          e+R+  L  E+   RP
gi|2198470   396 LDIRQNSQFHDRALAQLlkVAALPTDDLLGGDPERRRALLEREIVSPRPF 445

                lgsDLPktEEvkDvldafrvL....AELPiDsFGaYiismataPsDvLAv
                  +D P   E + v++ +rvL ++ A       G+ iism+    DvL v
gi|2198470   446 AHPDTPLDPEAAAVVGCYRVLashiARYGTSGLGPLIISMTRDVTDVLVV 495

                ELLqRECgvkqt........LrvvPLFEkLADLeAAPAavekLFsiDWYi
                 LL RE g+  +++++   +L+vvPLFE + DLe  P  ++ +      +
gi|2198470   496 YLLAREAGLAYAtpeglvcrLPVVPLFETIEDLEHSPQILAEILDHPVTR 545

                nri.....dGK..qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKky
                  ++ ++++G   q+vm+GYsDs KD G l+  W L +Aq  +  v
gi|2198470   546 RSLraqsqNGElvQQVMIGYSDSNKDGGILASQWALQRAQRAMSEVGAAR 595

                GvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsF
                Gv++  FHGRGGt+ RG GPt   i   PP  +nG lR t qGEvi + +
gi|2198470   596 GVRIRFFHGRGGTISRGAGPTNRFIAMLPPGSLNGDLRLTEQGEVIAQKY 645

                GEEnLCFrsLqRFtAA....tLEHGmnPPvsPkPEWRkLmeemAvvAtEE
                         L    A ++++tL H  +PP+ P+P    +me++   A
gi|2198470   646 ANRLTAAYNLELLLAGttthTLLHRRHPPL-PHP-LEPVMERLVQQARAA 693

                YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPW
                YR ++ ++  F+ +FR AtP     +  iGsRPa+R     +  LRAiPW
gi|2198470   694 YRNLIERDG-FITFFRQATPIDVIEQSRIGSRPARRTGQATLADLRAIPW 742

                iFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlD
                +F+W q RF LP W GvG A     d D      L     +WPF    l
gi|2198470   743 VFSWNQSRFYLPGWYGVGSALHALRDTDPAVWEELCAAQWNWPFLSYLLA 792

                LlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtkdlLLkiAG
                 +            y  L+  E L++ F   + ++++ t   L  i G
gi|2198470   793 NVSTSLLTAHRPTMHAYASLVEDEVLrRDFLTLIDAEFERTVAALEAIFG 842

                HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                   l    P L   l  R+  +  L   q   L+  R            +
gi|2198470   843 -MPLDRRWPQLAETLARRQIGLAPLHQQQIELLRQWR-----------A 879

                KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                +  Ad++   a+e   +            L+L +  iAAG+  tG
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  gi|2198470   880 QRAADDP---AAETTLID------------LLLLVNAIAAGLRTTG    910

gi|254459897|ref|ZP_05073313.1|: domain 1 of 1, from 1 to 879: score 101.6, E = 2.7e-27
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          + ++    v    +  +Y   L D   D+L        k ++
  gi|2544598     1    -----MNVVRACMVD--CEGQDYAKSLRDLLWDLL-------FKTVM 33

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                      +++A     +D + L++  +++     a  i           L  +
  gi|2544598    34 RRAPDIAAFLASPRDIESLQD--SQISDFLQAANI--------WFQLKKI 73

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  A+E      RR+         D a+      ++ t+ +++ k      +
  gi|2544598    74 ADENTAVRDRRNTETM-----DGAEC-----VDGTFAQVMAKIAEHAPDQ 113

                  Fe.ALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  Fe+A+   sv   ltAHPt + R  +L  + Ri   L  L  + +t+ ++
  gi|2544598   114 FEsAVASLSVGPTLTAHPTEAKRITILEIHRRIYRHLVALETQRLTPRER 163

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                      E L  E+   +   E+R  +P   DE+  G+ ++ + +++  P+
  gi|2544598   164 ANRVEDLRGEVDLLWLSGELRLERPSLSDEIDWGLQFFRDSLFDATPQLF 213

                  RRvDtALKniGinERlPYd....vPLikFssWmGGDRDGknPRvtPEvtR
                     D  L  iG+    P ++++  P ikF sW+GGDRDG nP vt   t+
  gi|2544598   214 ---DQFL--IGLENTFPTQprslRPCIKFHSWIGGDRDG-NPNVTVAATK 257

                  DvCLLaRmmAanlYisqvEDLmFElsmWRCndEL.RvRAEElyr.taard
                        R  A    i+ +      +s+     EL+ +    l + t ++d
  gi|2544598   258 SAMARGRDTAITKHIDDLSRAARHISISCDIAELpDIHVQLLASiTTRSD 307

                  kvvKyYiEFWKqv..PPtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                         EF   +++ P E +R  + ++                  i+ +
  gi|2544598   308 -------EFDALIkrNPGEVFRQAISAI-----------------IARL 332

                  sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                       yt+ +e +  L     +L   G + +    +  +   v  FG
  gi|2544598   333 EGRPLYTHTDELVSDLHEIENALFAIGAQQLSNRYIRPVRWRVEVFGFRT 382

                  vKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPL
                    LDiRq s   tDvl  i    e     +Ws   R E  + +L
  gi|2544598   383 TSLDIRQNSTVTTDVLAEIWGPGETYGSIKWSQRLRYEIAVDDLPDIDVE 432

                  lgsDLPktEEvkDvldafrvLAELPi.DsFGaYiismataPsDvLAvELL
                    s+  +  E+   l+a+    E   +D+ G +i+sm+ +  D LAv LL
  gi|2544598   433 ALSE--QAQELLNLLEAIVDAREGNDpDAIGCFILSMTRSTDDLLAVYLL 480

                  qRECgv...kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid...G
                   R  g +++   L+vvPLFE + DL+ AP  +  L ++   +  + +++
  gi|2544598   481 ARYAGAtgdTLDLPVVPLFETIEDLRNAPRILSDLIAVPTARRSLKrqgS 530

                  KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                  + evm+GYsDs KD G +   W L +Aq  i +  +  G     FHGRGG
  gi|2544598   531 RIEVMLGYSDSNKDGGFICSTWELEQAQRKIKQTLQGLGFVPAFFHGRGG 580

                  tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                   v RGG Pt  Ai +qP  t+nG+lR t qGEv+   +       r L
  gi|2544598   581 SVSRGGAPTGRAIAAQPSGTVNGALRTTEQGEVVSTKYANCGTALRELEQ 630

                  FtAAtLEHGmnPPvsPk..PEWRkLmeemAvvAtEEYRsvvvKEPRFvEY
                   +   L H      +P+++PE+ + ++ +  +    Y ++ +  P Fv Y
  gi|2544598   631 LASSALLHTALSHNAPQtnPEYDNALQALSGMSQVAYDAL-LNSPGFVQY 679

                  FRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvW
                  F  A P  E   + iGsRPa+R  +  +  LRAiPW+FaW q R  L  W
  gi|2544598   680 FQEASPVEELAMLKIGSRPARRFGASSLSDLRAIPWVFAWSQNRHLLTGW 729

                  LGvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                   G+GAA  ++A  +     ++L +m+ +   F   +D +E    + D  i
  gi|2544598   730 YGFGAACTsFAKVRGELGWKMLCDMFATSTLFQLMVDEVEKSLFQADMQI 779
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                  AaLyDkLLv.aEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                  Aa y  L  ++         + ++Y      + ki G   l    P L
  gi|2544598   780 AAKYAALSTdTASGTAILGMIEAEYASSVAAIQKITGQPSLAARFPNLTE 829

                  rlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkade
                  r      Y+ t+  +q   L+ +R                  En
  gi|2544598   830 RFEGNRRYLETIHTIQIKQLRALR-----------------REN------ 856

                  LvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       + +  P     L+  m  i AG+  tG
  gi|2544598   857 -----QSAETGP-----LLQSMNCISAGLGWTG    879

gi|18073876|emb|CAC84395.1|: domain 1 of 1, from 1 to 365: score 100.8, E = 4.8e-27
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807387     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807387     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807387     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807387     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807387     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807387     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807387     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807387     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807387     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807387     - ---------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807387     - ---------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|1807387     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+i vAKk+GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807387     9 RLSAAWQLYKAQEELIEVAKKHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEHGm PP+ P
  gi|1807387    59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHGMIPPLTP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+emAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
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  gi|1807387   109 KPEWRALMDEMAVVATERYRSIVFREPRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh idKD Knl
  gi|1807387   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFKHVIDKDNKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+ mY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL P G++
  gi|1807387   209 LMLQQMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELLPLGEE 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR  Y +tk +LLki GH ++LEGDP+LKqrl+LR +YittLnv+qAYtL
  gi|1807387   259 LRTAYNDTKSYLLKITGHNEILEGDPFLKQRLKLRTAYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|1807387   309 KRIRDPSYQVPVRPPIAKEISESSVSSANQLVKLNPTSEYAPGLEDTLIL 358

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807387   359 TMKGIAA------    365

gi|10303403|emb|CAA65117.1|: domain 1 of 1, from 1 to 363: score 100.3, E = 6.7e-27
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1030340     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1030340     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1030340     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1030340     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1030340     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1030340     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1030340     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1030340     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1030340     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1030340     - ---------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1030340     - ---------------------------------------------- -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1030340     1 ----------------------------------------SDSGKDAG 8
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                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYk qE++iKvAKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1030340     9 RLSAAWQLYKGQEDLIKVAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|1030340    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR L++emAvvAtEEYRs+v++EPRFvEY RlAtPElEYG+mniGsR
  gi|1030340   109 KPEWRTLLDEMAVVATEEYRSIVFQEPRFVEYGRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh   KDiKnl
  gi|1030340   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGTAFKHVSPKDIKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+EmY+eWPFFRvt+DL+EmvFAKG PGiA+Ly kLLv+ eL+ FG++
  gi|1030340   209 RILQEMYNEWPFFRVTIDLVEMVFAKGNPGIASLYGKLLVSSELWSFGER 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++Y+EtkdlLL++AGHk  L  +      + LRdsYittLnv+qAYtL
  gi|1030340   259 LRANYQETKDLLLQVAGHKVFLK-ESLSEAEVGLRDSYITTLNVCQAYTL 307

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDP+++v +rPh+sKE  d   k+a+eLvkLnpt+++aPGLEDtLiL
  gi|1030340   308 KRIRDPNFHVKVRPHISKEISDAS-KPAAELVKLNPTSEYAPGLEDTLIL 356

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1030340   357 TMKGIAA------    363

gi|18073862|emb|CAC84948.1|: domain 1 of 1, from 1 to 365: score 100.1, E = 7.4e-27
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807386     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807386     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807386     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807386     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807386     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807386     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807386     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807386     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807386     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
```

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  gi|1807386     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807386     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807386     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+i vAKk+GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807386     9 RLSAAWQLYKAQEELIEVAKKHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEHGm PP+ P
  gi|1807386    59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHGMIPPLTP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|1807386   109 KPEWRALMDEMAVVATERYRSIVFREPRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh idKD Knl
  gi|1807386   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFKHVIDKDNKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+ mY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL P G++
  gi|1807386   209 LMLQQMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELLPLGEE 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR  Y +tk +LLki GH ++LEGDP+LKqrl+LR +YittLnv+qAYtL
  gi|1807386   259 LRTAYNDTKSYLLKITGHNEILEGDPFLKQRLKLRTAYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|1807386   309 KRIRDPSYQVPVRPPIAKEISEGSVSSANQLVKLNPTSEYAPGLEDTLIL 358

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807386   359 TMKGIAA------    365

gi|148657218|ref|YP_001277423.1|: domain 1 of 1, from 1 to 908: score 98.7, E = 2e-26
                   *->siDAqLRlLvPGKvsedekLieYDA.LLlDkFLDiLqDLHGedLkEa
                             +  G +   +  +e D + L+D+F ++L  +  e+++ +
  gi|1486572     1    --------MNTGDIP-TQARVERDLhWLMDRFCEVLDTVNAEEVRVF 38

                   vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                                   k  ++L  +L   +P       +a++    L n
  gi|1486572    39 L--------------PWKEHGDLPDQLPERAP-------QAYSIAFQLLN 67

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   L EE   A  RR           ++ A        t+ +L   +  s +
  gi|1486572    68 LVEENAEAQARRAAETI------DGPAALRGLWGQTFMQLRNAG-LSDAQ 110

                   vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                   +  AL    v+ vltAHPt   R  +L     +   L +   +  t+ ++
  gi|1486572   111 IAAALPRIRVEPVLTAHPTENKRATVLAHYRELYLQLVKAENQMWTPLER 160

                   kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                   k + + +   +   +Rt +i   +     E+   + Y+     +
  gi|1486572   161 KGIADDVRTILERLWRTGDIFLERLEVTAELQNVIHYLRNVFPEALAMHD 210

                   RRvDtALKniGinERl...PYdvPLikFssWmGGDRDGknPRvtPEvtRD
                    R       iG    l ++P   P i F  W+GGDRDG +P vt   tR
  gi|1486572   211 QRLRQIWEEIGNDPALlddPDSLPSITFGTWVGGDRDG-HPLVTAGETRN 259

                   vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                     L  R  A  l  +q+  +   ls+    + L    + l  t +r
  gi|1486572   260 ALLELRSNALALLREQLTAIARHLSL---SNLLQTPPDILVDTIQRY--A 304
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                    KyYiEFWKqv...PPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                        E  +q  ++ P EP+R ++  +  +L                  +
  gi|1486572   305 ALLGEAGQQAlnrNPYEPWRQMVNLILARLPEP------------VGAPG 342

                    eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                       yt   e +  L +   sL   G   +A   +  l+R v tFG  L
  gi|1486572   343 PGRYTSAAELIADLRILDESLVSVGAIRLARSDVRPLIRSVRTFGFHLAV 392

                    LDiRqEseRqtDvlDAittHLei..GsYReWsEeKRqEWLlaELkGKRPL
                    LDiRq s  +   l  + t  +i++G Y +WsE +R+  L aEL+  RP
  gi|1486572   393 LDIRQNSAFHDRALAQLLTAAGIdgGDYPSWSETQRMALLEAELQSPRPF 442

                    lgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataPsDvLAv
                      s +    E + vl  +rvL E+ +   iD  Ga i+sm+   sD L +
  gi|1486572   443 TRSGMSLGMEAEAVLSCYRVLVEhvhmYGIDGLGALIVSMTRQLSDLLVI 492

                    ELLqRECgvkq........tLrvvPLFEkLADLeAAPAavekLF......
                     L  RE g+  ++++++  +L++vPLFE + DLe  P  +     ++  +
  gi|1486572   493 FLFARETGLLVstpegpicPLPIVPLFETIDDLERSPLILRDYLahpivq 542

                    .siDWYinr...idGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvA
                    +s++W + r++  +  q+vm+GYsDs KD G  +  W L +Aq  ++
  gi|1486572   543 rSLEWQRRRhgaAERVQQVMIGYSDSNKDGGIGASFWALKRAQQALAAEG 592

                    KkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviE
                    +  Gv++  FHGRGGt  RG GPt   i + P + + G lR+t qGE i
  gi|1486572   593 RAAGVRIRFFHGRGGTLSRGAGPTGRFIRALPVEALAGDLRMTEQGETIS 642

                    fsFGEEnLCFrsLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEY
                    + +              A      + P  +        +e +A      Y
  gi|1486572   643 QKYANRISAIYNFELLLAGVTGATLRPAPARPDHLAMALELIARESQKAY 692

                    RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWi
                    R ++  E RF+ +FR AtP        iGsRPa+R     +  LRAiPW+
  gi|1486572   693 RVLIEHE-RFIPFFREATPIDAIEASRIGSRPARRTGTRSLADLRAIPWV 741

                    FaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDL
                    F+W q RF L  W G+G       + +   +  L    +eW      l
  gi|1486572   742 FSWNQARFYLSGWYGIGSGLAVVQQEEPALFAELCARMREWAPVHYLLGN 791

                    lEmvFAKGDPGiAaLyDkLLv.aEeLkPFGksLRdkYvEtkdlLLkiAGH
                    +       D  i   y +L+ +a       +++ d++  t+ lL ++ G
  gi|1486572   792 VATSVMNADETIMCAYAELVNdATTRTVILQKILDEFARTRALLEQVYGG 841

                    kDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsK
                      l E  PY+  +l LR   +  L   q   L+  R     v  r +
  gi|1486572   842 T-LEEKRPYIARQLDLRREGLHRLHREQIARLRTWR----AVRDRDP--- 883

                    EyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    E  +E       Lv +n                  iAAG+  tG
  gi|1486572   884 EAGEEH--LRRVLVLIN-----------------AIAAGLRATG    908

gi|163849410|ref|YP_001637454.1|: domain 1 of 1, from 1 to 910: score 96.2, E = 1.1e-25
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            +  L   Kv      +++   LlD F  +L D+    + Ea
  gi|1638494     1    -----MQPLDQEKVD-----LDF-TFLLDCFARVLRDVDAGPVSEA- 35

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDai...lvAkailHmLnL
                                       L  LG+      P+D i+++ +A+a+     L
  gi|1638494    36 ------------------LPWLGSH----TPGDHIptrALAQALIIAFQL 63

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttE.sDiEEtlKkLvlklnKs
                     n+AEE      RR+  +         +   E     + l+kL   +  +
  gi|1638494    64 LNIAEENAAVQQRRVADRD-------PNIPPElGRWRDALQKLHQSG-LT 105

                    PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                     eE+  AL    v+ vltAHPt + R  +L     +   L     +   +
  gi|1638494   106 GEEIAAALPHVHVEPVLTAHPTEAKRATVLAHYRELYLLLVRRESQRWSP 155

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                     ++ E+   +   +   +Rt ++  ++P    E+R  + Y+     +  P
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  gi|1638494   156 AEQAEITADIETLLERLWRTGDVFLSKPGVPAEVRNVLHYLVNVFPDVLP 205

                    KFLRRvDtALKniGinERlPYdv.PLikFssWmGGDRDGknPRvtPEvtR
                            A +  G    l  d  P + F sW+GGDRDG +P vt E+t
  gi|1638494   206 VLDNQLRYAWQEAGFDPALLSDTwPKLSFGSWVGGDRDG-HPLVTAEITA 254

                    DvCLLaRmmAanlYisqvEDLmFElsmWR........CndELRvRAEEly
                          R+ A  l    +      ls+     +++++  d +R     l
  gi|1638494   255 QTLREMRLQALRLLRRRIRQAASHLSISDllvptppgLIDQIRRLSSGLG 304

                    rtaardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtG
                    +  a+  v +          P+EP+R  L      L   R       A
  gi|1638494   305 SRGAQA-VARN---------PNEPWRQAL-----NLMLARLPIDDAPAEA 339

                    iseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstF
                       + +   y   +e L  L      L   G   +AD  +  l+  v tF
  gi|1638494   340 ARLVDDPDRYRCADELLNDLREFAGYLRAVGAGRLADAEIRPLMQLVDTF 389

                    GLsLvKLDiRqEseRqtDvlDAittHLeiGs..YReWsEeKRqEWLlaEL
                    G  L  LD+Rq s+ +   l  + +  ++ s++      e+R+  L  E+
  gi|1638494   390 GFHLATLDVRQNSQFHDRALAQLLEAAGLSSddLIGGDPERRRALLEREV 439

                    kGKRPLlgsDLPktEEvkDvldafrvLAE....LPiDsFGaYiismataP
                       RP   +  P   E + v+d++rvLA +  +      G+ iism+
  gi|1638494   440 ASPRPFAHPNTPLDYEAAAVVDSYRVLANhiarYGTAGLGPLIISMTRDV 489

                    sDvLAvELLqRECgvkqt........LrvvPLFEkLADLeAAPAavekLF
                     DvL v LL RE g+  +++++   +L+vvPLFE + DLe  P  ++ +
  gi|1638494   490 TDVLVVYLLAREAGLAYAtpeglvcrLPVVPLFETIEDLEHSPRILADIL 539

                    siDW....YinridG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEii
                        ++++ i + +G++  q+vm+GYsDs KD G l+  W LY+Aq  +
  gi|1638494   540 DHPVtrrsLIAQAQGgelVQQVMIGYSDSNKDGGILASQWALYQAQRAMT 589

                    KvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGE
                     v +  G+++  FHGRGGt+ RG GPt   i   PP  +nG lR t qGE
  gi|1638494   590 EVGRARGIRIRFFHGRGGTISRGAGPTSRFISMLPPGSLNGDLRLTEQGE 639

                    viEfsFGEEnLCFrsLqRFtAAtLEHGm...nPPvsPkPEWRkLmeemAv
                    vi + +         L    A t  H + ++  P  P+P    ++  +A
  gi|1638494   640 VISQKYANRLTAAYNLELLIAGTTKHTLlqqRQPEEPHP-LEPVIGWLAE 688

                    vAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesL
                         YR +v ++  F+ +FR AtP     +  iGsRP++R     +  L
  gi|1638494   689 KSRIAYRELVERDG-FITFFRQATPIDVIEQSRIGSRPSRRTGQATLADL 737

                    RAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFF
                    RAiPW+F+W q RF LP W GvG A     +++     +L+     WP
  gi|1638494   738 RAIPWVFSWNQARFYLPGWYGVGSALTALQEQEPALWEQLRAEQWRWPLL 787

                    RvtlDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtkdlL
                    R  l  +              y  L+  +e+++ F + + +++  t+  L
  gi|1638494   788 RYLLANVGTSLQTAHRETMHAYAGLVEDDEIrRQFLNLIDAEFTRTEAAL 837

                    LkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtl
                      i G   +    P +   l  R+  +  L   q   L R R
  gi|1638494   838 TAIFG-MPIEQRRPRVTATLARRQIGLAPLHRRQIELLGRWR-------- 878

                    rPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqnt
                        ++  Ad++   a+e   +            L+L +  iAAG+  t
  gi|1638494   879 ----AQRAADDP---AAETTLID-----------LLLLVNAIAAGLRTT 909

                    G<-*
                    G
  gi|1638494   910 G    910

gi|7768226|emb|CAB90660.1|: domain 1 of 1, from 1 to 365: score 95.4, E = 1.9e-25
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768226     -    ---------------------------------------------- -
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|7768226    - ------------------------------------------------- -

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|7768226    - ------------------------------------------------- -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|7768226    - ------------------------------------------------- -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|7768226    - ------------------------------------------------- -

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|7768226    - ------------------------------------------------- -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|7768226    - ------------------------------------------------- -

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|7768226    - ------------------------------------------------- -

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|7768226    - ------------------------------------------------- -

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|7768226    - ------------------------------------------------- -

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|7768226    - ------------------------------------------------- -

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
gi|7768226    1 -------------------------------------------SDSGKDAG 8

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|7768226    9 RLSAAWQLYKAQEELIEVAKRHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEHGm PP+ P
gi|7768226   59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHGMIPPLTP 108

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                k EWR Lm+emAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
gi|7768226  109 KQEWRALMDEMAVVATERYRSIVFREPRFVEYFRLATPELEYGRMNIGSR 158

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh idKD Knl
gi|7768226  159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFKHVIDKDNKNL 208

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                 +L+ mY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+E+L P G++
gi|7768226  209 LMLQQMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVTEDLLPLGEQ 258

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR+ Y +tk +LLki GH ++LEGDP+LKqrlRLR++YittLnv+qAYtL
gi|7768226  259 LRAAYNDTKTYLLKITGHNEILEGDPFLKQRLRLRNAYITTLNVCQAYTL 308

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                KRiRDPsy+v +rP+++KE  d      +++vkLnpt+++aPGLEDtLiL
gi|7768226  309 KRIRDPSYQVPVRPPIAKEILDGAVFSTNQVVKLNPTSEYAPGLEDTLIL 358
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                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|7768226   359 TMKGIAA------    365

gi|18073902|emb|CAC84979.1|: domain 1 of 1, from 1 to 365: score 95.4, E = 2e-25
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807390     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807390     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807390     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807390     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807390     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807390     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807390     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807390     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807390     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807390     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807390     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807390     1 ----------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+i vAKk+GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807390     9 RLSAAWQLYKAQEELIEVAKKHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEHGm PP+ P
  gi|1807390    59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHGMIPPLTP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm++mAvvAtE YRs+v++EPRFvEYFR AtPElEYG+mniGsR
  gi|1807390   109 KPEWRALMDDMAVVATERYRSIVFREPRFVEYFRPATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh idKD Knl
  gi|1807390   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFKHVIDKDNKNL 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
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                    +L+ mY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL P G++
  gi|1807390   209 LMLQQMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELLPLGEQ 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR  Y +tk +LLki GH ++L GDP+LKqrl+LR++YittLnv+qAYtL
  gi|1807390   259 LRTAYNDTKSYLLKITGHNEILGGDPFLKQRLKLRNAYITTLNVCQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|1807390   309 KRIRDPSYQVPVRPPIAKEILEGSVTSANQLVKLNPTSEYAPGLEDTLIL 358

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|1807390   359 TMKGIAA------    365

gi|18073832|emb|CAC84933.1|: domain 1 of 1, from 1 to 365: score 94.9, E = 2.7e-25
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807383     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807383     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807383     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807383     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807383     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807383     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807383     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807383     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807383     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807383     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807383     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807383     1 ----------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+i vAKk+GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807383     9 RLSAAWQLYKAQEELIEVAKKHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEHGm PP+ P
  gi|1807383    59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHGMIPPLTP 108
```

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                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm++mAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|1807383   109 KPEWRALMDDMAVVATERYRSIVFREPRFVEYFRLATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh idKD Knl
  gi|1807383   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFKHVIDKDNKNL 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+ mY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL P G++
  gi|1807383   209 LMLQQMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELLPLGEQ 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR  Y +tk +LLki GH ++L GDP+LKqrl+LR +YittLnv+qAYtL
  gi|1807383   259 LRTAYNDTKSYLLKITGHNEILGGDPFLKQRLKLRTAYITTLNVCQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|1807383   309 KRIRDPSYQVPVRPPIAKEILEGSVTSANQLVKLNPTSEYAPGLEDTLIL 358

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|1807383   359 TMKGIAA------    365

gi|7768228|emb|CAB90661.1|: domain 1 of 1, from 1 to 365: score 93.8, E = 6.1e-25
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768228     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768228     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768228     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768228     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768228     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768228     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768228     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768228     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768228     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768228     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768228     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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                                                      sDsGKDAG
  gi|7768228     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768228     9 RLSAAWQLYKAQEELIEVAKRHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEHGm PP+ P
  gi|7768228    59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHGMIPPLTP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   k EWR Lm+emAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|7768228   109 KQEWRALMNEMAVVATERYRSIVFREPRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh idKD Knl
  gi|7768228   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFKHVIDKDNKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+ mY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+E+L P G++
  gi|7768228   209 LMLQQMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVTEDLLPLGEQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR+ Y +tk +LLki GH ++LEGDP+LKqrlRLR++YittLnv+qAYtL
  gi|7768228   259 LRAAYNDTKTYLLKITGHNEILEGDPFLKQRLRLRNAYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPsy+v +rP+++KE  d      +++vkLnpt+++aPGLEDtLiL
  gi|7768228   309 KRIRDPSYQVPVRPPIAKEILDGAVFSTNQVVKLNPTSEYAPGLEDTLIL 358

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|7768228   359 TMKGIAA------    365

gi|7768246|emb|CAB90654.1|: domain 1 of 1, from 1 to 365: score 93.8, E = 6.1e-25
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768246     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768246     - ------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768246     - ------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768246     - ------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768246     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768246     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768246     - ------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768246     - ------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768246     - ------------------------------------------------- -
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                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768246     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768246     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768246     1 -----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768246     9 RLSAAWQLYKAQEELIEVAKQHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  P Dti GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEHGm PP+ P
  gi|7768246    59 PADTIRGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHGMIPPLTP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  k EWR Lm+emAvvAtE YRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|7768246   109 KQEWRALMDEMAVVATERYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh i+KD Knl
  gi|7768246   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFKHLINKDNKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+ mY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL P G++
  gi|7768246   209 LMLQQMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELLPLGEQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR  Y +tk +LLki GH ++LEGDP+LKqrl+LR++YittLnv+qAYtL
  gi|7768246   259 LRTAYNDTKSYLLKITGHNEILEGDPFLKQRLKLRNAYITTLNVCQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDPs++v lrP+++KE        a++LvkLnpt+++aPGLEDtLiL
  gi|7768246   309 KRIRDPSHQVPLRPPIAKEVMGGSISSANQLVKLNPTSEYAPGLEDTLIL 358

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|7768246   359 TMKGIAA------    365

gi|254445406|ref|ZP_05058882.1|: domain 1 of 1, from 9 to 933: score 93.4, E = 8e-25
                  *->siDAqLRlLvPGK..vsedekLieYDALLlDkFLDiLqDLHGedLkE
                     +   + + L P ++ +s  e+ i      +D+ +D L     e L E
  gi|2544454     9    AQNEKAKNLLPEQqaMSFFEQHISTGLKKIDRDIDHLLACASEVLTE 55

                  avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                  +           G  +   L        +  Pa+    A+ ++    +
  gi|2544454    56 I------------GEPELAPLLNRQNPQSGAIPAEK--TAQVLSIAFQIM 91

                  nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                  nL EE       R+           a A t s     lK++      s
  gi|2544454    92 NLVEENVANQAGRNLETE-----KQATADTGS-WGYWLKRIAETS-PSKG 134

                  EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                  + F+ ++  sv  vlt HPt + R s+L ++ ++   L  L     t+ +
  gi|2544454   135 DLFQTIRRASVYPVLTGHPTEAKRPSVLAQHRKLYQLLVELENNMYTPVE 184

                  KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                  + E  + +   i   +R  Ei   +P    E    ++Y+       +
  gi|2544454   185 RGEFRDRIKATIELIWRSGEILVEKPDVASERDNILAYLTQKFPVAIEIS 234

                  LRRvDtALKniGin..ERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                    R   A+   Gi  +E      P ik  sW+GGDRDG +P vt +vt +
  gi|2544454   235 DSRFRAAMSQAGIEwdESDIASYPHIKLGSWVGGDRDG-HPFVTADVTAE 283

                  vCLLaRmmAanlYisqvEDLmFElsmWRCnd....ELRvRAEElyrtaar
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                     R  A      ++  L  ++ + +  +++++EL  R   l
  gi|2544454   284 TLANLRTAALDTLAKKLKQLARDMPLSKLFQtpppELLKRISQLDPKCDD 333

                    dkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseis
                           iE        EP++  +  vR+ L   R +  H      se+
  gi|2544454   334 P----NSIE--------EPWKRFVELVRENL--PRGKRAHKSYRQPSEVI 369

                    EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                     +            L     +L + G + +A   +L ++R   tFG  +
  gi|2544454   370 AD------------LQRLKNALQNAGARRLAVTYVLPIIRFLDTFGFHMA 407

                    KLDiRqEs...eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKR
                     LDiRq s+ ++R    l A     +   + eW E++R E+L  EL   R
  gi|2544454   408 ALDIRQNSgyhDRAMSQLLAAAGVTDGENFAEWTEQQRVEFLSEELTHAR 457

                    PLlgsDLPktE.EvkDvldafrvLAELPiD....sFGaYiismataPsDv
                    P +  D  + E E ++ +++++v+A    D ++ + G  iism+ + sD
  gi|2544454   458 P-FAQDHGQLElEAREAIGSLKVVANQIRDygraAIGQVIISMTRSLSDL 506

                    LAvELLqRECgvkqt........LrvvPLFEkLADLeAAPAavekLF...
                    L    L RE g+ + +++++   +++ PLFE L DLe     ++   +++
  gi|2544454   507 LVTYALCREAGLTRMtdrgniclVPISPLFETLDDLENSESIMDAFLshp 556

                    ....siDWYinridG.................KqevmvGYsDsGKDAGRls
                     ++ s+ W    +d +  + + ++++++ +  qe m+GYsDs KDAG ++
  gi|2544454   557 vtkaSLPWQQRALDEglanygvptpdpdaplIQEAMLGYSDSNKDAGIIA 606

                    AAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPD
                      W L+ Aq  +i  A k+Gv +  FHGRGGtv RG GPtH  + + P
  gi|2544454   607 SQWGLFNAQSRLIALAEKHGVAIRFFHGRGGTVSRGAGPTHRFLEALPAG 656

                    tinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGm.nPPvsPkP
                     +    Rvt qGEvi + +       rsL    A  +   +++ P  P P
  gi|2544454   657 SLTHGSRVTEQGEVIAQKYSNFLTAARSLELLIAGSVGPQLsESPNTPSP 706

                    EWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPa
                    E  + m  +       YRs+ ++E  F  ++R AtP     +  iGsRP+
  gi|2544454   707 ELVEAMSFLSEYSSKTYRSL-LQEENFLTFYRQATPIDALEQSRIGSRPS 755

                    KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqk
                    +R     ++ LRAiPW+F+W q RF +P W GvG     A++K+   l k
  gi|2544454   756 RRSGKPSLKDLRAIPWVFSWNQSRFYMPGWYGVGSSIT-ALKKEKPELYK 804

                    .LkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP.FGks
                     Lk   + WPF R  l  +E      D  +   y +L+  + ++ +F k
  gi|2544454   805 aLKKSARSWPFIRYVLYNVETSIESADTLMMQSYAELVSNDSIRDkFFKL 854

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    + d+   t++ L      ++lL G   L  r   R  +  tL
  gi|2544454   855 ITDERAATREAL------QELLNGP--LETR---RPRFFKTLHA------ 887

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                       RD         ++    A  +s   ++L ++
  gi|2544454   888 ---RDKWLDLLHAQQIELLAAWRQSGSEEDLRRVL--------------Q 920

                    tmKGiAAGmqntG<-*
                     +  iAAG+  tG
  gi|2544454   921 SINAIAAGLRTTG    933

gi|7768236|emb|CAB90652.1|: domain 1 of 1, from 1 to 365: score 92.2, E = 1.8e-24
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768236     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768236     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768236     - ---------------------------------------------- -
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                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768236     - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768236     - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768236     - ------------------------------------------------ -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768236     - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768236     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768236     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768236     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768236     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|7768236     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768236     9 RLSAAWQLYKAQEELIEVAKQHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEHGm PP+ P
  gi|7768236    59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHGMIPPLTP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  k EWR Lm+emAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|7768236   109 KQEWRALMDEMAVVATERYRSIVFREPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AF+h idKD Knl
  gi|7768236   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFRHVIDKDNKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+ mY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL P G++
  gi|7768236   209 LMLQQMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELLPLGEQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR  Y +tk +LL+i GH ++LEGDP+LKqrl+LR +YittLnv+qAYtL
  gi|7768236   259 LRTAYNDTKSYLLQITGHNEILEGDPFLKQRLKLRTAYITTLNVCQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|7768236   309 KRIRDPSYQVPVRPPIAKEIMEGSVSSANQLVKLNPTSEYAPGLEDTLIL 358

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|7768236   359 TMKGIAA------    365

gi|7768242|emb|CAB90658.1|: domain 1 of 1, from 1 to 365: score 91.4, E = 3.1e-24
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
```

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gi|7768242     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|7768242     - ---------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|7768242     - ---------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|7768242     - ---------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|7768242     - ---------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|7768242     - ---------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|7768242     - ---------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|7768242     - ---------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|7768242     - ---------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|7768242     - ---------------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|7768242     - ---------------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
gi|7768242     1 ------------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|7768242     9 RLSAAWQLYKAQEELIEVAKQHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEHGm PP+ P
gi|7768242    59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHGMIPPLTP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  k EWR Lm++mAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
gi|7768242   109 KQEWRALMDDMAVVATERYRSIVFREPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AF+h +dKD+Knl
gi|7768242   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFRHVMDKDSKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+ mY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL P G++
gi|7768242   209 LMLQQMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELLPLGEE 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR  Y +tk +LLki GH ++LEGDP+LKqrl+LR++YittLnv+qAYtL
gi|7768242   259 LRTAYNDTKSYLLKITGHNEILEGDPFLKQRLKLRNAYITTLNVCQAYTL 308
```

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                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|7768242   309 KRIRDPSYQVPVRPPIAKEIMEGSVSSANQLVKLNPTSEYAPGLEDTLIL 358

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|7768242   359 TMKGIAA------    365

gi|7768230|emb|CAB90644.1|: domain 1 of 1, from 1 to 365: score 91.3, E = 3.3e-24
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768230     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768230     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768230     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768230     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768230     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768230     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768230     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768230     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768230     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768230     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768230     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768230     1 ----------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768230     9 RLSAAWQLYKAQEELIEVAKQHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEHGm PP+ P
  gi|7768230    59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHGMIPPLTP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    k EWR Lm+emAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|7768230   109 KQEWRALMDEMAVVATERYRSIVFREPRFVEYFRLATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AF+h idKD Knl
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  gi|7768230   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFRHIIDKDNKNL 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+ mY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL P G++
  gi|7768230   209 LMLQQMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELLPLGEQ 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR  Y +tk +LLki GH ++LEGDP+LKqrl+LR++Yit Lnv+qAYtL
  gi|7768230   259 LRTGYNDTKSYLLKITGHNEILEGDPFLKQRLKLRNAYITALNVCQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|7768230   309 KRIRDPSYRVPVRPPIAKEIMEGSDSSANQLVKLNPTSEYAPGLEDTLIL 358

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|7768230   359 TMKGIAA------    365

gi|114769507|ref|ZP_01447133.1|: domain 1 of 1, from 9 to 907: score 91.2, E = 3.8e-24
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       si+   ++ +  K        +Y   L      +L ++ G    E++
  gi|1147695     9    SIEVAKKAEIFSKNT------HYSSWLRHLLWTLLCEVAGRRAPEII 49

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkai.lHmLnLAn
                         ls       D    eE    L         l A  i  H+L +A
  gi|1147695    50 P---VLS-------DKNIFEESNDELR-----QNFLHATNIwFHLLRIAE 84

                    LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkL....vlklnK
                      E + +  RR+i+       +D ++         t+ +L+++++ ++ K
  gi|1147695    85 --ENILVRARRKIE-------SDGGQGAVKGTFASTFLRLkehnIDLG-K 124

                    sPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvt
                     P+ vF   K q +   +tAHPt   R  +L  + Ri   +  L     t
  gi|1147695   125 IPNNVF---KTQ-ISPTITAHPTEGKRETILDIHRRIYRAIVDLESNRWT 170

                    veDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGv
                    + +++   E L  Ei   + t E+R  +PtP +E+     ++   +++
  gi|1147695   171 PFEREKHIENLRNEIDMLWLTGELRFERPTPAEEINWANRFFKNAIFQAQ 220

                    PKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                         +   AL  +Gi        P i F sW+GGDRDG + +vt  +t
  gi|1147695   221 IDIDEKFRRAL--VGIKSPEDKIFPSIMFHSWVGGDRDG-HTKVTAVIT- 266

                    DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                            + an   + +E L   ls     + ++      y  +  +
  gi|1147695   267 -----NQAIEANKR-NAIEALRDKLS-----SAIKNISISAYCYPFDQ-- 303

                    vKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                        +     v        i       ++     a       i +    A
  gi|1147695   304 -NTLVSLSSIVMKSGKLQDISKRNQGEVFRKSLTAIDFRLEAIINPENGA 352

                    v.ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                     +y   EeF   L+L    L     + i    +  +    s  G   + L
  gi|1147695   353 TpYASCEEFRKDLDLVDNVL-SLAAREISNQYIRPIQALHSSCGFRTMSL 401

                    DiRqEseRqtDvlDAittHLeiGsY....ReWsEeKRqEWLlaELkGKRP
                    DiRq s+  tD +  i   L+    + +++eWs+    E  l   +  +P
  gi|1147695   402 DIRQNSDVTTDAISNIWSFLGFDPIeygtKEWSDRIYDE--LKNSQEIKP 449

                    LlgsDLPktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvEL
                     +g     t E+ D  + +++  A +   + G++i+sm+ +  D L v L
  gi|1147695   450 NIGDLKETTVELLDLFGVIKdAKASVDPKCLGSFILSMTRSNDDLLGVML 499

                    LqRECgvkq........tLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                    + R  g+  ++ +++   L  vPLFE + DL+ AP  ++   s+   +
  gi|1147695   500 IARYAGLASgplgsdiiDLNLVPLFETIDDLRNAPNILKVYCSVPIIRRS 549

                    i...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                    +++ +  qevm+GYsDs KD G +   W + kAq  i+ +  +   K+
  gi|1147695   550 MkefNSVQEVMLGYSDSNKDGGFICSTWEVNKAQKNIVSIMNEIDTKVSF 599
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                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                    FHGRGG v RGG Pt  Ai +qP   i    R+t qGEv+   F
  gi|1147695   600 FHGRGGSVSRGGAPTGRAIAAQPAGSIGNCFRITEQGEVVSSKFANKGTA 649

                    FrsLqRFtAAtLEHGm....nPPvsPkPEWRkLmeemAvvAtEEYRsvvv
                     r L   +   L H + ++++P +   P++ + +e +  v    YR +
  gi|1147695   650 TRQLELLASSVLFHQIysnnEPELLATPDYDEALEALSGVSQAHYRNLLE 699

                    KEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtq
                     E  F+ YF  A P  E  k+niGsRP  R  +  ++ LRAiPW+FaW q
  gi|1147695   700 TEG-FINYFEQASPVKELAKLNIGSRPQTRFGASSLDDLRAIPWVFAWSQ 748

                    tRFHLPvWLGvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                     R  +  W G+G A K++   +       Lk m++e   FR  +D +E
  gi|1147695   749 NRHLITGWYGFGSALKsFRSYRGEAGDNILKSMFRESRIFRLIVDEVEKS 798

                    FAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlL
                        D  iA  y +L+    ++ +  k++ d+Y    ++LL +   k +
  gi|1147695   799 IYLTDLDIAKKYSDLVEDKVVRQkIFKKIEDEYRSSVNMLLWLCKDKSIA 848

                    EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                       P L+ +++ +d+ +      q  tL            +  l KE+
  gi|1147695   849 KRFPILQSQIKRKDPLLQ-----QSHTL------------QVSLLKEHRK 881

                    EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     +          n  e+++P     L+  m  iA G+  tG
  gi|1147695   882 LD----------N-NENISP----CLLQSMNCIATGLGWTG    907

gi|242309960|ref|ZP_04809115.1|: domain 1 of 1, from 1 to 883: score 90.4, E = 6.2e-24
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                  +   ++ i+    +     ++Lq++  e   +++
  gi|2423099     1    -------------MK--NRRIKEADFIFSLMCELLQEVAPEIKEDFI 32

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        +   +Y  K+   KL      L sL+  D   + ka+     L n+
  gi|2423099    33 SLKEDTTIDYQLKR---KL------LDSLESKDISKLIKAFTLYYLLLNI 73

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     +E     R  i++               + i  tl  L ++     e++
  gi|2423099    74 IDE-----RYFISLNS------------KAHIKPTLEELKSQQ-YDEEDI 105

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiR...nCLaqLsAKDvtve
                     + L+      v+tAHPt s RR  L     + ++ nC  q
  gi|2423099   106 KNVLRKIKFYPVFTAHPTESLRRTFLESYHEMYddlNCWFQFQDNNAKEH 155

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                     K  L       i        +R  +     E+   + ++   + +
  gi|2423099   156 LKYRLNLLWYSHI--------VRSEKIEVLFELDNLLYFMESSILQSGVN 197

                    FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                     L  v   L+       +P     i+  sW+GGDRDG nP vt  v  +v
  gi|2423099   198 VLEEVQNTLQ-------IPLKKSPIRLGSWIGGDRDG-NPYVTNGVMIEV 239

                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                               Y+ q++ L  Els+    +E      El     r+
  gi|2423099   240 MKRQHQTIIEHYLKQIDKLSRELSI---AQEYSQPTQELLDSLERE--KD 284

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                    y  +  K++  +EP+R  L  +R KL n R  a  L    + e     +y
  gi|2423099   285 YLDDMAKKLFLQEPFRAKLTCMRQKLQN-RILALNLPQSALYE-NKPYMY 332

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRq.vstFGLsLvKLDi
                     +  eF+  +++   sL    Dk    G  L  L+  v   G  L++LD
  gi|2423099   333 ENPKEFIKDIDMMIESL----DKR--SGIYLRKLKNlVLLAGFHLMQLDF 376

                    RqEseRqtDvlDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLlgs
                    Rq  +     l  i   L+ ++G +   +     E L + L    PLl
  gi|2423099   377 RQHRDVFWRALTEIFALLGYtqGDFSLLPPKEQTEILNTALNA--PLLDL 424

                    DL...PktEEvkDvlda...frvLAELPiD.sFGaYiismataPsDvLAv
                     +  +    E ++ l a  +f+   E  +D+   + iism+ +  D L v
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  gi|2423099   425 NIlygKLSKESQELLMAfinFKWAKERISDnIIDSCIISMCQSSNDLLCV 474

                   ELLqRECgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri
                       +  g+ ++++k  + + PLFE + DLe AP  +  L +   Y+  +
  gi|2423099   475 LWFAKQSGLwregkKTRISISPLFETIGDLENAPTILRELCANPQYVEYL 524

                   dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                   + ++++qe+m+GYsDs KD G +   + L kA   +i    +  +K  lF
  gi|2423099   525 QSRknnQEIMIGYSDSSKDGGIFTSNYSLRKAINNLIILESELKIKFRLF 574

                   HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                   HGRGG v RGGG    A+Ls P   + G l+ t qGEvi   +   +
  gi|2423099   575 HGRGGSVSRGGGALEDALLSSPDNSVAGFLKTTEQGEVISEKYLNPKKAE 624

                   rsLqRFtAAtL......EHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvv
                    s     A  L+++  +  G+n  +  + ++  +m+++       YR +v
  gi|2423099   625 YSFSSALATLLkksvydKYGINQQICNR-DFETIMQKVSEESFKAYRKLV 673

                   vKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWt
                   +    F+EYF++AtP     ++niGsRP+KRk    +e LRAiPW+FaWt
  gi|2423099   674 YETEGFIEYFKSATPIEFIQQLNIGSRPSKRKNTQNVEDLRAIPWVFAWT 723

                   qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                   q R  +P W G+G     A +   K +  L+E Y +  FF+ t+D +
  gi|2423099   724 QNRSIIPAWYGLGSGLEEASKICDKAI--LQECYTKDLFFKTTIDNISQA 771

                   FAKGDPGiAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlL
                   F K D  iA  y   +    L+ +  + +  +Y  t ++LL +   k+lL
  gi|2423099   772 FLKVDLEIARHYNAFVEDISLREkIWNMIESEYNLTLKWLLYVRQEKELL 821

                   EGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAd
                     +  ++  + LR s++ttL  fq Y +   +   y            +
  gi|2423099   822 TSEKCIQESILLRKSFLTTLSFFQFYLMEQYKKATY----------E 858

                   EnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   E+     + +               +i t+ GiA G+ ntG
  gi|2423099   859 EQ----RQRIAKQ-----------IITTIVGIAQGIRNTG    883

gi|18073898|emb|CAC84977.1|: domain 1 of 1, from 1 to 365: score 90.3, E = 6.7e-24
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807389     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807389     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807389     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807389     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807389     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807389     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807389     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807389     - ---------------------------------------------- -
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                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807389     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807389     - ------------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807389     - ------------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807389     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+i vAKk+GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807389     9 RLSAAWQLYKAQEELIEVAKKHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEHGm PP+ P
  gi|1807389    59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHGMIPPLTP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm++mAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|1807389   109 KPEWRALMDDMAVVATERYRSIVFREPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh id+D Knl
  gi|1807389   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFKHVIDQDNKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+ mY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL P G++
  gi|1807389   209 LMLQQMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELLPLGEQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR  Y +tk +LLki GH ++L GDP+LKqrl+LR++YittLnv+qAYtL
  gi|1807389   259 LRTAYNDTKSYLLKITGHNEILGGDPFLKQRLKLRNAYITTLNVCQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDPsy+  +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|1807389   309 KRIRDPSYQKPVRPPIAKEILEGSVTSANQLVKLNPTSEYAPGLEDTLIL 358

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807389   359 TMKGIAA------    365

gi|7768378|emb|CAB90717.1|: domain 1 of 1, from 1 to 363: score 90.1, E = 7.6e-24
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768378     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768378     - ------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768378     - ------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768378     - ------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768378     - ------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
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  gi|7768378     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768378     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768378     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768378     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768378     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768378     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768378     1 -----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYk qEE+++vAK++GvKL++FHGRGGtvGRGGGPtHL iLsq
  gi|7768378     9 RLSAAWQLYKTQEELVQVAKQFGVKLTMFHGRGGTVGRGGGPTHLGILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti GslRvtvqGEviE+ FGEE LCFr+LqRFt AtLEHGm+  +sP
  gi|7768378    59 PPDTILGSLRVTVQGEVIEQCFGEERLCFRTLQRFTVATLEHGMHHHISP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emAv+At EYRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|7768378   109 KPEWRSLMDEMAVIATKEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i KDi+nl
  gi|7768378   159 PAKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVITKDIRNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+EmY+ WPFFRvt+DL+EmvF KG PGiA+LyD+LLv+ +L  FG +
  gi|7768378   209 HILREMYNGWPFFRVTIDLIEMVFTKGNPGIASLYDELLVSNDLLSFGME 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   L+++Y+Etk lLL++AGHkDlLEGDP LKqrlRLRd+YittLnv+qAYtL
  gi|7768378   259 LKANYEETKRLLLQVAGHKDLLEGDPHLKQRLRLRDPYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiR+Psy+     h+s E   E  k a+eLvkLnpt+++aPGLEDtLi+
  gi|7768378   309 KRIREPSYHAMAPHHVSNE--TESRKSAAELVKLNPTSEYAPGLEDTLII 356

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|7768378   357 TMKGIAA------    363

gi|291277543|ref|YP_003517315.1|: domain 1 of 1, from 1 to 883: score 89.6, E = 1.1e-23
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                  +s+ e+  ++   L+ k L     L  e    ++
  gi|2912775     1    -------------MSDFEREKQFIMELMRKMLQSTDALAAEFFDAFI 34

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDail.vAkailHmLnLAn
                                    K e   + Lt +      l+v ka++    L n
  gi|2912775    35 LA-------------LNKQECTSSLLTQIIQNNKTLeVIKAFSLYNILLN 71

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   +  E     R  ik  k               i  t+  L+ ++   Pe+
  gi|2912775    72 IIQE-----RYNIKTAK-----------PLQKIAQTYEELIAQG-FDPED 104
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                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + e +       v+tAHPt s RR  L  +  i   L +     +
  gi|2912775   105 IQEIINKMEFYPVFTAHPTESRRRTFLEAHYAINRDLHK-----IFELHD 149

                    kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +EL E +   +   +Rt  +R  +     E+   +  i   + +   K L
  gi|2912775   150 EELIEDINYRLHLLWRTHLVRSQKLEVLFELDNLLYIIETSILNSAQKTL 199

                    RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                          L         P     i+  sW+GGDRDG nP v  E    v
  gi|2912775   200 NMLSALLPK-------PLSKSPIRLGSWIGGDRDG-NPFVSNELMTQVMK 241

                    LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyY
                        +  nlYi +vE L+ Els+    ++     EEl r  +r+   K
  gi|2912775   242 TQHKLLINLYIKKVEKLIRELSI---SQDFCNISEELLRSIQRE---KEH 285

                    iEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGi.seisEeAvyt
                    ++ ++ +   EP+R  L  ++ KL n     R +   Gi+ +  Ee vy
  gi|2912775   286 LDSFR-LYSKEPFRTKLFLIKKKLQN-----RFI---GInTNWREEFVYH 326

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                       e L  ++L   s  e   +     sL ++   v     sL  LD R
  gi|2912775   327 SAKELLADIDLLIDSAPEHCTR-----SLKEFRNLVLLADFSLLHLDFRE 371

                    EseRqtDvlDAittHLeiG..sYReWsEeKRqEWLlaELkGKRPLlgsDL
                          + +  i   L++ ++ + + sEeK+ E L   L   + +l   L
  gi|2912775   372 HKSVFQEAISEIFCLLGMCdnDFGSLSEEKKIEILNQALDSPKSILSEIL 421

                    P.ktEEvkDvldafrvLA....ELPiDsFGaYiismataPsDvLAvELLq
                    P+   + + v++ f  +A +++ +  +   ++i+sm+t  sD L +
  gi|2912775   422 PsLSRDTQNVIEIFVSIAwgkrHISEEILHSFILSMTTDASDLLTILWFI 471

                    RECgvkqt.....LrvvPLFEkLADLeAAPAavekLF...siDWYinrid
                    +   +  ++++ ++ + PLFE + DL+     +  L +++    Y
  gi|2912775   472 KQNRLWIPgqsaqIAITPLFETIQDLKHSKEILLTLSknpHYSLYLKDCA 521

                    GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRG
                      qe+mvGYsDs KD G ++  + L  A  ++iK      +   lFHGRG
  gi|2912775   522 STQEIMVGYSDSSKDGGIFASNYNLHSAIYDLIKLGESLKITFKLFHGRG 571

                    GtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEvi.........EfsFG
                    G v RGGG    A+L+ PP  +nG l+vt qGE+i+++  ++ + +f F
  gi|2912775   572 GSVSRGGGTLESALLAAPPRSVNGMLKVTEQGEIIgskylspmsaDFNFA 621

                    E...EnLCFrsLqRFtAAtLEH.GmnPPvsPkPE.WRkLmeemAvvAtEE
                     + +  L    L  F+   + H+ ++  +     + R  m+++
  gi|2912775   622 NtlsALLKKSCLDAFCTHDIAHdDLDAKMCEITRsHRGQMQKISEQSYLK 671

                    YRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPW
                    YR +v+    F++YF+ AtP     ++n+GsRP+KRk    +e LRAiPW
  gi|2912775   672 YRELVYGTAGFMDYFKAATPIEFIQQLNLGSRPSKRKDTAKVEDLRAIPW 721

                    iFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlD
                    +FaWtq R  +P W G+G       dK       L+  Y e  FFR t+D
  gi|2912775   722 VFAWTQNRSIIPAWYGLGSGLLAIEDKNA-----LRQSYLESDFFRATID 766

                    LlEmvFAKGDPGiAaLyDkLLvaEeL..kPFGksLRdkYvEtkdlLLkiA
                     +   F K D  iA+ y   +  E L++k +G  + ++Y  t +++L i
  gi|2912775   767 NISQAFLKVDLEIAGFYNAFIDDEALgnKIWG-MIAEEYDKTMEYILWIR 815

                    GHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhl
                       +lL   P +++ + +R + +  Ln +q   +KR     y
  gi|2912775   816 DESELLCSQPEIRKSILMRKPTVNALNLLQIELIKRYQKSHY-------- 857

                    sKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                          E  +k   L ++               t+ GiA G+ ntG
  gi|2912775   858 ------EK-QKTRLLEEIH--------------STIIGIAQGLRNTG    883

gi|255264237|ref|ZP_05343579.1|: domain 1 of 1, from 1 to 872: score 89.2, E = 1.5e-23
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                              +v           +Y   L D   D+L        k ++
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gi|2552642     1    --------MVDCEGQ------DYAKSLRDLLWDLL-------FKTVM 26

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                        +++A     +D + L++  +++     a  i           L  +
gi|2552642    27 RRAPDIAAFLASPRDIESLQD--SQISDFLQAANI--------WFQLKKI 66

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    A+E      RR+          ++    +      + k+       P+
gi|2552642    67 ADENTAVRDRRNTETT------DGVECVDGTFAQVMAKIAEHA---PDQF 107

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      A+   sv   ltAHPt + R  +L  + Ri   L  L  + +t+ ++
gi|2552642   108 ESAVASLSVGPTLTAHPTEAKRITILEIHRRIYRHLVALETQRLTPRERA 157

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                       E L  Ei   +   E+R  +P   DE+  G+ ++ + +++  P+
gi|2552642   158 NRVEDLRGEIDLLWLSGELRLERPSLSDEIEWGLQFFRDSLFDATPQLF- 206

                    RvDtALKniGinERlPYd....vPLikFssWmGGDRDGknPRvtPEvtRD
                      D  L  iG+    P ++++  P ikF sW+GGDRDG nP vt   t+
gi|2552642   207 --DQFL--IGLENTFPTQprslRPCIKFHSWIGGDRDG-NPNVTLAATKS 251

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndEL.RvRAEElyr.taardk
                         R  A    i+ +      +s+     EL+ +    l + t ++d
gi|2552642   252 AMARGRDTAITKHIDDLSRAARHISISSDIAELpDIHVQLLASiTTRSD- 300

                    vvKyYiEFWKqv..PPtEPYRviLGdvRDKLYntRERaRHLLAtGiseis
                          EF   +++ P E +R  + ++                  i+ +
gi|2552642   301 ------EFDALIkrNPGEVFRQAISAI-----------------IARLE 326

                    EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLv
                        y + +e +  L     +L   G + +    +  +   v  FG
gi|2552642   327 GRPLYSHTDELVSDLHEIENALFAIGAQHLSNRYIRPVRWRVEVFGFRTT 376

                    KLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLl
                     LDiRq s   tDvl  i    e     +Ws   R E  +  L
gi|2552642   377 SLDIRQNSTVTTDVLAEIWGPGETYGSIKWSQRLRYEIAVDVLPDIDVEA 426

                    gsDLPktEEvkDvldafrvLAELPi.DsFGaYiismataPsDvLAvELLq
                     s+  +  E+   l+a+    E   +D+ G +i+sm+ +  D LAv LL
gi|2552642   427 LSE--QAQELLNLLEAIVDAREGNDpDAIGCFILSMTRSTDDLLAVYLLA 474

                    RECgv...kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid...GK
                    R    +++   L+vvPLFE + DL+ AP  +  L ++   +  + +++ +
gi|2552642   475 RYAAAtgeTLDLPVVPLFETIEDLRNAPRILSDLIAVPTARRSLKrqgSR 524

                    qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                     evm+GYsDs KD G +   W L +Aq  i +  +  G     FHGRGG
gi|2552642   525 IEVMLGYSDSNKDGGFICSTWELEQAQRKIRQTLQGLGFVPAFFHGRGGS 574

                    vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                    v RGG Pt  Ai +qP  t+nG+lR t qGEv+   +       r L
gi|2552642   575 VSRGGAPTGRAIAAQPSGTLNGALRTTEQGEVVSTKYANCGTALRELEQL 624

                    tAAtLEHGmnPPvsPk..PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                    +   L H      +Pk++PE+ + ++ +  +    Y ++ +  P Fv YF
gi|2552642   625 ASSALLHTALSHNAPKtnPEYDNALQALSGMSQVAYDAL-LNSPGFVQYF 673

                    RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                      A P  E   + iGsRPa+R  +  +  LRAiPW+FaW q R  L  W
gi|2552642   674 QEASPVEELAMLKIGSRPARRFGASSLSDLRAIPWVFAWSQNRHLLTGWY 723

                    GvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiA
                    G+GAA  ++A  +     ++L +m+ +   F   +D +E    + D  iA
gi|2552642   724 GFGAACAsFAKVRGELGWKMLCDMFATSTLFQLMVDEVEKSLFQADMQIA 773

                    aLyDkLLv.aEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                    a y  L  ++         + ++Y      + ki G   l    P L  r
gi|2552642   774 AKYAALSTdTASGTAILGMIEAEYASSAAAIQKITGQPSLAARFPNLTER 823

                    lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
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                       Y+ t+  +q   L+ +R                  En
  gi|2552642   824 FEGNRRYLETIHTIQIKQLRALR-----------------REN------- 849

                   vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        + +  P     L+  m  i AG+  tG
  gi|2552642   850 ----QSAETGP-----LLQSMNCISAGLGWTG    872

gi|7768224|emb|CAB90648.1|: domain 1 of 1, from 1 to 365: score 86.7, E = 8e-23
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768224     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768224     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768224     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768224     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768224     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768224     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768224     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768224     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768224     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768224     - ---------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768224     - ---------------------------------------------- -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768224     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768224     9 RLSAAWQLYKAQEELIEVAKQHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEH m PP+ P
  gi|7768224    59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHSMIPPLTP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   k EWR Lm+emAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|7768224   109 KQEWRALMDEMAVVATERYRSIVFREPRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AF+h idKD Knl
  gi|7768224   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFRHVIDKDNKNL 208
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                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+ mY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL P G++
  gi|7768224   209 LMLQQMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELLPLGEQ 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR  Y +tk +LLki GH ++LEGDP+LKqrl+LR +YittLnv+qAYtL
  gi|7768224   259 LRTAYNDTKSYLLKITGHNEILEGDPFLKQRLKLRTAYITTLNVCQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|7768224   309 KRIRDPSYQVPVRPPIAKETMEGSISSANQLVKLNPTSEYAPGLEDTLIL 358

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|7768224   359 TMKGIAA------    365

gi|10303367|emb|CAA65112.1|: domain 1 of 1, from 1 to 367: score 84.9, E = 2.8e-22
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1030336     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1030336     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1030336     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1030336     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1030336     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1030336     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1030336     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1030336     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1030336     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1030336     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1030336     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1030336     1 ------------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+++vAKkyGvKL++FHGRGGtvGRGGGPtHLA+Lsq
  gi|1030336     9 RLSAAWQLYKAQEELVQVAKKYGVKLTMFHGRGGTVGRGGGPTHLALLSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
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                    PP+tinGslRvt+qGEviE+sFGEE LCFr+LqR+tAAtLEHGm PP+sP
  gi|1030336     59 PPETINGSLRVTIQGEVIEQSFGEERLCFRTLQRYTAATLEHGMRPPISP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR +++emAvvAt EYRs+ + EPRFvEYFRlAtPElEYG+mniGsR
  gi|1030336    109 KPEWRAILDEMAVVATAEYRSIEFGEPRFVEYFRLATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRF LPvWLG+GAAF     K  K l
  gi|1030336    159 PSKRKPSGGIESLRAIPWIFAWTQTRFLLPVWLGFGAAFNIYC-KGQKDL 207

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      LkEmY+eWPFFRvtlDLlEmvF  GDPGiAaLyDkLLv+++LkPFG++
  gi|1030336    208 RTLKEMYNEWPFFRVTLDLLEMVFXXGDPGIAALYDKLLVSDDLKPFGEQ 257

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Etk+lL +    + lLEG P LKqr+RLR+ Yit Lnv+q Y L
  gi|1030336    258 LRANYEETKQLLSQGCRPHGLLEGRPLLKQRIRLRERYITILNVCQVYSL 307

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+++v +rP+lsK y d n  k++eLvkLnp +++aPGLEDtLiL
  gi|1030336    308 KRIRDPNFHVHVRPPLSKRY-DSN--KPAELVKLNPRSEYAPGLEDTLIL 354

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|1030336    355 TMKGIAAGMQNTG    367

gi|7768232|emb|CAB90650.1|: domain 1 of 1, from 1 to 365: score 84.9, E = 3e-22
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768232      -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768232      - ------------------------------------------------ -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768232      - ------------------------------------------------ -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768232      - ------------------------------------------------ -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768232      - ------------------------------------------------ -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768232      - ------------------------------------------------ -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768232      - ------------------------------------------------ -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768232      - ------------------------------------------------ -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768232      - ------------------------------------------------ -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768232      - ------------------------------------------------ -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768232      - ------------------------------------------------ -
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                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|7768232     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768232     9 RLSAAWQLYKAQEELIEVAKQHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAA LEH m PP+ P
  gi|7768232    59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAAALEHSMIPPLTP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  k EWR Lm+emAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|7768232   109 KQEWRALMDEMAVVATERYRSIVFREPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AF+h idKD Knl
  gi|7768232   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFRHVIDKDNKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+ mY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL P G++
  gi|7768232   209 LMLQQMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELLPLGEQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR  Y +tk +LLki GH ++LEGDP+LKqrl+LR +YittLnv+qAYtL
  gi|7768232   259 LRTAYNDTKSYLLKITGHNEILEGDPFLKQRLKLRTAYITTLNVCQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|7768232   309 KRIRDPSYQVPVRPPIAKEIMEGSVSSANQLVKLNPTSEYAPGLEDTLIL 358

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|7768232   359 TMKGIAA------    365

gi|7768222|emb|CAB90647.1|: domain 1 of 1, from 1 to 365: score 84.6, E = 3.4e-22
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768222     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768222     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768222     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768222     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768222     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768222     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768222     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768222     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
```

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  gi|7768222     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768222     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768222     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768222     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768222     9 RLSAAWQLYKAQEELIEVAKQHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEH m PP+ P
  gi|7768222    59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHSMIPPLTP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   k EWR Lm+emAvvAtE YRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|7768222   109 KQEWRALMDEMAVVATERYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AF+h idKD Knl
  gi|7768222   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFRHVIDKDNKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+ mY+eW FFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL P G++
  gi|7768222   209 LMLQQMYNEWAFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELLPLGEQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR  Y +tk +LLki GH ++LEGDP+LKqrl+LR +YittLnv+qAYtL
  gi|7768222   259 LRTAYNDTKSYLLKITGHNEILEGDPFLKQRLKLRTAYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|7768222   309 KRIRDPSYQVPVRPPIAKETMEGSISSANQLVKLNPTSEYAPGLEDTLIL 358

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|7768222   359 TMKGIAA------    365

gi|2145451|emb|CAA62829.1|: domain 1 of 1, from 1 to 363: score 83.9, E = 5.5e-22
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                  s
  gi|2145451     1    --------------S------------------------------- 1

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2145451     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2145451     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2145451     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2145451     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                                                 D
  gi|2145451     2 --------------------------------DS---------------- 3
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                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2145451    - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2145451    - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2145451    - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|2145451    - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|2145451    - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                              KDAG
  gi|2145451    4 ---------------------------------------------KDAG 7

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2145451    8 RLSAAWQLYKAQEELVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 57

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti GslRvtvqGEviE+sFGEE LCF++LqR+t AtLEHGm+ P sP
  gi|2145451   58 PPDTILGSLRVTVQGEVIEQSFGEELLCFQTLQRYTTATLEHGMKLPFSP 107

                  kPEWRk.LmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                  kPEWR +Lm+emA+v t EYRs+v++EPRFvEY RlAtPElEYG+mniG
  gi|2145451  108 KPEWRAtLMDEMAIVSTNEYRSIVFQEPRFVEYLRLATPELEYGRMNIGI 157

                  RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                  RP+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD Kn
  gi|2145451  158 RPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIQKDQKN 207

                  lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                  lq L+EmY+eWPFFRvt+DL+EmvF KG PGiAaLyDkLLv+ eL PFG+
  gi|2145451  208 LQILREMYNEWPFFRVTIDLIEMVFTKGSPGIAALYDKLLVSPELLPFGE 257

                  sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                  +LR++Y+Etk lLL +AGHk+lLEGDPYLKqrlRLR +YittLnvfqAYt
  gi|2145451  258 QLRANYEETKRLLLMVAGHKELLEGDPYLKQRLRLRYPYITTLNVFQAYT 307

                  LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                  LKRiRDPsy+   +Phl  E    n  +a+eLv Lnpt+++aPGLEDtLi
  gi|2145451  308 LKRIRDPSYH-PAQPHLPTEIVHSN-NQAAELVNLNPTSEYAPGLEDTLI 355

                  LtmKGiAAGmqntG<-*
                  LtmKGiAA
  gi|2145451  356 LTMKGIAA------    363

gi|18073856|emb|CAC84945.1|: domain 1 of 1, from 1 to 365: score 81.8, E = 2.5e-21
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807385    -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807385    - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807385    - ------------------------------------------------ -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
```

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  gi|1807385     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807385     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807385     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807385     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807385     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807385     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807385     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807385     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807385     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+i vAKk+GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807385     9 RLSAAWQLYKAQEELIEVAKKHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEHGm PP+ P
  gi|1807385    59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHGMIPPLTP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|1807385   109 KPEWRALMDEMAVVATERYRSIVFREPRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KR PsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh idKD Knl
  gi|1807385   159 PSKREPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFKHVIDKDNKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+ mY+eWPFFRvt+DL+Em+FAKG PGiAaLyDkLLv+EeL P G++
  gi|1807385   209 LMLQQMYNEWPFFRVTIDLVEMMFAKGNPGIAALYDKLLVSEELLPLGEE 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR  Y +tk +LLki GH ++LEG P+LKqr +LR +YittLnv+qAYtL
  gi|1807385   259 LRTAYNDTKSYLLKITGHNEILEGNPFLKQRHKLRTAYITTLNVCQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPsy+  +rP+++KE  +     a  LvkLnpt+++aPGLEDtLiL
  gi|1807385   309 KRIRDPSYRGPVRPPIAKEISEGSVSSAKKLVKLNPTSEYAPGLEDTLIL 358

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807385   359 TMKGIAA------    365

gi|7739277|emb|CAB90713.1|: domain 1 of 1, from 1 to 362: score 81.2, E = 3.7e-21
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7739277     -    ------------------------------------------- -
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```
                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|7739277    - ------------------------------------------------ -

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|7739277    - ------------------------------------------------ -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|7739277    - ------------------------------------------------ -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|7739277    - ------------------------------------------------ -

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|7739277    - ------------------------------------------------ -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|7739277    - ------------------------------------------------ -

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|7739277    - ------------------------------------------------ -

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|7739277    - ------------------------------------------------ -

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|7739277    - ------------------------------------------------ -

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|7739277    - ------------------------------------------------ -

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
gi|7739277    1 -------------------------------------------SDSGKDAG 8

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLYk qEE+++vAK++GvKL++FHGRGGtvGRGGGPtHL iLsq
gi|7739277    9 RLSAAWQLYKTQEELVQVAKQFGVKLTMFHGRGGTVGRGGGPTHLGILSQ 58

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PPDti GslRvtvqGEviE+ FGEE LCFr+LqRFt AtLEHGm+  +sP
gi|7739277   59 PPDTILGSLRVTVQGEVIEQCFGEERLCFRTLQRFTVATLEHGMHHHISP 108

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                kPEWR Lm+emAv+At EYRs+v+++PRFvEYFRlAtPElEYG+mniGsR
gi|7739277  109 KPEWRSLMDEMAVIATKEYRSIVFQDPRFVEYFRLATPELEYGRMNIGSR 158

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i KDi+nl
gi|7739277  159 PAKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVITKDIRNL 208

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  L+EmY+ WPFFRvt+DL+EmvF KG PGiA+LyD+LLv+ +L  FG +
gi|7739277  209 HILREMYNGWPFFRVTIDLIEMVFTKGNPGIASLYDELLVSNDLLSFGME 258

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR++Y+Etk lLL++AGHkDlLEGDP LK rlRLRd+YittLnv+qAYtL
gi|7739277  259 LRANYEETKRLLLQVAGHKDLLEGDPHLK-RLRLRDPYITTLNVCQAYTL 307

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                KRiR+Psy+     h+s E   E  k a+eLvkLnpt+++aPGLEDtLiL
```

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  gi|7739277   308 KRIREPSYHAMAPHHVSNE--TESRKSAAELVKLNPTSEYAPGLEDTLIL 355

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|7739277   356 TMKGIAA------    362

gi|56696455|ref|YP_166812.1|: domain 1 of 1, from 10 to 879: score 78.4, E = 2.6e-20
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      s DA + +     v          A L   +L +L          +v
  gi|5669645    10   SADATVYA---AEVH---------ARLRLAWLRVLR-----RRAPVV 39

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA..
                       E  Ae+                + + a+ +  A    H+  + ++
  gi|5669645    40 ARAIEGGAEF---------------WDAAAYAEHLQAATIWFHLQQIMde 74

                   nLA.EEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                   nLA  E + A R    +   G Fa  a A  + D    +++L
  gi|5669645    75 NLAiREARQAERSGAARDVPGSFA-RALADADPDARREMRRLLAEA---- 119

                   eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                             sv   +tAHPt + R s++  + Ri   L q   +   ++
  gi|5669645   120 --------KLSVGPTITAHPTEAKRVSVMEIHRRIYRHLVQFESRRWSPQ 161

                   DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                   +   L+  L  Ei   + t E+R  +P    E+  G+ ++   +   vP+
  gi|5669645   162 EETRLEQRLEMEIDLLWLTGELRMERPSLAAEIDWGLQFYRTSLIAAVPR 211

                   FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      R   A+         P  + L kF sW+GGDRDG nP vt  vtR
  gi|5669645   212 LYERYRSAVEA-EFGPGFPGTACL-KFHSWIGGDRDG-NPNVTAQVTRLA 258

                   CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                      +R m   +Y+  +++++  ls+    ++  v      r a    v++
  gi|5669645   259 LERSRDMMRGVYVTALDEIVQRLSL----SDRLVPVPPAERAALERIVTR 304

                   yYiE..FWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA
                      ++    q  P+E +R                    A  i++  E
  gi|5669645   305 RADDpaACAQRNPNELFRQA------------------AAAIAQSVEGS 335

                   vytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLD
                    y +v +F+  LE   + L       +AD  +  l+ qv  FG     LD
  gi|5669645   336 RYAHVADFIADLETLDRGLQAIDAGLLADLLVRPLIWQVNVFGFRAHTLD 385

                   iRqEseRqtDvlDAittHLeiG...sYReWsEeKRqEWLlaEL.kGKRPL
                   iRq se  t  l  + +  +  +++    Ws   R E    +L+   R
  gi|5669645   386 IRQNSEVVTRALHDLWQVTGEApepLSPAWSARLRAELGKPDLpYVNRAR 435

                   lgsDLPktEEvkDvldafr.vLAELPiDsFGaYiismataPsDvLAvELL
                   lg   P   E+   l+ +r++       + G++i+sm+ +  D LAv LL
  gi|5669645   436 LG---PEAAELMALLELMReIRTGADPQAIGPFILSMTRSADDLLAVYLL 482

                   qRECgv...kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri...dG
                    R  g + ++ +L+vvPLFE + DL+AAPA +  +  +      ++++ G
  gi|5669645   483 ARYAGFgaeRLPLKVVPLFETIEDLRAAPAILRDVLEVPVAARSLrdgSG 532

                   KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                   + e+m+GYsDs KD G l   W L +Aq  i +   + G K v FHGRGG
  gi|5669645   533 QIEIMLGYSDSNKDGGFLCSTWSLDRAQRAITRALARSGLKPVFFHGRGG 582

                   tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                    v RGG Pt  Ai +qP  t+nG lR t qGEv+   +         L
  gi|5669645   583 SVSRGGAPTERAIAAQPRGTLNGTLRLTEQGEVVTAKYANTGTAAAQLEL 632

                   FtAAtLEHGmnPPv.sPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                    +   L H  +P  ++  PE  ++me +       Y  + ++ P F +YF
  gi|5669645   633 LASSVLRHSAQPAFeAVDPEAEDVMETLSSLSQTRYQTL-LQHPAFLDYF 681

                   RlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWL
                     A P  E   + iGsRPa+R  +  +  LRAiPW+FaW q R  +  W
  gi|5669645   682 NQASPVNELALLRIGSRPARRFGAQSLADLRAIPWVFAWSQNRHMISSWY 731
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                    GvGAAFK.hAidKDiKnlqkLkEmYkeWPFFRvtlDLlE..mvFAKGD..
                    G+G A  ++   +  +   +L+ +++  P FR  +D +E+++v A+ D
  gi|5669645   732 GFGSAVEdFCTVRGERGRAQLRRLFERVPLFRLIVDEVEksLVLARLDia 781

                    PGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                     G AaL  +   aE +     ++ ++    ++ +  + G
  gi|5669645   782 EGYAALVSDRAGAEAIF---ARIGAEHGCSRQAIEMLTG----------- 817

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                     q+                    +R P++       +++  A   +  a
  gi|5669645   818 -QG------------------NGVRFPNFL----GRVARNDATLRAAHA 843

                    deLvkLnptervaPGLED..tLiLtmKGiAAGmqntG<-*
                    +++  L  + r  PG + +  L+ tm  i AG+  tG
  gi|5669645   844 AQIGLLG-ALRADPGQDRriRLMQTMNCISAGLGWTG    879

gi|18073852|emb|CAC84943.1|: domain 1 of 1, from 1 to 366: score 77.8, E = 3.9e-20
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807385     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807385     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807385     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807385     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807385     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807385     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807385     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807385     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807385     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807385     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807385     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807385     1 ----------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYkAqEE+i vAK++GvKL++F GRGGtvGRGGGPtHLAiLsq
  gi|1807385     9 RLSAAWQLYKAQEELIEVAKQHGVKLTMFRGRGGTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLE Gm PP+ P
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  gi|1807385    59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEQGMIPPLTP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   k EWR Lm+emAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|1807385   109 KQEWRALMDEMAVVATERYRSIVFREPRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh i+KDi+n
  gi|1807385   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHVIKKDIRNH 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+EmY++WPFFRvt+DLlEmvFAKGDPGiAaLyDkLLv+++L+ FG++
  gi|1807385   209 SVLREMYNDWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVSDDLQSFGER 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvf.qAYt
                   LR++Y++tk  LL++AGHkDlLEGDP+LKqrl+LR +YittLnv++qAYt
  gi|1807385   259 LRANYEDTKRRLLEVAGHKDLLEGDPFLKQRLKLRTAYITTLNVCqQAYT 308

                   LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                   LKRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLi
  gi|1807385   309 LKRIRDPSYRVPVRPPIAKEIMEGSVSSANQLVKLNPTSEYAPGLEDTLI 358

                   LtmKGiAAGmqntG<-*
                   LtmKGiAA
  gi|1807385   359 LTMKGIAA------    366

gi|7768248|emb|CAB90645.1|: domain 1 of 1, from 1 to 365: score 75.3, E = 2.2e-19
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768248     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768248     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768248     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768248     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768248     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768248     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768248     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768248     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768248     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768248     - ---------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768248     - ---------------------------------------------- -
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                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768248     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768248     9 RLSAAWQLYKAQEELIEVAKQHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEHGm PP+ P
  gi|7768248    59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHGMIPPLTP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  k EWR  m emAvvAtE YRs+v++EPR+vEYFRlAt E EYG+mniGsR
  gi|7768248   109 KQEWRAXMXEMAVVATERYRSIVFREPRYVEYFRLATXEXEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AF+h idKD Knl
  gi|7768248   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFRHIIDKDNKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L+ mY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL P G++
  gi|7768248   209 LMLQQMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELLPLGEQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR  Y +tk +LLki GH ++LEGDP+LKqrl+LR++Yit Lnv+qAYtL
  gi|7768248   259 LRTGYNDTKSYLLKITGHNEILEGDPFLKQRLKLRNAYITALNVCQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|7768248   309 KRIRDPSYRVPVRPPIAKEIMEGSDSSANQLVKLNPTSEYAPGLEDTLIL 358

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|7768248   359 TMKGIAA------    365

gi|7768366|emb|CAB90709.1|: domain 1 of 1, from 1 to 369: score 74.4, E = 4.2e-19
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768366     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768366     - ---------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768366     - ---------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768366     - ---------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768366     - ---------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768366     - ---------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768366     - ---------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768366     - ---------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
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  gi|7768366     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768366     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768366     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768366     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAW ++k qE+++KvAK++G+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768366     9 RLSAAWEMFKCQEDLVKVAKEHGIKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP sP
  gi|7768366    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPRSP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kP WR+Lm+emA vAtEEYR vv+K P FvEYFR+AtPE+EYG+mniGsR
  gi|7768366   109 KPKWRELMDEMAKVATEEYRNVVFKHPQFVEYFRSATPETEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFK  + K + nl
  gi|7768366   159 PAKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKQSLAKSSTNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     ++EmY+eWPFFRvt+DL+EmvFAKGDP iAaLyD+LLv++eLkP G++
  gi|7768366   209 ALMREMYNEWPFFRVTIDLIEMVFAKGDPRIAALYDELLVSDELKPLGQK 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR  Y Et++lLLkiAGH D+L G P LKqrlRLR++Yit Ln +qA+tL
  gi|7768366   259 LRTMYAETRELLLKIAGHEDVLAGNPTLKQRLRLREPYITPLNLIQAFTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    +iRD +++vt +P   +    +++k++ eLv Ln t +++PGLEDtLi+
  gi|7768366   309 AKIRDQNFHVTEQPTTPR--SGDPAKQSSELVSLNRTTEYPPGLEDTLII 356

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|7768366   357 TMKGIAAGMQNTG    369

gi|18076776|emb|CAC84961.1|: domain 1 of 1, from 1 to 357: score 74.2, E = 4.9e-19
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807677     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807677     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807677     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807677     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807677     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807677     - ------------------------------------------------ -
```

```
                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807677     - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807677     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807677     - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807677     - ------------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807677     - ------------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807677     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYk  E+++K AK+yG KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807677     9 RLSAAWQLYKTHEDLVKGAKEYGAKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti GslRvtvqGEviE+sFGEE+LCF++LqRFtAAtLEHGm+ P+ P
  gi|1807677    59 PPDTILGSLRVTVQGEVIEQSFGEEQLCFKTLQRFTAATLEHGMQVPITP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+emA++At EYRs+v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|1807677   109 KPEWRALMDEMAIIATNEYRSIVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD Knl
  gi|1807677   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIQKDPKNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q+L+Em +eWPFFRvt+DLlEmvF +G PGiAaLyDkLLv+ eL PFG++
  gi|1807677   209 QMLREMHNEWPFFRVTIDLLEMVFTRGNPGIAALYDKLLVSPELLPFGEQ 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  L ++Y+Et++lLL++AGHk lLE DPYLKqrlRLR +YittLnvfqAYtL
  gi|1807677   259 LIANYEETQNLLLQVAGHKVLLESDPYLKQRLRLRYPYITTLNVFQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KR+RDPsy     Phls        k+adeLvkLnp +++ PGLEDtLiL
  gi|1807677   309 KRMRDPSY---AEPHLS-----NAHKPADELVKLNPISEYGPGLEDTLIL 350

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807677   351 TMKGIAA------    357

gi|1166446|emb|CAA61084.1|: domain 1 of 1, from 1 to 365: score 74.0, E = 5.6e-19
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1166446     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1166446     - ------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1166446     - ------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
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  gi|1166446     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1166446     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1166446     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1166446     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1166446     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1166446     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1166446     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1166446     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1166446     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1166446     9 RLSAAWQLYKAQEELIEVAKQHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEHGm PP sP
  gi|1166446    59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHGMIPPSSP 108

                   kPEWRk.LmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                   k EWR  Lm+emAvv tE YRs+v++EPRFvEYFRlAtPElEYG+mniGs
  gi|1166446   109 KQEWRAcLMDEMAVVTTERYRSIVFREPRFVEYFRLATPELEYGRMNIGS 158

                   RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                   RP+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AF+h idKD Kn
  gi|1166446   159 RPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFRHVIDKDNKN 208

                   lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                   l +L+ mY+eWPFFR t+DL+EmvFAKGDPGiAaLyDkLL +EeL+P G+
  gi|1166446   209 LLMLQQMYNEWPFFRATIDLVEMVFAKGDPGIAALYDKLL-SEELWPLGE 257

                   sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                   +LR  Y +tk +LLki GH ++LEGDP+LKqrl++R +YittLnv+qAYt
  gi|1166446   258 QLRTAYNDTKSYLLKITGHNEILEGDPFLKQRLKVRTAYITTLNVCQAYT 307

                   LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                   LKRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLi
  gi|1166446   308 LKRIRDPSYQVPVRPPIAKEIMEGSVSSANQLVKLNPTSEYAPGLEDTLI 357

                   LtmKGiAAGmqntG<-*
                   LtmKGiAA
  gi|1166446   358 LTMKGIAA------    365

gi|7768234|emb|CAB90651.1|: domain 1 of 1, from 1 to 365: score 71.7, E = 2.8e-18
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768234     -    ------------------------------------------- -
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|7768234    - ------------------------------------------------- -

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|7768234    - ------------------------------------------------- -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|7768234    - ------------------------------------------------- -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|7768234    - ------------------------------------------------- -

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|7768234    - ------------------------------------------------- -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|7768234    - ------------------------------------------------- -

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|7768234    - ------------------------------------------------- -

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|7768234    - ------------------------------------------------- -

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|7768234    - ------------------------------------------------- -

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|7768234    - ------------------------------------------------- -

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                      sDsGKDAG
gi|7768234    1 -------------------------------------------SDSGKDAG 8

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|7768234    9 RLSAAWQLYKAQEELIEVAKQHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                P Dti+GslRvt+qGEviE sFGE + CF++LqR+tAAtLEH m PP+ P
gi|7768234   59 PADTIQGSLRVTIQGEVIERSFGEAQSCFKTLQRYTAATLEHSMIPPLTP 108

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                k EWR Lm++mAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
gi|7768234  109 KQEWRALMDKMAVVATERYRSIVFREPRFVEYFRLATPELEYGRMNIGSR 158

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+KRkPsGGiesL AiPWiFaWtqtRFHLPvWLG+  AF+h idKD Knl
gi|7768234  159 PSKRKPSGGIESLCAIPWIFAWTQTRFHLPVWLGFXEAFRHVIDKDNKNL 208

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                 +L+ mY+eWPFFRvt+DL+EmvFAKG PGiAaLyDkLLv+EeL P G++
gi|7768234  209 LMLQQMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEELLPLGEQ 258

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR  Y +tk +LL+i GH ++LEGDP+LKqrl+LR +YittLnv+qAYtL
gi|7768234  259 LRTAYNDTKSYLLRITGHNEILEGDPFLKQRLKLRTAYITTLNVCQAYTL 308

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
gi|7768234  309 KRIRDPSYQVPVRPPIAKEIMEGSVSSANQLVKLNPTSEYAPGLEDTLIL 358
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                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|7768234   359 TMKGIAA------    365

gi|237752184|ref|ZP_04582664.1|: domain 1 of 1, from 1 to 880: score 71.4, E = 3.4e-18
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +D         K       i++   L+   LD +          a
  gi|2377521     1    -MD---------KLQ----EIKFIFALMCEQLDAV----------AP 23

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    q      A  EGK+    L+ L a   s      ++ A ++ H+  L n+
  gi|2377521    24 QILPLFLALKEGKE--IDLNTLSAIEIS-----NLIKAFTLYHL--LLNI 64

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                     +E     R R ++ k               i  t+  L  +     +++
  gi|2377521    65 IDE-----RHRLSQVK------------NGAILTTITELKAQK-YDNADI 96

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       LK      v+tAHPt s RR  L     +   L   +       D +
  gi|2377521    97 QSVLKKIRFYPVFTAHPTESLRRTFLESYHEMSDDLEAWF----KFSDTQ 142

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                       E L   +   +    +R  +     E+   + ++   + +     L+
  gi|2377521   143 A-KEHLKYRLNLLWNSHIVRSEKIEVLFELDNLLYFMESSILRSGASVLK 191

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     v  AL  +G  E l    P i+  sW+GGDRDG nP vt  v  +v
  gi|2377521   192 EVQEALAELGDKEVLK-KSP-IRLGSWIGGDRDG-NPYVTNAVMLEVMKR 238

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                            Y+  ++ L  Els+    +E  +    l      +    +
  gi|2377521   239 QHQTIIHQYLKHIDKLSRELSI---AQEFVAPSQALLESLETE--KEHLD 283

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                       K++  +EP+R  L  +R KL n R  a  L    + e     +y +
  gi|2377521   284 SMAKKLFLQEPFRAKLTCMRQKLEN-RILALNLPQSALNE-NKLYMYANA 331

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                     eF+  +++   sL e     + +   L +L      G  L++LD Rq
  gi|2377521   332 KEFIKDIDMMIESLDERSSIYLKELKNLAILA-----GFHLMQLDFRQHR 376

                    eRqtDvlDAittHLei..GsYReWsEeKRqEWLlaELkG....KRPLlgs
                    +     l  i  HL+  +G     +   R   L + L  +  +   L+g
  gi|2377521   377 DVFWNALAEIFSHLGYvqGDLLLLPQSERTKILNTALDAplldLNTLYGK 426

                    DLPktEEvkDvldafrvLAELPiD.sFGaYiismataPsDvLAvELLqRE
                       +t E       f+   +  +D+   + iism+ +  D L v    +
  gi|2377521   427 LSTQTQETILAFVNFKWAKDRISDnIIDSCIISMCQSANDLLCVLWFAKQ 476

                    Cgv.....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...
                     g+ ++++k  + + PLFE + DLe APA +  L +   Y   ++ +++
  gi|2377521   477 SGLwrkgkKTRISISPLFETIGDLESAPAILRELCANPHYAEYLQSRkny 526

                    qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                    qe+m+GYsDs KD G ++  + L +A   +i    +  +K  lFHGRGG
  gi|2377521   527 QEIMIGYSDSSKDGGIFASNYSLKQAIGNLIALEDELKIKFRLFHGRGGS 576

                    vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                    v RGGG    A+Ls P   + G l+ t qGEvi   +   +
  gi|2377521   577 VSRGGGALEDALLSSPTNSVAGFLKTTEQGEVISEKYLNPKKAESNFESA 626

                    tAAtLEHGmnPPvsPkPEWRkLmee..mAvvAtE...EYRsvvvKEPRFv
                     A  L   +      k E   +  e+ + ++ tE+ + YR +v+    F+
  gi|2377521   627 LATLLKKSVYDKFKMKFEQGGVDFEpiLQIISTEsykAYRKLVYETQGFI 676

                    EYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLP
                    EYF++AtP     ++niGsRP+KRk    +e LRAiPW+FaWtq R  +P
  gi|2377521   677 EYFKSATPIYFIQQLNIGSRPSKRKDTQNVEDLRAIPWVFAWTQNRAIIP 726

                    vWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPG
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                    W G+G     A  K+      L+  Y+   FF+ t+D +   F K D
  gi|2377521   727 AWYGLGSGLEAAF-KECGEKEFLRQCYQGNLFFKTTIDNISQAFLKVDLD 775

                    iAaLyDkLLvaEeLkP.FGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLK
                    iA  y   +   eL+ +  + + ++Y  t ++LL +     lL  +  ++
  gi|2377521   776 IAKRYNAFVENVELREkIWQMIEEEYHRTLEWLLYVRNEEHLLASEKLIQ 825

                    qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                      + LR +++t L  fq   ++  ++  y             +E+
  gi|2377521   826 ESILLRKPFLTSLSFFQLHLMRAYKEAHY-------------AEQ----K 858

                    eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    e +              ++ t+ GiA G+ ntG
  gi|2377521   859 ERIAKQ------------IVTTIVGIAQGIRNTG    880

gi|2145471|emb|CAA62826.1|: domain 1 of 1, from 1 to 357: score 70.6, E = 5.8e-18
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2145471     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2145471     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2145471     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2145471     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2145471     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2145471     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2145471     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2145471     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2145471     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|2145471     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|2145471     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|2145471     1 ----------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWqLYk qE+++KvAK+yGvKL++FHGRGGtvGRGGGP HLAiLsq
  gi|2145471     9 RLSAAWQLYKTQEDLVKVAKEYGVKLTMFHGRGGTVGRGGGPSHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti GslRvtvqGEviE+sFGEE+LCF++LqRFtAAtLEHGm+ P+ P
  gi|2145471    59 PPDTILGSLRVTVQGEVIEQSFGEEQLCFKALQRFTAATLEHGMQVPITP 108
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                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emA++At EYRs v+KEPRFvEYFRlAtPElEYG+mniGsR
  gi|2145471   109 KPEWRALMDEMAIIATNEYRSSVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P KRkP GGiesLRA PWiFaWtqtRFHLPvWLG+GAAFKh i+KD Knl
  gi|2145471   159 PLKRKPCGGIESLRANPWIFAWTQTRFHLPVWLGFGAAFKHVIQKDPKNL 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    q+L+Em +eWPFFRvt+DLlEmvF KG PGiAaLyDkLLv+  L PFG++
  gi|2145471   209 QMLREMHNEWPFFRVTIDLLEMVFTKGNPGIAALYDKLLVSPALLPFGEQ 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    L ++Y+Et++lLL++AGHk lLE DPYLKqrlRLR +YittLnvfqAYtL
  gi|2145471   259 LIANYEETQNLLLQVAGHKVLLESDPYLKQRLRLRYPYITTLNVFQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KR+RDPsy     Phls        k+adeLvkLnpt+++ PGLEDtLiL
  gi|2145471   309 KRMRDPSY---AEPHLS-----NAQKPADELVKLNPTSEYGPGLEDTLIL 350

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|2145471   351 TMKGIAA------    357

gi|2145354|emb|CAA62825.1|: domain 1 of 1, from 1 to 356: score 70.3, E = 7.1e-18
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2145354     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2145354     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2145354     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2145354     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2145354     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|2145354     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2145354     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2145354     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2145354     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|2145354     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|2145354     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
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                                                        sDsGKDAG
  gi|2145354     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYk qEE++ vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|2145354     9 RLSAAWQLYKTQEELVEVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                     Dti GslRvtvqGEviE+sFGEEnLCFr+LqRFtAAtLEHGm+ P+sP
  gi|2145354    59 ASDTILGSLRVTVQGEVIEQSFGEENLCFRTLQRFTAATLEHGMQLPISP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emA+vAt EYRs+v++EPRFvEYFRlAtPElE G+mniGsR
  gi|2145354   109 KPEWRALMDEMAIVATKEYRSIVFQEPRFVEYFRLATPELECGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+K   nl
  gi|2145354   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIEKTKNNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q L+EmY+eWPFFRvt+DL+EmvF KG  GiAaLy kLLv+EeL+PFG++
  gi|2145354   209 QILQEMYNEWPFFRVTIDLIEMVFTKGSTGIAALYNKLLVSEELQPFGEQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   L ++Y E k lLL++AGHk lLEGDPYLKqrlRLR +YittLnv+qAYtL
  gi|2145354   259 LIANY-ENKRLLLEVAGHKVLLEGDPYLKQRLRLRYPYITTLNVCQAYTL 307

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDP+y    +Phls    + n k+a+eLvkLnpt+++aPGLEDtLiL
  gi|2145354   308 KRIRDPNY---AKPHLS----NSN-KPAAELVKLNPTSEYAPGLEDTLIL 349

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|2145354   350 TMKGIAA------    356

gi|7768306|emb|CAB90681.1|: domain 1 of 1, from 1 to 367: score 66.5, E = 9.7e-17
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768306     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768306     - ------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768306     - ------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768306     - ------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768306     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768306     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768306     - ------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768306     - ------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768306     - ------------------------------------------------- -
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                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768306     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768306     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768306     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  Rl+AAW ++k qE+++K+AK+yG+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768306     9 RLAAAWSMFKCQEDLVKIAKQYGIKLTIFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|7768306    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR+Lm+e+  v tEEYRs+v+K P+Fv YFR AtPE+EYG+mniGsR
  gi|7768306   109 KPEWRELMDEISRVSTEEYRSIVFKHPKFVHYFRAATPETEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKhA +K  +n+
  gi|7768306   159 PAKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHAFEKSNQNV 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+ mY+eWPFFRvt+DL+EmvFAKGDP iAaLyD+LLv EeLkP G++
  gi|7768306   209 VLLRQMYNEWPFFRVTIDLIEMVFAKGDPRIAALYDELLVDEELKPLGEK 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR  Y Et+dlLLk+AGH D+L G P LKqrlRLR++Yit Lnv qA+tL
  gi|7768306   259 LRTMYAETRDLLLKVAGHEDVLQGNPTLKQRLRLREPYITPLNVQQAFTL 308

                  KRiRDPsykvtlrPhlsKEyAdEns.kkadeLvkLnptervaPGLEDtLi
                  K+iRD s++v +  +       Ens+k++ eLv Ln t +++PGLEDtLi
  gi|7768306   309 KKIRDQSFHVSPGTP-----KGENSgKQSSELVGLNTTTEYPPGLEDTLI 353

                  LtmKGiAAGmqntG<-*
                  +tmKGiAAGmqntG
  gi|7768306   354 ITMKGIAAGMQNTG    367

gi|10303371|emb|CAA65108.1|: domain 1 of 1, from 1 to 368: score 64.0, E = 5.5e-16
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1030337     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1030337     - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1030337     - ------------------------------------------------ -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1030337     - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1030337     - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1030337     - ------------------------------------------------ -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|1030337     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1030337     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1030337     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1030337     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1030337     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1030337     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAW ++kAqEE++ vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1030337     9 RLSAAWYMFKAQEELVEVAKQYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvt+qGEviE sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|1030337    59 PPDTINGSLRVTIQGEVIEHSFGEEHLCFRTLQRFTAATLEHGMHPPISP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWRk+m+ mA vAtEEYRsvv++ P Fv YFR AtPElEYG+mniGsR
  gi|1030337   109 KPEWRKVMDSMALVATEEYRSVVFQNPDFVSYFRTATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWt tRFHLPvWLG+G A  hA++ D  n+
  gi|1030337   159 PSKRKPSGGIESLRAIPWIFAWTXTRFHLPVWLGLGGALAHALQSDPSNI 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+ mY++WPFF vtlDL+EmvFAKGDP iAaL+D LLv+ eLkPFG +
  gi|1030337   209 VILHRMYNQWPFFHVTLDLVEMVFAKGDPRIAALNDSLLVSPELKPFGVE 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR kY+Et+ lLLk+AGHkD+LEGDPYLKqrlRLR++Yit Lnv qAYtL
  gi|1030337   259 LRRKYEETRSLLLKVAGHKDVLEGDPYLKQRLRLREPYITVLNVQQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAd.EnskkadeLvkLnptervaPGLEDtLi
                   K++RD + k+      + E+A++ + k+  eLv Lnp +++aPGLEDtLi
  gi|1030337   309 KKMRDEECKI----NCATEWAArKPGKRTTELVALNPMSEYAPGLEDTLI 354

                   LtmKGiAAGmqntG<-*
                   LtmKGiAAGmqntG
  gi|1030337   355 LTMKGIAAGMQNTG    368

gi|1166444|emb|CAA61083.1|: domain 1 of 1, from 1 to 365: score 62.9, E = 1.2e-15
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1166444     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1166444     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1166444     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1166444     - ------------------------------------------------ -
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                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1166444     - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1166444     - ------------------------------------------------ -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1166444     - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1166444     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1166444     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1166444     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1166444     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1166444     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAW LYkA EE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1166444     9 RLSAAWHLYKAEEELIEVAKQHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  P Dti+GslRvt+qGEviE sFGE +LCF++LqR+tAAtLEHGm PP sP
  gi|1166444    59 PADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAATLEHGMIPPSSP 108

                  kPEWRk.LmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                  k E R  Lm+emAvv tE YRs+v++EPRFvEYFRlAtPElEYG+mniGs
  gi|1166444   109 KQECRAcLMDEMAVVTTERYRSIVFREPRFVEYFRLATPELEYGRMNIGS 158

                  RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                  RP+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AF+h idKD Kn
  gi|1166444   159 RPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFRHVIDKDNKN 208

                  lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                  l +L+ mY+eWPFFRvt+DL+EmvFAKGDPGiAaLyDkLL +EeL+P G+
  gi|1166444   209 LLMLQQMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDKLL-SEELWPLGE 257

                  sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                  +LR  Y +tk +LLki GH ++LEGDP+LKqrl++R +YittLnv+qAYt
  gi|1166444   258 QLRTAYNDTKSYLLKITGHNEILEGDPFLKQRLKVRTAYITTLNVCQAYT 307

                  LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                  LKRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLi
  gi|1166444   308 LKRIRDPSYQVPVRPPIAKEIMEGSVSSANQLVKLNPTSEYAPGLEDTLI 357

                  LtmKGiAAGmqntG<-*
                  LtmKGiAA
  gi|1166444   358 LTMKGIAA------    365

gi|2145426|emb|CAA62827.1|: domain 1 of 1, from 1 to 361: score 62.2, E = 1.9e-15
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2145426     -    ------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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gi|2145426     - ------------------------------------------------- -

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|2145426     - ------------------------------------------------- -

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|2145426     - ------------------------------------------------- -

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|2145426     - ------------------------------------------------- -

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|2145426     - ------------------------------------------------- -

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|2145426     - ------------------------------------------------- -

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|2145426     - ------------------------------------------------- -

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|2145426     - ------------------------------------------------- -

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|2145426     - ------------------------------------------------- -

                 EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|2145426     - ------------------------------------------------- -

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                       sDsGKDAG
gi|2145426     1 -------------------------------------------SDSGKDAG 8

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 RlsAAWqLYkAqE+++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|2145426     9 RLSAAWQLYKAQEDLVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                 PPDti GslRvtvqGEviE+sFGEEnLCFr+LqR+t AtLEHGm+ P+sP
gi|2145426    59 PPDTILGSLRVTVQGEVIEQSFGEENLCFRTLQRYTVATLEHGMQIPISP 108

                 kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                 kPEWR Lm+emA+vAtEEYRs v+KEPRFvEYFRlAtPElEYG+mniGsR
gi|2145426   109 KPEWRALMDEMAIVATEEYRSFVFKEPRFVEYFRLATPELEYGRMNIGSR 158

                 PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                 P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFKh i+KD Knl
gi|2145426   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHVIEKDPKNL 208

                 qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   L+Em ++WPFFRvt+DL+EmvF KG  GiAaLyDkLLv+ eL PFG++
gi|2145426   209 LLLREMHNNWPFFRVTIDLIEMVFSKGNSGIAALYDKLLVSPELLPFGEQ 258

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                 LR++Y+EtkdlLL++AGHk lLEGDPYL qrlRLR +YittLnv+qA+tL
gi|2145426   259 LRANYEETKDLLLQVAGHKSLLEGDPYL-QRLRLRVPYITTLNVYQAFTL 307

                 KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                     D   k  l+Ph+s          a+eLvkLnp++++aPGLEDtLiL
gi|2145426   308 T---DQRTKHRLQPHVSNQSKLNSNNTAAELVKLNPASEYAPGLEDTLIL 354
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                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|2145426   355 TMKGIAA------    361

gi|7768368|emb|CAB90710.1|: domain 1 of 1, from 1 to 368: score 61.5, E = 3.1e-15
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768368     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768368     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768368     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768368     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768368     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768368     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768368     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768368     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768368     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768368     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768368     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768368     1 ----------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWq++kAqE+++KvAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768368     9 RLSAAWQMFKAQEDLVKVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGslRvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP++P
  gi|7768368    59 PPDTINGSLRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPIAP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+ mAvvAtEEYRs+v++ P+Fv YFR AtPE+EYG+mniGsR
  gi|7768368   109 KPEWRALMDSMAVVATEEYRSIVFQNPKFVAYFRAATPEMEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G A  hA+d D Kn+
  gi|7768368   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGLGRALSHALDTDPKNI 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+ mY++WPFFRvt+DL+EmvFAKGDP iAaLyD LLv+ e kPFG++
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  gi|7768368   209 TTLRQMYNKWPFFRVTIDLVEMVFAKGDPRIAALYDSLLVSPEFKPFGEE 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR+kY Et++ LL++AGH D+L G P LKqrlRLR++Yit Lnv qAYtL
  gi|7768368   259 LRQKYNETRNNLLRVAGHDDVLAGNPTLKQRLRLREPYITPLNVQQAYTL 308

                   KRiRDPs..ykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                   K++R+ +++  +t   +l+K     ++k+a eLvkLn t ++aP LEDtL
  gi|7768368   309 KKMREENkqLNITQNGELAK-----PTKRATELVKLNTTTEYAPRLEDTL 353

                   iLtmKGiAAGmqntG<-*
                   iLtmKGiAAGmqntG
  gi|7768368   354 ILTMKGIAAGMQNTG    368

gi|7768216|emb|CAB90662.1|: domain 1 of 1, from 1 to 368: score 61.5, E = 3.2e-15
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768216     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768216     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768216     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768216     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768216     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768216     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768216     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768216     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768216     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768216     - ---------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768216     - ---------------------------------------------- -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768216     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   Rl+AAW ++k qE+++KvAK++G+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768216     9 RLAAAWSMFKCQEDLVKVAKQFGIKLTIFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|7768216    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 108
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                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR+Lm+e+  v tEEYRs+v+K P Fv YFR AtPE+EYG+mniGsR
  gi|7768216   109 KPEWRELMDEISRVSTEEYRSIVFKHPQFVHYFRNATPETEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFK A +K  +n+
  gi|7768216   159 PAKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKAAFQKSNQNV 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+ mY+eWPFFRvt+DL+EmvFAKGDP iAaLyD+LLv++eLkP G++
  gi|7768216   209 VLLRQMYNEWPFFRVTIDLIEMVFAKGDPRIAALYDELLVSDELKPLGEK 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR  Y Et++lLLk+AGH D+L G P LKqrlRLR++Yit Lnv qA+tL
  gi|7768216   259 LRVMYAETRELLLKVAGHEDVLQGNPTLKQRLRLREPYITPLNVQQAFTL 308

                    KRiRDPsykvtlrPhlsKEyAdEns.kkadeLvkLnptervaPGLEDtLi
                    K+iRD s++v   P+  K    Ens+k++ eLv Ln t +++PGLEDtLi
  gi|7768216   309 KKIRDQSFHV-RDPETPK---GENSgKQSSELVGLNTTTEYPPGLEDTLI 354

                    LtmKGiAAGmqntG<-*
                    LtmKGiAAGmqntG
  gi|7768216   355 LTMKGIAAGMQNTG    368

gi|7768093|emb|CAB90612.1|: domain 1 of 1, from 1 to 367: score 59.3, E = 1.4e-14
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768093     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768093     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768093     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768093     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768093     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768093     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768093     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768093     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768093     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768093     - ------------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768093     - ------------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
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  gi|7768093     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   Rl+AAW ++k qE+++K+AK+yG+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768093     9 RLAAAWSMFKCQEDLVKIAKQYGIKLTIFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|7768093    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR+Lm+e+  v tEEYRs+v+K P+Fv YFR AtPE+EYG+mniGsR
  gi|7768093   109 KPEWRELMDEISKVSTEEYRSIVFKHPKFVHYFRAATPETEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKhA +K  +n+
  gi|7768093   159 PAKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHAFEKSNQNV 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+ mY+e PFFRvt+DL+EmvFAKGDP iAaLyD+LLv E+LkP G++
  gi|7768093   209 VLLRQMYNECPFFRVTIDLIEMVFAKGDPRIAALYDELLVDEDLKPLGEK 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR  Y Et+dlLLk+AGH D+L G P LKqrlRLR++Yit Lnv qA+tL
  gi|7768093   259 LRTMYAETRDLLLKVAGHEDVLQGNPTLKQRLRLREPYITPLNVQQAFTL 308

                   KRiRDPsykvtlrPhlsKEyAdEns.kkadeLvkLnptervaPGLEDtLi
                   K+iRD s++v +  +       Ens+k++ eL  Ln t +++PGLEDtLi
  gi|7768093   309 KKIRDQSFHVSPGTP-----KGENSgKQSSELAGLNTTTEYPPGLEDTLI 353

                   LtmKGiAAGmqntG<-*
                   LtmKGiAAGmqntG
  gi|7768093   354 LTMKGIAAGMQNTG    367

gi|7768259|emb|CAB90665.1|: domain 1 of 1, from 1 to 368: score 59.0, E = 1.8e-14
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768259     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768259     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768259     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768259     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768259     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768259     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768259     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768259     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768259     - ---------------------------------------------- -
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                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768259     - ------------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768259     - ------------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768259     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  Rl+AAW ++k qE+++KvAK+yG+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768259     9 RLAAAWSMFKCQEDLVKVAKQYGIKLTIFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|7768259    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR+Lm+e+  v tEEYRs+v+K P Fv YFR AtP +EYG+mniGsR
  gi|7768259   109 KPEWRELMDEISRVSTEEYRSIVFKHPQFVHYFRAATPGTEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFK A +K  +n+
  gi|7768259   159 PAKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKAAFQKSNQNV 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+ mY+eWPFFRvt+DL+EmvFAKGDP iAaLyD+LLv+EeLkP G++
  gi|7768259   209 VLLRQMYNEWPFFRVTIDLIEMVFAKGDPRIAALYDELLVSEELKPLGEK 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR  Y Et++lLLk+AGH D+L G P LKqrlRLR++Yit Lnv qA+tL
  gi|7768259   259 LRLMYAETRELLLKVAGHDDVLQGNPTLKQRLRLREPYITPLNVQQAFTL 308

                  KRiRDPsykvtlrPhlsKEyAdEns.kkadeLvkLnptervaPGLEDtLi
                  K+iRD s++v   P+  K    Ens+k++ eLv Ln t +++PGLEDtLi
  gi|7768259   309 KKIRDQSFHV-RDPETPK---GENSgKQSSELVGLNTTTEYPPGLEDTLI 354

                  LtmKGiAAGmqntG<-*
                  LtmKGiAAGmqntG
  gi|7768259   355 LTMKGIAAGMQNTG    368

gi|18073824|emb|CAC84917.1|: domain 1 of 1, from 1 to 365: score 56.6, E = 9.6e-14
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807382     -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807382     - ------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807382     - ------------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807382     - ------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807382     - ------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807382     - ------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
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  gi|1807382     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807382     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807382     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807382     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807382     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807382     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+i vAK++GvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807382     9 RLSAAWQLYKAQEELIEVAKQHGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   P Dti+GslRvt+qGEviE sFGE + CF++LqR+tAAtLEH m PP+ P
  gi|1807382    59 PADTIQGSLRVTIQGEVIERSFGEAQSCFKTLQRYTAATLEHSMIPPLTP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   k EWR Lm+emAvvAtE YRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|1807382   109 KQEWRALMDEMAVVATERYRSIVFREPRFVEYFRLATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesL AiPWiFaWtqtR HLPvWLG+G   +h idKD Knl
  gi|1807382   159 PSKRKPSGGIESLCAIPWIFAWTQTRVHLPVWLGFGESVRHVIDKDHKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+ mY+eWPFFRvt+DL+Emv AKG PGiAaLyDkLLv+EeL P G++
  gi|1807382   209 LMLQQMYNEWPFFRVTIDLVEMVVAKGNPGIAALYDKLLVSEELLPLGEQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR  Y +tk +LL+i GH ++LEGDP+LKqrl+LR +YittLnv qAYtL
  gi|1807382   259 LRTAYNDTKSYLLRITGHNEILEGDPFLKQRLKLRTAYITTLNVRQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   KRiRDPsy+v +rP+++KE  +     a++LvkLnpt+++aPGLEDtLiL
  gi|1807382   309 KRIRDPSYQVPVRPPIAKEIMEGSVSSANQLVKLNPTSEYAPGLEDTLIL 358

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807382   359 TMKGIAA------    365

gi|7768091|emb|CAB90611.1|: domain 1 of 1, from 1 to 371: score 55.2, E = 2.4e-13
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768091     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768091     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768091     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768091     - ------------------------------------------------ -
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                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768091    - ------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768091    - ------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768091    - ------------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768091    - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768091    - ------------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768091    - ------------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768091    - ------------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768091    1 -----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWq++kAqE+++KvAK+yGv+L++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768091    9 RLSAAWQMFKAQEDLVKVAKQYGVRLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGslRvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP++P
  gi|7768091   59 PPDTINGSLRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPIAP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR++m+ mAv  t EYRs+v++ P+FvEYFR AtPElEYG+mniGsR
  gi|7768091  109 KPEWREIMDTMAVASTKEYRSIVFQNPKFVEYFRAATPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G A +  ++ D +n+
  gi|7768091  159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGLGSALREVLQTDPRNI 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+ mY++WPFFRvt+DL+EmvFAKGDP iAaLyD+LLv+ eLkPFG++
  gi|7768091  209 AILRRMYNQWPFFRVTIDLVEMVFAKGDPRIAALYDNLLVSNELKPFGEE 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR kY Et+++LLk+AGH D+L G P LKqrlRLR++Y+t Lnv qA  L
  gi|7768091  259 LRRKYNETREFLLKVAGHEDILQGNPTLKQRLRLREPYLTALNVQQALVL 308

                  KRiRDPsyk.vtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                  K++RD s +   l+   s E    + ++a+eLv+Lnpt +++PGLEDtLi
  gi|7768091  309 KKMRDQSSQfCALQNGQSNEVPKSP-RRAAELVELNPTTEFPPGLEDTLI 357

                  LtmKGiAAGmqntG<-*
                  LtmKGiAAGmqntG
  gi|7768091  358 LTMKGIAAGMQNTG    371

gi|2145479|emb|CAA62828.1|: domain 1 of 1, from 1 to 362: score 53.8, E = 6.5e-13
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2145479    -    ------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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gi|2145479     - ------------------------------------------------ -

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|2145479     - ------------------------------------------------ -

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|2145479     - ------------------------------------------------ -

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|2145479     - ------------------------------------------------ -

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|2145479     - ------------------------------------------------ -

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|2145479     - ------------------------------------------------ -

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|2145479     - ------------------------------------------------ -

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|2145479     - ------------------------------------------------ -

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|2145479     - ------------------------------------------------ -

                 EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|2145479     - ------------------------------------------------ -

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                       sDsGKDAG
gi|2145479     1 -----------------------------------------SDSGKDAG 8

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 RlsAAW +Yk qEE+++vAK++GvKL++FHGRGGtvGRGGGPtHL iLsq
gi|2145479     9 RLSAAWPVYKTQEELVQVAKQFGVKLTMFHGRGGTVGRGGGPTHLGILSQ 58

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                 PPDti GslRvtvqGEviE+ FGEE LCFr+LqRFt AtLEHGm+  +sP
gi|2145479    59 PPDTILGSLRVTVQGEVIEQCFGEERLCFRTLQRFTVATLEHGMHHHISP 108

                 kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                 kPEWR Lm+emAv+At EYRs+v++EPRFvEYFRlAtPElEYG+mni sR
gi|2145479   109 KPEWRSLMDEMAVIATKEYRSIVFQEPRFVEYFRLATPELEYGRMNIKSR 158

                 PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                 PaKRkPsGGiesLRAiPWiFaWt tRFHLPvWLG+GAAFKh i KDi+nl
gi|2145479   159 PAKRKPSGGIESLRAIPWIFAWTHTRFHLPVWLGFGAAFKHVITKDIRNL 208

                 qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   L+EmY+ WPFFRvt+DL+EmvF KG PGiA+LyD+LLv+ +L  FG +
gi|2145479   209 HILREMYNGWPFFRVTIDLIEMVFTKGNPGIASLYDELLVSNDLLSFGME 258

                 LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                 LR++Y+Etk lLL++AGHkDlLEGDP LKqrlR Rd+YittLnv+qAYtL
gi|2145479   259 LRANYEETKRLLLQVAGHKDLLEGDPHLKQRLRPRDPYITTLNVCQAYTL 308

                 KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                 K iRD +     r h+s E   E  k a+eLvkLnpt+++aPGLEDtLiL
gi|2145479   309 KAIRD-QVTTQWRTHVSNE--TESRKSAAELVKLNPTSEYAPGLEDTLIL 355

                 tmKGiAAGmqntG<-*
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                  tmKGiAA
  gi|2145479   356 TMKGIAA------    362

gi|7768148|emb|CAB90635.1|: domain 1 of 1, from 1 to 371: score 52.0, E = 2.3e-12
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768148     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768148     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768148     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768148     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768148     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768148     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768148     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768148     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768148     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768148     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768148     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768148     1 ----------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWq++kAqE+++KvAK+yGv+L++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768148     9 RLSAAWQMFKAQEDLVKVAKQYGVRLTMFHGRGGTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGslRvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP++P
  gi|7768148    59 PPDTINGSLRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPIAP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR++m++mAv+ t EYR+vv++ P+FvEYFR AtPElEYG+mniGsR
  gi|7768148   109 KPEWREIMDKMAVISTKEYRAVVFQTPKFVEYFRTATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G A K  ++ D +n+
  gi|7768148   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGLGSALKEVLQTDPRNI 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+ mY++WPFFRvt+DL+EmvFAKGDP iAaLyD+LLv++e+kPFG++
  gi|7768148   209 AILRRMYNQWPFFRVTIDLVEMVFAKGDPRIAALYDNLLVSDEIKPFGDE 258
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                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR kY Et+++LL++AGH D+L G P LKqrlRLR++Y+t Lnv qA  L
  gi|7768148   259 LRRKYNETREYLLRVAGHEDILQGNPTLKQRLRLREPYLTALNVQQALVL 308

                    KRiRDPsyk.vtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    K++RD s +   l+   s E    + ++a+eLv+Lnpt +++PGLEDtLi
  gi|7768148   309 KKMRDSSSQfCALQNGHSGEVPKSP-RRAEELVELNPTTEFPPGLEDTLI 357

                    LtmKGiAAGmqntG<-*
                    LtmKGiAAGmqntG
  gi|7768148   358 LTMKGIAAGMQNTG    371

gi|7768308|emb|CAB90705.1|: domain 1 of 1, from 1 to 371: score 51.5, E = 3.2e-12
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768308     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768308     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768308     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768308     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768308     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768308     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768308     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768308     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768308     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768308     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768308     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768308     1 ----------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWq++kAqE+++KvAK+yGv+L++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768308     9 RLSAAWQMFKAQEDLVKVAKQYGVRLTMFHGRGGTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP++P
  gi|7768308    59 PPDTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPIAP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
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                    kPEWR++m++mAv+ t EYR+vv++ P+FvEYFR AtPElEYG+mniGsR
  gi|7768308   109 KPEWREIMDKMAVISTKEYRAVVFQNPKFVEYFRTATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G A K  ++ D +n+
  gi|7768308   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGLGSALKEVLQTDPRNI 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+ mY++WPFFRvt+DL+EmvFAKGDP iAaLyD+LLv++e+kP G++
  gi|7768308   209 AILRRMYNQWPFFRVTIDLVEMVFAKGDPRIAALYDNLLVSDEVKPLGDE 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR kY Et+++LL++AGH D+L G P LKqrlRLR++Y+t Lnv qA  L
  gi|7768308   259 LRRKYNETREYLLRVAGHEDILQGNPTLKQRLRLREPYLTALNVQQALVL 308

                    KRiRDPsyk.vtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    K++RD s +   l+   s E    + ++a+eLv+Lnpt +++PGLEDtLi
  gi|7768308   309 KKMRDSSSQfCALQNGNSGEVPKSP-RRAAELVELNPTTEFPPGLEDTLI 357

                    LtmKGiAAGmqntG<-*
                    LtmKGiAAGmqntG
  gi|7768308   358 LTMKGIAAGMQNTG    371

gi|7768302|emb|CAB90679.1|: domain 1 of 1, from 1 to 369: score 51.0, E = 4.5e-12
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768302     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768302     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768302     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768302     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768302     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768302     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768302     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768302     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768302     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768302     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768302     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768302     1 -----------------------------------------SDSGKDAG 8
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                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWq++kAqE+++KvAK+yG++L++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768302      9 RLSAAWQMFKAQEDLVKVAKQYGIRLTMFHGRGGTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGslRvt+qGEviE+sFGEE+LCF++LqRFtAAtLEHGm+PP++P
  gi|7768302     59 PPDTINGSLRVTIQGEVIEQSFGEEHLCFKTLQRFTAATLEHGMHPPIAP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    k EWR+Lm+ mAv AtEEYRs v++ P+FvEYFR AtPE+EYG+mniGsR
  gi|7768302    109 KLEWRNLMDSMAVAATEEYRSFVFQNPKFVEYFRAATPEMEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAA +hAid D++nl
  gi|7768302    159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGLGAALRHAIDTDSQNL 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L  mY++WPFFRvt+DL+EmvFAKGDP iAaLyD+LLv+EeL+P G++
  gi|7768302    209 AMLCRMYDQWPFFRVTIDLVEMVFAKGDPRIAALYDNLLVSEELRPLGDE 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR kY+Et++lLL++A H D+L G P LKqrlRLR++Yit Lnv qA+tL
  gi|7768302    259 LRRKYEETRNLLLRVARHSDILQGNPTLKQRLRLREPYITALNVQQAFTL 308

                    KRiRDPs.ykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                    K++R+ ++ k     + s      + k+a eLv Lnpt +++PGLEDtLi
  gi|7768302    309 KKMREQNsCKLETSQPGS---PLKPVKRAMELVTLNPTTEFPPGLEDTLI 355

                    LtmKGiAAGmqntG<-*
                    LtmKGiAAGmqntG
  gi|7768302    356 LTMKGIAAGMQNTG    369

gi|10303358|emb|CAA65114.1|: domain 1 of 1, from 1 to 365: score 50.3, E = 7.3e-12
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1030335     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1030335     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1030335     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1030335     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1030335     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1030335     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1030335     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1030335     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1030335     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|1030335     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1030335     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1030335     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAW ++kAqEE+iKvAK++ +K+++FHGRGGtvGRGGGPtHLAiLsq
  gi|1030335     9 RLSAAWEMFKAQEELIKVAKHHDIKITMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP+sP
  gi|1030335    59 PPDTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPISP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR  m +mA +AtEEYRs+v+KEPRFvEYFRlAtPE+EYG+mniGsR
  gi|1030335   109 KPEWRARMAKMAAIATEEYRSIVFKEPRFVEYFRLATPEMEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkP GGi+sLRAiPWiFa tqtRFHLPvWLG+GAAFK+ +   +Kn
  gi|1030335   159 PSKRKPTGGIDSLRAIPWIFACTQTRFHLPVWLGFGAAFKYVVTENSKNS 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+EmY++WPFFRvtlDL+EmvF KGDP iA LyD+LLv+E L+ FG+
  gi|1030335   209 NTLREMYNQWPFFRVTLDLVEMVFTKGDPRIAELYDRLLVSETLHAFGEH 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR+kY Et+++LLk+AGH ++L G P LKqrlRLR++Yit Lnv qAYtL
  gi|1030335   259 LRAKYAETRNFLLKVAGHTEILAGNPTLKQRLRLREPYITVLNVQQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   K++RD s        +       n k+a+eLv Ln t++++PGLEDtLiL
  gi|1030335   309 KKMRDESQYCSFPGSVTL-----N-KPAAELVTLNTTSEYPPGLEDTLIL 352

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|1030335   353 TMKGIAAGMQNTG    365

gi|7768304|emb|CAB90680.1|: domain 1 of 1, from 1 to 369: score 47.9, E = 3.8e-11
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768304     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768304     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768304     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768304     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768304     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768304     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768304     - ------------------------------------------------ -
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                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768304    - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768304    - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768304    - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768304    - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|7768304    1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWq++kAqE+++KvAK+yG++L++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768304    9 RLSAAWQMFKAQEDLVKVAKQYGIRLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGslRvt+qGEviE+sFGEE+LCF++LqRFtAAtLEHGm+PP++P
  gi|7768304   59 PPDTINGSLRVTIQGEVIEQSFGEEHLCFKTLQRFTAATLEHGMHPPIAP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR+Lm+ mAv AtEEYRs v++ P+FvEYFR AtPE+EYG+mniGsR
  gi|7768304  109 KPEWRNLMDSMAVAATEEYRSFVFQNPKFVEYFRAATPEMEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFa tqtRFHLPvWLG+GAA +hAid D++nl
  gi|7768304  159 PSKRKPSGGIESLRAIPWIFACTQTRFHLPVWLGLGAALRHAIDTDSQNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   +L  mY++WPFFRvt+DL+EmvFAKGDP iAaLyD LLv+EeL+P G++
  gi|7768304  209 AMLCRMYDQWPFFRVTIDLVEMVFAKGDPRIAALYDSLLVSEELRPLGDE 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR kY Et++lLL++A H D+L G P LKqrlRLR++Yit Lnv qA+tL
  gi|7768304  259 LRRKYDETRNLLLRVARHSDILQGNPTLKQRLRLREPYITALNVQQAFTL 308

                  KRiRDPs.ykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                  K++R+ ++ k     + s      + k+a eLv Lnpt +++PGLEDtLi
  gi|7768304  309 KKMREQNsCKLETSQPGS---PLKPVKRAMELVTLNPTTEFPPGLEDTLI 355

                  LtmKGiAAGmqntG<-*
                  LtmKGiAAGmqntG
  gi|7768304  356 LTMKGIAAGMQNTG    369

gi|7768310|emb|CAB90706.1|: domain 1 of 1, from 1 to 375: score 47.6, E = 4.9e-11
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768310    -    ------------------------------------------------ -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768310    - ------------------------------------------------ -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768310    - ------------------------------------------------ -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768310    - ------------------------------------------------ -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|7768310     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768310     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768310     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768310     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768310     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768310     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768310     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768310     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAW ++k qE+++KvAK++G+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768310     9 RLSAAWEMFKCQEDLVKVAKEFGIKLTIFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDt++GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP sP
  gi|7768310    59 PPDTVHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPRSP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    PEWR Lm+emA vAtEEYR vv+K P FvEYFR AtPE+EYG+mniGsR
  gi|7768310   109 EPEWRVLMDEMALVATEEYRNVVFKHPQFVEYFRAATPETEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh + K   n+
  gi|7768310   159 PAKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHVLAKNNSNV 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+ mY+eWPFFRvt+DL+EmvFAKGDP iAaLyD+LLv++eLkP G++
  gi|7768310   209 VLLRKMYNEWPFFRVTIDLIEMVFAKGDPRIAALYDELLVSDELKPLGEK 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR+ Y Et++lL+ iAGH D+L G P LKqrlRLR++Yit Ln +qA+tL
  gi|7768310   259 LRAMYGETRELLMTIAGHEDVLAGNPTLKQRLRLREPYITPLNLIQAFTL 308

                   KRiRDPsykvtlrP....hlsKEyAdEnskkadeLvkLnptervaPGLED
                   ++iRD s ++ +r  ++++     A E  k++  Lv Ln   +++PGLED
  gi|7768310   309 QKIRDQSNHISVREagdrPSTPPKAGESGKQSSHLVTLNKKTEFPPGLED 358

                   tLiLtmKGiAAGmqntG<-*
                   tLi+tmKGiAAGmqntG
  gi|7768310   359 TLIITMKGIAAGMQNTG    375

gi|7768370|emb|CAB90711.1|: domain 1 of 1, from 1 to 371: score 47.2, E = 6.5e-11
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768370     -    ------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768370     - ------------------------------------------------ -
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```
                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|7768370    - ------------------------------------------------ -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|7768370    - ------------------------------------------------ -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|7768370    - ------------------------------------------------ -

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|7768370    - ------------------------------------------------ -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|7768370    - ------------------------------------------------ -

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|7768370    - ------------------------------------------------ -

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|7768370    - ------------------------------------------------ -

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|7768370    - ------------------------------------------------ -

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|7768370    - ------------------------------------------------ -

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                      sDsGKDAG
gi|7768370    1 -----------------------------------------SDSGKDAG 8

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWq++kAqE+++KvAK+yGv+L++FHGRGGtvGRGGGPtHLAiLsq
gi|7768370    9 RLSAAWQMFKAQEDLVKVAKQYGVRLTMFHGRGGTVGRGGGPTHLAILSQ 58

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PPDtinGslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtL HGm+PP++P
gi|7768370   59 PPDTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLGHGMHPPIAP 108

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                kPEWR++m++mAv+ t EYR+vv++ P+FvEYFR AtPElEYG+mniGsR
gi|7768370  109 KPEWREIMDKMAVISTKEYRAVVFQNPKFVEYFRTATPELEYGRMNIGSR 158

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G A K  ++ D +n+
gi|7768370  159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGLGSALKEVLQTDPRNI 208

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  L+ mY++WPFFRvt+DL+EmvFAKGDP iAaLyD+LLv++e+kP G++
gi|7768370  209 AILRRMYNQWPFFRVTIDLVEMVFAKGDPRIAALYDNLLVSDEVKPLGDE 258

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR kY Et+++LL++AGH D+L G P LKqrlRLR++Y+t Lnv qA  L
gi|7768370  259 LRRKYNETREYLLRVAGHEDILQGNPTLKQRLRLREPYLTALNVQQALVL 308

                KRiRDPsyk.vtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                K++RD s +   l+   s E    + ++a+eLv+Lnpt +++PGLEDtLi
gi|7768370  309 KKMRDSSSQfCALQNGNSGEVPKSP-RRAAELVELNPTTEFPPGLEDTLI 357

                LtmKGiAAGmqntG<-*
                LtmKGiAAGmqntG
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  gi|7768370   358 LTMKGIAAGMQNTG    371

gi|7768146|emb|CAB90632.1|: domain 1 of 1, from 1 to 375: score 44.9, E = 3.2e-10
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768146     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768146     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768146     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768146     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768146     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768146     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768146     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768146     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768146     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768146     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768146     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768146     1 ----------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWq++kAqE+++KvAK+yGv+L++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768146     9 RLSAAWQMFKAQEDLVKVAKQYGVRLTMFHGRGGTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGslRvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP++P
  gi|7768146    59 PPDTINGSLRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPIAP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR+Lm+ mAv  t EYRs+v++ P FvEYFR AtPElEYG+mniGsR
  gi|7768146   109 KPEWRELMDAMAVASTKEYRSIVFQNPSFVEYFRAATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkP GGiesLRAiPWiFaWtqtRFHLPvWLG+G A K A++ D +n+
  gi|7768146   159 PSKRKPNGGIESLRAIPWIFAWTQTRFHLPVWLGLGSALKQALQTDPRNI 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+ mY++WPFFRvt+DL+EmvFAKGDP iAaLyD+LLv+++LkP G++
  gi|7768146   209 ATLRRMYNQWPFFRVTIDLVEMVFAKGDPRIAALYDNLLVSDQLKPLGEE 258
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                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR+kY Et+dlLLki  H ++L G P LKqrlRLR++Yit Lnv qA  L
  gi|7768146   259 LRQKYNETRDLLLKITFHDEILQGNPSLKQRLRLREPYITALNVQQALVL 308

                  KRiRDPs..ykvtlrPhlsKEyAdEns..kkadeLvkLnptervaPGLED
                  K++RD s ++        sK+  + ++++k+a+eLv+Lnpt +++PGLED
  gi|7768146   309 KKMRDQSlqFCALQNSSSSKDQSELPTtpKRAAELVELNPTTEFPPGLED 358

                  tLiLtmKGiAAGmqntG<-*
                  tLiLtmKGiAAGmqntG
  gi|7768146   359 TLILTMKGIAAGMQNTG    375

gi|7768257|emb|CAB90664.1|: domain 1 of 1, from 1 to 366: score 44.9, E = 3.2e-10
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768257     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768257     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768257     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768257     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768257     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768257     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768257     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768257     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768257     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768257     - ---------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768257     - ---------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|7768257     1 -----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWq++kAqE+++KvAK+yGv+L++FHGRGGtvGRG GPtHLAi sq
  gi|7768257     9 RLSAAWQMFKAQEDLVKVAKQYGVRLTMFHGRGGTVGRGRGPTHLAIFSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDtinGslRvt+qGEv E+sFGEE+LCFr+LqRFtAAtLEHGm+PP++P
  gi|7768257    59 PPDTINGSLRVTIQGEVFEQSFGEEQLCFRTLQRFTAATLEHGMHPPIAP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR+Lm+ mAv AtEEYRs+v+K PRFvEYFR AtPElEYG+mniGsR
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  gi|7768257   109 KPEWRDLMDSMAVAATEEYRSIVFKNPRFVEYFRTATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtq RFHLPvWLG+GAAFK A++    n+
  gi|7768257   159 PSKRKPSGGIESLRAIPWIFAWTQNRFHLPVWLGLGAAFKTALEAKPENM 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L  mY++WPFFRvt+DL+EmvFAKGDP iA LyD LLv EeL+PFG++
  gi|7768257   209 NTLARMYDQWPFFRVTIDLVEMVFAKGDPRIAQLYDTLLVKEELRPFGEE 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR kY Etk  LLkiA H D+L G P LKqrl LR++Yit Lnv qAYtL
  gi|7768257   259 LRRKYNETKLHLLKIARHTDILQGNPTLKQRLLLREPYITALNVQQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   K++R+ +    ++P+  K     ++k+a eLv Lnpt ++aPGLEDt+iL
  gi|7768257   309 KKMREQNSSQPPQPESPK-----PTKPASELVTLNPTTEFAPGLEDTVIL 353

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|7768257   354 TMKGIAAGMQNTG    366

gi|7768095|emb|CAB90613.1|: domain 1 of 1, from 1 to 371: score 43.8, E = 6.9e-10
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768095     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768095     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768095     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768095     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768095     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768095     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768095     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768095     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768095     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768095     - ---------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768095     - ---------------------------------------------- -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768095     1 -----------------------------------------SDSGKDAG 8
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                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWq++kAqE+++KvAK+yGv+L++FHGRG tvGRGGGPtHLAiLsq
  gi|7768095     9 RLSAAWQMFKAQEDLVKVAKQYGVRLTMFHGRGRTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGslRvt+qGEviE+sFGEE+LCF++LqRFtAAtLEHGm+PP++P
  gi|7768095    59 PPDTINGSLRVTIQGEVIEQSFGEEHLCFKTLQRFTAATLEHGMHPPIAP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR+Lm+ mA+ AtEEYRsvv++ PRFvEYFR AtPElEYG+mniGsR
  gi|7768095   109 KPEWRELMDSMAITATEEYRSVVFQNPRFVEYFRTATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GA  K A+     n+
  gi|7768095   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGLGAGLKQALAAKPENM 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L  mY++WPFFRvt+DL+EmvFAKGDP iA LyD LLva eL+PFG++
  gi|7768095   209 NILSRMYDQWPFFRVTIDLVEMVFAKGDPRIAELYDTLLVAPELRPFGDE 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR  Y Etk  LLkiA H D+L G P LKqrlRLR++Yit Lnv qA+tL
  gi|7768095   259 LRRLYNETKLHLLKIARHTDILQGNPTLKQRLRLREPYITALNVQQAFTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    K++R+ + +      +s+     + k a eLv Lnpt ++aPGLEDt+iL
  gi|7768095   309 KKMREQNPHQVASTNISQPDSPKPMKAASELVTLNPTTEFAPGLEDTMIL 358

                    tmKGiAAGmqntG<-*
                    tmKGiAAGmqntG
  gi|7768095   359 TMKGIAAGMQNTG    371

gi|7768382|emb|CAB90719.1|: domain 1 of 1, from 1 to 363: score 43.5, E = 8e-10
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768382     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768382     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768382     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768382     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768382     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768382     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768382     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768382     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768382     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|7768382     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768382     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768382     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYk qEE+++vAKk+ v L++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768382     9 RLSAAWQLYKCQEELVQVAKKFDVVLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   P Dt+nGslRvtvqGEviE+sFGEE+LCF++LqRFtAAtLEHGm+PP sP
  gi|7768382    59 PRDTVNGSLRVTVQGEVIEQSFGEEHLCFKTLQRFTAATLEHGMHPPTSP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   k EWRkLm+em  + tE YRsvv++EP+Fv YFR+AtPElEYG+mniGsR
  gi|7768382   109 KEEWRKLMDEMGAISTEVYRSVVFQEPKFVSYFRMATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+ RkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++ DiKnl
  gi|7768382   159 PSNRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGTAFKHVVQEDIKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+EmY+eWPFFRvt+DL+EmvFAKGDP iAaLyD LLv+ +L+  Gk+
  gi|7768382   209 RILQEMYEEWPFFRVTVDLVEMVFAKGDPRIAALYDSLLVSPDLQEIGKQ 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR+kY+ t++lLL++AGHk+lLEG P LKqrlRLR+++ittLnv qAYtL
  gi|7768382   259 LRAKYEQTQKLLLQVAGHKELLEGNPTLKQRLRLREPFITTLNVQQAYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   K++R  +      P+       ++ k+a+eLv Ln t ++aPGLEDt+iL
  gi|7768382   309 KKMRQAD----SDPPA----VVDPRKPAAELVNLNKTTEYAPGLEDTVIL 350

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|7768382   351 TMKGIAAGMQNTG    363

gi|139438299|ref|ZP_01771852.1|: domain 1 of 1, from 46 to 889: score 43.4, E = 9.1e-10
                   *->siDAqLR.lLvPGKvsedekLieYD...ALLlDkFL..DiLqDLHGe
                       i   LR+ L+     e   L eYD++ A L Dk L+ +i+     +
  gi|1394382    46    EIPEELRdNLALFLRLERRVLSEYDpeiADLFDKILsaEIVANAGNP 92

                   dLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHm
                     + a     E          +    E+   + sL      ++ +a+
  gi|1394382    93 GTRAADEAVDEQGVPTADEPTAVAFREVVDLIDSLPLDKQQVIVRAFTSF 142

                   LnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkln
                     LAnL EE    yR    + +    + +++     ++   + +Lv  l
  gi|1394382   143 FHLANLSEE---NYRVAQLREREAGASTDTEVDPANELTVAYHQLVNEL- 188

                   KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLa...qLsA
                      e   e L       v+tAHPt + R+++  K  Ri n L +++ L
  gi|1394382   189 -GVEGANELLGKLEFHPVFTAHPTEARRKAVEGKIRRISNLLEerpRLGG 237

                   KDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtv
                    D+  ++++ L      Ei A  Rt  i   +PtP +E    +  +  t+
  gi|1394382   238 SDLVENERHML-----QEIDALVRTSPIALKKPTPVEEADTIIDIFDNTL 282

                   WkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtP
                   ++ +P   RR D  +         P      +  sW+G DRDG nP vt
  gi|1394382   283 FDVIPVIYRRFDDWVLGDKAGTVPPLCPAFFHPGSWIGSDRDG-NPNVTA 331

                   EvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaa
                    v R+v       Aa  +   v  L  E    R    L   A   +  a
  gi|1394382   332 KVSREV-------AAKYFTHMV--LKLEDKCRRIGRNLTLEATYSKPSAE 372
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                    rdkvvKyYiEF.......WKqvPPtEPYRviLGdvRDKLYntRERaRHLL
                       +  + +E +++ + +   +   EP R ++  + D+L  t  R
  gi|1394382   373 LINLWNHQVEMsprytarAELISEHEPHRAVMLVMADRLNATVRRI---- 418

                    AtGiseisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqv
                             + +y   +eFLE L +  +sL  CG    A G +  ++ qv
  gi|1394382   419 --------TDTMYHSADEFLEDLRVVQRSLAACGAVRAAYGPVQTIIWQV 460

                    stFGLsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaE
                      FG  +v ++ Rq s  +   l  i +
  gi|1394382   461 ESFGFHMVEMEFRQHSVVHARALKDIHEN---------------------- 489

                    LkGKRPLlgsDLPktEEvkDvldaf.rvLAELPiDsFGaYiismataPsD
                          + g   P+t Ev D   a++ +           Yiis + +
  gi|1394382   490 -----GIHGDLQPMTREVIDTFRAIgSIQKRYGKKMAHRYIISFTKSAQH 534

                    vLAvELLqRECgvkq....tLrvvPLFEkLADLeAAPAavekLFsiDWYi
                    v  v  L      ++++ + L v+PLFE+L DLe     ++++  +
  gi|1394382   535 VADVFELAHLSFAHEedvpELDVIPLFEQLEDLEGCVDVLDQMLTLPVVQ 584

                    nri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKL
                     r+ +++ + evm+GYsDs KDAG   A   L  AqE i+K A k  + L
  gi|1394382   585 KRLaqtNRRMEVMLGYSDSSKDAGPTTAMLALHSAQERIAKWAEKNDIDL 634

                    vlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEn
                    vl HGRGG vGRGGGP   A+L+qP   +n   + t qGEvi   +G
  gi|1394382   635 VLMHGRGGAVGRGGGPANKAVLAQPKGSVNCFFKLTEQGEVIFARYGNRT 684

                    LCFrsLqRFtAAtLEHGmnPPvsPkPE....WRkLmeemAvvAtEEYRsv
                    L  r +   +AAtL             E+++++ ++ e++     E Y  +
  gi|1394382   685 LAQRHVESVAAATLLQSAPSVEKTNTEttqkFWDMAEKLNTASHERYLDL 734

                    vvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsG.GiesLRAiPWiFa
                       E  F  +F   tP +E G + iGsRPaKR  + + ++ LR iPWiF+
  gi|1394382   735 LNTED-FTPWFSTVTPLTEVGLLPIGSRPAKRGLGAkSLDDLRTIPWIFS 783

                    WtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlE
                    W q R  L  W G+G A           l +Lk  Y+eWPFFR  +D +E
  gi|1394382   784 WSQARINLAAWYGLGTAC-----EQLGDLDQLKAAYQEWPFFRTFIDNIE 828

                    mvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDl
                    m  AK D  iA +y +L    +L    +++  + + t++++L i G
  gi|1394382   829 MSIAKTDQRIAKMYLHLGDRQDLS---EKVFTEMQLTRKWVLAIVG---- 871

                    LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA

  gi|1394382     - ------------------------------------------------- -

                    dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    dE    a    +L
  gi|1394382   872 DEWPAAAPSRARLR-----------------------RPCT    889

gi|7768134|emb|CAB90628.1|: domain 1 of 1, from 1 to 368: score 42.5, E = 1.7e-09
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768134     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768134     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768134     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768134     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|7768134     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768134     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768134     - ------------------------------------------------ -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768134     - ------------------------------------------------ -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768134     - ------------------------------------------------ -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768134     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768134     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768134     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWq++kAqE+++KvAK+yGv+L++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768134     9 RLSAAWQMFKAQEDLVKVAKQYGVRLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvt+qGEviE+sFGE +LCFr+LqRFtAAtLEHGm+PP++P
  gi|7768134    59 PPDTINGSLRVTIQGEVIEQSFGEQHLCFRTLQRFTAATLEHGMHPPIAP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR++m+ mAv  t EYRs+v++ P+FvEYFR AtPElEYG+mniGsR
  gi|7768134   109 KPEWREIMDVMAVASTKEYRSIVFQNPKFVEYFRAATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkP GGiesLRAiPWiFaWtqtRFHLPvWLG+G A + A++ D +n+
  gi|7768134   159 PSKRKPNGGIESLRAIPWIFAWTQTRFHLPVWLGLGSALREALETDPRNI 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+ mY++WPFFRvt+DL+EmvFAKGDP iAaLyD+LLv++eLkP G++
  gi|7768134   209 AILRRMYNQWPFFRVTIDLVEMVFAKGDPRIAALYDNLLVSDELKPLGEE 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR kY Et+dlLL++AGH D+L G P LKqrlRLR++Y+t Lnv qA  L
  gi|7768134   259 LRRKYSETRDLLLRVAGHEDILQGNPTLKQRLRLREPYVTALNVQQALVL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   K++RD s +       s      + k+a+eLv+Lnpt +++PGLEDtLiL
  gi|7768134   309 KKMRDQSTQFCALQNGSE--VKSP-KRAAELVELNPTTEFPPGLEDTLIL 355

                   tmKGiAAGmqntG<-*
                   tmKGiAAGmqntG
  gi|7768134   356 TMKGIAAGMQNTG    368

gi|2145352|emb|CAA62830.1|: domain 1 of 1, from 1 to 355: score 40.2, E = 8.1e-09
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2145352     -    ------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2145352     - ------------------------------------------------ -
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                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|2145352    - ------------------------------------------------- -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|2145352    - ------------------------------------------------- -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|2145352    - ------------------------------------------------- -

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|2145352    - ------------------------------------------------- -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|2145352    - ------------------------------------------------- -

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|2145352    - ------------------------------------------------- -

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|2145352    - ------------------------------------------------- -

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|2145352    - ------------------------------------------------- -

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|2145352    - ------------------------------------------------- -

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                      sDsGKDAG
gi|2145352    1 -----------------------------------------SDSGKDAG 8

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                RlsAAWqLYk qEE++ vAK+yGvKL++FHGRGGtvGRGGGPtHLAiLsq
gi|2145352    9 RLSAAWQLYKTQEELVEVAKEYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PPDti GslRvtvqGEviE+sFGEEnLCFr+LqRFtAAtLEHGm+ P+sP
gi|2145352   59 PPDTILGSLRVTVQGEVIEQSFGEENLCFRTLQRFTAATLEHGMQLPISP 108

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                kPEWR Lm+emA+vAt EYRs+v++EPRFvEYFRlAtPElEYG+mniGsR
gi|2145352  109 KPEWRALMDEMAIVATKEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 158

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFK   ++    +
gi|2145352  159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKQSSKRTKIIF 208

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                +  k    eWPFFRvt+DL+EmvF KG  GiAaLy kLLv+ +L+PFG++
gi|2145352  209 KYYKRCTIEWPFFRVTIDLIEMVFTKGSTGIAALYNKLLVSADLWPFGEQ 258

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR++Y Et+ lLL++AGHk lLEGDPYLKqrlRLR +YittLnv+qAYtL
gi|2145352  259 LRANY-ETQRLLLEVAGHKVLLEGDPYLKQRLRLRYPYITTLNVCQAYTL 307

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                KRiRDP+y    +Phls    + n k+a+eLvkLnpt+++aPGLE tLiL
gi|2145352  308 KRIRDPNY---AKPHLS----NSN-KPAAELVKLNPTSEYAPGLE-TLIL 348

                tmKGiAAGmqntG<-*
                tmKGiAA
gi|2145352  349 TMKGIAA------    355
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gi|7768198|emb|CAB90642.1|: domain 1 of 1, from 1 to 379: score 39.8, E = 1e-08
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768198     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768198     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768198     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768198     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768198     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768198     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768198     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768198     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768198     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768198     - ---------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768198     - ---------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|7768198     1 -----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAW ++k qE+++KvAK++G+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768198     9 RLSAAWEMFKCQEDLVKVAKEFGIKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP +P
  gi|7768198    59 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPRAP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                     WR++m+emA vAtEEYR +v+K P+FvEYFR AtPE+EYG+mniGsR
  gi|7768198   109 ERKWREVMDEMAKVATEEYRNIVFKHPKFVEYFRAATPETEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh + K   n+
  gi|7768198   159 PAKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHVLAKSNSNV 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+EmY+eW FFRvt+DL+EmvFAKGD  iAaLyD+LLv++eLkP G+
  gi|7768198   209 VLLREMYNEWSFFRVTIDLIEMVFAKGDSRIAALYDELLVSDELKPLGEH 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
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                  LR+ Y Et++lLLkiAGH D+L G P LKqrlRLR++Yit Ln +qA tL
  gi|7768198   259 LRAMYAETRELLLKIAGHEDVLAGNPTLKQRLRLREPYITILNLIQASTL 308

                  KRiRDPsykvtlrP..hlsKEyAdEns......kkadeLvkLnptervaP
                   +iRD ++++t +P+++ + +    +++++ ++k ++eLv Ln t +++P
  gi|7768198   309 CKIRDQNFHITEQPttPRAGDSSSQPTtpraggKHSAELVTLNRTTEYPP 358

                  GLEDtLiLtmKGiAAGmqntG<-*
                  GLEDtLi+tmKGiA GmqntG
  gi|7768198   359 GLEDTLIITMKGIATGMQNTG    379

gi|88799804|ref|ZP_01115377.1|: domain 1 of 1, from 1 to 517: score 39.1, E = 1.8e-08
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                             s
  gi|8879980     1    --------------S------------------------------- 1

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|8879980     - ------------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                                                    L+  +
  gi|8879980     2 -------------------------------------LIAVG------- 6

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|8879980     - ------------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|8879980     - ------------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|8879980     - ------------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                                                   l r a  d
  gi|8879980     7 ----------------------------------LDRVANAD------- 14

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|8879980     - ------------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                                           LLD +R v  FG+ Lv LDiRq+s
  gi|8879980    15 --------------------------LLDTIRRVHCFGINLVPLDIRQDS 38

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  eR+   lD i + +++G Y +WsE+ RqE+Ll  Lk KRPL++
  gi|8879980    39 ERHVKALDEIVRYVGLGEYESWSEDERQEFLLNQLKSKRPLIPRRWQPSA 88

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                  + ++vld+ +v+AE P ++   Yiisma  PsDvLAv LL +E gv   +
  gi|8879980    89 DTQEVLDTCQVVAEEPEETLSHYIISMAQQPSDVLAVALLLKEAGVTWNV 138

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                  ++vPLFE L DL+ AP  +++L+s  WY     G+q vm+GYsDs KDAG
  gi|8879980   139 PIVPLFETLDDLDRAPDVMQRLWSNHWYSQYSHGRQTVMIGYSDSAKDAG 188

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  ++ A W  YkAqE ++  A ++ + L+lFHGRGGtvGRGGGP   A+ sq
  gi|8879980   189 KITATWAQYKAQEALVELAGEHEIALMLFHGRGGTVGRGGGPVEKAMASQ 238

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP  + G +Rvt qGE+i + FG   +  rsL  + AAtL   ++P  +P
  gi|8879980   239 PPGSVPGEIRVTEQGEMIRYKFGQPRVAVRSLAVYVAATLRATLEPNPAP 288

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  k  WR L+e m       YR +v  + RFv YFR+ tPE E Gk+ +GsR
  gi|8879980   289 KQSWRSLIESMSQKSLKHYRQIVREDERFVPYFRSLTPEQELGKLALGSR 338
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                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    PaKRk  GG+esLRAiPW+FaW q R  LP WLG   A +hA+d +
  gi|8879980   339 PAKRKATGGVESLRAIPWVFAWMQVRLNLPAWLGATQALQHAVDEEP--- 385

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+Em ++WPFF   +DLlEmv  K D  iA  y++ Lv E  +  Gk+
  gi|8879980   386 ELLQEMVEQWPFFAAYIDLLEMVLGKADCSIAEYYEQQLVDEAYQDLGKQ 435

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++ +   dl+ +i    +lL  DP L q + +R +Y   Ln +qA  L
  gi|8879980   436 LRADLQTCADLMNRIKQQDELLISDPLLAQSVEVRAPYTDPLNYLQAELL 485

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KR                    E         k+    ++   LE  L +
  gi|8879980   486 KR--------------------ER--------KMG---QIDHDLEQALKV 504

                    tmKGiAAGmqntG<-*
                    tm Gi AGm ntG
  gi|8879980   505 TMAGISAGMRNTG    517

gi|7768097|emb|CAB90616.1|: domain 1 of 1, from 1 to 369: score 35.5, E = 2.2e-07
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768097     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768097     - ------------------------------------------------ -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768097     - ------------------------------------------------ -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768097     - ------------------------------------------------ -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768097     - ------------------------------------------------ -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768097     - ------------------------------------------------ -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768097     - ------------------------------------------------ -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768097     - ------------------------------------------------ -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768097     - ------------------------------------------------ -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768097     - ------------------------------------------------ -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768097     - ------------------------------------------------ -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768097     1 ----------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
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                    RlsAAWq++kAqE+++KvAK+yGv+L++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768097      9 RLSAAWQMFKAQEDLVKVAKHYGVRLTMFHGRGGTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDtinGs Rvt+qGEviE+sFGEE+LCF++LqRFtAAtLEHGm+PP++P
  gi|7768097     59 PPDTINGSFRVTIQGEVIEQSFGEEHLCFKTLQRFTAATLEHGMHPPIAP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR+Lm+ mAv AtEEYRsvv++ PRFvEYFR AtPElEYG+mniGsR
  gi|7768097    109 KPEWRELMDLMAVTATEEYRSVVFQNPRFVEYFRTATPELEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAA K A+     n+
  gi|7768097    159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGLGAALKQALAANPENV 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L  mY++WPFFRvt+DL+EmvFAKGDP iA LyD LLva eL+PFG++
  gi|7768097    209 TILSRMYDQWPFFRVTIDLVEMVFAKGDPRIAELYDTLLVAPELRPFGDE 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR  Y +tk  LLkiA H D+L G P LKqrlRLR++Yit Lnv qA+tL
  gi|7768097    259 LRRLYNDTKLHLLKIARHTDILQGNPTLKQRLRLREPYITALNVQQAFTL 308

                    KRiRDPs.ykvt..lrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                    K++R+ ++ +v + ++P   K     + k a eLv Lnpt ++aPGLEDt
  gi|7768097    309 KKMREQNtQHVAniPQPDSPK-----PMKAASELVTLNPTTEFAPGLEDT 353

                    LiLtmKGiAAGmqntG<-*
                    +iLtmKGiAAGmqntG
  gi|7768097    354 MILTMKGIAAGMQNTG    369

gi|237750822|ref|ZP_04581302.1|: domain 1 of 1, from 1 to 931: score 35.1, E = 2.8e-07
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                       +++L +Y+  L    L+++ +   +++kE
  gi|2377508      1    ---------------MQQELCKYE-FLKTILLEVIEE-NSPEVKETF 30

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       +    +     D+ K+ +L   +   +    ++ A ++  +  + n+
  gi|2377508     31 LMLFNSLRDKN--TDSTKIKDLFHEISESQYLMGVIKACSLHNI--ILNI 76

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEt.lKkLvlklnKsPeE
                     EE e A    +++           At    +EE ++ ++
  gi|2377508     77 YEEQEQAKIASVSRSI---------ATAYKNLEEEgFDRIDCDR------ 111

                    vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLs......AKD
                    v e ++      v+tAHPt s RR  L  +  i   L ++ + +  +
  gi|2377508    112 VLESIRFYP---VFTAHPTESRRRTFLEAHQEITRELEKIEqfsympSEQ 158

                    vtveDKkELD..EALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtv
                    +   D++   ++E +   +   ++   +R  +     E+   +  i   +
  gi|2377508    159 IPYKDREIAQsrESIKYRLHLLWKSHLVRSEKLEVIFELDNLLFIIENSI 208

                    WkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtP
                         + L  v   L         P  +  ik  sW+GGDRDG nP v
  gi|2377508    209 LPSALRVLNQVSNRLNK-------PLKISPIKLGSWIGGDRDG-NPFVSN 250

                    EvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaa
                    E+   v  +   +    Yi  +  L+ Els+     +      El++  +
  gi|2377508    251 EMMTRVMKMQHELIIQTYIKEINKLIRELSL---SVDFCTPSKELQKSLQ 297

                    rdkvvKyYiEFWK.qvPPtEPYRviLGdvRDKLYntRERaRHLL.AtGis
                    ++   K Y+     ++   EP+R  L  ++ KL n      HLL+   +
  gi|2377508    298 KE---KSYLNQTSlKLHEREPFRAKLNLIKLKLQN------HLLkVNAVG 338

                    eisEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGL
                    e+  +  y +  e LE +++   sL       iA   L  l   v   G
  gi|2377508    339 EV--DFTYQNPKELLEDIDMLIASL-----DSIAAKRLKSLRNLVLLGGF 381

                    sLvKLDiRqEseRqtDvlDAittHLeiG..sYReWsEeKRqEWLlaELkG
                     L++LD R   +     +  +   L+  ++ +    E K+ E L   L+
  gi|2377508    382 HLMQLDFREHRDMYMNAVSEVLCLLGYTdsDFIHRHESKKIEILNKVLSE 431
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                    KRPLlgsDL.PktEEvkDvldaf.rvL...AELPiDsFGaYiismataPs
                        l s L       +  l+af r+L  +  +  D   + i+sm+t  s
  gi|2377508   432 PPLNLNSILwEVSSQTRHTLNAFlRILwakKAISKDILKSVIVSMTTRAS 481

                    DvLAvELL.......qR.........ECgvkq...tLrvvPLFEkLADLe
                    D LAv  L   ++  q+++ ++++++EC +k +++ + + PLFE + DLe
  gi|2377508   482 DLLAVLYLaycsglwQKgkvkttdngECIIKDgksGIFITPLFETIEDLE 531

                    AAPAavekLFsiDWYinridG...KqevmvGYsDsGKDAGRlsAAWqLYk
                     A   +e L   + Y+  +  +++ q++m+GYsDs KD G +   + LYk
  gi|2377508   532 NAQEILEVLSKNEHYRQYLKDsgnAQQIMIGYSDSSKDGGIFTSNYSLYK 581

                    AqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslR
                    A   ++K  ++ G+  +lFHG+GG + RGGG    A+L+ P   i   l+
  gi|2377508   582 AISNLVKLEQRLGIHFMLFHGKGGSISRGGGQLESALLAFPRGSIGTTLK 631

                    vtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnP.............
                     t qGE+i   +    +  rs     A  L   ++ +   + +++++++
  gi|2377508   632 TTEQGEIISSRYLNPRVAIRSFALTLASLLKKAVHDnfcanlnpnsnggv 681

                    .............PvsPkPE...WRkLmeemAvvAtEEYRsvvvKEPRFv
                    +++++ ++   ++ +  k + +++   +ee+  +    YR +v+  P Fv
  gi|2377508   682 qntknldsvlvdkNIQIKCDvdpYLPKLEELSRISYRTYRDLVYETPNFV 731

                    EYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLP
                     YF+ AtP      +n+GsRP+KRk    +e LRAiPW+FaWtq R  +P
  gi|2377508   732 SYFKQATPIEFIQNLNLGSRPSKRKDTQRVEDLRAIPWVFAWTQNRSIIP 781

                    vWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPG
                     W G+G A K   dK     q L++ Yk+  FF+ t+D +   F K D
  gi|2377508   782 AWYGLGSALKGIGDK-----QLLQDCYKDSVFFKTTIDNIVQGFIKVDME 826

                    iAaLyDkLLvaEeLk.PFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLK
                    iA +y + +    Lk+    ++ ++Y Et ++LL      +lL+    ++
  gi|2377508   827 IAEMYNDFVQDFGLKqSIWSKIHNEYNETLEWLLITRNENELLDSNKEVR 876

                    qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                      +  R + i  L  +q   +++ +  +y              E+
  gi|2377508   877 ETILTRMPNIKALSLLQIELVRKYKQAQY--------------ED----- 907

                    eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                        L    r    +  t+i    GiA G+ ntG
  gi|2377508   908 ----LR--HRLMEQIHGTII----GIAQGIRNTG    931

gi|255588103|ref|XP_002534501.1|: domain 1 of 1, from 6 to 852: score 34.3, E = 5e-07
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       +  A + +          + i    +LlDk   iL ++ Ge++   +
  gi|2555881     6    AASATMSVAMASAETRLSENITLLGVLLDK--AIL-EVEGEEISRKI 49

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                         +  +   +D +   +L   L +L    ++ v +a+     L nL
  gi|2555881    50 AAIRQAALRFHQTHDQQASLDLEQLLAGLSLEHTVRVVRALAYFKHLVNL 99

                    AEEv...elAyRRRikkkkhGDFaDEasAttEsDi.EEtlKkLvlklnKs
                    AE+  +++l +   +     G  +       E+ i+ +t+K+L      s
  gi|2555881   100 AEDLygqQLGHCQQNTPAP-GMLSYTLLQIKEAGIpADTIKHLLEDALIS 148

                    PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                    P              vltAHPt   R+s+L  +  i   La   A+   v
  gi|2555881   149 P--------------VLTAHPTEVQRKSVLDIERLIAELLA---ARAAMV 181

                    eDKkELDEALHRE..iqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                     +++     L   + + A + t  +R ++     E+   + Y+  t  +
  gi|2555881   182 SERQLARNTLLLQgaVSALWQTRMMRYSKLSVLNEIENALTYYESTFLHV 231

                    vPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                    +P  L  ++  L  +     lP     ++  sW+GGDRDG nP v
  gi|2555881   232 IPEILQDIECDLADVLPDAALP---GFLRMGSWIGGDRDG-NPFVNGGTL 277

                    RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk
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                    R+   L  +    +Y++ +  L  El++      +      l +t++ +
  gi|2555881   278 RESVRLQAITLFKFYLQELSALKRELAVSTRVVGVDDAVLQLSKTSRDQ- 326

                    vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                              q    EPYR  L  + D+L  t   a  LL +G   ++E+
  gi|2555881   327 ---------SQHRLDEPYRLALNGIHDRLLAT---ANTLLPQGGWVLAED 364

                    Av...ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                       ++y   E  L PL     sL      ++    L  l++ + tFG  L
  gi|2555881   365 MAadpYETPEALLAPLQTIADSLRAHQGEALIYPRLGKLIKAIATFGFHL 414

                    vKLDiRqEseRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRP
                      +DiRq s+ +  v+  + +  +    Y  + E+ +   Ll ELk  R
  gi|2555881   415 ATVDIRQSSDVHEAVITELLQKAGHDfDYAGFNEDEKIGILLEELKQPRL 464

                    LlgsDLPktEEvkDvldafrvLAELPiDsFG.....aYiismataPsDvL
                    L+ +     E v   ++ +  + E+  + FG++  + Yiis + + sD L
  gi|2555881   465 LFSPFQQYSELVHKEIGVLVAVREM-RERFGehavrQYIISHTETLSDLL 513

                    AvELLqRECg..........vkqtLrvvPLFEkLADLeAAPAavekLFsi
                     v LLqRE g  ++  ++ +++  L +vPLFE +ADL+ AP  +
  gi|2555881   514 EVALLQREAGllrgvwgsanIQVDLNIVPLFETIADLRDAPMIM------ 557

                    DWYinridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvK

  gi|2555881     - ------------------------------------------------- -

                    LvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEE
                         G  G   R G               +G +R t qGE+i   + +
  gi|2555881   558 -----GHHGATQRHG---------------DGQIRLTEQGEIISTRYADP 587

                    nLCFrsLqRFtAAtLEHGmnPP....vsPkPEWRkLmeemAvvAtEEYRs
                     +  + L    AAtL+  + P ++ +   +  +  +me +   A   YRs
  gi|2555881   588 VVGRQHLETLIAATLDATLFPAdqleSGKRRAFEGVMETLSATAMTSYRS 637

                    vvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFa
                    +v+  P F EYF   tP  E   +n+GsRPa Rk    ie LRAiPW F+
  gi|2555881   638 LVYETPGFAEYFFNTTPINEIAELNLGSRPAARKSTRRIEDLRAIPWGFS 687

                    WtqtRFHLPvWLGvGAAFKhAidKD....iKnlqkLkEmYkeWPFFRvtl
                    W q R  LP W G+G A  h +++D+  +   l +L Em   WP F   +
  gi|2555881   688 WGQCRLLLPGWYGLGSAIHHFLQQDpalkEARLAMLLEMQAHWPLFNTLI 737

                    DLlEmvFAKGDPGiAaLyDkLLvaEeLk.PFGksLRdkYvEtkdlLLkiA
                      ++mv AK D  +A  y +LL   eL++    ++ ++ + t d +  +
  gi|2555881   738 QNVDMVLAKTDLIVARHYAHLLEDRELReEIFSRIAQEHKLTTDAVNLLL 787

                    GHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhl
                    G    L   P + + +R R +Y+  +n +q   ++R R  +
  gi|2555881   788 GTTQRLATQPVIAKSIRDRLPYLDPMNHLQVEMIQRYRNGE--------- 828

                    sKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                         dE                   L   + Lt+ GiA  + ntG
  gi|2555881   829 ----TDEK-------------------LKWAIPLTINGIATSLRNTG    852

gi|18073654|emb|CAC81270.1|: domain 1 of 1, from 1 to 358: score 31.0, E = 4.8e-06
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807365     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807365     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807365     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807365     - ------------------------------------------------- -
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                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807365     - ------------------------------------------------ -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807365     - ------------------------------------------------ -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807365     - ------------------------------------------------ -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807365     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807365     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807365     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807365     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807365     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqL+k qE++i vAK++GvKL +FHGRGGtvGRGGGPtHLAiLsq
  gi|1807365     9 RLSAAWQLFKSQEDLISVAKQFGVKLNMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PPv P
  gi|1807365    59 PPDTIHGSLRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPVKP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+emA v tEEYRs+v+KEPRF+EYF +AtP lEYG+mniGsR
  gi|1807365   109 KPEWRALMDEMALVSTEEYRSIVFKEPRFMEYFHSATPVLEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+  ++KD  nl
  gi|1807365   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFQAVLKKDPNNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+EmY+eWPFFRvt+DL+EmvFAKGDP iAaLyD+LLv +eLk FG
  gi|1807365   209 IVLQEMYNEWPFFRVTIDLVEMVFAKGDPRIAALYDELLVNDELKFFGTV 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR+kY+Etk+lLLk+AGH +lLEG PYLKqrl LRd+YittLn  qAYtL
  gi|1807365   259 LRAKYEETKELLLKVAGHEELLEGNPYLKQRLALRDPYITTLNLQQAYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  K++R+   +v     l K  A      a+eLv Ln t+++aPGLEDt+iL
  gi|1807365   309 KKMREG--HVGKSSSLLK--ARSS---AAELVSLNTTSEYAPGLEDTMIL 351

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807365   352 TMKGIAA------    358

gi|119504081|ref|ZP_01626162.1|: domain 1 of 1, from 1 to 626: score 25.8, E = 0.00017
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                             + P   s+  +L +    L +    ++q      L Eav
  gi|1195040     1    --------MTPSSTSNTAQLRQNVRHLGEILGQVIQSQGDAGLFEAV 39

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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                     s +    +D    e L a Lt L+    + vA+a++H LnLAn+
gi|1195040    40 EAIRLQSKQ---SRDDDDQEALRALLTQLNEKQILDVARAFSHFLNLANI 86

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                   AE          + +   D++      t s +E  +++L        +
gi|1195040    87 AE--------QHHTLA--DYSQSLFSATAS-LESAFQQLLKDH--EHNCL 123

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      LKn s+DLvltAHPt   RR L+ K++ i  CL+ L
gi|1195040   124 NTVLKNLSIDLVLTAHPTEITRRTLIHKHGEINDCLTRLEILNDKAAASS 173

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                        L   i   + t+E R  +P P DE R   + i   +W+ vP+FLR
gi|1195040   174 KDHSRLKELISQIWHTEEFRSDRPKPIDEARWAFAVIENSLWDAVPQFLR 223

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    vD       +    P   P i+ ssW+GGDRDG nP vt  vtR+v LL
gi|1195040   224 VVDDICERYALPIPPPNWSP-IRISSWIGGDRDG-NPNVTAKVTREVLLL 271

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                   a   A  l  + +  L  Els+      L    EE    a
gi|1195040   272 AQWQACTLLENDIVTLYEELSVTTASTAL----EEATEGAL--------- 308

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                            EPYR +L   RD+L       R  + + + + s       +
gi|1195040   309 ---------EPYRFLLKPLRDRL----QGQRLNIEKALNDQSLAPAPLTL 345

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    e ++PLE CY sL      v+A G LLD LR v  FG  L++LDiRqEs
gi|1195040   346 SEIVDPLEACYESLQAVNLDVLARGYLLDTLRRVHCFGPYLIQLDIRQES 395

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                    R+t  +  +t+ L +G YR+W E +R +WL  EL   RPL+++    t
gi|1195040   396 ARHTQAIAELTEALALGDYRDWNEGQRCDWLRGELDNPRPLIPAGWKPTP 445

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E ++v+d+f v+AE P  + G+Y+isma   sDvLAv +L +  g    +
gi|1195040   446 ETQEVIDTFLVIAETPQSALGSYVISMAAEASDVLAVQVLLKATGCTTNM 495

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                    v PLFE L DLe AP  ve L s   Y+ r d +  vm+GYsDs KDAG
gi|1195040   496 LVAPLFETLDDLESAPRVVEELLSDNAYRDRCDHQIMVMIGYSDSAKDAG 545

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    l+A W  Y+AqE +  v Kk+ vKL lFHGRGG +GRGG P H A+Lsq
gi|1195040   546 MLAAGWAQYRAQESLLSVCKKFAVKLQLFHGRGGSIGRGGAPAHDALLSQ 595

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP  ++  lRvt qGE+i    G
gi|1195040   596 PPGSLENGLRVTEQGEMIRTKLG--------------------------- 618

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

gi|1195040     - ------------------------------------------------- -

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

gi|1195040     - ------------------------------------------------- -

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

gi|1195040     - ------------------------------------------------- -

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

gi|1195040     - ------------------------------------------------- -

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                                          L  L             +iL
gi|1195040   619 ------------------------------LTPLA------------VIL 626
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                  tmKGiAAGmqntG<-*

  gi|1195040     - -------------    -

gi|149019670|ref|ZP_01834989.1|: domain 1 of 1, from 1 to 709: score 19.6, E = 0.013
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1490196     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                                                                 m+
  gi|1490196     1 ----------------------------------------------MI----- 2

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                            R kk+k          t E  i   +    +
  gi|1490196     3 ----------REKKLK---------VTNE--ITNAMEYYNSSF------- 24

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                            L    H t   +R L q ++     L    AK +t
  gi|1490196    25 ----------LKAVPHLTTEYKR-LAQAHG-----LNLKQAKPIT----- 53

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                                                +Gm
  gi|1490196    54 -------------------------------MGM---------------- 56

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                                           W+GGDRDG nP vt    +   L
  gi|1490196    57 --------------------------WIGGDRDG-NPFVTAKTLKQSALT 79

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                     +  n Y  ++  L  E+s+      +     E+ r ++ +     Y
  gi|1490196    80 QCEVIMNYYDKKIYQLYREFSLSTSIVNVSKQVREMARQSKDN---SIYR 126

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                  E        E YR  L d+  K+  t+          i +       y
  gi|1490196   127 E-------KELYRRALFDIQSKIQATK-------TYLIEDEEVGTRYETA 162

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                   +F   L     sL e     +  G  ++lL  v  FG  L  +D+Rq+s
  gi|1490196   163 NDFYKDLIAIRDSLLENKGESLISGDFVELLQAVEIFGFYLASIDMRQDS 212

                  eRqtDvlDAittHLeiGs.YReWsEeKRqEWLlaELkGK.RPLlgsDLPk
                        +  + +  +i s+Y e sEe + + Ll EL+  +R L      k
  gi|1490196   213 SVYEACVAELLKSAGIHSrYSELSEEEKCDLLLKELEEDpRILSATHAEK 262

                  tEEvk...DvldafrvLAE.LPiDsFGaYiismataPsDvLAvELLqREC
                   E ++++  +  + rvL ++L  D     iis at+ sD+L   +L +E
  gi|1490196   263 SELLAkelAIFKTARVLKDkLGDDVIRQTIISHATSLSDMLELAILLKEV 312

                  gv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...qe
                  g+ ++++  +++vPLFE + DL+    ++ k  s+   +  id +++ qe
  gi|1490196   313 GLvdteRARVQIVPLFETIEDLDHSEETMRKYLSLSLAKKWIDSRnnyQE 362

                  vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                  +m+GYsDs KD G ls  W LYkAq  +  +  ++GvK++ FHGRGGtvG
  gi|1490196   363 IMLGYSDSNKDGGYLSSCWTLYKAQQQLTAIGDEFGVKVTFFHGRGGTVG 412

                  RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                  RGGGPt  Ai sqP   i+  +R t qGEvi   +G  +  +  L
  gi|1490196   413 RGGGPTYEAITSQPLKSIKDRIRLTEQGEVIGNKYGNKDAAYYNLEMLVS 462

                  AtLEHGmnPPvsPk...PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                  A +   +    s  +++  +  +m+++     + YR +v+    F +YF
  gi|1490196   463 AAINRMITQKKSDTntpNRYEAIMDQVVDRSYDIYRDLVFGNEHFYDYFF 512

                  lAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG
                     P       niGsRPa Rk    i  LRAiPW+F+W q R   P W G
  gi|1490196   513 ESSPIKAISSFNIGSRPAARKTITEIGGLRAIPWVFSWSQSRVMFPGWYG 562

                  vGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaL
                  vG  FK  i+K   n+  L++mY++WPFF   l  ++mv  K    iA
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  gi|1490196   563 VGSSFKEFINKNPENIAILRDMYQNWPFFQSLLSNVDMVLSKSNMNIAFE 612

                   yDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRL
                   y kL   E++k   + + ++++ tk+ +L i GH +lL   PYLK  l
  gi|1490196   613 YAKLCEDEQVKAIYETILNEWQVTKNVILAIEGHDELLADNPYLKASLDY 662

                   RdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkL
                   R +Y   Ln +q   +KR R        r +ls +  +E       L+++
  gi|1490196   663 RMPYFNILNYIQLELIKRQR--------RGELSSD--QER------LIHI 696

                   nptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                   + GiA G+ n G
  gi|1490196   697 T----------------INGIATGLRNSG    709

gi|19070128|gb|AAL83719.1|AF236126_1: domain 1 of 1, from 1 to 339: score 18.9, E = 0.022
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                   s
  gi|1907012     1    --------------S------------------------------- 1

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1907012     - ------------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1907012     - ------------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1907012     - ------------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1907012     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1907012     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                                                          ar
  gi|1907012     2 ---------------------------------------ARA------- 4

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1907012     - ------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1907012     - ------------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1907012     - ------------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1907012     - ------------------------------------------------- -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG

  gi|1907012     - ------------------------------------------------- -

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                                              +FHGRGGtvGRGGGP  L
  gi|1907012     5 --------------------------MFHGRGGTVGRGGGPPILLYCLS 27

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PPvsP
  gi|1907012    28 PPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPVSP 77
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                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+emAv+At EYRs+v++EPRFvEYFRlAtPElEYG+mniGsR
  gi|1907012     78 KPEWRALMDEMAVIATKEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSR 127

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh i +D +nl
  gi|1907012    128 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHVIGRDPRNL 177

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     +L+ mY+eWPFFRvt+DL+EmvFAKGDPGiAaLyD+LLv+EeL+ FGk+
  gi|1907012    178 PMLQQMYNEWPFFRVTIDLVEMVFAKGDPGIAALYDRLLVSEELWLFGKR 227

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y+Etk lLL+iAGH+DlLEGDPYLKqrlRLRd+YittLnv+qAYtL
  gi|1907012    228 LRTNYEETKRLLLQIAGHRDLLEGDPYLKQRLRLRDAYITTLNVCQAYTL 277

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    KRiRDP+y+v  rPhlsKE   E sk+a+eLvkLnpt+++aPG+EDtLiL
  gi|1907012    278 KRIRDPNYHVMERPHLSKEIM-ESSKPAAELVKLNPTSEYAPGMEDTLIL 326

                    tmKGiAAGmqntG<-*
                    tmKGiAAG+qntG
  gi|1907012    327 TMKGIAAGLQNTG    339

gi|10303354|emb|CAA65110.1|: domain 1 of 1, from 1 to 371: score 16.1, E = 0.15
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1030335     -    ------------------------------------------------ -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1030335     - ------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1030335     - ------------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1030335     - ------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1030335     - ------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1030335     - ------------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1030335     - ------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1030335     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1030335     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1030335     - ------------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1030335     - ------------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
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  gi|1030335     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   R+sAAWqLYkAqEE++KvA +yG+KL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1030335     9 RFSAAWQLYKAQEELVKVAHHYGIKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDt++Gsl vt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP  P
  gi|1030335    59 PPDTVHGSLAVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPTPP 108

                   kPEWRkLmeemAvvA.tEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                   k   R+Lm++m v+ +tE +Rs v++ PRFvEYFR AtPE+EYG+mniGs
  gi|1030335   109 KEVRRRLMDKMGVICtTEAFRSFVFQNPRFVEYFRTATPEMEYGRMNIGS 158

                   RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                   RPaKRkPsGGiesLRAiPWiF WtqtRFHLPvWLG+G AFK  id D Kn
  gi|1030335   159 RPAKRKPSGGIESLRAIPWIFRWTQTRFHLPVWLGFGEAFKTVIDEDPKN 208

                   lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                   +  L+EmY++WPFFRvt+DL+EmvF KGDP iA LyD+LLvaE+L+  G+
  gi|1030335   209 FCVLREMYENWPFFRVTIDLVEMVFKKGDPRIAELYDHLLVAEDLQDLGN 258

                   sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                    LR+kY+Et++lLL++AGHk+lL G P LKq+lRLR++Y+ttLnv qAYt
  gi|1030335   259 TLRQKYKETENLLLQVAGHKELLAGNPTLKQKLRLREPYLTTLNVQQAYT 308

                   LKRiR..DPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt
                   L+++R+ D s+   +r  +       n  ka+eLv Lnpt ++aPGLEDt
  gi|1030335   309 LRKMRhlDTSFSSSPR-TVDGGTPRAN--KAAELVSLNPTTEYAPGLEDT 355

                   LiLtmKGiAAGmqntG<-*
                   LiLtmKGiAAGmqntG
  gi|1030335   356 LILTMKGIAAGMQNTG    371

gi|18072440|emb|CAC84970.1|: domain 1 of 1, from 1 to 339: score 14.2, E = 0.53
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807244     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807244     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807244     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807244     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807244     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807244     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807244     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807244     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807244     - ---------------------------------------------- -
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                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807244     - ------------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807244     - ------------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|1807244     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqLYkAqE+++KvAKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1807244     9 RLSAAWQLYKAQEDMMKVAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PP tinGs+Rvt+qGEviE+s GEE LCF++
  gi|1807244    59 PPGTINGSIRVTIQGEVIEQSCGEERLCFKT------------------- 89

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                        L++emAvvAt EYRs+v++EPRFvEYFRlAtPE+EYGkmniG R
  gi|1807244    90 ------LLDEMAVVATKEYRSIVFQEPRFVEYFRLATPETEYGKMNIGGR 133

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKh ++KD Kn+
  gi|1807244   134 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGVGAAFKHIMEKDKKNF 183

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q L+EmY+ WPFFRvt+DLlEmvFAKG P iAaLyDkLLv+E+L+PFG++
  gi|1807244   184 QTLREMYNVWPFFRVTIDLLEMVFAKGNPDIAALYDKLLVSEDLQPFGER 233

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR++YvEtk lLL++AGHkDlLEGDPYLKqrlRLR++YittLnv+qAYtL
  gi|1807244   234 LRNNYVETKSLLLQVAGHKDLLEGDPYLKQRLRLRNAYITTLNVCQAYTL 283

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  KRiRDP y v lrP lsK+  +   k+a+e + Lnpt+++aPGLEDtLiL
  gi|1807244   284 KRIRDPTYNVNLRPRLSKDVTERR-KPAAEFLTLNPTSEYAPGLEDTLIL 332

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807244   333 TMKGIAA------    339

gi|256370921|ref|YP_003108745.1|: domain 1 of 1, from 1 to 772: score 12.3, E = 2
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2563709     -    ------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                                                        m n+ n+
  gi|2563709     1 ----------------------------------------MFNVLNV 7

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                  AE  +             D +D a     s     l ++ l
  gi|2563709     8 AEGAD-------------DVTDLAKLAPRS-----LGRIRLTP------- 32

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                            vltAHPt   RR +L    Ri           v + D +
  gi|2563709    33 -----------VLTAHPTETKRRTILHTLQRIAH-----APNAVDPSDLR 66

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   L           + t+E+R  +    DE+  G+ Y+   +++ +P   R
  gi|2563709    67 LL-----------WFTEELRSRRLEVADEVHTGLFYLTTSLFDAIPVVYR 105

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                      A         +P     ++F sW+GGDRDG nP vt Evt+   +
  gi|2563709   106 QLAAARGVDADAIGVP-----VRFGSWIGGDRDG-NPLVTAEVTKAAFVA 149

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                         + s ++ +   l        +     E  r    d    +
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  gi|2563709   150 NATACLEAFRSRLDAVKRRLTHSMHFAAVSDAIVESIRNDEHD--FVHLA 197

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                     + +     EPY       R K+Y    R    L     +     +   v
  gi|2563709   198 PYVRTHYVDEPY-------RQKIYYLLARIDNQLHRLHNDPEALDIAPLV 240

                    EeFLE.PLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                       LE+ L L   sL   GD ++A+G L Dl+ q  tFG  L  LDiRqE
  gi|2563709   241 GPDLEtALRLIRDSLAAHGDTALAEGPLQDLVWQAATFGTHLASLDIRQE 290

                    se.RqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    s   +  +l+       +  Y e   + R   Lla L    P   +  P+
  gi|2563709   291 STvHHQAILELFGDDPRLAGYWEADADDRLSMLLACLD-HPP--HARTPR 337

                    tEEvkDvldafrvL....AELPiDsFGaYiismataPsDvLAvELLqREC
                    t  v+D +  f  L++ +AEL   + G+Y+ism+   +Dv+Av ++ R
  gi|2563709   338 TTLVADLVALFDTLttveAELGPAAIGSYVISMTHHAADVIAVLVIARAL 387

                    gvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridG...KqevmvG
                    g  + L + PLFE +ADLe     +e+LF +  Y  +++ +  +qevm+G
  gi|2563709   388 GADH-LDITPLFETIADLECLESVMEQLFTLPAYLAHLERralRQEVMLG 436

                    YsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGG
                    YsDs KD G  + A+ LY+AqE +i    ++ + + lFHGRGGtvGRGGG
  gi|2563709   437 YSDSTKDGGMAASAYALYRAQEALIGLGERHAITVELFHGRGGTVGRGGG 486

                    PtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLE
                    P      + P   + G +R+t qGE i   +   +    +L   tA
  gi|2563709   487 PIAQVARAHPRAALRGTIRITEQGETISHRYATTDRASATL--LTALGAF 534

                    HGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElE
                     G +   +P      + e +A      YR++      F  YFR+ tP  E
  gi|2563709   535 GGADDDTAPTDRAVMVTELVARSSEHAYRALTTSAG-FDAYFRSVTPFPE 583

                    YGkmniGsRPaKRkPs.GGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFK
                      ++ iGsRPa+R+ ++ G+ ++RAiPW+FaW q R  LP W G+G
  gi|2563709   584 LTQLRIGSRPARRHQAdTGLATIRAIPWVFAWAQSRHTLPAWFGIGTGL- 632

                    hAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLv
                     A  ++      ++E    WPF    lD + +  AK D  +A  y +L
  gi|2563709   633 -ATAREAHGDHAIREARASWPFVAGMLDNVQIALAKADMRLARRYLDL-- 679

                    aEe...LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRds
                    a+++++       + ++Y+ t    L+  G + lL   P L   l +R+
  gi|2563709   680 ADDpttAAAIFAVIEEEYERTVAETLRATGQRRLLAWSPTLADSLTVRNR 729

                    YittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpt
                     +  Ln +q   L   R                    s+ +d+L
  gi|2563709   730 VLAELNPLQVTALGAWR------------------SSRNPDDL------ 754

                    ervaPGLEDtLiL.tmKGiAAGmqntG<-*
                             tL+L+ +  iA   +n G
  gi|2563709   755 ---------TLVLrSINAIATVQKNSG    772

gi|6119717|emb|CAB59571.1|: domain 1 of 1, from 1 to 335: score 10.9, E = 3
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       siDAqLRlL+P Kvsed+kL+eY ALLlD+FLDiLqDLHGe ++E v
  gi|6119717     1    SIDAQLRLLAPAKVSEDDKLVEYVALLLDRFLDILQDLHGEVVRETV 47

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    qE YElsAeYE K+D+kKL+ELG  L sLdP+ +i++A++++HmLnLAnL
  gi|6119717    48 QELYELSAEYESKHDPKKLDELGNLLISLDPGNSIVIASSFSHMLNLANL 97

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    AEEv++A+RRRik+kk GDFaDEasAttEsD EEtlK+Lv kl K+P+E+
  gi|6119717    98 AEEVQIAFRRRIKLKK-GDFADEASATTESDFEETLKRLVGKLKKTPQEI 146

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    F+ALKnq+vDLvltAHPtqsvRRsLLqK++RiRnCL+qL+AKD+t++DK+
  gi|6119717   147 FDALKNQTVDLVLTAHPTQSVRRSLLQKHGRIRNCLTQLYAKDITPDDKQ 196
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                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                    ELDEALHREiqAAFRtDEiRR +PtPqDEmRaGmsY+HEt+WkGvP+FLR
  gi|6119717   197 ELDEALHREIQAAFRTDEIRRIPPTPQDEMRAGMSYFHETIWKGVPQFLR 246

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                    RvDtALKn+GinERlPY++PLi+FssWmGGDRDG nPRvtPEvtRDvCLL
  gi|6119717   247 RVDTALKNLGINERLPYNAPLIQFSSWMGGDRDG-NPRVTPEVTRDVCLL 295

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    aRmmAanlY+sq+EDLmFElsmWRC dELR RA+El+r   +
  gi|6119717   296 ARMMAANLYFSQIEDLMFELSMWRCSDELRLRADELQR---SS------- 335

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|6119717     - ------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|6119717     - ------------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|6119717     - ------------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|6119717     - ------------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG

  gi|6119717     - ------------------------------------------------- -

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq

  gi|6119717     - ------------------------------------------------- -

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP

  gi|6119717     - ------------------------------------------------- -

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR

  gi|6119717     - ------------------------------------------------- -

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl

  gi|6119717     - ------------------------------------------------- -

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks

  gi|6119717     - ------------------------------------------------- -

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL

  gi|6119717     - ------------------------------------------------- -

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|6119717     - ------------------------------------------------- -

                    tmKGiAAGmqntG<-*

  gi|6119717     - -------------    -

gi|7768255|emb|CAB90663.1|: domain 1 of 1, from 1 to 372: score 2.4, E = 3.3
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768255     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
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gi|7768255     - ------------------------------------------------ -

                 AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|7768255     - ------------------------------------------------ -

                 FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|7768255     - ------------------------------------------------ -

                 ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|7768255     - ------------------------------------------------ -

                 RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|7768255     - ------------------------------------------------ -

                 aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|7768255     - ------------------------------------------------ -

                 EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|7768255     - ------------------------------------------------ -

                 EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|7768255     - ------------------------------------------------ -

                 eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|7768255     - ------------------------------------------------ -

                 EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|7768255     - ------------------------------------------------ -

                 rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
gi|7768255     1 ----------------------------------------SDSGKDAG 8

                 RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                 RlsAAWq++kAqE+++KvAK+yGv+L++FHGRGGtvGRGGGPtHLAiLsq
gi|7768255     9 RLSAAWQMFKAQEDLVKVAKQYGVRLTMFHGRGGTVGRGGGPTHLAILSQ 58

                 PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                 PPDtinG lRvt+qGEviE+sFGE +LCFr+LqRFtAAtLEHGm+PP++P
gi|7768255    59 PPDTINGRLRVTIQGEVIEQSFGEQHLCFRTLQRFTAATLEHGMHPPIAP 108

                 kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                 kPEWR Lm+ mA v t EYRsvv++ P FvEYFR AtPElEYG+mniGsR
gi|7768255   109 KPEWRGLMDSMAEVSTKEYRSVVFQNPNFVEYFRTATPELEYGRMNIGSR 158

                 PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                 P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G A + A++ + +n+
gi|7768255   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGLGYALRQALESEPRNI 208

                 qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkP.FGk
                   L+ mY++WPFFRvt++L+EmvFAKGDP iAaLyD+LLv++eL  ++G+
gi|7768255   209 GHLRRMYNQWPFFRVTIELVEMVFAKGDPRIAALYDDLLVSDELVSrYGE 258

                 sLRdk.YvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAY
                 +L +++  Et+dlL ++AGH D+L G P LKqrlRLR++Yit Lnv qA
gi|7768255   259 ELSARsIYETRDLLSQVAGHEDILQGNPTLKQRLRLREPYITALNVQQAL 308

                 tLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                  LK++RD s +  +           + k+a+eLv+Lnpt +++PGLEDtL
gi|7768255   309 VLKKMRDQSSQFCVIDNGTPKAPKSP-KRAAELVELNPTTEFPPGLEDTL 357

                 iLtmKGiAAGmqntG<-*
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                  iLtmKGiAAGmqntG
  gi|7768255   358 ILTMKGIAAGMQNTG    372

gi|18073660|emb|CAC81273.1|: domain 1 of 1, from 1 to 358: score -2.8, E = 3.4
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807366     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807366     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807366     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807366     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807366     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807366     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807366     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807366     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807366     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807366     - ---------------------------------------------- -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807366     - ---------------------------------------------- -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                        sDsGKDAG
  gi|1807366     1 -----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWqL+k qE++i vAK++GvKL +FHGRGGtvGRGGGPtHLAiLsq
  gi|1807366     9 RLSAAWQLFKSQEDLISVAKQFGVKLNMFHGRGGTVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PPv P
  gi|1807366    59 PPDTIHGSLRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPVKP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+++  +At+ YR vv++EPRF+EYF +AtP lEYG+mniGsR
  gi|1807366   109 KPEWRALMDDITPIATDAYRGVVFQEPRFMEYFHSATPVLEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+GAAF+  ++KD  nl
  gi|1807366   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFQAVLKKDPNNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    L+EmY+eWPFFRvt+DL+EmvFAKGDP iAaLyD+LLv +eLk FG
  gi|1807366   209 IVLQEMYNEWPFFRVTIDLVEMVFAKGDPRIAALYDELLVNDELKFFGTV 258
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                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR+kY+Etk+lLLk+AGH +lLEG PYLKqrl LRd+YittLn  qAYtL
  gi|1807366   259 LRAKYEETKELLLKVAGHEELLEGNPYLKQRLALRDPYITTLNLQQAYTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    +  R+   +v     l K     +      Lv Ln t+++aPGLEDt+iL
  gi|1807366   309 RQGREG--HVGKSSSLLKARSSVE-----KLVSLNTTSEYAPGLEDTMIL 351

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|1807366   352 TMKGIAA------    358

gi|255037677|ref|YP_003088298.1|: domain 1 of 1, from 1 to 860: score -6.1, E = 3.5
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +       v  K       i     L   +  i q   G  L
  gi|2550376     1    -MNNSFQDAVVTKYN-----IFNSLFLSLPYRGIFQT--GSLLPILT 39

                    qECYElsAeYEGKkDtkKLeELGakL..tsLdPaDailvAkailHmLnLA
                    q         EGK   + +e   + L +t+     a l+   i  +
  gi|2550376    40 QQSEN--GFQEGKSPKEIIEHFFSELleTATPKERADLLFAFIQYIERQV 87

                    nLAEEve.lAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                     L + ve+ A+     +  +G  +  ++   EsD  E  KkL  kl
  gi|2550376    88 VLFDSVEdAAFDETHDLTGKGSVTYLTE-RLESD--ELKKKLLAKL---- 130

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                     E F      sv +vltAHPtq     +L     i n L       +  +
  gi|2550376   131 -EDF------SVRIVLTAHPTQFYSGKVLG----IINDLED----AIKEN 165

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    D  E+   L    + AF    i   +PtP DE      ++    ++ +P
  gi|2550376   166 DFAEVNQLLLQLGKTAF----INHEKPTPFDEAVSLCWFLENVYYDAIPS 211

                    FLRRvDtALKniGinER.lPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                     L +    +  +G+   + PY   + +   W GGDRDG nP v P++t
  gi|2550376   212 ILEKL---INGLGMSVHdWPYPN-VFRLGFWPGGDRDG-NPFVNPDITLK 256

                    vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                    v    R      Y+  +  L   l      d +      + +t
  gi|2550376   257 VAARLRETLLRGYYRDLRQLKRRLTFKGVDDAISLAEKKMNST------- 299

                    KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                                      i G   +   n  E     L   +    E  v
  gi|2550376   300 ------------------IFGPFEEGYNNAQE-----LIDEFLKAREVLV 326

                    ytkvEeFLEPLELCYksLCeCGDkviADGsLLD.lLRqvstFGLsLvKLD
                      +   F+E                     LLD+++ +   FG     LD
  gi|2550376   327 NKHQGLFVE---------------------LLDnFILKLNLFGFFFASLD 355

                    iRqEseRqtDvlDAittHLe.......iGsYReWsEeKRqEWLlaELkGK
                    +Rq+s ++    + i + Le++ +  +   Y  W E K+ + L   L+
  gi|2550376   356 VRQDSRKHGKAWEDILKRLEkkipllkYSDYEGWDEAKKIDLL---LSLN 402

                    RPLlgsDLPktEEvkDvldafrvLAELPiDs..FGa..YiismataPsDv
                     PL   D    E  kD+l+++r +  +    ++ Ga++Y+is  t+   v
  gi|2550376   403 IPLRDEDY-EDELTKDILGSIRAIKTIQEANgeKGAhrYVISNNTSALNV 451

                    LAvELLqRECgv....kqtLrvvPLFEkLADLeAAPAavekLFsiDWYin
                    + v  L +    ++ +k +L vvPLFE + DL  AP  +  L+  D+Y+n
  gi|2550376   452 MQVVALAKNLIAdeagKLALDVVPLFETVDDLANAPGIMRTLYENDYYRN 501

                    ri...dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLv
                    ++++++  q +mvG+sD  KD G l A W +Y+A+EE+ Kv +++G+K++
  gi|2550376   502 HLsnrENHQTIMVGFSDGTKDGGYLRANWSIYRAKEELTKVSREFGIKVT 551

                    lFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnL
                     F GRGG   RGGG  H    s   D  +  +  tvqG  i   +G
  gi|2550376   552 FFDGRGGPPARGGGNNHNFYSSLGKDIEDKEIQLTVQGQTISSNYGTVTT 601

                    CFrsLqRFtAAtLEHGm...nPPvsPkPEWRkLmeemAvvAtEEYRsvvv
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                       L R   A LE  + +++         ++L+eemA +A   Y  +
  gi|2550376   602 AMYNLERLFTAGLENHLfkgHREDELTEADKELIEEMAEIAYNSYLDL-K 650

                   KEPRFvEYFRlAtPElEYGkmniGsRPaKR...kPsGGiesLRAiPWiFa
                     P Fv Y    tP   YG+ niGsRP+KR+++  +   e LRAiP++ +
  gi|2550376   651 NHPMFVKYLDKKTPLRFYGQTNIGSRPTKRgndDEGLKFEDLRAIPFVGS 700

                   WtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlE
                   W q +  +P + G+G A +  + K  K +  +k +Y++  FFR  ++
  gi|2550376   701 WAQMKQNVPGFYGFGTAIRE-LGKTNK-VDEIKKLYQKSLFFRTLIENSM 748

                   mvFAKG.DPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkD
                       K   P    L D+    Ee + F +++ +++  t++lLL++ G k+
  gi|2550376   749 QSLSKAfFPATKYLRDE----EEYREFWDKMYEEFLLTRELLLEVSGQKE 794

                   lLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEy
                   lL+     K  ++ R+  +  L  +q Y L+              ls +
  gi|2550376   795 LLDSNNVTKVSIKTRERIVLPLITIQQYALQ------------MLSGDP 831

                   AdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    d +       v +             +i  m Gi     n
  gi|2550376   832 KDLP-------VDVE-------TYNQLIIRAMFGIINAARNSA    860

gi|18073658|emb|CAC81272.1|: domain 1 of 1, from 1 to 360: score -9.9, E = 3.7
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807365     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807365     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807365     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807365     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807365     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807365     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807365     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807365     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807365     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807365     - ---------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807365     - ---------------------------------------------- -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807365     1 -----------------------------------------SDSGKDAG 8
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                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWq++k qE+ +Kv  ++G+KL+lFHGRGG vGRGGGPtHLAiLsq
  gi|1807365      9 RLSAAWQVFKTQEDCVKVGHQFGIKLTLFHGRGGSVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP +P
  gi|1807365     59 PPDTIHGSLRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMQPPRAP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR Lm+++  +At+ YR vv++EP Fv YFR  tPElEYG+m iGsR
  gi|1807365    109 KPEWRALMDDITPIATDAYRGVVFQEPQFVQYFRAVTPELEYGRMDIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkP GGiesLRAiPWiFaWtqtRFHLPvWLG+G A K+A++KD Knl
  gi|1807365    159 PSKRKPDGGIESLRAIPWIFAWTQTRFHLPVWLGIGSALKYALNKDKKNL 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+EmY+ WPFFR t+DL+EmvFAKGDP iAaLyDkLLv+E+L+ FG+s
  gi|1807365    209 HVLQEMYNGWPFFRATIDLIEMVFAKGDPRIAALYDKLLVSEDLQQFGDS 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR++Y+Et+dlLL +AGH DlL G P LKqrl+LR++Yit Lnv q  tL
  gi|1807365    259 LRARYEETRDLLLLVAGHSDLLQGNPTLKQRLKLREPYITVLNVQQVHTL 308

                    KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    ++iR+    v      sK     n k+a+eLv Lnpt+++aPGLEDtLiL
  gi|1807365    309 RKIREGGVPVNS----SKSPVSQN-KPAAELVSLNPTSEYAPGLEDTLIL 353

                    tmKGiAAGmqntG<-*
                    tmKGiAA
  gi|1807365    354 TMKGIAA------    360

gi|18073656|emb|CAC81271.1|: domain 1 of 1, from 1 to 360: score -10.6, E = 3.7
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807365      -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807365      - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807365      - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807365      - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807365      - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807365      - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807365      - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807365      - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807365      - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|1807365     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807365     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807365     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWq++k qE+ +Kv  ++G+KL+lFHGRGG vGRGGGPtHLAiLsq
  gi|1807365     9 RLSAAWQVFKTQEDCVKVGHQFGIKLTLFHGRGGSVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDti+GslRvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP +P
  gi|1807365    59 PPDTIHGSLRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMQPPRAP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+++  +At+ YR vv++EP Fv YFR  tPElEYG+mniGsR
  gi|1807365   109 KPEWRALMDDITPIATDAYRGVVFQEPQFVQYFRAVTPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkP GGiesLRAiPWiFaWtqtRFHLPvWLG+G A K+A+ K  Knl
  gi|1807365   159 PSKRKPDGGIESLRAIPWIFAWTQTRFHLPVWLGIGSALKYALYKGQKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+ mY+ WPFFR t+DL+EmvFAKGDP iAaLyDkLLv+E+L+ FG+s
  gi|1807365   209 HVLQGMYNGWPFFRATIDLIEMVFAKGDPRIAALYDKLLVSEDLQQFGDS 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Et+dlLL +AGH DlL G P LKqrl+LR++Yit Lnv q  tL
  gi|1807365   259 LRARYEETRDLLLLVAGHSDLLQGNPTLKQRLKLREPYITVLNVQQVHTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   ++iRD +y    +   sK     n k+a+eLv Lnpt+++aPGLEDtLiL
  gi|1807365   309 RKIRDEEY----QYNSSKSPVSQN-KPAAELVSLNPTSEYAPGLEDTLIL 353

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807365   354 TMKGIAA------    360

gi|18076788|emb|CAC84974.1|: domain 1 of 1, from 1 to 357: score -11.7, E = 3.7
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807678     -    ------------------------------------------------ -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807678     - ------------------------------------------------ -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807678     - ------------------------------------------------ -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807678     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807678     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807678     - ------------------------------------------------ -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807678     - ------------------------------------------------ -
```

```
                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807678     - ------------------------------------------------ -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807678     - ------------------------------------------------ -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807678     - ------------------------------------------------ -

                  EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807678     - ------------------------------------------------ -

                  rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807678     1 ----------------------------------------SDSGKDAG 8

                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWq++k qE+ +KvA ++GvKL+lFHGRGG vGRGGGPtHLAiLsq
  gi|1807678     9 RLSAAWQVFKTQEDCVKVANQFGVKLTLFHGRGGSVGRGGGPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+ FGEE+LCFr+LqRFtAAtLEHGm PP +P
  gi|1807678    59 PPDTIHGSLRVTVQGEVIEQCFGEEHLCFRTLQRFTAATLEHGMPPPRAP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+e+  +At+EYR vv KEPRFv YFR  tPElEYG+mniGsR
  gi|1807678   109 KPEWRALMDEITPIATDEYRGVVSKEPRFVKYFRAVTPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G A +hA++KD +nl
  gi|1807678   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGIGSALQHALNKDKRNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q L+EmY+eWPFFR t+DL+EmvFAKGDP iAaLyDk Lv+ +L+ FG++
  gi|1807678   209 QLLQEMYNEWPFFRATIDLIEMVFAKGDPRIAALYDKYLVSGDLQQFGDE 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR kY +t+dlLL +AGH +lL G P LKqrl+LR++Y+t Lnv q YtL
  gi|1807678   259 LRKKYGDTRDLLLLVAGHSELLQGNPTLKQRLKLREPYLTVLNVQQVYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  +++RD  y   ++ + s+      sk+a eLv Ln t+++aPGLEDtLiL
  gi|1807678   309 RKMRDAGY--IPKSPTSQ------SKPASELVSLNTTSEYAPGLEDTLIL 350

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807678   351 TMKGIAA------    357

gi|213580501|ref|ZP_03362327.1|: domain 1 of 1, from 1 to 584: score -15.8, E = 3.9
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFL.DiLqDLHGedLkEa
                      +  q  +L    vs           +l k L++ ++D  Ge + +
  gi|2135805     1    -MNEQYSALR-SNVS-----------MLGKVLgETIKDALGEHILDR 34

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                  v     ls       ++ + +EL + L  L   + + vA+a++  LnLAn
  gi|2135805    35 VETIRKLSKSSRAGNEANR-QELLTTLQNLSNDELLPVARAFSQFLNLAN 83

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                   AE  +      i+ k       Ea    E  i  tl+kL  + +   +
  gi|2135805    84 TAEQYH-----SISPKG------EAASNPEV-IAHTLRKLKNQPDLNDAT 121

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                  +  A+   s +LvltAHPt   RR L+ K + i nCL qL   D+   ++
  gi|2135805   122 IKKAVESLSLELVLTAHPTEITRRTLIHKMGEINNCLKQLDNTDIADYER 171

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
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                    + +   L   i   + tDEiR+ +P P DE + G + +   +W+GvP +L
  gi|2135805   172 HQVMRRLRQLIAQSWHTDEIRKQRPSPVDEAKWGFAVVENSLWQGVPNYL 221

                    RRvDtAL.KniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    R     L+ n+G   +lP d   ++F+sWmGGDRDG nP vt E+tR v
  gi|2135805   222 RELNEQLeENLGY--KLPVDFVPVRFTSWMGGDRDG-NPNVTAEITRHVL 268

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    LL+R  A+ l++  +  L+ Elsm     EL +   E     a++
  gi|2135805   269 LLSRWKATDLFLKDIHVLVSELSMVDATPELLALVGE---EGASE----- 310

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeA.vy
                                PYR ++   R +L  t       L      ++  A+
  gi|2135805   311 ------------PYRYLMKKLRARLMATQSWLEARLKG--EKLPKPAgLL 346

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                    t+ E+  EPL  CY+sL  CG  +iA G LLD LR v  FG+ Lv++DiR
  gi|2135805   347 TQNEQLWEPLYACYQSLQACGMGIIANGELLDTLRRVKCFGVPLVRIDIR 396

                    qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    qEs R+t+ l  it+ L+iG Y +WsE  +q +L+ EL  KRPLl+
  gi|2135805   397 QESTRHTEALGEITRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWE 446

                    ktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvk
                       + ++vl++ +v+AE P  s  aY+isma +PsDvLAv LL +E g+
  gi|2135805   447 PSNDTREVLETCKVIAEAPKGSIAAYVISMAKTPSDVLAVHLLLKEAGIG 496

                    qtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGK
                     +++v PLFE L DL+ A   + +L  iDWY+  i+GKq vm+GYsDs K
  gi|2135805   497 FAMPVAPLFETLDDLNNADDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAK 546

                    DAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAi
                    DAG ++A W  Y+Aq+ +iK   k G+ L+lFHGRGG
  gi|2135805   547 DAGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGS------------ 584

                    LsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPP

  gi|2135805     - ------------------------------------------------- -

                    vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmni

  gi|2135805     - ------------------------------------------------- -

                    GsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi

  gi|2135805     - ------------------------------------------------- -

                    KnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPF

  gi|2135805     - ------------------------------------------------- -

                    GksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqA

  gi|2135805     - ------------------------------------------------- -

                    YtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDt

  gi|2135805     - ------------------------------------------------- -

                    LiLtmKGiAAGmqntG<-*

  gi|2135805     - ----------------    -

gi|10303360|emb|CAA65115.1|: domain 1 of 1, from 1 to 371: score -15.8, E = 3.9
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1030336     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1030336     - ------------------------------------------------- -
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                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1030336    - ------------------------------------------------ -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1030336    - ------------------------------------------------ -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1030336    - ------------------------------------------------ -

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1030336    - ------------------------------------------------ -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1030336    - ------------------------------------------------ -

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1030336    - ------------------------------------------------ -

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1030336    - ------------------------------------------------ -

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

gi|1030336    - ------------------------------------------------ -

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

gi|1030336    - ------------------------------------------------ -

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                      sDsGKDAG
gi|1030336    1 -----------------------------------------SDSGKDAG 8

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                R+sAAWqLYkAqEE++KvA +yG+KL++FHGRGGtvGRGGGPtHLAiLsq
gi|1030336    9 RFSAAWQLYKAQEELVKVAHEYGIKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                PPDt++GslRvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP  P
gi|1030336   59 PPDTVHGSLRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPTPP 108

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                k E  +Lm++m v+AtE YRs+v++ PRFvEYFR  tPE+EYG+mniGsR
gi|1030336  109 KLEHARLMDKMGVIATEAYRSIVFQHPRFVEYFRALTPEMEYGRMNIGSR 158

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDi.Kn
                P+KR+PsGG+++     WiFaWtqtRFHL vWLG+G AFK  +d+D +Kn
gi|1030336  159 PSKRRPSGGLNT-SCYTWIFAWTQTRFHLLVWLGFGEAFKLTVDRDDpKN 207

                lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                +  L+Em   WPFFRvt+DL+EmvF KGDP iA LyD+LLv+ +L+  Gk
gi|1030336  208 VDILREMSAHWPFFRVTIDLVEMVFKKGDPRIAELYDHLLVSPDLQDLGK 257

                sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                 LR+kY+Et++lLL++AGH +lL G P LKqrlRLR++Y+ttLnv qA t
gi|1030336  258 TLRQKYKETENLLLQVAGHNELLAGNPTLKQRLRLREPYLTTLNVQQAHT 307

                LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                L+++RD +      P           k a+eLv Lnpt ++aPGLEDtLi
gi|1030336  308 LRKMRDRENVFCSSPRTVDGGTPRANKSAAELVTLNPTTEYAPGLEDTLI 357

                LtmKGiAAGmqntG<-*
                LtmKGiAAGmqntG
```

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  gi|1030336   358 LTMKGIAAGMQNTG    371

gi|120435841|ref|YP_861527.1|: domain 1 of 1, from 2 to 857: score -16.8, E = 3.9
                  *->siDAqLRlLvPGKvsedekLieYDALLlDk.FLDiLqDLHGedLkEa
                       +  L        +   k   Y  + l  ++ Di +      L
  gi|1204358     2    HREPRLDRFNDNVLA---KYQVYNSIFLTLpYSDIRK---TGALLPL 42

                  vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                   qE  E    +   + ++++ +L     + +P++   v   +  +  +
  gi|1204358    43 FQEICE--TGFNNNENPSQIVDLFFEKYGENPSEEEKVDLLFRFIQYIER 90

                  LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeE
                       +       +         ++  t  s  EE   k   k      E
  gi|1204358    91 QVVLFDAIEDASFSIVN----NMDGRGTLRSVKEEAEAK--QKV----GE 130

                  vFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDK
                    + LK   v   ltAHPtq     +L          ++ L  K +  +D
  gi|1204358   131 LKDYLKRFNVRPTLTAHPTQFYPGTVL-------GIITDLD-KAIQKNDL 172

                  kELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFL
                    +   L    +  F     ++ +PtP DE    + Y+    ++   K
  gi|1204358   173 VKIRQLLAQLGKTPF----FKKEKPTPYDEAVNLIWYFENVFYQSASKIH 218

                  RRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCL
                    +    +ni   E +  +v  + F  W GGDRDG nP vt E+t  v
  gi|1204358   219 NYIQ---QNIFDGEDIGNQVVNLGF--WPGGDRDG-NPFVTTEITLRVAK 262

                  LaRmmAanlYisqvEDLmFElsmWRCndELRvRAEE.lyrtaardkvvKy
                    R      Y+  +  L   l  +R   EL    E +ly  a ++
  gi|1204358   263 RLRRTILLNYYRDIRKLKRRLT-FREVHELMTEIEKgLYDSAISK----- 306

                  YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                                +  L d + KL   +           s + E
  gi|1204358   307 ----------SGSIKLTLEDFKSKLLKIK----------SILIEKHQSL 335

                  kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                   +Ee                       + D+L +v  FG     LDiRq
  gi|1204358   336 FIEE----------------------VDDMLNKVHLFGYHFATLDIRQ 361

                  EseRqtDvlDAitt...HLeiGsYReWsEeKRqEWLlaELkGKRPLlgsD
                  +s  + +vl  i + ++ L    Y +  ++     +l+ +kGK   l ++
  gi|1204358   362 DSSIHEEVLAEISKlnpELIPSNYNDLNDDEQIK-ILSNVKGK---LDPE 407

                  LPktEEvkDvldafrvLAELPiDs..FGa..YiismataPsDvLA.vELL
                        +k  + ++  + E+   s++ Ga++Yiis + +   vL +   L
  gi|1204358   408 EMEEGMMKATISSMFAMQEIQEKSgeLGAnrYIISNCGSVQGVLQpFAFL 457

                  qRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid...GKqe
                  +     k ++ vvPLFE + DL+ A   +ekL+    Y+ ++ +++ Kq
  gi|1204358   458 KMTGWEKPSVDVVPLFETVPDLQDAHNVMEKLYTNPVYKDHLKrrgNKQT 507

                  vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                  +m+G+sD  KD G l A W +YkA+E + K+ ++yG+K+v F GRGG
  gi|1204358   508 IMLGFSDGTKDGGYLMANWSIYKAKESLTKISREYGIKVVFFDGRGGPPA 557

                  RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                  RGGG tH    s  P   n  +  tvqG  i   FG  + C   L
  gi|1204358   558 RGGGKTHQFYASLGPTIENEEIHLTVQGQTISSNFGTKDSCTYNLEQLLS 607

                  AtL..EHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRl
                    +++E   n     k + Rk m e+A +  E Y     K PRF+ Y
  gi|1204358   608 SGVsnEIFSNGKNVLKDDDRKTMTELAEISYETYTNF-KKHPRFIPYLEK 656

                  AtPElEYGkmniGsRPaKRkPsGGies..LRAiPWiFaWtqtRFHLPvWL
                        Y k niGsRP+KR  s  ++ ++LRAiP++ +W q +  +P +
  gi|1204358   657 MSTLKYYAKTNIGSRPSKRNQSAELNLsdLRAIPFVGSWSQLKQNVPGFF 706

                  GvGAAFKhAidKDiKn..lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                  GvG     A++K  Kn+++ k+k +Y++  FFR  l+   m   K    +
  gi|1204358   707 GVGT----AMEKLEKNgeFAKVKQLYDNSEFFRTLLENSMMSLTKSFFPL 752
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                    AaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                     a   +    Ee   F + + ++++ tk++LLk+ G   l+   P  +
  gi|1204358   753 TAYMKN---DEEFGEFWQLIHEEFERTKKMLLKVTGYNVLMQNQPAGRAS 799

                    lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                    +  R+  +  L  +q   L+ + +          lsK    En     eL
  gi|1204358   800 IQARERIVLPLLTIQQHALRQVQE----------LSKN--PEN--AGKEL 835

                    vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                +   + G      n
  gi|1204358   836 ETFE----------KMVTRSLYGNINASRNSA    857

gi|18076784|emb|CAC84972.1|: domain 1 of 1, from 1 to 357: score -20.9, E = 4
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807678     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807678     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807678     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807678     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807678     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807678     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807678     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807678     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807678     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807678     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807678     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                           sDsGKDAG
  gi|1807678     1 ----------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWq++k qE+ +KvA ++GvKL+lFHGRGG vGRGGGPtHLAiLsq
  gi|1807678     9 RLSAAWQVFKTQEDCVKVANQFGVKLTLFHGRGGSVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDti+GslRvtvqGEviE+ FGEE+LC r+LqRFtAAtLEHGm+PP +P
  gi|1807678    59 PPDTIHGSLRVTVQGEVIEQCFGEEHLCLRTLQRFTAATLEHGMQPPRAP 108

                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                    kPEWR L +e+  +At+EYR vv+KEPRFv YFR  tPElEYG+mniGsR
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  gi|1807678   109 KPEWRALTDEITPIATDEYRGVVFKEPRFVKYFRAVTPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G A +hA++KD +nl
  gi|1807678   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGIGSALQHALNKDKRNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L+EmY+eWPFFR t+DL+EmvFAKGDP iAaLyDk Lv+ +L+ FG++
  gi|1807678   209 PLLQEMYNEWPFFRATIDLIEMVFAKGDPRIAALYDKYLVSGDLQQFGDE 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR kY +t+dlLL +AGH +lL G P LKqrl+LR++Y+t Lnv q YtL
  gi|1807678   259 LRKKYGDTRDLLLLVAGHSELLQGNPTLKQRLKLREPYLTVLNVQQVYTL 308

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                   +++RD  y   ++ + s+      sk+a eLv Ln t+++aPGLEDtLiL
  gi|1807678   309 RKMRDAGY--IPKSPTSQ------SKPASELVSLNTTSEYAPGLEDTLIL 350

                   tmKGiAAGmqntG<-*
                   tmKGiAA
  gi|1807678   351 TMKGIAA------    357

gi|18076786|emb|CAC84973.1|: domain 1 of 1, from 1 to 357: score -22.0, E = 4.1
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1807678     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1807678     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1807678     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1807678     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1807678     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1807678     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1807678     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1807678     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1807678     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1807678     - ---------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1807678     - ---------------------------------------------- -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|1807678     1 ----------------------------------------SDSGKDAG 8
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                  RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                  RlsAAWq +k qE+ +KvA ++GvKL+lFHGRGG vGRGG PtHLAiLsq
  gi|1807678     9 RLSAAWQAFKTQEDCVKVANQFGVKLTLFHGRGGSVGRGGFPTHLAILSQ 58

                  PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                  PPDti+GslRvtvqGEviE+ FGEE+LCFr+LqRFtAAtLEHGm+PP +P
  gi|1807678    59 PPDTIHGSLRVTVQGEVIEQCFGEEHLCFRTLQRFTAATLEHGMQPPRAP 108

                  kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  kPEWR Lm+e+  +At+EYR vv+KEPRFv YFR  tPElEYG+mniGsR
  gi|1807678   109 KPEWRALMDEITPIATDEYRGVVFKEPRFVKYFRAVTPELEYGRMNIGSR 158

                  PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                  P+KRkPsGGiesLRAiP iFaWtqtRFHLPvWLG+G A +hA++KD +nl
  gi|1807678   159 PSKRKPSGGIESLRAIPRIFAWTQTRFHLPVWLGIGSALQHALNKDKRNL 208

                  qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  q L+EmY+eWPFFR t+DL+EmvFAKGDP iAaLyDk Lv+ +L+ FG++
  gi|1807678   209 QLLQEMYNEWPFFRATIDLIEMVFAKGDPRIAALYDKYLVSGDLQQFGDE 258

                  LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                  LR kY +t+dlLL +AGH +lL G P LKqrl+LR++Y+t Lnv q YtL
  gi|1807678   259 LRKKYGDTRDLLLLVAGHSELLRGNPTLKQRLKLREPYLTVLNVQQVYTL 308

                  KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                  ++i+D  y   ++ + s+      sk+a eLv Ln t+++aPGLEDtLiL
  gi|1807678   309 RKIKDAGY--IPKSPTSQ------SKPASELVSLNTTSEYAPGLEDTLIL 350

                  tmKGiAAGmqntG<-*
                  tmKGiAA
  gi|1807678   351 TMKGIAA------    357

gi|7768111|emb|CAB90623.1|: domain 1 of 1, from 1 to 401: score -24.0, E = 4.1
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768111     -    ---------------------------------------------- -

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768111     - ---------------------------------------------- -

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768111     - ---------------------------------------------- -

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768111     - ---------------------------------------------- -

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768111     - ---------------------------------------------- -

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768111     - ---------------------------------------------- -

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768111     - ---------------------------------------------- -

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768111     - ---------------------------------------------- -

                  EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768111     - ---------------------------------------------- -

                  eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
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  gi|7768111     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768111     - ------------------------------------------------ -

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768111     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWq++kAqE+++KvA+++ v+L++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768111     9 RLSAAWQMFKAQEDLVKVAQDHKVRLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvt+qGEviE+sFGEE+LCFr+LqRFtAAtLEHGm+PP++P
  gi|7768111    59 PPDTINGSLRVTIQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHPPIAP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR+Lm+ mAv AtEEYRs+v+K PRFvEYFR AtPElEYG+mniGsR
  gi|7768111   109 KPEWRDLMDSMAVAATEEYRSIVFKNPRFVEYFRTATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G A K Ai+ D +n+
  gi|7768111   159 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGLGGALKQAIEVDPRNM 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     L  mY++WPFFRvt+DL+EmvFAKGDP iA LyD LLv E  +PFG++
  gi|7768111   209 NTLARMYDQWPFFRVTIDLVEMVFAKGDPRIAELYDTLLVKESSQPFGED 258

                   LRdkYvEtkdlL.....................................
                   LR kY Etk+lL + + + + ++ + +  +++++++  +    +   + +
  gi|7768111   259 LRRKYNETKNLLlqvpfpipfkhfsvkffsrrrnpeclqilmlqvlipvt 308

                   LkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtl
                   L+iA H D+L G P LKqrlRLR++Yit Lnv qA tLK++R+   +  +
  gi|7768111   309 LQIARHTDILQGNPTLKQRLRLREPYITALNVQQACTLKKMREQRSQPQP 358

                   r.PhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqn
                    +P+lsK           eLv Ln + ++aPGLEDt+iLtmKGiAAGmqn
  gi|7768111   359 EsPKLSK---------TSELVTLNRATEFAPGLEDTVILTMKGIAAGMQN 399

                   tG<-*
                   tG
  gi|7768111   400 TG    401

gi|86135028|ref|ZP_01053610.1|: domain 1 of 1, from 2 to 859: score -24.4, E = 4.2
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                      s   +L        s   k   Y  + +    D +    G  L  +
  gi|8613502     2    STLPKLTKFNDNVLS---KYQIYNSIFITLPFDTINN-TGVLLPLFH 44

                   qECYElsAeYEGKkDtkKLeELGakL..tsLdPaDailvAkailHmLnLA
                   + C     +  GK  t+ +e    k ++t  +     l+ + i  +
  gi|8613502    45 KVCEKGFKN--GKNPTELVEKFFKKYqdTPSEKDKKDLLFQFIQYIERQV 92

                   nLAEEve.lAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                    L + +e+ A+   +     G      +  t s  +E lKk
  gi|8613502    93 VLFDAIEdAAFPVVNNMDGFGTLRNSKESATLSGKDEALKKYLEDF---- 138

                   eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                              v +vltAHPtq    s+L         ++ L  K +  +
  gi|8613502   139 ----------KVRVVLTAHPTQFYPGSVL-------GIITDLD-KAIQND 170

                   DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                   D   +   L    +  F     ++++PtP DE    + Y+    ++ v K
  gi|8613502   171 DLLLIKKLLAQLGKTPF----YKKSKPTPFDEAVSLIWYLENVFYHSVSK 216

                   FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                       +        + +  P +  +i    W GGDRDG nP vt  +t Dv
  gi|8613502   217 IHNYIQEH-----VYDGQPTENEIIDLGFWPGGDRDG-NPFVTTQITLDV 260
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                    CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                        R                        + LR    ++ r  +r
  gi|8613502   261 AERLR----------------------QSILRNYYRDVRRLKRRF---- 283

                    yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                                +    iL  v  +LY    R+               v
  gi|8613502   284 ----------TFDGVQEILSRVEKRLYKHVVRSY------------AKVN 311

                    tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                       E  LE LE     +    D    D  L D++ +v  FG     LDiR
  gi|8613502   312 FSKEILLEELENAREIVIKNHDSLFID-ELNDVINKVRIFGFHFATLDIR 360

                    qEseRqtDvlDAittHLeiG.......sYReWsEeKRqEWLlaELkGKR.
                    q+s  +      i   L   ++++ ++ Y   s e   E +la +kG  +
  gi|8613502   361 QDSRVHHKAFTQIVDDLLASgdttfpkNYQRLSPEEQVE-VLALVKGNId 409

                    PLlgsDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvEL
                    P + sD      ++ +     +           Yiis   +   v+
  gi|8613502   410 PSIFSDEMSVKTIESIYALKTIQQRNGESGANRYIISNNQTALNVMQTFA 459

                    LqRECgvkqtLr..vvPLFEkLADLeAAPAavekLFsiDWYinri...dG
                    +   Cg  + L+ +v+PLFE + DLe A   +  L+s   Y+ +++++
  gi|8613502   460 MLNLCGFENELPvdVIPLFETVDDLENASDVMRTLYSNKAYRYHLskrKD 509

                    KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                    Kq +m+G+sD  KD G  l A W ++kA+E + Kv +++ + ++ F GRGG
  gi|8613502   510 KQTIMLGFSDGTKDGGYLMANWGIFKAKEALTKVSREFDIEVIFFDGRGG 559

                    tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                       RGGG tH    s  P   +  +  t+qG  i   FG  +     L
  gi|8613502   560 PPARGGGKTHQFYASLGPTIEDKEIQLTIQGQTISSNFGTLDSSQFNLEQ 609

                    FtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKE.PRFvEYF
                         +   +          R++++++A      Y  v +K +P F  Y
  gi|8613502   610 LISSGIKNEVFTKDQINDTNREIINDLANTSYKTY--VDFKNhPQFLSYL 657

                    RlAtPElEYGkmniGsRPaKRkPsGGie..sLRAiPWiFaWtqtRFHLPv
                            Y k niGsRP+KR  s  ++ ++LRAiP++ +W q +  +P
  gi|8613502   658 EKMSTLKYYAKTNIGSRPSKRSNSDTLDfsALRAIPFVGSWSQLKQNVPG 707

                    WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                    + GvG A K     D   +  +   Y+   FF+  l+   m   K   G+
  gi|8613502   708 FFGVGTALKK--YEDADRFDEIVAFYNASDFFKTLLENSMMSLTKSFFGL 755

                    AaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                     a   +  v  e +   k + ++Y+ tk lLLk+ GHk+l+E  P  K
  gi|8613502   756 TAYMADDPVYGEFW---KLIYEEYKTTKRLLLKLTGHKELMENYPEGKAS 802

                    lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                    + +R+s +  L  +q + LK+i D          l +   +E
  gi|8613502   803 IAMRESIVLPLLTIQQFALKKIQD----------LQQSEGNEA------E 836

                    vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    +++          E  ++  + G      n
  gi|8613502   837 IEVY---------EKMVMRSLFGNINASRNSA    859

gi|149278227|ref|ZP_01884365.1|: domain 1 of 1, from 6 to 862: score -24.8, E = 4.2
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           q   L    v    +   Y  L l      ++D  G  L  ++
  gi|1492782     6    RAKGQRESLFNNEVI--SRFQLYNSLFLTLPFYKIKD-TGTLLPLFI 49

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDai..lvAkailHmLnLA
                    + C +     E  k ++ ++    k t  + +  i +l+ + i  +
  gi|1492782    50 KYCEDGVNKRE--KPAEIIDAFFKKYTQNNSTKDIidLLFRFIQYIERQV 97

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                     L + ve A      k+     aDE      s     lKk v       +
  gi|1492782    98 VLFDAVEDA---SFNKLN----ADEEHSALLS----YLKKGVDNA-SLNN 135

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                     +   +   s+ LvltAHPtq    s+L         ++ L A  +  +D
```

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  gi|1492782   136 KIEKLIEEFSMRLVLTAHPTQFYPGSVL-------SIITDLTAA-IKKND 177

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                       +D  L    q   +t    +  PtP DE      Y+    +
  gi|1492782   178 ISSIDLLL----QQLGKTPFFNKKSPTPVDEALSLAWYLENVFYFAAANI 223

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                       vD  L    +  +      +i+   W GGDRDG nP v  + t  v
  gi|1492782   224 QSEVDKSLNDYNLESK-----KIIELGFWPGGDRDG-NPNVHIDSTIQVA 267

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                     + R +    Y+     L   +      d+L    + ly+ a
  gi|1492782   268 RMLRQILFRCYYRDFKNLKRRITFRGVEDDLALIHDVLYKNAFDP----- 312

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                                                       tG  +i+
  gi|1492782   313 ------------------------------------NTGSENIA------ 320

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                      E  +E L      L +  D    D  + Dl+R+v  +G     LDiRq
  gi|1492782   321 --EFLIEHLNKIKTTLNDGHDGLFTD-VVSDLIRKVELYGSHFASLDIRQ 367

                    EseRqtDvlDAittHLeiGs.....YReWsEeKRqEWLl...aELkGKRP
                    +s    Dv         + s  +++Y e sE  + + ++ ++a +
  gi|1492782   368 DSRILRDVHTYCRNNKPLVSifpenYDELSEAEKIDTMVfksAKINFTQE 417

                    LlgsDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvL.AvEL
                      +  L     ++++ +  +   EL    F   iis +   sD+L+ +EL
  gi|1492782   418 PDPLTLDTLQTIAEIKQIQQSNGELACHRF---IISNCQEASDILqLIEL 464

                    LqRECgvkqtLrv..vPLFEkLADLeAAPAavekLFsiDWYinrid...G
                                L v+ vPLFE + DLe A   +e L+s  +Y+ ++++++G
  gi|1492782   465 FLWNGWTEDELTVdfVPLFETVHDLEGAAEIMETLYSHPFYKKHLEsrgG 514

                    KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                    Kq++m+G+sDs KD G l A W ++ A+  +   A k+ ++L  F GRGG
  gi|1492782   515 KQHIMLGFSDSTKDGGYLMANWSIFNAKVSLTATANKHNIQLAFFDGRGG 564

                    tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                       RGGG tH    s   +  n  +  t+qG  i   +G  +     +
  gi|1492782   565 PPSRGGGKTHRFYASMGKEIANKNIQLTIQGQTISSQYGSIDSAEFNIEQ 614

                    FtAAtLEHGmnPP..vsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEY
                       A +  Gm+  +++   P  ++L+++mA    E + s+  K P F  Y
  gi|1492782   615 MINAGISAGMKEThnILLDPLHKDLLDNMARDSYEAFVSL-RKHPLFLSY 663

                    FRlAtPElEYGkmniGsRPaKRkPsGG..iesLRAiPWiFaWtqtRFHLP
                         P +   k+ i sRP KR  +   ++e LRAi ++ aW q +  +P
  gi|1492782   664 LEKFSPLTLLSKITISSRPVKRNSGEAlkLEDLRAISFVTAWSQLKQNIP 713

                    vWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPG
                     + G+G A K   +K+  n   +   Y+e  +F+  +D   m   K D
  gi|1492782   714 GFYGIGTALKN--QKEKGNWDNIVKTYQESGYFKTIIDNCMMSMSKSDFA 761

                    iAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                    i a + +     e   F k L d+++  k++LL + GH  l+E  P  K
  gi|1492782   762 ITAHFAN---DKEYGDFWKMLHDEFELSKNMLLSLSGHETLMENYPVEKR 808

                    rlRLRdsYittLnvfqAYtLKRiR.DPsykvtlrPhlsKEyAdEnskkad
                     + +R+  +  L  +q Y L  + +DP+              +E     +
  gi|1492782   809 SIAVREKIVLPLVLIQHYALEQLQnDPE-------------GAEK----Q 841

                    eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       kL              i t+ Gi     n
  gi|1492782   842 AFEKLA-------------IRTVYGIVNAGRNLA    862

gi|88801380|ref|ZP_01116908.1|: domain 1 of 1, from 2 to 859: score -28.4, E = 4.3
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s+  +L        s   k   Y  + +    D +    G  L  +
  gi|8880138     2    SVLPKLARFNENVLS---KYQIYNSVFMTLPFDTINN-TGVLLPLFH 44
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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                  C       EGK  t+ +     k    +P++   +A  +
gi|8880138    45 ELCKK--GFQEGKNPTEIITAFFNKYQE-NPTEKEKIALLFQF------- 84

                AEEvelAyRRRikkkkhGDFaDEas..AttEsDiEEtlK..kLvlklnKs
                     + y  R   +   D  ++a  +     D   tl+++k +  l+
gi|8880138    85 -----IQYIERQVVLF--DAIEDAAfpIVNNMDGIGTLRnsKEIAILEDK 127

                PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                 e     L    v +vltAHPtq     +L                +t
gi|8880138   128 KEALKAHLEDFKVRVVLTAHPTQFYPGTVLGI---------------ITD 162

                eDK..kELDEALHREiqAAF.RtDEiRRaqPtPqDEmRaGmsYiHEtvWk
                 DK  +E D  L + + A  ++t   ++++P P DE    + Y+    ++
gi|8880138   163 LDKaiQEDDLLLIKKLLAQLgKTPFYKKSKPSPFDEAVSLIWYLENVFYH 212

                GvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEv
                 + K    +     ni   E  P +  +i    W GGDRDG nP +t E+
gi|8880138   213 AISKIYNYIQ---NNIYDGE--PMNNEIIDLGFWPGGDRDG-NPFITTEI 256

                tRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaard
                t  v    R                       + LR    ++ r  +r
gi|8880138   257 TLNVAERLR----------------------QSILRNYYRDVRRLKRRF 283

                kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                                +    iL  v  +LY    R+   L    s + E
gi|8880138   284 --------------TFDGVQEILASVEKRLYKHVVRSYGKLNFSQSILLE 319

                eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                e   tk            + +     + +    L D++ +v  FG
gi|8880138   320 E--LTKA-----------RKIIAGKHQSLFIEELDDFINKVKIFGFHFAT 356

                LDiRqEseRqtDvlDAittHLe.iG......sYReWsEeKRqEWLlaELk
                LDiRq+s  +      i + L++iG+++ ++ Y   sE+   E +la +k
gi|8880138   357 LDIRQDSRVHHQAFTQIVKDLQtIGdtpfprNYAHLSEQEQIE-ILAVVK 405

                GKR.PLlgsDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvL
                G  +P    D      ++ +    ++           Yiis   +   v+
gi|8880138   406 GNIdPKTLTDDTSVSTIESIYALKEIQLRNGERGANRYIISNNQTALNVM 455

                AvELLqRECgvkqtLr..vvPLFEkLADLeAAPAavekLFsiDWYinri.
                    +   Cg k+ L+ +v+PLFE + DLe A   ++ L+    Y+ +++
gi|8880138   456 ETFAMLNLCGFKNELPvdVIPLFETVEDLENAETVMQTLYTNRSYRYHLe 505

                ..dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                +++ Kq +m+G+sD  KD G l A W ++kA+E + K+ + + + ++ F
gi|8880138   506 krENKQTIMLGFSDGTKDGGYLMANWGIFKAKEALTKISRAFDIEVIFFD 555

                GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                GRGG   RGGG tH    s  P   +  +  tvqG  i   FG  n
gi|8880138   556 GRGGPPARGGGKTHQFYASLGPTIEDKEIQLTVQGQTISSNFGTKNSAQF 605

                sLqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKE.PRF
                 L       +   +        E Rk++e++A    E Y  v +K +P+F
gi|8880138   606 NLEQLLSSGIKNEIFTKDQLNDENRKIIEDLAATSYETY--VAFKNhPKF 653

                vEYFRlAtPElEYGkmniGsRPaKRkPsGGie..sLRAiPWiFaWtqtRF
                  Y         Y k niGsRP+KR  s  ++ ++LRAiP++ +W q +
gi|8880138   654 LPYLEKMSTLKYYAKTNIGSRPSKRSNSATLDfsALRAIPFVGSWSQLKQ 703

                HLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKG
                 +P + GvG A K     D   +  +   Y+   FF+  l+   m   K
gi|8880138   704 NVPGFFGVGTALKK--YEDANRFEEVIAFYNASDFFKTLLENSMMSLTKS 751

                DPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPY
                   + a   +     e   F k + ++Y+ tk lLLki GHk+l+E  P
gi|8880138   752 FFELTAYMAD---DAEFGAFWKLIHEEYKTTKRLLLKISGHKELMENFPV 798

                LKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskk
                 K  + +R+  +  L  +q + LK i + +         s E
gi|8880138   799 GKASIEIREQIVLPLLTIQQFALKQIQELQ---------STEGNTAA--- 836
```

```
                  adeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      +++          E  ++  + G      n
  gi|8880138   837 ----IEVY---------EKMVMRSLFGNINASRNSA    859

gi|118377471|ref|XP_001021914.1|: domain 1 of 1, from 58 to 926: score -32.0, E = 4.4
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                     ++     lL   K     k +    +Ll  F   +q L  + L
  gi|1183774    58    AMKRTFDLLNDQKKL---KSVTNKEILLANFESRVQ-LRYQLLNSLF 100

                  qECYElsAeYEGKkDtkKLeELGak..LtsLdPaDai.lvAkailHmLnL
                  q    +    E       L     k+   +L P + i+   k +
  gi|1183774   101 Q-TLPVDQINETSMLIPILTHACQKglESGLSPEEVIdKFFKEYDQNQIY 149

                  AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiE.....EtlKkLvlk
                        ++  +R      +     D  +    s i + +++E l  L+ +
  gi|1183774   150 NTEQKKIDFLFRVVQFVERQVVLVDALEDANYSQINdlhgpESLGNLIER 199

                  lnKs..PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLs
                    + +  +E    L   +v +vltAHPtq   + +L     i n L
  gi|1183774   200 IRRHnlDDELLKQLSRFAVRVVLTAHPTQFYPKQVLS----IINDLNE-- 243

                  AKDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEt
                     +  +D   +   L    +  F      R +PtP DE  + + Y+
  gi|1183774   244 --AIQSNDITQIQYLLWQLAKTPF----FQREKPTPLDEAQFLIQYLENV 287

                  vWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvt
                   ++ v     R    L       +       + F  W GGDRDG nP v
  gi|1183774   288 FYDAVGTLQDRLRKVLGSKFDKQKEFHKFYTLGF--WPGGDRDG-NPFVR 334

                  PEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrta
                        v  L R      Yi  v  +   ls     + L    EE+
  gi|1183774   335 ------VAKLLRTSILKCYIRDVRQVKKRLSFKGIYELL----EEIENDF 374

                  ardkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGise
                   ++         +   P      v L +  +KL   R +
  gi|1183774   375 GSN---------FSYKPS-----VSLEQLYEKLDFIRQK----------- 399

                  isEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLs
                       + t+      P+                    + R+v tFG
  gi|1183774   400 -----IITDHNGLFLPI------------------FENFQRKVHTFGYH 425

                  LvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRP
                     +DiRq+s        A+ + +      ++ E   q  L   L+ K P
  gi|1183774   426 FASIDIRQDSRVLDKTFKALQEKVPYMLPYNFEELPVQQKLDLLLSLK-P 474

                  LlgsDLPktEEvkDvldafrvLAELPiDs..FGaY..iismataPsDvLA
                  L        E + D l++f+ + E+  + ++FG+Y+ iis +  P Dv
  gi|1183774   475 LNTVPQLDDEVLNDTLQTFNAMREIQEENgeFGSYrfIISNCRGPLDVAK 524

                  vELLqRECg...vkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri.
                  v  +    g+ +    + vvPLFE + DL+ A  +++ LFs   Y  +++
  gi|1183774   525 VYAMSQLTGgwsGNSKIDVVPLFETIDDLKSADKSMKELFSNGIYQKHLk 574

                  ..dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                   +  +q +m G+sD  KD G l A W +Y+A+E + K+ ++yGv  + F
  gi|1183774   575 frKMRQTIMCGFSDGTKDGGYLGANWGIYQAKENLSKISRDYGVEAIFFD 624

                  GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                  GRGG   RGGG  HL   sq P   n  + +t+qG  i   FG  + C +
  gi|1183774   625 GRGGPPARGGGNKHLYYASQGPTIENHEIQITIQGQTISSNFGVTDSCLH 674

                  sLqRFtAAtLEHGm..nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKE.P
                   L     A L   + ++P        R+L++e+  v    Y  + +K +P
  gi|1183774   675 NLELLMSAGLQNNVleDPKRVLTQSQRDLLNELSEVSLKSY--LEFKNhP 722

                  RFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWtqt
                  +F+ Y     P   YG  niGsRPaKR  +G ++ e LRAiP++ aW q
  gi|1183774   723 KFMPYLLEKSPLKYYGEANIGSRPAKRSAGGEMkfEDLRAIPFVGAWSQL 772

                  RFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFA
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                    +  +P + G+G A K         l    ++Yk+  FF+  +    m
  gi|1183774   773 KQNVPGFYGLGTALKKL--EAEGRLNEAADLYKDSLFFKALVQNSMMSMC 820

                    KGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGD
                    K       L   +L   +   F +++ ++++Et+ lLL i   k lL+ +
  gi|1183774   821 K---TYFPLTHYMLKDKQYSEFWNQIYNEFQETERLLLLITEQKQLLDNE 867

                    PYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEns
                    P +Kq ++LR+  +  L  +q + L+Ri              K++ ++
  gi|1183774   868 PVIKQSIKLREQIVLPLLTIQQFALQRI-------------NKDHQEDLH 904

                    kkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    k  ++L+                   + G      n
  gi|1183774   905 KSYQNLIIRS----------------LFGSINATRNAA    926

gi|7768261|emb|CAB90666.1|: domain 1 of 1, from 1 to 371: score -33.5, E = 4.5
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|7768261     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|7768261     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|7768261     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|7768261     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|7768261     - ---------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|7768261     - ---------------------------------------------- -

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|7768261     - ---------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|7768261     - ---------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|7768261     - ---------------------------------------------- -

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|7768261     - ---------------------------------------------- -

                    EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|7768261     - ---------------------------------------------- -

                    rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                          sDsGKDAG
  gi|7768261     1 ----------------------------------------SDSGKDAG 8

                    RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    RlsAAWq++k qEE+++vAK+yGv+L++FHGRGGtvGRGGGPtHLAiLsq
  gi|7768261     9 RLSAAWQMFKSQEELVQVAKQYGVQLTVFHGRGGTVGRGGGPTHLAILSQ 58

                    PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                    PPDt+nGslRvt+qGEviE+sFGE++LCFr+LqRFtAAtLEHGm+PP++P
  gi|7768261    59 PPDTVNGSLRVTIQGEVIEQSFGEDELCFRTLQRFTAATLEHGMHPPLAP 108
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                    kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                     PEWR Lm++mA v t EYR +v+  P Fv YFR AtP lEYG+mniGsR
  gi|7768261   109 EPEWRALMDDMAAVSTAEYRKIVFNNPQFVRYFRKATPVLEYGRMNIGSR 158

                    PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                    P+KRkP GGiesLRAiPWiFaWtqtRFHLPvWLG+GAAFK  ++ D   +
  gi|7768261   159 PSKRKPKGGIESLRAIPWIFAWTQTRFHLPVWLGMGAAFKQVLKADDIII 208

                    qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                      L+ mY++WPFFRvt+DL+EmvFAKGDP i aLyD+LLv +eL   G +
  gi|7768261   209 TILRKMYNQWPFFRVTVDLVEMVFAKGDPRISALYDRLLVDDELEHIGVE 258

                    LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                    LR +Y Etk+lL ++  H +lL G P+LK +lRLR+ +i  Lnv q YtL
  gi|7768261   259 LRSRYDETKELLHQVVEHDELLAGSPFLKHKLRLREYFISPLNVQQVYTL 308

                    KRiRDPsykvt..lrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtL
                    K++RD   ++ ++l+  +  E       ++ eLv  n t + +PGLEDtL
  gi|7768261   309 KKMRDSRSQICdpLQEAILEELRSGK--ESSELVTRNTTTEHPPGLEDTL 356

                    iLtmKGiAAGmqntG<-*
                    iLtmKGiAAGmqntG
  gi|7768261   357 ILTMKGIAAGMQNTG    371

gi|146300556|ref|YP_001195147.1|: domain 1 of 1, from 6 to 861: score -33.6, E = 4.5
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           ++        s   k   Y  + +    D + D  G  L  +
  gi|1463005     6    ----KIERFNKDVLS---KYHIYNSVFITLPFDSI-DNTGVLLPLFT 44

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                      C      +  ++ +k + +  +                    Ln A
  gi|1463005    45 ETC---ETGFKKQETPKEIFDFFSN-----------------KFLNNASE 74

                    AEEvelAyRRRikkkkhGDFaD..EasAttEsDiEEtlKkLvlklnKsPe
                     E ++l +R      +     D  E  A  E    E    L    +Ks +
  gi|1463005    75 TEKIDLMFRFIQYIERQIVLFDaiEDAAFPEVNNMEGRGSLRDIKEKSDA 124

                    .....EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKD
                    +++++E  + L    v  vltAHPtq     +L     i n L+
  gi|1463005   125 kekddELVDFLESFNVRTVLTAHPTQFYPGPVLG----IINDLTE----A 166

                    vtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWk
                    +  +D   +   L    +  F    i   +P P DE    + Y+    +
  gi|1463005   167 IRQNDLLQIKQLLAQLGKTPF----IQHEKPNPYDEAVSLIWYLENVFYA 212

                    GvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEv
                         +      L      +  P    Lik   W GGDRDG nP vt E+
  gi|1463005   213 TAGEIVHYLQKNLH-----DGNPIKNQLIKLGFWPGGDRDG-NPFVTTEI 256

                    tRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaard
                    t  v                           d LR      y    r+
  gi|1463005   257 TLKVA----------------------------DRLRTSILKCYYVEMRN 278

                    kvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisE
                       K  + F            ++ d   KLY    R+           s
  gi|1463005   279 --LKRKLTF-------SGVDTLVSDLEHKLY----RSVFY--------SK 307

                    eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                      ++  ++e L  L      + e       D  L  lL ++  FG
  gi|1463005   308 GEIFITLDELLTQLNTIRTIIIEKHQSLYLD-ELEALLVKINLFGFHFAT 356

                    LDiRqEseRqtDvl.DAittHLeiGs......YReWsEeKRqEWLlaELk
                    LDiRq s  +  v +D +   L+ Gs+  +++Y +  E+++ + +l+ ++
  gi|1463005   357 LDIRQNSKIHNAVFkDVVNYYLNSGSdifpknYYDLTEDQKID-VLSKVQ 405

                    GKRPLlgsDL..PktEEvkDvldafrvL.AELPiDsFGaYiismataPsD
                    G   L ++D ++  t    + ++a++ ++A    +    Yiis   +
  gi|1463005   406 GN--LNPADFenEITRSTLESVQAIKTIqANNGEEGANRYIISNNESALN 453

                    vLAvELLqRECgvkq.tLrvvPLFEkLADLeAAPAavekLFsiDWYinri
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                    v+    + R    k++t+ ++PLFE + DL+ A   +e+L+    Y  ++
  gi|1463005   454 VMETFAMIRLNNWKNpTVDIIPLFESVDDLQNAHQIMEQLYTNPEYSKHL 503

                    dGK...qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                      ++++q +m+G+sD  KD G l A W +Y+A+  +  + +kyG+K + F
  gi|1463005   504 KSRgneQTIMLGFSDGTKDGGYLMANWSIYQAKISLTEISRKYGIKAIFF 553

                    HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                     GRGG   RGGG tH    s  P   n  + +tvqG  i   FG  + C
  gi|1463005   554 DGRGGPPARGGGKTHKFYASLGPKIENKEIQITVQGQTISSNFGTLDSCR 603

                    rsLqRFtAAtLEHGm..nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKE.
                      +     A +   + ++       E  +++ ++A    E Y s  +K +
  gi|1463005   604 FNIENLLSAGVTNQVfgKEKNELSAEETQILTQLADLGYEKYLS--FKNh 651

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGie..sLRAiPWiFaWtq
                    P+F+ Y         Y k niGsRP+KR  s  ++   LRAiP++ +W q
  gi|1463005   652 PKFIPYLEKMSTLKYYSKTNIGSRPSKRSKSESLDfaDLRAIPFVGSWSQ 701

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     +  +P + GvG A Kh  +  +    k+ ++Y++  FF+  l+   m
  gi|1463005   702 LKQNVPGFFGVGTALKHFEK--SGQWHKVSDLYHNSLFFKTLLENSMMSL 749

                    AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                    AK    + a   k     e   F + + d++ Etk lLLkiAGHk l+E
  gi|1463005   750 AKSFLPLTAYMRK---DPEFGEFWQIIHDEFSETKRLLLKIAGHKTLMEN 796

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                     P     + +R+  +  L  +q Y L +i +          l KE
  gi|1463005   797 YPDGIASIQIRERIVLPLLTIQQYALSKINE----------LNKE----- 831

                    skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    s + +eL+k+          E  +   + G      n
  gi|1463005   832 SSPNEELIKVY---------EKIVTRSLFGNTNASRNSA    861

gi|2695868|emb|CAA75817.1|: domain 1 of 1, from 1 to 328: score -40.5, E = 4.8
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2695868     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2695868     - ---------------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                                                                  l
  gi|2695868     1 ----------------------------------------L------- 1

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|2695868     - ---------------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2695868     - ---------------------------------------------------- -

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                                                +G
  gi|2695868     2 --------------------------------EG---------------- 3

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2695868     - ---------------------------------------------------- -

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|2695868     - ---------------------------------------------------- -

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2695868     - ---------------------------------------------------- -
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                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|2695868     - ------------------------------------------------ -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                                                 Av LL        tL
  gi|2695868     4 ----------------------------------AVALL--------TL 10

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +
  gi|2695868    11 PSC------------------------------------------------ 13

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                                                                 sq
  gi|2695868    14 ------------------------------------------------SQ 15

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PPDtinGslRvtvqGEviE+sFGEE+LCFr+LqRFtAAtLEHGm PP+sP
  gi|2695868    16 PPDTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPISP 65

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR L++emAvvAtEEYRs+v++EPRFvEYFRlAtPE+EYG+mniGsR
  gi|2695868    66 KPEWRALLDEMAVVATEEYRSIVFQEPRFVEYFRLATPETEYGRMNIGSR 115

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG+G AFKh ++KDi+n+
  gi|2695868   116 PSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHILKKDIRNF 165

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                    +L+EmY+eWPFFRvt+DL+EmvFAKG PGiAaLyD+LLv+E L+P G++
  gi|2695868   166 HMLQEMYNEWPFFRVTIDLVEMVFAKGNPGIAALYDRLLVSEGLQPLGEK 215

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR++Y+Et++lLL++AGHkDlLEGDPYLKqrlRLRd+Yitt+nv+qAYtL
  gi|2695868   216 LRANYEETQKLLLQVAGHKDLLEGDPYLKQRLRLRDAYITTMNVCQAYTL 265

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpte.rvaPGLEDtLi
                   KRiRDP+y+v  rPhlsKE  d   k+a+eLv Lnp+   +aPGLEDtLi
  gi|2695868   266 KRIRDPDYHVAFRPHLSKEVMDTS-KPAAELVTLNPGRvSYAPGLEDTLI 314

                   LtmKGiAAGmqntG<-*
                   LtmKGiAAG+qntG
  gi|2695868   315 LTMKGIAAGLQNTG    328

gi|163787422|ref|ZP_02181869.1|: domain 1 of 1, from 1 to 835: score -42.2, E = 4.8
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           L      K            +Ll  F            +E
  gi|1637874     1    ---MTLPFDTITKTG----------VLLPLF------------HETC 22

                   qECYElsAeYEGKkDt..kKLeELGakLtsLdPaDailvAkailHmLnLA
                   q  +E   +     Dt  kK +   +    ++     l+ + i  +
  gi|1637874    23 QKGFENQENPTTIVDTffKKYQARRSPKSQIN-----LLFRFIQYIERQV 67

                   nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    L + +e A    +           +  t  s     lK  v k nK  e
  gi|1637874    68 VLFDAIEDAAFPVVNNMD-------GIGTLRS-----LKESVAKDNKL-E 104

                   EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                        L    v +vltAHPtq    s+L         ++ L    +  +D
  gi|1637874   105 TLQKYLEEFKVRIVLTAHPTQFYPGSVL-------GIITDLTTA-IREND 146

                   KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                      + + L    +  F     +  +PtP DE    + Y+    +k    F
  gi|1637874   147 LLKINDLLAQLGKTPF----FKHKKPTPYDEAVSLIWYLENVFYKS---F 189

                   LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                       D   +ni     +  d+  i F  W GGDRDG nP vtPE+t  v
  gi|1637874   190 GTIYDYIQQNIFDGKQIDNDIINIGF--WPGGDRDG-NPFVTPEITLNVA 236

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
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                      R      Y+     L   l      + + v   Ely+    +
  gi|1637874   237 KRLRDTVIKNYYRDARRLRRKLTFAGVEERIIVLETELYKIITNK----- 281

                      YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                                 E +   L  ++D + n            +se+
  gi|1637874   282 -----NSNLTAESFASELKIIKDVIVNEHQ------SLYVSEVNS----- 315

                      kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                                                lL ++  FG     LDiRq
  gi|1637874   316 -------------------------------LLNKIHLFGFHFANLDIRQ 334

                      EseRqtDvl.DAittHLeiGs......YReWsEeKRqEWLlaELkGKRPL
                      +s ++    +D + t +e Gs+  +++Y +  E K q  +l+ ++G   L
  gi|1637874   335 DSRKHAQFFnDMVNTLIESGSeifpknYHDLLE-KEQIKILSKVEGEVDL 383

                      lgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAv
                          L k EE    l +++ +  + ++++  +   Yiis   +   v+
  gi|1637874   384 ---SLIKDEETLKALKTMKAIKTIQgtngEKAANRYIISNNQTTLHVMQL 430

                      ELLqRECgvkqtLrv..vPLFEkLADLeAAPAavekLFsiDWYinridG.
                        + +    +  + v+  PLFE + DLe APA +e L+    Y  ++  +
  gi|1637874   431 FAMLKLVAFQDEMTVdiGPLFETITDLENAPAVMEELYTNPQYAAHLKSr 480

                      ..KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                      ++Kq +m+G+sD  KD G l A W +YkA+E + +v +++G+K+v F GR
  gi|1637874   481 gnKQTIMLGFSDGTKDGGYLMANWAIYKAKENLTRVSREHGIKVVFFDGR 530

                      GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                      GG   RGGG tH    s  P   +  +  t+qG  i   FG  +     L
  gi|1637874   531 GGPPARGGGKTHNFYASLGPTIEDKEVQLTIQGQTISSNFGTLESSQYNL 580

                      qRFtAAtLEHGm.nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvE
                             +   +++  +s  PE R++m ++       Y s     P+F+
  gi|1637874   581 EQLISSGIHNSLsDSDLSMLPENRDVMTDLSERSYKAY-SDFKAHPKFIT 629

                      YFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWtqtRFHL
                      Y         Y k niGsRP+KR  s G+  e LRAiP++ +W q +  +
  gi|1637874   630 YLEHMSTLKYYAKTNIGSRPSKRGKSEGLvfEDLRAIPFVGSWSQLKQNV 679

                      PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                      P + GvG A Kh    D+  + k++ ++k+  FF+  ++   m   K
  gi|1637874   680 PGFFGVGTALKH--YEDVGEFEKVQTLFKTSDFFKTLIENSMMSLSK--- 724

                      GiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLK
                          L   +    e   F   + ++Y+  k l+Lk+ G k+l+  +P  K
  gi|1637874   725 SFFDLTRYMAEDPEYGEFWTIIYNEYETSKRLILKLTGYKELMQEEPAGK 774

                      qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                        + +R+s +  L  +q Y LK+i              +E   E  k+ d
  gi|1637874   775 ASIAVRESIVLPLLTIQQYALKKI--------------QELEKEGVKPND 810

                      eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      e +k+  ++ v   L         G      n
  gi|1637874   811 EQMKIY-ASMVTRSL--------FGNINASRNSA    835

gi|126648531|ref|ZP_01721018.1|: domain 1 of 1, from 1 to 844: score -43.4, E = 4.9
                      *->siDAqLRlLvPGKvsedekLieYDALLlDk.FLDiLqD.LHGedLkE
                             +       v+   +   Y  L lD +F Di   +   + L
  gi|1266485     1    -----MHKTYDTEVA--KRFTIYNSLFLDLpFDDIYRTgTLLPILGT 40

                      avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                      a q  +                      +L P +  ++   +  m+
  gi|1266485    41 ACQKGFQ--------------------NGLTPKE--IIHGFFEEMMAGN 67

                      nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEE.....tlKkLvlkl
                         E  +l ++      +     D  +      i + ++++ +K L+ +
  gi|1266485    68 SKTEQNNLLFKMIQYVERQVVLFDSIEDAAYEKINDlsgkgSIKALIDRA 117

                      ..nKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsA
                      +++   e   e LK  sv L ltAHPtq    s+L   + + n
  gi|1266485   118 dnDHKREALIEKLKSFSVRLTLTAHPTQFYPGSVLGIITDLENA------ 161
```

```
                    KDvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtv
                      +  +D   +   L    +  F    i R +P P +E    + ++
  gi|1266485   162 --IRSDDIGKINLLLKQLGKTGF----INREKPSPYEEAVSLIWFLENVF 205

                    WkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtP
                    ++ +   + R    L  + i      +  L+k   W GGDRDG nP vt
  gi|1266485   206 YQSISDIMIRL---LSSLDIPLHTWDNPGLLKIGFWPGGDRDG-NPFVTH 251

                    EvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaa
                    E t  v                                    AE l++
  gi|1266485   252 ETTVKV-----------------------------------AERLQKWIL 266

                    rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                    r     yY +  K        R     v DK+  t ER   +  t + +
  gi|1266485   267 RC----YYRDLRKI-----KRRLTFKHVEDKVL-TIERN--IYNTLFED- 303

                    sEeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsL
                      +Avyt  E+ L+ L     sL +       D  L  ++ +v  FGL
  gi|1266485   304 --QAVYTSKEQLLDDLIEVRDSLIQYHNSMFVD-VLDQFILKVKIFGLHF 350

                    vKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPL
                      +D Rq+s ++    + i    +i    +W E       +  + G   L
  gi|1266485   351 AYMDARQDSRKHDSLWEEIFSIQGI----NWKETEDDQ--IEQIMGVESL 394

                    lgsDLPktEE..vkDvldafrvLAELP....iDsFGaYiismataPsDvL
                      +DL k  ++   ++l +f v+  + ++++ D+   Yiis + +    L
  gi|1266485   395 --PDLEKFQDdfHIEMLKTFGVIRTVQnsngEDALHRYIISNCQSRKHLL 442

                    AvELLqRECgvkq....tLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                     v  L +    k++++ +L +vPLFE + DL  AP  +  L+ +  Y+ +
  gi|1266485   443 EVYKLAKLTVGKEekqlPLDIVPLFETIDDLAEAPGIMTSLYQMPEYRAH 492

                    idG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                    +  +++Kq +m+G+sD  KD G l A W + +A+EE+ +v ++  + +v
  gi|1266485   493 LASrgnKQTIMLGFSDGTKDGGYLQANWSILRAKEELTRVSRENDIEVVF 542

                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                    F GRGG   RGGG  H    s      n  + vt+qG  i   +G    C
  gi|1266485   543 FDGRGGPPARGGGNMHNFYASLGEKVENSEIQVTIQGQTISANYGKQASC 592

                    FrsLqRFtAAtLEHGmnPPvsPkPE..WRkLmeemAvvAtEEYRsvvvK.
                             A LE  +        +++ R L+ee+  vA E Y+   +K+
  gi|1266485   593 TYNFEQLLSAGLENHLYSDSENNLDekQRALIEELSSVAYESYKD--FKs 640

                    EPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWt
                     P+Fv Y    tP   +G  niGsRP KR  +GG++ e LRAiP++ +W
  gi|1266485   641 HPKFVPYLEHVTPLKYFGMTNIGSRPLKRGKGGGLkfEDLRAIPFVGSWA 690

                    qtRFHLPvWLGvGAAFKhAidKDiKn..lqkLkEmYkeWPFFRvtlDLlE
                    q +  +P + GvG     AidK    +++  ++ +Yk+  FFR  l
  gi|1266485   691 QMKQNIPGFYGVGT----AIDKLESEgrIDEVRKLYKNSLFFRALLGNSM 736

                    mvFAKG.DPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkD
                        K   P  A L D+    E    F + + ++Y    d  Lk+    D
  gi|1266485   737 QSLNKCfYPATAYLKDN----EAYGQFWEIMYAEYHKSIDK-LKLVSEMD 781

                    lLEGDPYL.KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKE
                     L GD  ++K+ + +R+  +  L  +q Y ++ +
  gi|1266485   782 ELMGDNQVsKKSIAIREKIVLPLITIQQYAIQTM---------------- 815

                    yAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       E  + ++ L kL              +  m Gi     n
  gi|1266485   816 --LETGQNSELLQKLI-------------LRSMFGIINAARNAA    844

gi|227366515|ref|ZP_03850064.1|: domain 1 of 1, from 1 to 844: score -45.8, E = 5
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        i  q R+    ++  ++k   Y  L +    D +  +    L  +
  gi|2273665     1    MIHDQ-RAEKFRQIV-ENKFQIYNSLFMSLPYDKMTNI--GMLLPFL 43

                    qECYElsAeYE.GKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
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                E  E    YE GK     +eE     t L+  +             L
gi|2273665    44 YE--ESRTGYEaGKTPENIVEEFFKNHTDLQTEEQ-----------KLEL 80

                LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLv..lklnKsP
                L   ++   R  +      + a   +   EsD   t+  L ++++ +
gi|2273665    81 LFKIIQYIERQVVLFDS-IEDAAFPNLHSESD-NGTVTNLFerSLQDHKI 128

                eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                e v e LK  sv +v+tAHPtq    s+     Ri     q     +t +
gi|2273665   129 EKVREKLKDFSVKVVFTAHPTQFYPSSV----QRI----IQDLRGAITSD 170

                DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPK
                    +D  L    q   +t  + + +PtP DE    +sY+    ++ +
gi|2273665   171 SVTQIDMLL----QQLGKTPFVNKEKPTPIDEALSIISYLRYVYYDTIGE 216

                FLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDv
                      t +K    n        +i+   W GGDRDG nP vt +vt+ v
gi|2273665   217 LF----TKIKKTFGNGHFHLHEDIIQLGFWPGGDRDG-NPFVTADVTKRV 261

                CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                    R      Y+s +  +   ls     + L    EEly      k +K
gi|2273665   262 AEELRSAILKSYYSHLKFIRRRLSFRGVSEVLTQLSEELYAAIFDGKDIK 311

                yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                                       D L    E  + L+    s
gi|2273665   312 ---------------------AEDILKRAAEAEKILINEHNS-------- 332

                tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                     FL+                      L+ +   v+ FG     LDiR
gi|2273665   333 ----LFLD--------------------LLVNFRDRVMIFGTHFATLDIR 358

                qEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                q+s  +  v+D +   +  G      E+K     l  ++ K  + + D
gi|2273665   359 QDSRIHQKVIDEVYAKV-YGNEEADYEQKFNK--LIQISEK--INPEDF- 402

                ktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvELLqRE
                  + vkD l ++  + ++ + ++      Yiis + a  Dv+ v    +
gi|2273665   403 -EDIVKDTLLTVSQVTDIQhlngLRGMNRYIISNSDAVKDVMNVYAFFKV 451

                Cgvkqt...LrvvPLFEkLADLeAAPAavekLFsiDWYinrid..GKqe.
                Cg k  + ++ +vPLFE +  L  A   +  L+    Y+ +++++G q++
gi|2273665   452 CGYKDEdinMDIVPLFETMEGLANAEHVMSELYQNPVYKKHLEkrGNQQt 501

                vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                +m+G+sD  KD G l A W +YkA+E + K   +  +K+v F GRGG
gi|2273665   502 IMLGFSDGTKDGGYLKANWEIYKAKEVLTKLSEQNNIKVVFFDGRGGPPA 551

                RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                RGGG tH    sq     n  +  t+qG  i   FG  +
gi|2273665   552 RGGGKTHDFYASQGKTIANNKIELTIQGQTITSIFGNKEQAKYNFEQLLT 601

                AtLEHGm..nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRl
                A +E  + +n         R L+ e+A +    Y s     P Fv Y
gi|2273665   602 AGVENDVfkNAKKELTEKERALIIELADISYKKY-SDLKAHPMFVPYLQE 650

                AtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWtqtRFHLPvWL
                      YGk niGsRP+KR  +  ++ e LRAiP++ +W q +  +P +
gi|2273665   651 MSTLEYYGKTNIGSRPSKRGNGSELkfEDLRAIPFVGSWSQLKQNVPGFF 700

                GvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAa
                G+G A +    K+   +  + E+Yk   FF+ tl L  m+
gi|2273665   701 GFGYAMQKM--KEQGRFEEVIELYKGSDFFK-TLVLNSMMSM--NKSYFP 745

                LyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                L   +        F + L d+Y+  +d++L++ G k l E DP  ++ ++
gi|2273665   746 LTYYIKNNPKFGAFWNVLFDEYELSRDIMLELTGFKMLQEEDPLSRKSVK 795

                LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                +R+  +  L  +q Y L +i         + +  KE A E       Lv
gi|2273665   796 IREKIVLPLLSIQQYALMKIQ--------KGEGNKE-AYEK------LVT 830
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                    LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                                       + G      n
  gi|2273665   831 RS----------------LFGNINASRNSA    844

gi|11596397|gb|AAG38601.1|AF317284_1: domain 1 of 1, from 37 to 811: score -45.8, E = 5
                    *->siD.AqLRlLvP.........GKvsed.ekLieYDALLlDkFL.DiL
                        +D+A  R L+P++  + +++G+  ed+++ +  D   l + L+D++
  gi|1159639    37    KLDgAAARPLAPtnaasakpqGRTREDkDRPLFEDIRYLGRLLgDVV 83

                    qDLHGedLkEavqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvA
                     +  G+ + ++v      +  +    D    + L   L  L P  ++ v
  gi|1159639    84 REQEGDAVFDVVETIRQTAVKFRREDDKAAAQTLEKMLRKLTPEQTVSVV 133

                    kailHmLnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKk
                    +a++    LAn+AE+ +   RRRi+ +        +sA     +   l k
  gi|1159639   134 RAFSYFSHLANIAEDRHHNRRRRIHALA-------GSAAQAGTVAYALDK 176

                    LvlklnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaq
                    L   ++ s + + +      +  vltAHPt   R+s+L  +  i    a
  gi|1159639   177 LKQAGDASSKTIKQFFEGALIVPVLTAHPTEVQRKSILDAQHDI----AR 222

                    LsAKDvtveDKkEL..DEALHRE.iqAAFRtDEiRRaqPtPqDEmRaGms
                    L A    +   +EL + EAL R ++   + t  +R a+ t  DE+   +s
  gi|1159639   223 LLAERDQPLTARELahHEALLRArVTTLWQTRMLRDARLTVADEIENALS 272

                    YiHEtvWkGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGk
                    Y+  t  +  P     ++ AL   G+  R+P      +  sW+GGDRDG
  gi|1159639   273 YYRATFLDELPALYADIEEALAEHGLRARVP---AFFQMGSWIGGDRDG- 318

                    nPRvtPEvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEE
                    nP vt     +       +    Y++qv  L  Els+    + L v A +
  gi|1159639   319 NPNVTAATLDEAISRQAAVIFEHYLEQVHKLGAELSV----SNLLVGASD 364

                    lyrtaardkvvKyYiEFWKqvP..PtEPYRviLGdvRDKLYn.tRER...
                      +  a            q P++  EPYR  L  v  +L  + R R ++
  gi|1159639   365 ALKALAAA--------SPDQSPhrVDEPYRRALIGVYTRLAAsARVRlge 406

                    .aRHLLAtGiseisEeAv.ytkvEeFLEPLELCYksLCeCGDkviADGsL
                    ++  +   G    +  A +y + EeF   L +   sL       +A   L
  gi|1159639   407 gTVPVRSAGRGAAPVRATpYADAEEFAADLRVLTDSLALHHGESLATPRL 456

                    LDlLRqvstFGLsLvKLDiRqEseRqtDvlDAittHLeiGs.YReWsEeK
                      l+R    FG  L  +D+Rq s+ +  v+  +    ++ ++Y   +E
  gi|1159639   457 APLMRAAEVFGFHLASIDLRQSSDIHEAVVAELLARGGVEAdYAALPEAD 506

                    RqEWLlaELkGKRPLlgsDLPktEEvkDvldafr....vLAELPiDsFGa
                    +   Lla L   RPL  + L   +  k  l+ +++ + + A     +
  gi|1159639   507 KLRVLLAALADPRPLRSPYLDYSDLAKSELGVLErahaIRAQFGARAVRN 556

                    YiismataPsDvLAvELLqRECgv.............kqtLrvvPLFEkLA
                    Yiis + + sD + v LLq+E g+ +++ ++++ + ++ L v+PLFE +A
  gi|1159639   557 YIISHTETVSDLVEVLLLQKETGLfegtlgtphanaRNGLMVIPLFETIA 606

                    DLeAAPAavekLFs...iDWYinridGKqevmvGYsDsGKDAGRlsAAWq
                    DL+ A   +   F+ +++     +    qevm+GYsDs KD G l   W
  gi|1159639   607 DLRNASDIMRAFFAlpgVGELLAHQGHEQEVMLGYSDSNKDGGFLTSNWE 656

                    LYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinG
                    LY+A   ++    + G+KL lFHGRGGtvGRGGGPt  AiLsqPP t+nG
  gi|1159639   657 LYRAELALVDLFDERGIKLRLFHGRGGTVGRGGGPTYQAILSQPPGTVNG 706

                    slRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPv.sPk..PEW
                     +R t qGEvi   F   ++  r L    AAtLE  + P  ++Pk+ P +
  gi|1159639   707 QIRLTEQGEVIASKFANPEIGRRNLETVVAATLEATLAPHSnAPKqlPAF 756

                    RkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKR
                       m+ +   A   YR++v+  P F +YF + tP +E   +niGsRPa R
  gi|1159639   757 EAAMQTLSDAAMASYRALVYETPGFTDYFFSSTPITEIAGLNIGSRPASR 806

                    kPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLk
                    k
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  gi|1159639   807 K---------------------------------------------- 807

                   EmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdk

  gi|1159639     - ---------------------------------------------- -

                   YvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiR
                                                                  +
  gi|1159639   808 ----------------------------------------------LQ 809

                   DPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKG
                   DP
  gi|1159639   810 DP---------------------------------------------- 811

                   iAAGmqntG<-*

  gi|1159639     - ---------    -

gi|260063588|ref|YP_003196668.1|: domain 1 of 1, from 2 to 848: score -46.9, E = 5.1
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          q+  L   K s  +k   Y  L l         + G  +
  gi|2600635     2    ---SQVERLKEFKKSVRNKFNIYNSLFLNLPYTEGENV-GIYIPLLF 44

                   qECYElsAeYEGKkDtkKLeELGakLt.sLdPaDai.lvAkailHmLnLA
                   q C        GK  t+ L++     t++ d  + i+l+ + i  +
  gi|2600635    45 QQCDR--GLKSGKNPTEILDDFFENFTqATDEKERIdLMFRIIQYVERQV 92

                   nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                    L + ve A   R +        D  s      i + ++    k nK  +
  gi|2600635    93 VLYDSVEDAAFPRLHVHT-----DSLS------IRDYFQ--LAKKNKRWD 129

                   EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    v   L   s  +vltAHPtq    ++L   a +R          +  +
  gi|2600635   130 KVSKKLESFSARIVLTAHPTQFYTPAVLDIIAELRTL--------ILENK 171

                   KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                     E+D  L    q    t  i   +PtP DE +  +  +    ++ v
  gi|2600635   172 IDEIDVTL----QQLGLTSLINSKKPTPLDEAKNIIYTLRHVYYQAVGDL 217

                   LRRvDtALKniGinERlPYdvP.LikFssWmGGDRDGknPRvtPEvtRDv
                      +   + n        Yd P++ik   W GGDRDG nP vt ++t Dv
  gi|2600635   218 YAYIKGSIENDA------YDNPdIIKLGFWPGGDRDG-NPYVTADITMDV 260

                   CLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvK
                       R      Y++ +  L   +s        R   E +++   +
  gi|2600635   261 ADELRTTLMKCYYNDLKTLQKRIS-------FRGVQEQMQQLRGKA---- 299

                   yYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvy
                    Y+  +     t  Y  ++   R                   ei E  v
  gi|2600635   300 -YVAMF-DTSKTLSYEEMIETLR------------------EIREILVR 328

                   tkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                        +L  L+                     ++ +v  F      LDiR
  gi|2600635   329 DYYGLYLKELD-------------------HFIDKVRLFKTHFATLDIR 358

                   qEseRqtDvlDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLlgsD
                   q+  ++  v++ + +H ++ + s  e +Ee+  E L  E     P    D
  gi|2600635   359 QDHSKHYQVVETVLRHHGLikESLDELPEERLVELLTRESLELDPSAYDD 408

                   LPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvELLq
                    P    vkD l  +  L E+ ++++ D    Yiis +     vL v  L
  gi|2600635   409 -PI---VKDTLVNMAQLEEIQrkngEDGCNRYIISNSEDIFSVLFVFGLL 454

                   RECgvkq...tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...
                   R  g k+++ t  ++PLFE +  +  A   ++ LF +  Y+ ++  +++
  gi|2600635   455 RWSGWKNrdlTFDIIPLFETMKGMAEAESVMQTLFDLPEYRAHVAQRrdl 504

                   qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                   q +m+G+sD  KD G l A W ++k +E + +v ++  +K + F GRGG
  gi|2600635   505 QTIMLGFSDGTKDGGYLKANWSIFKTKETLSRVCRRNKIKAIFFDGRGGP 554
```

```
                    vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                      RGGG tH    +q     n  +  tvqG  i   FG  +L  +
  gi|2600635   555 PARGGGKTHRFYAAQTKAIANHEIQLTVQGQTITSTFGTKELFMHNSEQL 604

                    tAAtLEHGm..nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                      A L   + ++  v  k   R+L+e +     E Y ++   E  F  Y
  gi|2600635   605 LTAGLSNTIfgKENVIDKSQ-RDLLETLSELSFEKYNALKQHE-LFLPYL 652

                    RlAtPElEYGkmniGsRPaKR..kPsGGiesLRAiPWiFaWtqtRFHLPv
                           Y   niGsRP KR++k       LRAi ++ +W q +  +P
  gi|2600635   653 ENRSTLKYYSNANIGSRPGKRgnKAKLEFSDLRAISFVGSWSQLKQNVPG 702

                    WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                    + G+G A K    KD   +  Lk mYke  FFR  +    m   K    +
  gi|2600635   703 YYGIGTALKQL--KDEGRMPELKKMYKEVAFFRALMLNSMMSLTKCYFEL 750

                    AaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                     +   +    E  k F + L  +Y+  k++LL++ G k l+E +   +
  gi|2600635   751 TSYMKE---DEVYKGFWEMLYREYKLSKQMLLQLSGYKVLMENESVSRES 797

                    lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                    +++R+  +  L v+q Y L Ri               E  d
  gi|2600635   798 VKIRENIVLPLLVIQQYALHRI--------------AEGTDRK------- 826

                    vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     +L          E  +   + G      n
  gi|2600635   827 -ELY---------EKIVTRSLYGNINASRNSA    848

gi|255534738|ref|YP_003095109.1|: domain 1 of 1, from 1 to 846: score -47.4, E = 5.1
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        +  q +     ++  ++k   Y  L +    D +  +    L  +
  gi|2555347     1    -MQNQEKTEKFRQIV-ENKFQIYNSLFMSLPYDKMTNI--GMLLPFL 43

                    qECYElsAeYE.GKkDtkKLeELGakLtsLdP..aDailvAkailHmLnL
                     E  E  A YE+GK   + +eE  +k t+L+ ++  + l+ k i  +
  gi|2555347    44 YE--ESKAGYEnGKNPVEIVEEFFSKHTGLESegQKTELLFKIIQYI--- 88

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                         E ++     i+      Fa+   A     +   + +   +
  gi|2555347    89 -----ERQVVLFDSIEDAA---FAELHPAGETGTLLQLYDRSLQQH--QL 128

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKD.vtv
                    e     +K  +v +v+tAHPtq    s+     Ri   L     KD+vt
  gi|2555347   129 EATRAKMKDFAVRVVFTAHPTQFYPSSV----QRILHDLRSAIMKDsVT- 173

                    eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                        E+D  L    q   +t  + R +PtP DE    + Y+    ++
  gi|2555347   174 ----EIDMLL----QQLGKTPFLNREKPTPLDEAMSIIFYLRYVYYDSLG 215

                    KFLRRvDtALKn.iGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtR
                        ++    Kn+ G  + +P    + +   W GGDRDG nP vt E t
  gi|2555347   216 ELYAKI----KNsFGDGDFVP-PHDIFQLGFWPGGDRDG-NPFVTAETTL 259

                    DvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkv
                     v                                   A El +      v
  gi|2555347   260 QV-----------------------------------AKELNS-----SV 269

                    vKyYiEFWKqvPPtEPYR...viLGdvRDKLYntRERaRHLLAtGiseis
                     K Y E  K++     +R+ + +L    D LY    +  H        i
  gi|2555347   270 LKSYYEHLKKLRRRLSFRgvsEVLDMLSDALYDAIFKDQH--------IT 311

                    EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLL.DlLRqvstFGLsL
                     + +  ++ e    L      L          G LL+D+   v  FG
  gi|2555347   312 SDEILNRIHEAQQILNGKHNGLF---------GDLLdDFEDRVKIFGTHF 352

                    vKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPL
                      LDiRq+s  +  v+D i          +   e +  WL   L+    L
  gi|2555347   353 ATLDIRQDSRVHQNVIDEIVMKKSDLQSENIMNEDKLKWL---LETDVIL 399

                    lgsDLP.ktEEvkDvldafrvLAELP.iDsFGaYiismataPsDvLAvEL
                     + D  + t +    +  ++ +  + +      Yiis +    DvL v
```

```
  gi|2555347   400 NPEDFEgITQDTLRNICNIKDIQKINgARGMSRYIISNSDGIKDVLNVFG 449

                   LqRECgvkq...tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK.
                   L R Cg k+++  + +vPLFE +  L+A    +  L+ +  Y+ +++ ++
  gi|2555347   450 LFRLCGYKEddiNIDIVPLFETMEGLDAGEGVMRELYELPVYRKHLERRg 499

                   ..qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRG
                   + q +m+G+sD  KD G l A W +Y  +E + Kv  +  +K++ F GRG
  gi|2555347   500 naQTIMLGFSDGTKDGGYLKANWEIYETKEQLTKVSDENNIKVIFFDGRG 549

                   GtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLq
                   G   RGGG tH    sq     n  + +t+qG  i   FG  +
  gi|2555347   550 GPPARGGGKTHDFYASQGKTIANNKIEITIQGQTITSVFGNKDQAKYNFE 599

                   RFtAAtLEHGm..nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvE
                       A +E  + +n         R+L+ e+A +    Y s     P Fv
  gi|2555347   600 QLLTAGIENDVfkNSKKDLTENERNLIRELAEISFKKY-SDLKAHPMFVP 648

                   YFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWtqtRFHL
                   Y         YGk niGsRP+KR     ++ e LRAiP++ +W q +  +
  gi|2555347   649 YLQEMSTLQYYGKTNIGSRPSKRAGNDELkfEDLRAIPFVGSWSQLKQNV 698

                   PvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDP
                   P + G+G A      K    +  ++ +Yk   FF+  +    m   K
  gi|2555347   699 PGFFGFGFALHQL--KMQGRFDEIRALYKGSDFFKTLVLNSMMSMNKSYF 746

                   GiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLK
                    +     + L     +     L ++Y+  k l+L++ G k l+E +P  +
  gi|2555347   747 PLTYYMKNNLRFGGFWSI---LFEEYELSKALMLELTGFKMLMEEEPLSR 793

                   qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                   + +++R+  +  L  +q Y L +i                   E  ++a
  gi|2555347   794 KSVKIREKIVLPLLSIQQYALMKIQK----------------GEGNREAY 827

                   eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   e + +                 + G      n
  gi|2555347   828 EKLVMR--------------SLFGNINASRNSA    846

gi|629594|pir||PC2170: domain 1 of 1, from 1 to 368: score -47.5, E = 5.1
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|629594|     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|629594|     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|629594|     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                                                i+ CLaqL+ KD+t++DK+
  gi|629594|     1 ------------------------------IKDCLAQLYTKDITPDDKQ 19

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   ELDE L REiqAAFRtDEi+R +Pt qDEmRa msY+HE +W+GvPKFLR
  gi|629594|    20 ELDESLQREIQAAFRTDEIKRMPPTSQDEMRAXMSYFHERIWNGVPKFLR 69

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                   R   ALKniGi ER+PY++PLi+ ssWmGGDRD
  gi|629594|    70 R---ALKNIGIDERVPYNAPLIQLSSWMGGDRD----------------- 99

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|629594|     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    FWK +PPtEPY v+LGdvRD LY tRER+R LL  Gis+i+EeA +t+v
  gi|629594|   100 -FWKTIPPTEPYSVVLGDVRDTLYHTRERTRQLLSNGISDIPEEATFTDV 148
```

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                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+FLEPLELCY+sLC  GD+ iADG LLD+LRqvstFGLsLv+LDiRqEs
  gi|629594|   149 EQFLEPLELCYRSLCSSGDRPIADGTLLDFLRQVSTFGLSLVRLDIRQES 198

                    eRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgsDLPkt
                    eR+ DvlD it+H + G+sYR+WsEe+RqEWLlaEL+GKRPL+g DLPkt
  gi|629594|   199 ERHNDVLDDITKHXNTGsSYRDWSEERRQEWLLAELRGKRPLFGLDLPKT 248

                    EEvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqt
                    EE++Dvld+f+v+ ELP+D+FGaYiismat+PsDvL vELLqREC+vk++
  gi|629594|   249 EEIADVLDTFKVISELPSDCFGAYIISMATSPSDVLVVELLQRECHVKKP 298

                    LrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDA
                    LrvvPLFEkLADLeAAPAav +
  gi|629594|   299 LRVVPLFEKLADLEAAPAAVSR---------------------------- 320

                    GRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLs
                                        +L l
  gi|629594|   321 -------------------------QLLLL-------------------- 325

                    qPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvs
                            s+  t q
  gi|629594|   326 --------SMGXTLQ---------------------------------- 332

                    PkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGs
                                                    FRl
  gi|629594|   333 ---------------------------------FRL-------------- 335

                    RPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKn
                          PsG
  gi|629594|   336 -----NPSG---------------------------------------- 339

                    lqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGk
                                    l L+E
  gi|629594|   340 ---------------ALCLME---------------------------- 345

                    sLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYt
                               +LL +    Dl
  gi|629594|   346 -----------WLLLLPRSIDL--------------------------- 356

                    LKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLi
                                        +   n         L
  gi|629594|   357 --------------------WSSKN---------LD-------------- 363

                    LtmKGiAAGmqntG<-*
                             +  t
  gi|629594|   364 ---------LSSTS    368

gi|255534144|ref|YP_003094516.1|: domain 1 of 1, from 6 to 862: score -48.3, E = 5.1
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           q   +    v    +   Y  L l      ++D  G  L  ++
  gi|2555341     6    RAKGQRESIFNNEVV--SRFELYNSLFLTLPFYKVKD-TGTLLPLFI 49

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDai..lvAkailHmLnLA
                    + C +   +   +  +  ++    k t  +    i +l+ + i  +
  gi|2555341    50 KYCEDGINNH--QTPATIIDAFFKKYTQNNSNKDIidLLFRFIQYIERQV 97

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                     L + ve A    +k+      aDE +A     +   lKk +       +
  gi|2555341    98 VLFDAVEDA--SFNKLNA----ADEHNA-----LLSYLKKGIDNK-ALND 135

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                     +   +   s  LvltAHPtq    s+L   + i    + L   D+
  gi|2555341   136 KIEKLIDEFSLRLVLTAHPTQFYPGSVL---SIITDLTTALKTNDIST-- 180

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                           +   +q   +t    +  PtP DE      Y+    +
  gi|2555341   181 -------INLLLQQLGKTPFFNKKSPTPVDEALSLAWYLENVFYFAAANI 223

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                       +D  L    +  +      +i+   W GGDRDG nP v  + t  v
```

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  gi|2555341   224 QSEIDKSLNDYNLESK-----KIIELGFWPGGDRDG-NPNVHTDSTIQVS 267

                   LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                    + R +    Y+     L   +      + + +  + ly+ a
  gi|2555341   268 KMLRQILFRCYYRDFRNLKRRITFRGVEEHIAIVQDVLYKNAFDP----- 312

                   YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                                                        +i  e
  gi|2555341   313 ----------------------------------------NIETE---- 317

                   kvEeFL.EPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiR
                   ++ +FL E L      L +  D   AD +  Dl+R+v  +G     LDiR
  gi|2555341   318 NIADFLiENLNNIRATLMDDHDGLFADLA-SDLIRKVELYGSHFASLDIR 366

                   qEseRqtDvlDAittHLeiGs.....YReWsEeKRqEWL......laELk
                   q+s    Dv     +   i s  +++Y + sE  +   L+ ++ ++   +
  gi|2555341   367 QDSRVLRDVHAFCRQRKPIISlfpenYDSLSEAEKIKALsfksarINYSE 416

                   GKRPLlgsDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvL.
                    K  L+   L    E+k + ++   LA         +iis +   sD+L+
  gi|2555341   417 NKDSLINDTLQTITEIKQIQESNGELA------CHRFIISNCQQASDILq 460

                   AvELLqRECgvkqtLrv..vPLFEkLADLeAAPAavekLFsiDWYinrid
                    +EL          L ++ vPLFE + DL  A   +e L++  +Y+ ++
  gi|2555341   461 LMELFLWNGWEETDLSIdfVPLFETVHDLADAGGIMETLYAHPFYKKHLK 510

                   ...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                   +++ Kq++m+G+sDs KD G l A W ++ A+  +   A k+ ++L  F
  gi|2555341   511 rrgNKQHIMLGFSDSTKDGGYLMANWSIFNAKVALTETANKHNIQLAFFD 560

                   GRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFr
                   GRGG   RGGG tH    s   +  n  +  t+qG  i   +G  +
  gi|2555341   561 GRGGPPSRGGGKTHRFYASMGKEIANKNIQLTIQGQTISSQYGSIDSAEF 610

                   sLqRFtAAtLEHGmnPP..vsPkPEWRkLmeemAvvAtEEYRsvv..vKE
                    +     A +  G++  +++   P  ++L++   v+A E Y + v+  K
  gi|2555341   611 NIEQLINAGISAGIKEThnILLDPLHKELLD---VMAKESYEAFVdlRKH 657

                   PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGG..iesLRAiPWiFaWtq
                   P F  Y     P     k+ i sRP KR  +G  ++e LRAi ++ aW q
  gi|2555341   658 PLFLSYLEKFSPLSLLSKITISSRPVKRNSGGAlkLEDLRAISFVTAWSQ 707

                   tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                    +  +P + G+G A K   +    n  k+   Y+e  +F+  +D   m
  gi|2555341   708 LKQNIPGFYGMGTALKN--QEKLGNWDKVVKTYQESGYFKTIIDNCMMSM 755

                   AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                    K D  i a + +     e   F k L d+++  k +LLk+ GH  l+E
  gi|2555341   756 SKSDFAITAHFAN---DKEYGAFWKMLHDEFELSKSMLLKLSGHETLMEN 802

                   DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                    P  K  + +R+  +  L  +q Y L R             l  E  +E+
  gi|2555341   803 YPVEKRSIAVREKIVLPLVLIQHYALER-------------LQTEITAEE 839

                   skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       +   kL              i t+ Gi     n
  gi|2555341   840 ---QQSYEKLA-------------IRTVYGIVNAGRNLA    862

gi|126662794|ref|ZP_01733793.1|: domain 1 of 1, from 6 to 857: score -51.3, E = 5.3
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                          ++        s   k   Y  + +    D +    G  L  +
  gi|1266627     6    ----KIERFNQNVAS---KYNIYNSVFITLPFDEINN-TGVLLPLFS 44

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                     C        G k  +  eE+     s    D     +  + m
  gi|1266627    45 EVC------ENGFKNNQSPEEIFDTFVS-KYLDNPTQQEKESLMFRFIQY 87

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                    E  ++     i+      F+   +      + + +K    + nK  eE
  gi|1266627    88 IER-QVVLFDAIEDAA---FSVVNNLEGRGSLRD-MKENAEQKNKQ-EEL 131
```

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                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     e L n  +  vltAHPtq    s+L         ++ L    +  +
  gi|1266627   132 KEFLENFKIRTVLTAHPTQFYPGSVL-------GIITDL-TEAIRENNLN 173

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     + E L    +  F    i+  +PtP DE    + Y+    ++     +
  gi|1266627   174 SIKELLAQLGKTPF----IKHEKPTPYDEAVSLIWYLENVFYETAGAMMQ 219

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     +    Kni +   +P +  ++    W GGDRDG nP vt E+t  v
  gi|1266627   220 YIQ---KNI-LKGEMPKN-DILNLGFWPGGDRDG-NPYVTTEITLKVADR 263

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                     R      Y++ +  L   l                  a  d
  gi|1266627   264 LRTSILKSYYNDIRKLKRKLTF-----------------AGVD------- 289

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                                +i+ d+  KLY    R+           s   ++  +
  gi|1266627   290 -------------IIIADIESKLY----RSVFY--------SQGEIFITL 314

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                    E+  + L L  k L     + +    +  lL +   FG     LDiRq s
  gi|1266627   315 EDLKDKL-LQVKMLVTTKHQSLYIDEIDLLLNKLNLFGFHFATLDIRQNS 363

                    eRqtDvlDAittHLei...GsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                      +  v DAi      + +  Y+  sE+ +  +L    +    L   D
  gi|1266627   364 KIHARVFDAIIANKKTnfpENYKTLSEDDKFHFLSNVFSD---LDVTDF- 409

                    ktEEvkDvldafrvLAELPiD....sFGaYiismataPsDvLAvELLqRE
                      E vk  +++++ +  +   +++++   Yiis   +   v     +
  gi|1266627   410 EDEIVKSTIGSIKAMKTIQQNngekASNRYIISNNESALHVFETLSMFHL 459

                    Cgvkq.tLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK...qevm
                    Cg k++t+ +vPLFE + DLe A   +e+L+  + Y n++  ++++q +m
  gi|1266627   460 CGWKNpTVDIVPLFESVEDLEKADRVMEQLYTNETYANHLKMRgneQTIM 509

                    vGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRG
                    +G+sD  KD G l A W +YkA+E +  + +ky +K+v F GRGG   RG
  gi|1266627   510 LGFSDGTKDGGYLMANWGIYKAKEALTAISRKYDIKVVFFDGRGGPPARG 559

                    GGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAt
                    GG t     s  P   n  +  tvqG  i   FG  + C   L     A
  gi|1266627   560 GGKTNKFYASLGPTIENQQIQLTVQGQTISSNFGTIDSCRYNLENLLSAG 609

                    LEHGm..nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAt
                        + ++       E +++++++  +    Y      E  Fv Y
  gi|1266627   610 AKNQVftKNENELTSEEKEVLQNLSEISYQKYVDFKNHE-MFVPYLERMS 658

                    PElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWtqtRFHLPvWLGv
                        Y k niGsRP+KR  s  ++   LRAiP++ +W q +  +P + Gv
  gi|1266627   659 TLNYYAKTNIGSRPSKRNASDKLnfADLRAIPFVGSWSQLKQNVPGFFGV 708

                    GAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLy
                    G A K     D    qk+ ++Y++  FF+  ++   m   K    + a
  gi|1266627   709 GTALKN--YEDNNEWQKVSDLYHNSLFFKTLIENSMMALSKSFFPLTAYM 756

                    DkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLR
                     +     e   F + +  ++ Etk lLLk+ G   l+E  P  K  + LR
  gi|1266627   757 KN---DKEFGEFWQLIYTEFLETKRLLLKLSGYSALMENYPDGKASVELR 803

                    dsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLn
                    +  +  L  +q Y L +i              KE  + +  + +  + +
  gi|1266627   804 EKIVLPLLTIQQYALLKI--------------KELKESE-TPNEKQIAIY 838

                    ptervaPGLEDtLiLtmKGiAAGmqntG<-*
                              E  +   + G      n
  gi|1266627   839 ---------EKIVTRSLFGNINASRNSA    857

gi|149926183|ref|ZP_01914445.1|: domain 1 of 1, from 1 to 849: score -51.7, E = 5.3
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                            ++    G  +   + ie D    ++       LH   + E+v
```

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gi|1499261     1    -----MKFEQAGELA---EQIEADEPDFEH-------LHAR-VEEFV 31

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    q     s   +     + L  L ++L  L  a+  l A
gi|1499261    32 Q-----SNKNDPEIIVSALKYLNSQLMILSAAERHLKAND---------- 66

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                              ++ + hG                 lK L+       e +
gi|1499261    67 --------SPANQSLMHG-----------------LKTLIDHATSRGESI 91

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                     + L n ++  v+tAHPt         K       L+qL   D+
gi|1499261    92 IQKLSNTTISPVFTAHPTN------FNKPQASAVVLSQLD--DIATPHGN 133

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                           +  q  + t  +R  +P  qDE     s i      G     +
gi|1499261   134 A------KVCQELWQTQGVRELKPSVQDEANQFSSNIRHLHSSG-RNIHK 176

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                     +   L   G+   l    PL++   W+GGDRDG nP +   v +Dv +
gi|1499261   177 QINQQLS--GLPNNLKLSKPLVEAGNWVGGDRDG-NPNIDAAVLKDV-VK 222

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                    +   Aa  Y++q           +   E       l     +
gi|1499261   223 TLSTAAFDYFEQ-----------KIGKEKTTQPGSLGNLLSKA------- 254

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                                  LG +R+KL  tR    HL+  G   i  +  y +
gi|1499261   255 ----------GHSESLGLIREKLARTRA---HLVGEGPLPIQGD-LYLNA 290

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLR.qvstFGLsLvKLDiRqE
                     e L  LE       +  Dk i     LDlL+      G      DiRq
gi|1499261   291 NELLHDLESLNIGNLDTDDKRIVQEK-LDLLKlDADSIGFHGASTDIRQN 339

                    seRqtDvl.DAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    s  +   +++ + +  +   Y +  E  +q  L   L      +  D P
gi|1499261   340 SAMNEKTVgELLRRSGGPRNYESLGELEKQTLLTHLLLDTSKTVLNDAPI 389

                    tEEvk....DvldafrvLAELPiDsFGaYiismataP.....sDvLAvEL
                       + +++ D   a+        Ds+G+  +  + + ++++ sD+L v L
gi|1499261   390 DGQIDnpefDREIALIKSYKTIHDSYGPQALKNCITAntetlSDMLEVML 439

                    LqRECgvkq....tLrvvPLFEkLADLeAAPAavekLFsiDWYinridG.
                    L +  g+  +++  + vvPL E + DL+  P  ++ +    WY+  ++ +
gi|1499261   440 LLKHAGLADgdgvKMNVVPLIETVDDLHNGPTILNSMLNHPWYRQALQAs 489

                    ..KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    +++q++mvGYsDs +  G l+  W +Y     +  vAK+ GvKL +FHGR
gi|1499261   490 gnQQQIMVGYSDSNRLDGPLASSWAVYEGTAKMLEVAKQNGVKLHVFHGR 539

                    GGtvGRGGGPtHLA.iLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrs
                    GGt  RG G     +i s     +   +R t qGE +   FG   +
gi|1499261   540 GGTEARGSGDSYAQeIKSGNGASLLTGMRQTEQGEEVPAKFGTKIISQSN 589

                    LqRFtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvE
                    L      tLE     P      + + me +A  A + Y s+ +  P
gi|1499261   590 LADMVGSTLETMATGPDQQLAKYANTMELLAQHARDSYQSL-YTNPELPQ 638

                    YFRlAtPElEYGkmniGsRPaKRkPsGG....iesLRAiPWiFaWtqtRF
                    +F   tP    Gk n GsRPa R  s  ++  ++ LRAiPW+ aW q
gi|1499261   639 FFQRSTPIEFVGKSNAGSRPASRANSAEgslvLDKLRAIPWVGAWYQSGS 688

                    HLPvWLGvGAAFKhAidKD.......iKnlqkLkEmYkeWPFFRvtlDLl
                     +P + G G A K  +d+ +++++++ +   +L+ mY+eWPFF+  +D
gi|1499261   689 AMPAFFGTGSALKNFVDQStdtnttpAQRTEQLQTMYREWPFFKSFVDRT 738

                    EmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkD
                         K D  iA  y kL  a     F ++++++Y+ tk+++L i    D
gi|1499261   739 ATALQKADMQIAQQYAKLAPAKSQGVF-EKIKNEYELTKEMILNIKQTND 787

                    lLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEy
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```
                  l++  P     l ++ +       +q   LK
  gi|1499261   788 LMDHNPVDAEILTVKKPLTQAAHAMQIGLLK------------------- 818

                  AdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                  A  +            + ++   L + +++ m+ i       G
  gi|1499261   819 AHQQ-----------AGPEIQNKLVEPIVMSMQAISSS-NRFG    849

gi|88713052|ref|ZP_01107136.1|: domain 1 of 1, from 2 to 847: score -54.7, E = 5.4
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                         +   L   K s ++k   Y  L l             +L
  gi|8871305     2    ---HKTERLEEFKKSVNNKFNVYNSLFL-------------NLPYRN 32

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   E   +       +  k L        +L+P D  ++ + +   +n+ n
  gi|8871305    33 IENVGMVVPLLLHQSVKGLK------SGLNPQD--ILESFFQNYVNIENE 74

                  AEEvelAyRRRikkkkhGDFaD..EasA......ttEsDiEEtlKkLvlk
                   + ++  +R      +     D+ E  A ++ ++  Es     + +Lv k
  gi|8871305    75 KDRIDFMFRIIQYVERQVVLYDsvEDAAfpklqeHSESLSIKDYFQLVNK 124

                  lnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK
                    Ks + v e L   s  +vltAHPtq    ++L   + +R  +
  gi|8871305   125 T-KSWDKVAEKLSSFSARIVLTAHPTQFYTPAVLDIMSDLRELIEENKID 173

                  DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvW
                  D+ +             +q    t  +   +PtP DE +  +  +    +
  gi|8871305   174 DIDIT------------LQQLGLTSLMNSKKPTPLDEAKNIIYILRHVYY 211

                  kGvPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPE
                  + +      +        i +    +  ++k   W GGDRDG nP vt +
  gi|8871305   212 DAMGDLYSYIKEN-----IDDEDFQNHNIMKLGFWPGGDRDG-NPFVTAD 255

                  vtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaar
                  +tR v    R+     Y++ +  L   l       EL v   El
  gi|8871305   256 ITRNVSDELRISLMKCYYNDLKTLQKKLTF----KELQVHVREL------ 295

                  dkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseis
                                           RDK Y          A  +   +
  gi|8871305   296 --------------------------RDKFY----------AAMFN--P 306

                  EeAvytkvEeFLEPLELCYksLCeCGDkviADGsLLD.lLRqvstFGLsL
                  E  v  k E+ +E L      L +  D      s LD+++ +v  F
  gi|8871305   307 ETIV--KYENIIETLSNIRGLLID--DYHGLYLSELDhFIDKVKIFKTHF 352

                  vKLDiRqEseRqtDvlDAittH..LeiGsYReWsEeKRqEWLla.ELkGK
                    LDiRq+   +  v+  i   +++ i    e sEe     L+ ++Lk
  gi|8871305   353 ATLDIRQDHSMHIRVVQEILVKneIIIADISELSEEDLVKVLINkDLK-- 400

                  RPLlgsDLPktEEvkDvldafrvLAELP....iDsFGaYiismataPsDv
                    +   D   t  +kD l  +  LA + ++++ +    Yiis +     v
  gi|8871305   401 --VNSNDYEGT--IKDTLVNISQLAAIQekngEEGCNRYIISNSEDIFSV 446

                  LAvELLqRECgvkq...tLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                  L v  L R Cg k ++ t  ++PLFE +  ++ A A+++ L+ +  Y+ +
  gi|8871305   447 LFVFGLFRWCGWKTnkiTFDIIPLFETMKGMDNAEATMQYLYDLPIYREH 496

                  id...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                  +++++ Kq +m+G+sD  KD G l A W + k +E + Kv Kk  +K
  gi|8871305   497 LErrgDKQTMMLGFSDGTKDGGYLKANWSILKTKEVLSKVSKKQHIKALF 546

                  FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFG.EEnL
                  F GRGG   RGGG tH    +q  D  n  +  t+qG  i   +G+ E+
  gi|8871305   547 FDGRGGPPARGGGKTHRFYAAQTKDIANNEIQLTIQGQTITSTYGtKEQF 596

                  CFrsLqRFtAAtLE..HGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvK
                     s q  tA    +  G +  +s   E+RkL+ee+       Y ++  K
  gi|8871305   597 MHNSEQLLTAGLSNnlFGKENVIS--KEYRKLLEELSELSFNKYDAL-KK 643

                  EPRFvEYFRlAtPElEYGkmniGsRPaKR..kPsGGiesLRAiPWiFaWt
                     F+ Y         Y k niGsRP KR++k    ++ LRAi ++ +W
  gi|8871305   644 HEMFIPYLENRSTLKYYQKANIGSRPGKRgnKKQLELTDLRAISFVGSWS 693
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                    qtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmv
                    q +  +P + G+G A K    K+   l +Lk mYke PFF+  +    m
  gi|8871305   694 QLKQNVPGYFGIGTAIKSL--KETGKLRQLKKMYKEVPFFKALMLNSMMS 741

                    FAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLE
                      K    + +   +     e +   + L ++Y+   d+LL+i G   l+E
  gi|8871305   742 LTKCYFELTSYMKEDQKYGEFW---QILHEEYQLSIDMLLQISGSNILME 788

                    GDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdE
                     +   +  + +R+  +  L v+q Y L++i             s Ey +
  gi|8871305   789 NEAISRESIEIRENIVLPLLVIQQYALQKIGQ----------STEYKEL 827

                    nskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                         + +v                  + G      n
  gi|8871305   828 Y----EKIVTRS----------------LYGNINASRNSA    847

gi|256420516|ref|YP_003121169.1|: domain 1 of 1, from 6 to 855: score -54.7, E = 5.4
                    *->siDAqL.RlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEa
                           qL + Lv  K    + L  + AL   k      +  G  L  +
  gi|2564205     6    NNTLQLfKNLVGTKFQLYNSL--FTALPFHKV-----ERTGVFLSLF 45

                    vqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                       C E  A    K   + L+    + ts          + +  m
  gi|2564205    46 LIHCEEGYAK--EKSPQEILNSYFQQYTSCSNEQ-----QKLDLMFRFVQ 88

                    LAE.EvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                     AE+ v l         +     D   A t s +   l  + +    + e
  gi|2564205    89 YAErQVVLFDALEDAAFR--QIHDVHGAGTLSHL---LSEITSEQ--AGE 131

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                         L+  sv LvltAHPtq     +L     i n L+     D t +
  gi|2564205   132 QLAKKLQDYSVRLVLTAHPTQFYPGGVLT----IINDLSRALINDNTAQV 177

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                       L        q   +t   ++ +PtP DE    + ++  t +    +
  gi|2564205   178 NAYL--------QQLGKTPFFKKEKPTPYDEAISLIWFLENTFYPAAGRI 219

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                    + +             +  + P+i+   W GGDRDG nP vt ++t
  gi|2564205   220 ISKLKSQFPAA-----VNSNNPVIRMGFWPGGDRDG-NPFVTADITLRTA 263

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                       R      Y+  v  L   l      +EL    E ly         K
  gi|2564205   264 EALRGGIIKCYYLDVRRLKRRLTFKGIEQELNMLEEKLYNNLFIP-GHKT 312

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                     i                       +  t  R R +L      i E+
  gi|2564205   313 NIS------------------QKEILDTLARVRIIL------IEENNGL- 337

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                        FL  L+                    Dl+  v  FGL    LDiRq
  gi|2564205   338 ----FLTMLD--------------------DLVSRVELFGLFFATLDIRQ 363

                    EseRqtDvlDAittHLei..GsYReWsEeKRqEWLlaELkGKRPLlgsDL
                    +s  +   lD i +  ++ +  Y++ +++ +   Ll  +kG      +++
  gi|2564205   364 DSSVHGPLLDCIAEKTDLlpKNYKDLPDNEKITHLL-NIKGTA---NPEV 409

                    PktEEvkDvldafrvLAELPiDs..FGa..YiismataPsDvLAvELLqR
                          kD l ++  + ++    ++FG ++Yiis +     v+ v  L
  gi|2564205   410 LEDSLHKDTLATIAAVKDIQQNNgeFGChrYIISHSMNALNVMEVYGLFL 459

                    ECgv...kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid...GKq
                      g ++++ ++ +vPLFE + DL+ A   +  L+    Y+ ++ ++  Kq
  gi|2564205   460 ASGWqkdRLSVDIVPLFETIDDLRQAGNVMRELYDNAAYRAHLKkryNKQ 509

                    evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                     +m+G+sD  KD G l A W +YkA+ E+ ++ ++y + +v F GRGG
  gi|2564205   510 TIMLGFSDGTKDGGYLMANWSIYKAKQELTRISREYEIDVVFFDGRGGPP 559

                    GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
```

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                     RGGG tH    s   D  n  +  t+qG  i   FG  +     +
  gi|2564205   560 ARGGGKTHQFYASMGRDIANEEIQLTIQGQTISSNFGTVDSAQFNIEQLV 609

                    AAtLEHGmnPPvsPkPEWRkLmeemAv..vAtEEYRsv..vvKEPRFvEY
                     A +    n   s +        e   ++ A E Y + ++    P F +Y
  gi|2564205   610 HAGI---ANELFSSREQTMSGAGEALLqsLADEGYVAFnkLKHHPDFLDY 656

                    FRlAtPElEYGkmniGsRPaKRkPsG..GiesLRAiPWiFaWtqtRFHLP
                       A P   Y   niGsRP+KR  + +  ++ LRA+P++ aW q +  +P
  gi|2564205   657 LDFASPLRYYAETNIGSRPSKRNAAAklNLNDLRAVPYVGAWSQLKQNVP 706

                    vWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPG
                     + GvG A   A++K  K    L+ +Yk+  FFR  l    m   K
  gi|2564205   707 GFYGVGSALE-ALEKAGK-WEELRQLYKDSLFFRTLLGNCQMAMKKSYFP 754

                    iAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKq
                    + a y k     e++   + + d+ + t+ l+Lk+ G  +l+   P
  gi|2564205   755 LTAAYGKHPRFGEVW---NMIHDEHKRTRTLILKLVGETELMAAYPIDAL 801

                    rlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkade
                     + +R+  +  L  +q   L RiR+
  gi|2564205   802 SIQMRERIVLPLLTIQQAALARIRE------------------------ 826

                    LvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       Ln       GL +t    +     G+ n G
  gi|2564205   827 ---LN-EAGNGDGLKETYEKLVVRCSFGIINAG    855

gi|163755567|ref|ZP_02162686.1|: domain 1 of 1, from 15 to 862: score -55.0, E = 5.4
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLk..E
                       s   q+   +      de  i    +Ll  F +i       d  ++E
  gi|1637555    15    SSKYQIYNSIFMTLPFDE--ISNTGVLLPLFSEICEKGYALDKNpsE 59

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                    +v   +E   e + K +t+K++               l+ + i  +
  gi|1637555    60 IVHKFFERYVEKD-KTETEKIN---------------LLFRFIQYIERQV 93

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                     L + ve A    +           +  t     EE   k      K+
  gi|1637555    94 VLFDAVEDAAFPIVNNMD-------GRGTLRNIKEEAEEKQKIGALKTYL 136

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                    E F       +  vltAHPtq          + +   ++ L A  +  +D
  gi|1637555   137 ERFK------IRPVLTAHPTQFY-------PGQVLGIITDL-AEAIEKDD 172

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                       +   L    +  F     ++ +PtP DE    + Y+    ++   K
  gi|1637555   173 LLAIKKLLAQLGKTPF----FKKEKPTPYDEAVSLIWYLENVFYHAASKI 218

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                       +    +ni   E l  +  +i    W GGDRDG nP vt E+t+ v
  gi|1637555   219 YNYIQ---QNIFKDEEL--NNQVIDLGFWPGGDRDG-NPFVTTEITKKVA 262

                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                       R      Y   +  L   l      d +  R   l r    +
  gi|1637555   263 ERLRSTILLNYHRDIRKLKRRLTF----DGVEKRLAKLERMLYDN----- 303

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                                           +Y  +E     LA   +e+   A+
  gi|1637555   304 ----------------------VYLRKEEGMLSLAAFEAEL--KAIKD 327

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                     v +    L   +++  e            Dl+ +v  FG     LDiRq
  gi|1637555   328 IVVKKHQSL---FRAEIE-----------DLINKVKLFGYHFAMLDIRQ 362

                    EseRqtDvlDAittHLe........iGsYReWsEeKRqEWLlaELkGKRP
                    +s  +  v + i + + ++++   +i    +  EeK +     + k
  gi|1637555   363 DSRVHQGVFENIVETMKnrgealfsIDYVNSSEEEKIKVLTHIDKKVEEK 412

                    LlgsDLPktEEvkDvldafrvLAELPiD.sFGaYiismataPsDvLAvEL
                     +  ++  t      + a++ + +   ++    Yiis   +   v+
  gi|1637555   413 YFENEI--TNATISSIYAMKTIQDRNGErGANRYIISNNQSALHVMEAFT 460
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                    LqRECgvkqt.LrvvPLFEkLADLeAAPAavekLFsiDWYinrid...GK
                    + R C  kq+++ v PLFE + DL+AA A ++ L+  + Y  ++ +++ K
  gi|1637555   461 MLRLCDWKQPdVDVSPLFETVPDLQAAQAVMKTLYTNEAYAAHLKrrgNK 510

                    qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                    q +m+G+sD  KD G l A W ++kA+EE+  + ++yG+K++ F GRGG
  gi|1637555   511 QYIMLGFSDGTKDGGYLMANWSIFKAKEELTAISREYGIKVIFFDGRGGP 560

                    vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                      RGGG tH    s      +  +  tvqG  i   FG  + C   L
  gi|1637555   561 PARGGGKTHQFYASLGSTVEDEEIQLTVQGQTISSNFGTLDSCQYNLEQL 610

                    tAAtLEHGmnPPvsPk..PEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                        +   +        + E +k me +A v  + Y +   K P F  Y
  gi|1637555   611 LSSGISNEIFSSTEAEfsEEDKKTMEALASVSYDTYVAF-KKHPMFLPYL 659

                    RlAtPElEYGkmniGsRPaKRkPsGGie..sLRAiPWiFaWtqtRFHLPv
                            Y k niGsRP+KR  s   + + LRAiP++ +W q +  +P
  gi|1637555   660 ERMSTLKYYAKTNIGSRPSKRSKSKEFNfsDLRAIPFVGSWSQLKQNVPG 709

                    WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                    + GvG A  h  +  +  +  ++ +Y++  FFR  l+   m   K    +
  gi|1637555   710 FYGVGTALEHMEK--SGQFEAVEKLYQNSSFFRTLLENSMMSLTKSFFKL 757

                    AaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqr
                     a   +    Ee   F   + ++Y+ tk +LLk+ G  +l+E     K
  gi|1637555   758 TAYMKD---NEEFGSFWTIIFEEYERTKRMLLKLTGYNELMENQQEGKAS 804

                    lRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeL
                    +  R+  +  L  +q Y L++i              +E   ++
  gi|1637555   805 IHAREKIVLPLLTIQQYALRKI--------------QELQKDP------- 833

                    vkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       n +e+     E  +   + G      n
  gi|1637555   834 ---NASEEELKTFEKMVTRSLFGNINASRNSA    862

gi|86143373|ref|ZP_01061775.1|: domain 1 of 1, from 2 to 861: score -55.8, E = 5.5
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s   +L        s   k   Y  L +      + D  G  L  +
  gi|8614337     2    SRQPKLERFNNLVKS---KYQVYNSLFMTLPFQGITD-TGVLLPLFD 44

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDai...lvAkailHmLnL
                      C      Y+    ++K+          d ++  + +l+ + i  +
  gi|8614337    45 RIC---TRGYDKHYNPEKIVNYFFDKYQRDVSEEErydLLFRFIQYIERQ 91

                    AnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsP
                      L + +e A  R +               t   i E        +
  gi|8614337    92 VVLFDAIEDAAYRTVNNMD--------GRGTLRNIKEEAEAQSKTG---- 129

                    eEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtve
                     E  e L+   +  vltAHPtq    ++L   + i    a +    v
  gi|8614337   130 -ELKEYLQDFKIRPVLTAHPTQFYPGAVL---GIINDLSAAINENNV--- 172

                    DKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG...
                          E + + +    +t   ++ +PtP DE    + Y+    +k +++
  gi|8614337   173 ------EMIKKLLSQLGKTPFFKKEKPTPYDEAVSLIWYLENVFYKAssh 216

                    vPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                    +  +LR      +n+   E   +d  +i    W GGDRDG nP vt E+t
  gi|8614337   217 IYNYLR------QNVFKGEF--FDNEVIDLGFWPGGDRDG-NPFVTTEIT 257

                    RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk
                      v    R      Y+  +  L                        +r
  gi|8614337   258 LKVASRLRNTIIKNYYRDIRSL-----------------------RRR- 282

                    vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                         i F   v  +E     L d   +LY                ++ +
  gi|8614337   283 -----ITF---VGTEEA----LADLEKRLYDS------------IFLPGD 308

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
```

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                     v   +Ee LE   L  + +       +    + D+L +v  FG     L
  gi|8614337   309 EVTVSLEE-LETTLLRIRKIVVERHESLFLEEIDDILNKVKMFGYHFAVL 357

                    DiRqEseRqtDvlDAittH.....Lei..GsYReWsEeKRqEWLlaELkG
                    DiRq+s  +  v+D i +   +++L+i +  Y + sEe     +l +++G
  gi|8614337   358 DIRQDSRVHMHVMDEIVKQcakdnLGIfpENYLDLSEEEQIK-ILQDVRG 406

                    KR.PLlgsDLPktEEvkDvldafrvLAELPiDsFGaYiismataPsDvL.
                    K +P    D      ++ +    ++       s   Yiis   +   v++
  gi|8614337   407 KVdPATLEDDIARKTLESIYAMQEIQKQNGERSCNRYIISNNQTGLNVMq 456

                    AvELLqRECgvkqtLrvvPLFEkLADLeAAPAavekLFsiDWYinri...
                    A  ++        t+ +vPLFE + DL+ A   +  L+    Y  +++++
  gi|8614337   457 AFSMIHLTGWEDPTVDIVPLFETVPDLKIAKEVMRGLYTNPAYAAHLkkr 506

                    dGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGR
                    + Kq +m+G+sD  KD G l A W ++kA+EE+ +v +++G+K++ F GR
  gi|8614337   507 NMKQTIMLGFSDGTKDGGYLMANWSIFKAKEELTQVSREFGIKVIFFDGR 556

                    GGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsL
                    GG   RGGG tH    s      +  + vtvqG  i   FG  + C   L
  gi|8614337   557 GGPPARGGGKTHQFYASLGETIEDEEIQVTVQGQTISSNFGTPDSCQYNL 606

                    qRFtAAtLEHGm..nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFv
                           +  G+ ++   +   E Rk mee+A +    Y s     P+F
  gi|8614337   607 EQLLSSGIFNGVfsQKTKAFPDEDRKTMEELAEISYQAY-SDFKAHPKFL 655

                    EYFRlAtPElEYGkmniGsRPaKRkPsGGie..sLRAiPWiFaWtqtRFH
                     Y         Y k niGsRP+KR  s  ++ + LRAiP++ +W q +
  gi|8614337   656 GYLERMSTLKFYAKTNIGSRPSKRGGSDKLNfsDLRAIPFVGSWSQLKQN 705

                    LPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGD
                    +P + GvG A     ++    + +++ +Y++  FFR  l+   m   K
  gi|8614337   706 VPGFFGVGTAIEKLEERG--EFDRVQSLYNNSMFFRTLLENSMMSLTK-- 751

                    PGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYL
                        aL   +    e   F + + ++Y+  k  LLk+ G  +l+E +
  gi|8614337   752 -SFFALTAYMKDDPEFGAFWELIHEEYERSKRVLLKVTGYSELMEDEQAG 800

                    KqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskka
                    K  +  R+  +  L  +q + LK+i              +E   E+
  gi|8614337   801 KASIQERERIVLPLLTIQQFALKKI--------------QEMQREE---- 832

                    deLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                          np e+     E  +   + G      n
  gi|8614337   833 ------NPDEKKLEMFEKMVTRSLFGNINASRNSA    861

gi|89890758|ref|ZP_01202267.1|: domain 1 of 1, from 1 to 848: score -59.0, E = 5.6
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqD..LHGedLkE
                        +  q R ++  K s ++k   Y  L l      +   ++  + L E
  gi|8989075     1    -MQDQNR-IAEFKKSVQNKFNIYNSLFLNLPYSNIENvgMLIPLLME 45

                    avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLA
                      q         EG    + +e        L           i  m  +
  gi|8989075    46 QSQKGLK-----EGLNPKEIIEAFFNGFANLHTEQ-----DRIDFMFRII 85

                    nLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPe
                       E   + y               +s     D    + +Lv    Ks +
  gi|8989075    86 QYVERQVVLYDSVEDAAF-PKLQQHSSSRSLKD----YFQLVEEN-KSWD 129

                    EvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveD
                     +   L n s  +vltAHPtq    ++L   + +R          +  +
  gi|8989075   130 AIEKQLNNFSARIVLTAHPTQFYTPAVLDIITNLRTL--------INDNN 171

                    KkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKF
                      E+D AL    q    t  +   +PtP DE +  +  +    ++ +
  gi|8989075   172 IDEIDVAL----QQLGLTSLVNSKKPTPLDEAKNIIHTLRHVYYDAIGEM 217

                    LRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvC
                       +   + n         +  ++k   W GGDRDG nP vt  +t++v
  gi|8989075   218 YTHIKSSVGNAQFD-----NHDIVKLGFWPGGDRDG-NPFVTASITKEVM 261
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                    LLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKy
                       R+     Y++ + +L    ls             E++      k + y
  gi|8989075   262 NELRVTLMKCYYNELKELQRKLSF-----------KEIQEAITDLKNTLY 300

                    YiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvyt
                       F   +  t  Y+ i+      L   RE    LL   +  +
  gi|8989075   301 EAMFDTSIHVT--YKEIIAP----LIHIRE----LLVAQYHGL------- 333

                    kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                        +L  L+L                    ++ +v  F      +DiRq
  gi|8989075   334 ----YLKDLDL-------------------FIDKVKIFKTHFATIDIRQ 359

                    EseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                    +   +t v+ A+ +    G  +e  Ee  q  L+  L      l +
  gi|8989075   360 DHSMHTVVMQAVLK--KYGYIKESIEELTQLQLIDILLQESISLDPNDYE 407

                    tEEvkDvldafrvLAELP....iDsFGaYiismataPsDvLAvELLqREC
                     + vkD +  +  L  + ++++      Yiis +     vL v  L R C
  gi|8989075   408 EDIVKDTIVNISQLSTIQesngEQGCNRYIISNSEDVYSVLYVFALFRWC 457

                    gvkq...tLrvvPLFEkLADLeAAPAavekLFsiDWYinri...dGKqev
                    g  +++ t  ++PLFE +  ++    ++e+LF +D Y+ ++  ++ Kq +
  gi|8989075   458 GWENrdiTFDIIPLFETMKGMDDSRSTMEQLFELDAYRKHVafrNNKQTI 507

                    mvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGR
                    m+G+sD  KD G l A W + k +E +  v  ++ v  + F GRGG   R
  gi|8989075   508 MLGFSDGTKDGGYLKANWSILKTKETLSEVCSDHDVAAIFFDGRGGPPAR 557

                    GGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFG.EEnLCFrsLqRFtA
                    GGG tH    +q     n  +  t+qG  i   +G+ E+    s q  tA
  gi|8989075   558 GGGKTHRFYAAQTSKVANNEIQLTIQGQTITSTYGtKEQFKHNSEQLLTA 607

                    AtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAt
                          ++  +      R L+ee+  +    Y ++   + +F+ Y
  gi|8989075   608 GLSNSILDNEITISASSRSLIEELSEMSFKKYDALKHHD-KFMPYLENMS 656

                    PElEYGkmniGsRPaKR..kPsGGiesLRAiPWiFaWtqtRFHLPvWLGv
                        Y k niGsRP KR++k    ++ LRAi ++ +W q +  +P + G+
  gi|8989075   657 TLKYYTKANIGSRPGKRghKAKLELTDLRAISFVGSWSQLKQNVPGYFGI 706

                    GAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLy
                    G A +    +    +  ++ +Yk+ PFF+  +    m   K    + +
  gi|8989075   707 GTALQTM--QQQGRFDEVQQLYKDVPFFKALMLNSMMSLSKCYFELTSYM 754

                    DkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLR
                     +    Ee   F + L d+Y   k +LL++ G   l+E +   +  +++R
  gi|8989075   755 KE---NEEYGAFWQILEDEYLLSKRMLLELSGMEILMEKETVSRESIKIR 801

                    dsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLn
                    ++ +  L v+q Y L+ i                A+ n
  gi|8989075   802 EAIVLPLLVIQQYALQMI-----------------AQHN----------- 823

                    ptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       +  P  E  +   + G      n
  gi|8989075   824 ---EHQPQYEKIVTRSLYGNINASRNSA    848

gi|86130467|ref|ZP_01049067.1|: domain 1 of 1, from 2 to 859: score -59.7, E = 5.7
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       s + ++        s   k   Y  + +    D +    G  L  +
  gi|8613046     2    SREPKIERFNANVKS---KYEVYNGIFMTLPFDGISN-TGVLLPLFH 44

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDai......lvAkailHm
                      C       EG kD k   E+          Da ++++++++ k i  +
  gi|8613046    45 SIC------KEGYKDNKNPTEIIEYFFERYMRDATekeredILFKFIQYI 88

                    LnLAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlkln
                         L + +e A  R +               t   i E       k
  gi|8613046    89 ERQVVLFDAIEDASYRIVNNMD--------GRGTLRNIKEEAEATGKKE- 129

                    KsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDv
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                      E    L   ++  vltAHPtq     +L     i n L+    +D
  gi|8613046   130 ----ELISYLNRFTIRPVLTAHPTQFYPGVVLG----IINDLSA-AIRDN 170

                    tveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkG
                      eD k L   L        +t   ++ +PtP DE    + Y+    ++
  gi|8613046   171 RLEDIKTLLAQLG-------KTPFFKKEKPTPYDEAVSLIWYLENVFYHS 213

                    vPKFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                               L    i +   +   L+    W GGDRDG nP vt  +t
  gi|8613046   214 AGAIYDYLHRHL----IQDE-SFSNTLVDLGFWPGGDRDG-NPFVTTAIT 257

                    RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk
                      v    R      Y+  +  L   +        L    + +y    ++
  gi|8613046   258 LKVARKLRSSVLRNYYREIKQLRRRITFRGTEAPLSELEDQVYTAIFSE- 306

                    vvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEe
                      K          P      iL   +D     R++   L
  gi|8613046   307 -EK----------PAISQASILKTLKDIRDIVRDKHQSLYLD-------- 337

                    AvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKL
                        k++  +  +EL                          FGL    L
  gi|8613046   338 ----KIDSLIHKVEL-------------------------FGLHFASL 356

                    DiRqEseRqtDvlDAittHLei.Gs......YReWsEeKRqEWLlaELkG
                    DiRq+s  +  v + i +   i+Gs+  +++Y   sE+   ++L   ++G
  gi|8613046   357 DIRQDSSIHKIVFEQIVENATInGSkifpegYLALSENEQIDFL-NNVHG 405

                    KRPLlgsDLPktEEvkDvldafrvLAELPiDsFGa.....YiismataPs
                        l ++    E v   l+++  +  +  D  G +++++Yiis + +
  gi|8613046   406 A---LDPESFEEEVVTKTLGSIYAMKTI-QDENGErgsnrYIISNSQSAL 451

                    DvLAvELLqRECgvkq.tLrvvPLFEkLADLeAAPAavekLFsiDWYinr
                     v+      R C    +t  v PLFE + DL AAPA +e L+    Y  +
  gi|8613046   452 HVMQAFTFLRLCDWESpTADVAPLFETVPDLIAAPAVMEALYTNPTYSKH 501

                    idG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvl
                    +  ++ +q +m+G+sD  KD G l A W ++kA+E +  + +kyGv ++
  gi|8613046   502 LKSrgmRQTIMLGFSDGTKDGGYLMANWSIFKAKEAMTAMSRKYGVTVIF 551

                    FHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLC
                    F GRGG   RGGG tH    s  P      + +tvqG  i   FG  + C
  gi|8613046   552 FDGRGGPPARGGGKTHQFYASLGPNIEAQEIQITVQGQTISSNFGTVDSC 601

                    FrsLqRFtAAtLE....HGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvv
                       L       + ++   G +  +sP    R+ +e +A    E Y +  +
  gi|8613046   602 QYNLEQLLSSGVNnevfKGAHNDISPSD--RETLEALAQKSYEAYTA--F 647

                    K.EPRFvEYFRlAtPElEYGkmniGsRPaKR..kPsGGiesLRAiPWiFa
                    K+  +F  Y         Y k niGsRP+KR++k       LRAiP++ +
  gi|8613046   648 KgHDKFLPYLERMSTLKYYAKTNIGSRPSKRsqKSTLDFGDLRAIPFVGS 697

                    WtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlE
                    W q +  +P + GvG A   A   D   l  +k +Yk+  FFR  l+
  gi|8613046   698 WSQLKQNVPGFYGVGTAL--ASFEDAGKLEDVKQLYKNSSFFRTLLENSM 745

                    mvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDl
                    m   K   G+ a   +     e   F k L ++Y+  k l+L++AG  +l
  gi|8613046   746 MSLTKSFFGLTAYMQE---DQEFGEFWKLLFEEYKRSKRLMLEVAGLTEL 792

                    LEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyA
                    +E +   K  +  R+  +  L  +q Y L+ i D +         s E
  gi|8613046   793 MENEKAGKASIQERENIVLPLLTIQQYALRAIQDMQR--------SGEQT 834

                    dEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                    d   k  + +v                  + G      n
  gi|8613046   835 DKA-KVYERMVTRS----------------LFGNINASRNSA    859

gi|225011063|ref|ZP_03701527.1|: domain 1 of 1, from 2 to 847: score -60.9, E = 5.7
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                           q Rl v  K   ++    Y  L l      +  +
  gi|2250110     2    ---QQQRLEVFKKTV-NNTFNVYNSLFLNLPYRNIENVGMLIPLLLD 44
```

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                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                q    l A   GK   + Le       +L   ++      i  m  +
gi|2250110    45 QSKKGLEA---GKNPQQILEGFFKDYAGLTTEES-----QIDFMFRIIQY 86

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                 E   + y    +      F           i + ++  +   nKs +Ev
gi|2250110    87 VERQVVLY---DSVED-AAFPKLHKHSSSLSIKDYFQ--IIDKNKSWDEV 130

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                 e L n s  ++ltAHPtq    ++L   + +R        K +  +
gi|2250110   131 AEKLSNFSARIILTAHPTQFYTPAVLDIMTDLR--------KLIVENNIT 172

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                E+D  L    q    t  +   +PtP DE +  +  +    ++ +
gi|2250110   173 EIDKSL----QQLGLTSLLNSKKPTPLDEAKNIIHILRNVYYDAIGDLFS 218

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                 + t +  +  n    Y++  +k   W GGDRDG nP vt E+t
gi|2250110   219 YIKTNIPQVDFNN---YNI--VKLGFWPGGDRDG-NPFVTTEMT------ 256

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                          +qv D +    m     +L++    l  ta ++
gi|2250110   257 ----------DQVADELRTTLMKCYYKDLKALHQKLSFTALQE------- 289

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                               L   R  LY     a  L       ++ +    ++
gi|2250110   290 --------------PLIGLRKALYDSMFDANAL-------VPYDFLIGEL 318

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                 +  + L   Y  L       + D  L  l+ +v  F      LDiRq+
gi|2250110   319 QKIKDLLVSKYFGL------YLKD--LDALIDKVKIFKTHFATLDIRQDH 360

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                  +   + Ai +H +i   +e  Ee   E L   L      + +D
gi|2250110   361 SIHFNSITAILKHAGI--IKESLEELSPEALTDKLLHLDLEVYPDEFEDA 408

                EvkDvldafrvLAELPi....DsFGaYiismataPsDvLAvELLqRECgv
                 v D l  +r L  +  ++++D    Yiis +     vL v  L R  g
gi|2250110   409 LVSDTLKNIRNLKNIQAkngqDGCNRYIISNSEDKFSVLFVWALFRWSGY 458

                kqt...LrvvPLFEkLADLeAAPAavekLFsiDWYinrid...GKqevmv
                k+++ +  +vPLFE +  ++    +++ LF +  Y+ ++ +++ K  +m+
gi|2250110   459 KEAdihFDIVPLFETMHGMDTSEQSMQELFQTTAYMQHVKkrgNKHTIML 508

                GYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGG
                G+sD  KD G + A W + k +E +  v K+y v  v F GRGG   RGG
gi|2250110   509 GFSDGTKDGGYVKANWSILKTKENLTSVCKQYDVSAVFFDGRGGPPARGG 558

                GPtHLAiLsqPPDtinGslRvtvqGEviEfsFG.EEnLCFrsLqRFtAAt
                G tH    +q  +  n  +  t+qG  i   +G+ ++  +   q  tA
gi|2250110   559 GKTHRFYAAQTKEIANNEIQLTIQGQTITSTYGtRDQFVYNCEQLLTAGL 608

                LEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPE
                               R Lme +       Y ++  + P+F+ Y
gi|2250110   609 SNNIFSKENTISIAHRALMETLSERSFTKYDAL-KQHPKFMPYLENRSTL 657

                lEYGkmniGsRPaKR..kPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGA
                  Y k niGsRP KR++k    +  LRAi ++ +W q +  +P + G+G
gi|2250110   658 KYYTKANIGSRPGKRgqKAKLELSDLRAISFVGSWSQLKQNVPGYFGIGS 707

                AFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDk
                A   A       l  L+Em+ke P+F+  +    m  AK    + +   +
gi|2250110   708 AI--ASLEAEGKLGELQEMFKEVPYFKALMQNSMMALAKCYFELTSYMKE 755

                LLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRds
                     e   F + L d+Y   k+ LL i G   l+E +   +  + +R+
gi|2250110   756 ---DPEYGDFWQILHDEYTLSKEKLLLISGLNILMEKEAVSRESVLIREN 802

                YittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnpt
                 +  L v+q Y L++i                   n    + L ++
```

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  gi|2250110   803 IVLPLLVIQQYALQKI------------------GQN----APLKEIY-- 828

                   ervaPGLEDtLiLtmKGiAAGmqntG<-*
                          E  +   + G      n
  gi|2250110   829 -------EKIVTRSLYGNINASRNSA    847

gi|224368853|ref|YP_002603015.1|: domain 1 of 1, from 2 to 850: score -62.5, E = 5.8
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       +    R+ +  K    +k   Y  L l      +  + G  +
  gi|2243688     2    TMNKPRRIQAFEKSV-KNKFYVYNSLFLNLPFQKISNI-GMLIPLLL 46

                   qECYElsAeYE.GKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAn
                     C     + E+GK   + L+   +  t ++        + i  m  +
  gi|2243688    47 HVCRN---DLEsGKAPLEILNSFFSDHTKIQSE-----REKIDFMFRV-- 86

                   LAEEvelAyRRRikkkkhGDFaDEasAttEsDiEE.tlKkLvlkl.nKsP
                         + y  R   +      D a A       E  lK  + + +nK
  gi|2243688    87 ------IQYVERQVVLY-DSVEDSAFAQLRTHGNElSLKDYIHLSdNKRK 129

                   eEvF.eALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                     v ++ L    s+ +v+tAHPtq    s+L     i n  + + A  +
  gi|2243688   130 RGVLsDKLDTFSIRIVFTAHPTQFYSPSVLDI---IDNLRTLIAANNI-- 174

                   eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                       E+D AL    q    t  i   +PtP DE +  + ++    ++ v
  gi|2243688   175 ---NEIDLAL----QQLGMTSLINARKPTPCDEAKNIIYFLKSVYYDAVG 217

                   KFLRRvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRD
                        +   ++n      +  +  +i+   W GGDRDG nP vt E+t
  gi|2243688   218 EMYSYIKRNVQN-----SVFDNPEIIQLGFWPGGDRDG-NPFVTSEITMA 261

                   vCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvv
                   v    Rm     Y+  +E L    l      d +      ++ t      +
  gi|2243688   262 VADELRMTLMGCYYREIEGLERKLTFRGVDDIITTLKTCVHDTMFDP--T 309

                   KyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv
                   K  + F   + P       L  +RD L  t          G+
  gi|2243688   310 KT-LTFEDIITP-------LYTIRDALVST--------FNGL-------- 335

                   ytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDi
                         +LE L           Dk i           v  F      LDi
  gi|2243688   336 ------YLEDL-----------DKLID---------RVKLFRTHFAILDI 359

                   RqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDL
                   Rq    +   +  i +  +     e  +e  +  L++ L     L+ +D
  gi|2243688   360 RQNHAVHKQAIQEILKQKN--RIEESLDELEKNELISILVHENFLVEADQ 407

                   PktEEvkDvldafrvLAELPi....DsFGaYiismataPsDvLAvELLqR
                    +   vkD ++ +  +A + +++++     Yiis +     vL v  L R
  gi|2243688   408 FQDKIVKDTVQIISQIAAIQMkngeKGCNRYIISNSEDIFSVLFVHGLFR 457

                   ECgv...kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinrid...GKq
                    C  +++k ++ +vPLFE +  +  A   ++ LF i  Y+ ++ +++ +q
  gi|2243688   458 WCCRdsgKIAVDIVPLFESMEGMVHAGTIMQELFDIPEYRSHVSqrrNRQ 507

                   evmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtv
                    +m+G+sD  KD G l A W ++k +E +  v  +  vK + F GRGG
  gi|2243688   508 TMMLGFSDGTKDGGYLQANWSIFKTKEHLSAVCDHNNVKAIFFDGRGGPP 557

                   GRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFt
                    RGGG tH    sq     n ++  t+qG  i   +G      +
  gi|2243688   558 ARGGGKTHRFYASQSQKISNHAIQLTIQGQTITSHYGSKAHFMHNCEQLL 607

                   AAtLEHGm...nPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYF
                    A L   + ++   +s +   R+ ++ +A    E Y ++      F+ Y
  gi|2243688   608 TAGLSNSLyeqRNAISNQS--RQTLDTLARLSFEKYTALKNHK-MFIPYL 654

                   RlAtPElEYGkmniGsRPaKRkPsGGies..LRAiPWiFaWtqtRFHLPv
                           YG  niGsRP++R   G +e ++LRAiP++ +W q +  +P
  gi|2243688   655 ENKSTLKYYGETNIGSRPTRRTSKGKLELkdLRAIPFVGSWSQLKQNVPG 704
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                    WLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGi
                    + G+G   K  +  D   l  L+ ++k+ PFF+  +    m   K    +
  gi|2243688   705 YFGIGTSLKAFV--DDGRLNELRQLFKDVPFFKALIFNSMMSLSKCNFAL 752

                    AaLyDkLLvaEe..LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLK
                     +      +aE+++ k F   L ++Y   k+++L i     l+E +P  K
  gi|2243688   753 TG-----YIAEDpnYKEFWTLLFNEYTLSKQMVLLISDQSTLMEEEPVSK 797

                    qrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkad
                      + +R+  +  L ++q Y L+ i                E+
  gi|2243688   798 RSIEIREQIVLPLLIIQQYALQMI------------------EQ----- 823

                    eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                            + ++   E  +   + G      n
  gi|2243688   824 -------KSGYSGDYEKIVRRSLYGNINASRNSA    850

gi|227540600|ref|ZP_03970649.1|: domain 1 of 1, from 2 to 858: score -66.7, E = 6
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                  K s  +k   +   +l +F ++ + L        v
  gi|2275406     2    ------------KLS--QKEATFQNEVLTRF-ELFKSLFLTLPFQRV 33

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                    +    l   +   +  k +eE       L+P +  ++ + +
  gi|2275406    34 KHTGTL-LPFFTTHCEKGVEE------HLAPEE--IIDSFFGQYEQYVQE 74

                    AEEvelAyRRRikkkkhGDFaDEas........AttEsDiEEtlKkLvlk
                     + v+l +R      +     D  ++++ ++ +   E+ + E l +
  gi|2275406    75 EDRVDLLFRIVQYVERQVVLFDAVEdssfqsigRADEAGLLEPLFRQTET 124

                    lnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK
                      K  + + + LK  sv LvltAHPtq    ++L   + i   +  +
  gi|2275406   125 NSKLRKQIVNKLKDFSVRLVLTAHPTQFYPGAVL---SIINDLIEAIKDN 171

                    DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvW
                    D+           +H  +q   +t  i + +PtP DE      Y+    +
  gi|2275406   172 DI---------NNIHLLLQQLGKTPFINKLKPTPVDEAASLAWYLENVFY 212

                    kGvPKFLRRvDtALKniGinERlPYdv.PLikFssWmGGDRDGknPRvtP
                    k        +D  L      E    dv+ Li+   W GGDRDG nP vt
  gi|2275406   213 KVASEIQATIDDEL------EMPTEDVkQLIELGFWPGGDRDG-NPNVTV 255

                    EvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaa
                    E tR v  + R +                 ++RC
  gi|2275406   256 ESTRKVATMLRTI-----------------LFRC---------------- 272

                    rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                          yY +F          Rvi    R   +   E     L   + e
  gi|2275406   273 ------YYRDF----------RVI---KRRITFRGVEQYMDTLQELFYEN 303

                    sEeAvyt...kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFG
                    s + v  ++++ ++ L  L    k L e       D  + Dl+R+v tFG
  gi|2275406   304 SFNPVENpkdETDRILTNLKAIKKVLIEKHNSLFID-VVEDLIRKVVTFG 352

                    LsLvKLDiRqEseRqtDvlD.AittHLeiGsYReWsEeKRqEWLlaELkG
                         LDiRq+s    D +   it+H       e  E       l+E
  gi|2275406   353 CYFTTLDIRQDSRVLRDTITyLITKHQKKTGLAEDFEG------LSETAK 396

                    KR..PLlgsDLPktEEvkDvl.dafrvLAEL.PiDsFGa......Yiism
                    +++ P    DL   E+ +  ++d+++v+  L+ i   G+++  +++iis
  gi|2275406   397 QKgfPFSELDLEVGEDAALLVkDTLEVIPLLkSIQNAGSeraaqrFIISN 446

                    ataPsDvLAvELLqRECgvkq...tLrvvPLFEkLADLeAAPAavekLFs
                    +   sD+L    L    g k+++ t+  vPLFE + DL  A   ++ L+
  gi|2275406   447 CQQASDILGLMQLFLWSGWKKeelTIDFVPLFETVDDLVRAGDVMKALYT 496

                    iDWYinridG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKk
                       Y+ ++  +++Kq +m+G+sDs KD G l A W +YkA+ ++  +A++
  gi|2275406   497 HPAYVAHLKSrgnKQTIMLGFSDSTKDGGYLMANWSIYKAKMDLTAIARD 546

                    yGvKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfs
                    y v Lv F GRGG   RGGG t     s   +  n  +  t+qG  i
```

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  gi|2275406   547 YEVDLVFFDGRGGPPARGGGKTQRFYASMGREIENKHIQLTIQGQTISSQ 596

                   FGEEnLCFrsLqRFtAAtL..EHGmnPPvsPkPEWRkLmeemAvvAtEEY
                   +G  +     +     A + +E   n         ++++++mA v  E +
  gi|2275406   597 YGSLDTAKYNIEQLLHAGIisEIRQNEGDTLTAKQKNVIDQMAEVSYEKF 646

                   RsvvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGG..iesLRAiP
                    s+  K+P F  Y     P      +ni sRP KR      ++e LRAi
  gi|2275406   647 MSL-RKDPLFLNYLENLSPLKVLSTINISSRPVKRNSDKElkLEDLRAIS 695

                   WiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtl
                   ++ +W q +  +P + GvG A ++A +        ++ +Y+    F   +
  gi|2275406   696 FVTSWSQLKQNIPGFFGVGSALQFAEENNL--WSYVRNLYEHSGMFNTII 743

                   DLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAG
                   D   m   K    i +        E+   F k L ++Y+ tk+++Lk+
  gi|2275406   744 DNCMMSMTKSNFDITSYMQ---FDEQYGDFWKMLHAEYELTKKYVLKLSN 790

                   HkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhls
                    k l+E  P  +  +  R+  i  L ++q Y +++
  gi|2275406   791 TKILMENYPVERESILAREKIILPLLIIQHYAIRK--------------Q 826

                   KEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                   K    E+  k d   kL                t+ G+     n
  gi|2275406   827 KQLETED-PKYDVYSKLI-------------ARTIYGVVNAGRNLA    858

gi|1552966|gb|AAB08698.1|: domain 1 of 1, from 1 to 305: score -69.5, E = 6.2
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1552966     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1552966     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|1552966     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|1552966     - ---------------------------------------------- -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|1552966     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|1552966     - ---------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|1552966     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|1552966     - ---------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|1552966     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|1552966     - ---------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL

  gi|1552966     - ---------------------------------------------- -
```

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                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                                                              sDsGKDAG
  gi|1552966     1 ----------------------------------------SDSGKDAG 8

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                   RlsAAWqLYkAqEE+i+vAKkyGvKL++FHGRGGtvGRGGGPtHLAiLsq
  gi|1552966     9 RLSAAWQLYKAQEELIQVAKKYGVKLTMFHGRGGTVGRGGGPTHLAILSQ 58

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP+tinGs+RvtvqGEviE+sFGEE LCFr+LqRFtAAtLEHGm PP+sP
  gi|1552966    59 PPETINGSIRVTVQGEVIEQSFGEERLCFRTLQRFTAATLEHGMRPPISP 108

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR Lm+emAvvAt++YRs+v+K+PRFvEYFR+AtPElEYG+mniGsR
  gi|1552966   109 KPEWRALMDEMAVVATDDYRSIVFKDPRFVEYFRSATPELEYGRMNIGSR 158

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   P+KRkPsGGiesLRAiPWiFaWtqt+FHLPvWLG+G AFKh i KD Knl
  gi|1552966   159 PSKRKPSGGIESLRAIPWIFAWTQTKFHLPVWLGFGSAFKHVIGKDPKNL 208

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                   q+L+EmY+eWPFFRvt+DL+EmvFAKGDP iAa+yDkLLv+ +L+PFG+
  gi|1552966   209 QMLQEMYNEWPFFRVTIDLVEMVFAKGDPVIAAMYDKLLVSKDLQPFGEC 258

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR+kY EtkdlLLk+AGHkDlLEGDPYLKqrl LRdsYit Ln +qA
  gi|1552966   259 LREKYTETKDLLLKVAGHKDLLEGDPYLKQRLQLRDSYITALNACQA--- 305

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL

  gi|1552966     - ---------------------------------------------------- -

                   tmKGiAAGmqntG<-*

  gi|1552966     - -------------    -

gi|241892653|ref|ZP_04779949.1|: domain 1 of 1, from 2 to 858: score -70.3, E = 6.2
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                                  K s  +k   +   +l +F ++ + L        v
  gi|2418926     2    ------------KLS--QKEATFQNEVLTRF-ELFKSLFLTLPFQRV 33

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                   +    l   +   +  k +eE       L+P +  ++ + +
  gi|2418926    34 KHTGTL-LPFFTTHCEKGVEE------HLAPEE--IIDSFFGQYEQYVQE 74

                   AEEvelAyRRRikkkkhGDFaDEas........AttEsDiEEtlKkLvlk
                    + v+l +R      +     D  ++++ ++ +   E+ + E l +
  gi|2418926    75 EDRVDLLFRIVQYVERQVVLFDAVEdssfqsigRADEAGLLEPLFRQTET 124

                   lnKsPeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAK
                     K  + + + LK  sv LvltAHPtq    ++L   + i   +  +
  gi|2418926   125 NSKLRKQIVNKLKDFSVRLVLTAHPTQFYPGAVL---SIINDLIEAIKDN 171

                   DvtveDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvW
                   D+           +H  +q   +t  i + +PtP DE      Y+    +
  gi|2418926   172 DI---------NNIHLLLQQLGKTPFINKLKPTPVDEAASLAWYLENVFY 212

                   kGvPKFLRRvDtALKniGinERlPYdv.PLikFssWmGGDRDGknPRvtP
                   k        +D  L      E    dv+ Li+   W GGDRDG nP vt
  gi|2418926   213 KVASEIQATIDDEL------EMPTEDVkQLIELGFWPGGDRDG-NPNVTV 255

                   EvtRDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaa
                   E tR v  + R +                 ++RC
  gi|2418926   256 ESTRKVATMLRTI-----------------LFRC---------------- 272

                   rdkvvKyYiEFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGisei
                         yY +F          Rvi    R   +   E     L   + e
  gi|2418926   273 ------YYRDF----------RVI---KRRITFRGVEQYMDTLQELFYEN 303

                   sEeAvyt...kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFG
                   s + v  ++++ ++ L  L    k L e       D  + Dl+R+v tFG
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  gi|2418926   304 SFNPVENpkdETDRILTNLKAIKKVLIEKHNSLFID-VVEDLIRKVVTFG 352

                   LsLvKLDiRqEseRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGK
                        LDiRq+s     vl    t L     ++       E L    k K
  gi|2418926   353 CYFTTLDIRQDSR----VLRNTLTYLITKDQKKTGLTEDFEGLSETAKQK 398

                   .RPLlgsDLPktEEvkDvl.dafrvLAEL.PiDsFGa......Yiismat
                   + P    DL   E+ +  ++d+++v+  L+ i   G+++  +++iis +
  gi|2418926   399 gFPFSELDLEVGEDAALLVkDTLEVIPLLkSIQNAGSeraaqrFIISNCQ 448

                   aPsDvLAvELLqRECgvkq...tLrvvPLFEkLADLeAAPAavekLFsiD
                     sD+L    L    g k+++ t+  vPLFE + DL  A   ++ L+
  gi|2418926   449 QASDILGLMQLFLWSGWKKkelTIDFVPLFETVDDLIRAGDVMKALYTHP 498

                   WYinridG...KqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyG
                    Y+ ++  +++Kq +m+G+sDs KD G l A W +YkA+ ++  +A++y
  gi|2418926   499 AYVAHLKSrgnKQTIMLGFSDSTKDGGYLMANWSIYKAKMDLTAIARDYD 548

                   vKLvlFHGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFG
                   v Lv F GRGG   RGGG t     s   +  n  +  t+qG  i   +G
  gi|2418926   549 VDLVFFDGRGGPPARGGGKTQRFYASMGREIENKHIQLTIQGQTISSQYG 598

                   EEnLCFrsLqRFtAAtL..EHGmnPPvsPkPEWRkLmeemAvvAtEEYRs
                     +     +     A + +E   n         ++++++mA v  E + s
  gi|2418926   599 SLDTAKYNIEQLLHAGIisEIRQNEGDTLTAKQKDVIDQMAEVSYEKFMS 648

                   vvvKEPRFvEYFRlAtPElEYGkmniGsRPaKRkPsGG..iesLRAiPWi
                   +  K+P F  Y     P      +ni sRP KR      ++e LRAi ++
  gi|2418926   649 L-RKDPLFLNYLENLSPLKVLSTINISSRPVKRNSDKElkLEDLRAISFV 697

                   FaWtqtRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDL
                    +W q +  +P + GvG A ++A +        ++ +Y+    F   +D
  gi|2418926   698 TSWSQLKQNIPGFFGVGSALQFAEENNL--WSYVRNLYEHSGMFNTIIDN 745

                   lEmvFAKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHk
                     m   K    i +        E+   F k L ++Y+ tk+++Lk+   k
  gi|2418926   746 CMMSMTKSNFDITSYMQ---FDEQYGDFWKMLHAEYELTKKYVLKLSNTK 792

                   DlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKE
                    l+E  P  +  +  R+  i  L ++q Y +++               K
  gi|2418926   793 ILMENYPVERESILAREKIILPLLIIQHYAIRK--------------QKQ 828

                   yAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      E+  k d   kL                t+ G+     n
  gi|2418926   829 LETED-PKYDVYSKLI-------------ARTIYGVVNAGRNLA    858

gi|225012795|ref|ZP_03703229.1|: domain 1 of 1, from 2 to 862: score -70.6, E = 6.2
                   *->siDAqLRlLvPGKvsedekLieYDALLlDk.FLDiLq.DLHGedLkE
                      +   ++        s   +   Y  L l  +F  i  + L  +   +
  gi|2250127     2    ARKPKIERFNEKILS---RFQIYNSLFLTLpFKNIKEtSLFLPLFAD 45

                   avqECYElsAeYEGKkDtkKLeELGakLtsLdPaDai..lvAkailHmLn
                   a +  YE      G+k    +     +      aD  ++l+   i  +
  gi|2250127    46 ACKVGYE-----KGQKPNDIVKSFFNRYVPDFEADKQkdLLFNFIQYIER 90

                   LAnLAEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKs
                      L + +e A    +   +       +  t     EE   k  +
  gi|2250127    91 QVVLFDAIEDAGFSYVNNMH-------GRGTLRNIKEEANNKQLSEV--- 130

                   PeEvFeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtv
                        e +K   v +vltAHPtq     +L     i n L+   AKD
  gi|2250127   131 ---LSEYIKRFNVRIVLTAHPTQFYPDNVLV----IINELSNAIAKD--- 170

                   eDKkELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvP
                       +LD      +q   +t    + +PtP  E    + ++ E v
  gi|2250127   171 ----DLDNIKKLLVQLG-KTPFYNKEKPTPFNEA-VSLIWFLENV----- 209

                   KFLRRvDtALKniG..inERlPYdvPLikFssWmGGDRDGknPRvtPEvt
                    F     t    i ++i +   ++ P+  F  W GGDRDG nP vt ++t
  gi|2250127   210 -FYHSASTIYDYITehIIDSKQFENPIFDFGFWPGGDRDG-NPFVTADIT 257
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                    RDvCLLaRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardk
                                   i     L F +        LR      yr  ++
  gi|2250127   258 ---------------IKTAKRLQFSI--------LR----NYYRDLRKL- 279

                    vvKyYiEFWKqvPPtEPYRviLGd.vRDKLYntRERaRHLLAtGiseisE
                      K  i F    P  E     L + v   L+     +   +A   se+
  gi|2250127   280 --KRKITF----PGVEQRVANLEElVFNELFYPERNTDFSIAILTSEM-- 321

                    eAvytkvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvK
                    +Av       LE + L    L +   k         ++ ++  FGL
  gi|2250127   322 DAV-------LESVILDHSGLYQEEVK--------NMIHKIKLFGLHFAS 356

                    LDiRqEseRqtDvlDAittHLeiGs........YReWsEeKRqEWLlaEL
                    LDiRq+s  +  v   i  H +i s++++ +++Y e   eKR E L
  gi|2250127   357 LDIRQDSRVHHSVFTEIVSHPDIQShttgvpknYLELTSEKRCEALSLMQ 406

                    kGKRPLlgsDLPktEEvkDvldafrvLAELPiD.sFGaYiismataPsDv
                        P +  D   t    + + a++ +     ++    Yiis + +   +
  gi|2250127   407 GDVSPTIYND-EITHQTLESIRAMQSIQKTNGErGSNRYIISNCQTLENI 455

                    LAvELLqRECgvkq.tLrvvPLFEkLADLeAAPAavekLFsiDWYinrid
                    L    + R     ++t+  +PLFE + DLe A A +e LF    Y+ +++
  gi|2250127   456 LELFAMCRLSNWGNpTVDFIPLFETIPDLESAEAVMEGLFNNPVYKTHLQ 505

                    ...GKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFH
                    +++ Kq vm+G+sD  KD G + A W +YkA+E +   A kyG+ +  F
  gi|2250127   506 krkNKQTVMLGFSDGTKDGGYFMANWSIYKAKEALSGLASKYGITMAFFD 555

                    GRGGtvGRGGGPtHLAiLsqPPDtinG.slRvtvqGEviEfsFGE.EnLC
                    GRGG   RGGG tH    s   Dti+ + +  t+qG  i   FG  +
  gi|2250127   556 GRGGPPARGGGNTHEFYASM-GDTIQSdDIQLTIQGQTISSNFGTlDSSQ 604

                    FrsLqRFtAAtLEHGmnPPvsPkPEW.RkLmeemAvvAtEEYRsvvvK.E
                    F   q          +nP      + +R+ me +A      Y    +K
  gi|2250127   605 FNLEQLLSSGIASQILNPGKNNLSDAdRQTMESIADYSYQSYQD--FKaH 652

                    PRFvEYFRlAtPElEYGkmniGsRPaKRkPsGGi..esLRAiPWiFaWtq
                    P F+ Y         Y k niGsRP+KR  s G++ e LRAiP++ +W q
  gi|2250127   653 PMFIPYLERMSTLPYYAKTNIGSRPSKRGKSKGLqfEDLRAIPFVGSWSQ 702

                    tRFHLPvWLGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvF
                     +  +P + GvG    h ++    n+  +k +Yk+  FFR  l    m
  gi|2250127   703 LKQNVPGFYGVGSSINHFVKEG--NIDAVKQLYKNSRFFRTLLFNSMMSL 750

                    AKGDPGiAaLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEG
                     K    + a   +     e   F + + ++Y+ tk lLL++ G   l+E
  gi|2250127   751 TKSFFQLTAYMKD---DKEFGSFWELIFEEYKLTKSLLLEVSGFESLMEN 797

                    DPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEn
                    +P  K  +R R+  +  L  +q + L  +         +   sK+  d
  gi|2250127   798 EPAGKESIRAREEIVQPLLTIQQFALMELQ--------KLRQSKD-TDPK 838

                    skkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                            k+         LE  +   + G      n
  gi|2250127   839 --------KIE-------DLEAMVTRSLFGNINASRNSA    862

gi|207723607|ref|YP_002254005.1|: domain 1 of 1, from 1 to 682: score -78.7, E = 6.7
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2077236     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2077236     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                                                              +
  gi|2077236     1 ----------------------------------------MG------- 2

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
```

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  gi|2077236     - ------------------------------------------------ -

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2077236     - ------------------------------------------------ -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                                           sW+GGDRDG nP vt    R
  gi|2077236     3 -------------------------SWIGGDRDG-NPFVTAQTLRHAARR 26

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                      +    Y++ +  L  Elsm    + + v AE l    ++     +
  gi|2077236    27 QASVILTWYLDEIHALGAELSM--STSLVDVSAELLALAERSPDHSEHRA 74

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLA..tGiseisEeAvyt
                   +        EPYR  L  v  +L  t    R L  ++ G   +     yt
  gi|2077236    75 D--------EPYRRALIGVYARLAAT---CRELTGedAGRHAVGPAPAYT 113

                   kvEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRq
                     E+    + +   sL      ++AD  L  l R +  FG  L  +D+Rq
  gi|2077236   114 SPEDLRADIRIVIDSLAAHHGEALADARLTSLARAIDVFGFHLASIDLRQ 163

                   EseRqtDvlDAittHLei.GsYReWsEeKRqEWLlaELkGKRPLlgsDLP
                    s+ +   +  + +  +++G+Y   sE  ++  Ll EL+  R L  +
  gi|2077236   164 VSDVHEATVAELLKVAGVeGAYAALSEADKRTLLLRELQQPRLLTLPFHT 213

                   ktEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAvELLqRE
                     E  +  l+ fr  ++v A   +     Yiis + + sD L v LLq+E
  gi|2077236   214 YGETTASELEIFRaareVRARYGSRIVRNYIISHTETLSDLLEVMLLQKE 263

                   Cgv.kq.........tLrvvPLFEkLADLeAAPAavekLFsi...DWYi
                    g+ +++++++++ +  + v+PLFE + DL+ AP  +  L ++++ D
  gi|2077236   264 SGMfRHgtnggggaglDVMVIPLFETIEDLRNAPQIMGDLLALpgfDAVL 313

                   nridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                      d  qevm+GYsDs KD G l   W LYkA   ++    ++Gv+L lF
  gi|2077236   314 AAQDNEQEVMLGYSDSNKDGGFLTSNWELYKAELALVDLFERHGVRLRLF 363

                   HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                   HGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGE+i   F   ++
  gi|2077236   364 HGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEIISSKFANPEIGR 413

                   rsLqRFtAAtLEHGmnPPvs.Pk..PEWRkLmeemAvvAtEEYRsvvvKE
                   r L    AAtLE  + P   +Pk+  E+   m+ +   A   YR +v+
  gi|2077236   414 RNLETIVAATLEATLLPTRNrPKglEEFEAAMQALSNHAFSAYRNLVYET 463

                   PRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....GiesLRAiPWiFaW
                   P F +YF   tP +E   +n+GsRPa Rk   ++++ ie LRAiPW F+W
  gi|2077236   464 PGFKDYFFATTPITEIADLNLGSRPASRKLMDkkqrRIEDLRAIPWGFSW 513

                   tqtRFHLPvWLGvGAAFKhAidKD......iKnlqkLkEmYkeWPFFRvt
                    q R  LP W G+G A +  +d  ++ + +   l  Lk m k+WPFF
  gi|2077236   514 GQCRLLLPGWFGFGSAVQRWLDEAgsakakAARLATLKRMHKQWPFFANL 563

                   lDLlEmvFAKGDPGiAaLyDkLLvaEeLk.PFGksLRdkYvEtkdlLLki
                   l  ++mv  K D  +A+ y +L     L++    ++ +++  t ++L  i
  gi|2077236   564 LSNMDMVLSKADLNVASRYAQLCDDRKLRnAVFSRISAEFTLTGQMLAAI 613

                   AGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPh
                    G  + L   P L   ++ R +Y+  Ln +q   LKR R
  gi|2077236   614 TGQSERLADNPLLARSIKNRFPYLDPLNHLQVELLKRFRSGK-------- 655

                   lsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-
                        A  n  +    ++L                + GiAAG+ n G
  gi|2077236   656 -----AGSNDARVRRGIHLS----------------INGIAAGLRNSG   682

                   *

  gi|2077236     -   -
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gi|268685594|ref|ZP_06152456.1|: domain 1 of 1, from 1 to 653: score -84.4, E = 7

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                *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                               +s
gi|2686855     1    -------------MS-------------------------------- 2

                qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

gi|2686855     - ------------------------------------------------- -

                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|2686855     - ------------------------------------------------- -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                             tA      R      na      +   A  v    +
gi|2686855     3 -------------TAASARCCR------NANAAPMPTRWHADAVFRFYRS 33

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                ELD  L RE+                                    P  +R
gi|2686855    34 ELDK-LYREL-----------------------------------PLSIR 47

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                Rv                                         v  Dv  L
gi|2686855    48 RV---------------------------------------KVNDDVMAL 58

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                a +                       dE  +R EE yr a
gi|2686855    59 AAL---------------------SPDEEIARTEEPYRRAIAY------- 80

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHL.LAtGiseisEeAvytk
                              i+     K       aR L+L  G      e  y
gi|2686855    81 --------------IMARAMGK-------ARSLgLGMGCKFGFLEP-YAS 108

                vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                  +FL+ L    +sL + G + +A+G L Dl+R vs FG  ++ LD+Rq
gi|2686855   109 AQKFLDDLKKLQRSLIDNGSRLLAEGRLADLIRSVSVFGFHMMPLDLRQH 158

                seRqtDvlDAittHLeiGsYReWsEeKRqEWLlaElkGKRPLlgsDLPkt
                + ++ Dv+  + +H ++  Y +  Ee++q  Ll EL  +RPL+ + +
gi|2686855   159 AGKHADVVAELFQHAGLEDYNSLNEEQKQAALLRELGHQRPLYSPFITYS 208

                E....EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECg
                +++++E++   +a ++  E   D+    iis +  P D LA  LL +E g
gi|2686855   209 DhtrrELAIFNEARKIKDEFGEDAVTQSIISNCEQPGDLLALALLLKESG 258

                v........kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGK..
                +   ++++++  + +vPLFE +  Le A   +e +F +DWY   ++ +++
gi|2686855   259 LlavengkpHSRINIVPLFETIEALENACPVMETMFRLDWYDALLESRgn 308

                .qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGG
                 qe+m+GYsDs KD G +   W L +A   ++   Kky v++ lFHGRGG
gi|2686855   309 iQEIMLGYSDSNKDGGYVTSSWCLHQAELGLVELFKKYDVRMRLFHGRGG 358

                tvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqR
                 vGRGGGP   AiL+qP   + G +R+t qGEvi   + +     r L
gi|2686855   359 SVGRGGGPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQRNLET 408

                FtAAtLEHGmnPPvsPkPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                  AAtLE  + P    k    kLm+ +  v    YR ++   P F++YF
gi|2686855   409 LVAATLEASILP--DKKDPDAKLMQALSDVSFKYYRELITH-PDFIDYFL 455

                lAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG
                   P  E   +n+GsRPa Rk    i+ LRAiPW+F+W q R  LP W G
gi|2686855   456 QTSPIQEIATLNLGSRPASRKTLARIQDLRAIPWVFSWMQNRLMLPAWYG 505

                vGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaL
                +G A     +     l  L+   ++ PFF   l  +E v AK D  +A
gi|2686855   506 FGSAVETLCEGSPETLAALRGHAQNNPFFQAMLSNMEQVMAKTDITLAEN 555

                yDkLLva.EeLkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                y  L  ++E  k     ++++Y   ++ LL +    +lL     L   l
gi|2686855   556 YAGLSESpEKAKVIFGMIKEEYRRSRKALLDLLQTEELLRDNRSLARSLA 605
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                  LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                  LR +Y+  Ln +q   LK +R                  E+   +  L+
  gi|2686855   606 LRIPYLNALNGLQVAMLKLLR-----------------KEP-DNPHALLM 637

                  LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                  +               Lt+ G+A G+ ntG
  gi|2686855   638 VH--------------LTINGVAQGLRNTG    653

gi|257139898|ref|ZP_05588160.1|: domain 1 of 1, from 1 to 671: score -98.7, E = 7.9
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        A L          de + +  A++ +++L+
  gi|2571398     1    --AATL----------DEAINRQAAVIFEHYLE-------------- 21

                  qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                                ++  LGa L                    + nL
  gi|2571398    22 ----------------QVHKLGAELS------------------VSNL 35

                  AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                                                       Lv
  gi|2571398    36 -------------------------------------LVGAS------- 40

                  FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                   +ALK  +      A P qs  R
  gi|2571398    41 -DALKALA-----AASPDQSPHR-------------------------- 57

                  ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                   +DE
  gi|2571398    58 -VDE------------------------------------------- 60

                  RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                                PY   Li           G              +
  gi|2571398    61 ---------------PYRRALI-----------G--------------VY 70

                  aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                  +R+ A+                       RvR  E     ++
  gi|2571398    71 TRLAASA----------------------RVRLGEGAVPVRSA------- 91

                  EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAv.ytk
                                                    G    +  A +y +
  gi|2571398    92 ----------------------------------GRGAAPVRATpYAD 105

                  vEeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqE
                   EeF+  L +   sL       +A   L  l+R    +G  L  +D+Rq
  gi|2571398   106 AEEFVADLRVLTDSLAVHHGESLATPRLAPLMRAAEVYGFHLASIDLRQS 155

                  seRqtDvlDAittHLeiG.sYReWsEeKRqEWLlaELkGKRPLlgsDLPk
                  s+ +  v+  +    ++ + Y   +E  +   Lla L   RPL  + L
  gi|2571398   156 SDIHEAVIAELLARGGVEpDYAALPEADKLRVLLAALADPRPLRSPYLDY 205

                  tEEvkDvldafr....vLAELPiDsFGaYiismataPsDvLAvELLqREC
                   +  k  l+ +++ + + A     +   Yiis + + sD + v LLq+E
  gi|2571398   206 SDLAKSELGVLErahaIRAQFGARAVRNYIISHTETVSDLVEVLLLQKET 255

                  gv............kqtLrvvPLFEkLADLeAAPAavekLFs...iDWYi
                  g+ +++ + ++ + ++ L v+PLFE +ADL+ A   +   F+ +++
  gi|2571398   256 GLfegtlgaphanaRNGLMVIPLFETIADLRNASDIMREFFAlpgVGELL 305

                  nridGKqevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlF
                   +    qevm+GYsDs KD G l   W LY+A   ++    + G+KL lF
  gi|2571398   306 AHQGHEQEVMLGYSDSNKDGGFLTSNWELYRAELALVDLFHERGIKLRLF 355

                  HGRGGtvGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCF
                  HGRGGtvGRGGGPt  AiLsqPP t+nG +R t qGEvi   F   ++
  gi|2571398   356 HGRGGTVGRGGGPTYQAILSQPPGTVNGQIRLTEQGEVIASKFANPEIGR 405

                  rsLqRFtAAtLEHGmnPPv.sPk..PEWRkLmeemAvvAtEEYRsvvvKE
                  r L    AAtLE  + P  ++Pk+ P +   m+ +   A   YR++v+
  gi|2571398   406 RNLETVVAATLEATLAPHSnAPKqlPAFEAAMQTLSDAAMASYRALVYET 455

                  PRFvEYFRlAtPElEYGkmniGsRPaKRkPsG....GiesLRAiPWiFaW
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                    P F +YF + tP +E   +niGsRPa Rk   ++++ ie LRAiPW F+W
  gi|2571398   456 PGFTDYFFSSTPITEIAELNIGSRPASRKLQDpkhrKIEDLRAIPWGFSW 505

                    tqtRFHLPvWLGvGAAFKhAid......KDiKnlqkLkEmYkeWPFFRvt
                     q R  L  W G+G A    +d+ ++     K +  L+ m k+WPFF
  gi|2571398   506 GQCRLLLTGWYGFGGAVAAYLDgapdaaERGKRVALLRKMNKTWPFFANL 555

                    lDLlEmvFAKGDPGiAaLyDkLLvaEeL.kPFGksLRdkYvEtkdlLLki
                    l  ++mv AK D  +A+ y +L+    L+k   +++ +++  t   L +i
  gi|2571398   556 LSNMDMVLAKTDLAVASRYAQLVADKKLrKHVFERIVAEWHRTASALAEI 605

                    AGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtLKRiRDPsykvtlrPh
                     G +  L   P L   ++ R +Y+  Ln +q   +KR R
  gi|2571398   606 TGAQARLAANPLLARSIKNRFPYLDPLNHLQVELIKRHR----------- 644

                    lsKEyAdEnskkadeLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-
                         A +           n   r   G+     Lt+ GiAAG+ ntG
  gi|2571398   645 -----AGDT----------N--ARLRRGIH----LTINGIAAGLRNTG   671

                    *

  gi|2571398     -   -

gi|241667414|ref|ZP_04754992.1|: domain 1 of 1, from 5 to 844: score -101.3, E = 8.1
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       si   L       v    k      L l   LD         L  +
  gi|2416674     5    SIQNELVESYKSEVE--LKYKMLNGLFLSTPLDKEHNAN-AMLATFA 48

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                      C +l    E  kD+  +e +      +     + +   +   +
  gi|2416674    49 NICKDL---IENAKDP--IETIENLYPEMSEEQKLQIFVKFIRYIE---- 89

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                       v +         k  D   E s t        l + v + +K  +
  gi|2416674    90 RQTVLIDALEEAAYAKTHDLNGEYSIT-------RLARRVERHDKQNA-L 131

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      AL+     LvltAHPtq   + +L     ++        K +  +D
  gi|2416674   132 SRALQEYKTRLVLTAHPTQFYAKLVLPIIHDLK--------KAIIANDIN 173

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     + +      +  F      +++PtP DE    + Y+    ++ +P
  gi|2416674   174 KIQDIFLQMGKTKFSN----KTKPTPEDEAVSIIWYLNNIFYNVIPE--- 216

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                              i  +l  d   i+   W GGDRDG nP vt  vt+ v
  gi|2416674   217 ----------IQHKLTNDSTNIEIGFWPGGDRDG-NPFVTANVTKKVSKH 255

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                     R    n Y   +  L+  l      +EL             +
  gi|2416674   256 LRTNILNSYNKDLKRLIKKLTFENVHEEL------------TK------- 286

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                                    +R +L   +                    y +
  gi|2416674   287 ------------------IRKRLKTNK------------------YPNA 299

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                      FL+ L      +    D    D  L  l+ +v  FG    KLDiRq +
  gi|2416674   300 QTFLDNLVKVKNVVDSEYDSLFVD-KLDNLILKVKIFGFHFAKLDIRQNA 348

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGK..RPL.lgsDLP
                      +      +        Y    E  +   L+   k K+ + L++ sDL
  gi|2416674   349 KIHNQFFNELFSDNYNLDYQALNESEKIKHLIELAKQKsfKELeVNSDLA 398

                    ktEEvkDvldafrvLAELP.iDsFGaYiismataPsDvLAv....ELLqR
                    +  E+ + ++ ++ +    + D+   Yiis a +   +L v +   L  +
  gi|2416674   399 R--ELLETIEVIQYIQQHSgYDAIQRYIISNADSTVSILEVltifKLFNK 446

                    ECgv..kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqe...
                    +   ++k  + vvPLFE + DL+     ++ L  i  Y   +   q++++
  gi|2416674   447 DIDTnnKIKIEVVPLFETMEDLKNSTKILDELLKIQLYTDNLKAWQNtqt 496
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                    vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                    +m+G+sD  KD G + A W +  A+  + K     G+K + F GRGG
  gi|2416674   497 IMLGFSDGTKDGGYFMANWSILEAKRALSKYLSSKGIKPIFFDGRGGPPS 546

                    RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                    RGGG   L          n  + +t+qG  i   FG  n     L
  gi|2416674   547 RGGGDMFLFYKGLSNVVSNHDVQITIQGQSISSKFGNTNSAQYNLEQILT 596

                    AtLEHGmnPPvsPk..PEWRkLmeemAvvAtEEYRsvvvKE.PRFvEYFR
                      L   +n   + + +P    L++e+     + Y  + +K +P F++Y
  gi|2416674   597 SGLYGKLNLHNAHRlnPTETSLINELGKLSFDTY--INLKNhPQFIDYIT 644

                    lAtPElEYGkmniGsRPaKRkPsG..GiesLRAiPWiFaWtqtRFHLPvW
                      tP      mn+GsRPaKR  s +  ++ LRAiP+  aWtq R  +  +
  gi|2416674   645 EITPLKYISEMNVGSRPAKRNSSDkfKLDDLRAIPYGAAWTQMRQNILAF 694

                    LGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiA
                     G+G A    + KD  nl  L+ +Yk     +   D      A+    i
  gi|2416674   695 YGLGTAISTVVTKDNNNLTALQKIYKRSLIIKGIFDNALQSIAQTNFNIT 744

                    aLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkD.lLEGDPYLKqr
                        k         F ++L d+ +  k++LL +    ++ L   P
  gi|2416674   745 KHISK---DPKYSAFWQQLFDEHQLAKKYLLAVTEKDEsFLHANPVKERS 791

                    lRLRdsYittLnvfqAYtLKRiR.DPsy.kvtlrPhlsKEyAdEnskkad
                    +++Rd     L ++q Y L  +R+ P++++  l   + K   + n
  gi|2416674   792 IKMRDDITLPLVILQQYALDCLRkNPNHkHKKLLKTIIKKSLAAN----- 836

                    eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      +  n                        qn
  gi|2416674   837 --INAN-----------------------QNSI    844

gi|254875963|ref|ZP_05248673.1|: domain 1 of 1, from 7 to 846: score -101.3, E = 8.1
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                       si   L       v    k      L l   LD         L  +
  gi|2548759     7    SIQNELVESYKSEVE--LKYKMLNGLFLSTPLDKEHNAN-AMLATFA 50

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                      C +l    E  kD+  +e +      +     + +   +   +
  gi|2548759    51 NICKDL---IENAKDP--IETIENLYPEMSEEQKLQIFVKFIRYIE---- 91

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                       v +         k  D   E s t        l + v + +K  +
  gi|2548759    92 RQTVLIDALEEAAYAKTHDLNGEYSIT-------RLARRVERHDKQNA-L 133

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                      AL+     LvltAHPtq   + +L     ++        K +  +D
  gi|2548759   134 SRALQEYKTRLVLTAHPTQFYAKLVLPIIHDLK--------KAIIANDIN 175

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                     + +      +  F      +++PtP DE    + Y+    ++ +P
  gi|2548759   176 KIQDIFLQMGKTKFSN----KTKPTPEDEAVSIIWYLNNIFYNVIPE--- 218

                    RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                              i  +l  d   i+   W GGDRDG nP vt  vt+ v
  gi|2548759   219 ----------IQHKLTNDSTNIEIGFWPGGDRDG-NPFVTANVTKKVSKH 257

                    aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                     R    n Y   +  L+  l      +EL            +
  gi|2548759   258 LRTNILNSYNKDLKRLIKKLTFENVHEEL------------TK------- 288

                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                                     +R +L   +                  y +
  gi|2548759   289 ------------------IRKRLKTNK-------------------YPNA 301

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                      FL+ L      +    D    D  L  l+ +v  FG    KLDiRq +
  gi|2548759   302 QTFLDNLVKVKNVVDSEYDSLFVD-KLDNLILKVKIFGFHFAKLDIRQNA 350

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGK..RPL.lgsDLP
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                     +      +        Y    E  +   L+   k K+ + L++ sDL
  gi|2548759   351 KIHNQFFNELFSDNYNLDYQALNESEKIKHLIELAKQKsfKELeVNSDLA 400

                     ktEEvkDvldafrvLAELP.iDsFGaYiismataPsDvLAv....ELLqR
                     +  E+ + ++ ++ +    + D+   Yiis a +   +L v +   L  +
  gi|2548759   401 R--ELLETIEVIQYIQQHSgYDAIQRYIISNADSTVSILEVltifKLFNK 448

                     ECgv..kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqe...
                     +   ++k  + vvPLFE + DL+     ++ L  i  Y   +   q++++
  gi|2548759   449 DIDTnnKIKIEVVPLFETMEDLKNSTKILDELLKIQLYTDNLKAWQNtqt 498

                     vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                     +m+G+sD  KD G + A W +  A+  + K     G+K + F GRGG
  gi|2548759   499 IMLGFSDGTKDGGYFMANWSILEAKRALSKYLSSKGIKPIFFDGRGGPPS 548

                     RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                     RGGG   L           n  + +t+qG  i   FG  n     L
  gi|2548759   549 RGGGDMFLFYKGLSNVVSNHDVQITIQGQSISSKFGNTNSAQYNLEQILT 598

                     AtLEHGmnPPvsPk..PEWRkLmeemAvvAtEEYRsvvvKE.PRFvEYFR
                       L   +n   + + +P    L++e+     + Y  + +K +P F++Y
  gi|2548759   599 SGLYGKLNLHNAHRlnPTETSLINELGKLSFDTY--INLKNhPQFIDYIT 646

                     lAtPElEYGkmniGsRPaKRkPsG..GiesLRAiPWiFaWtqtRFHLPvW
                       tP      mn+GsRPaKR  s +  ++ LRAiP+  aWtq R  +  +
  gi|2548759   647 EITPLKYISEMNVGSRPAKRNSSDkfKLDDLRAIPYGAAWTQMRQNILAF 696

                     LGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiA
                      G+G A    + KD  nl  L+ +Yk     +   D      A+    i
  gi|2548759   697 YGLGTAISTVVTKDNNNLTALQKIYKRSLIIKGIFDNALQSIAQTNFNIT 746

                     aLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkD.lLEGDPYLKqr
                         k         F ++L d+ +  k++LL +    ++ L   P
  gi|2548759   747 KHISK---DPKYSAFWQQLFDEHQLAKKYLLAVTEKDEsFLHANPVKERS 793

                     lRLRdsYittLnvfqAYtLKRiR.DPsy.kvtlrPhlsKEyAdEnskkad
                     +++Rd     L ++q Y L  +R+ P++++  l   + K   + n
  gi|2548759   794 IKMRDDITLPLVILQQYALDCLRkNPNHkHKKLLKTIIKKSLAAN----- 838

                     eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                       +  n                        qn
  gi|2548759   839 --INAN-----------------------QNSI    846

gi|167626833|ref|YP_001677333.1|: domain 1 of 1, from 5 to 844: score -103.1, E = 8.3
                     *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav
                        si   L       v    k      L l   LD         L  +
  gi|1676268     5    SIQNELVESYKSEVE--LKYKMLNGLFLSTPLDKEHNAN-AMLATFA 48

                     qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL
                       C +l    E  kD+  +e +      +     + +   +   +
  gi|1676268    49 NICKDL---IENAKDP--IETIENLYPEMSEEQKLQIFVKFIRYIE---- 89

                     AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv
                        v +         k  D   E s t        l + v + +K  +
  gi|1676268    90 RQTVLIDALEEAAYAKTHDLNGEYSIT-------RLARRVERHDKQNA-L 131

                     FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                       AL+     LvltAHPtq   + +L     ++         K +  +D
  gi|1676268   132 SRALQEYKTRLVLTAHPTQFYAKLVLPIIHDLK--------KAIIANDIN 173

                     ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
                      + +      +  F      +++PtP DE    + Y+    +  +P
  gi|1676268   174 KIQDIFLQMGKTKFSN----KTKPTPEDEAVSIIWYLNNIFYSVIPE--- 216

                     RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                               i  +l  d   i+   W GGDRDG nP vt  vt+ v
  gi|1676268   217 ----------IQHKLTNDSTNIEIGFWPGGDRDG-NPFVTASVTKKVSKH 255

                     aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi
                      R    n Y   +  L+  l      +EL             +
  gi|1676268   256 LRTSILNSYNKDLKRLIKKLTFENVHEEL------------TK------- 286
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                    EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                                      +R +L   +                   y +
  gi|1676268   287 ------------------IRKRLKTNK------------------YPNA 299

                    EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs
                      FL+ L +  ks+ +     +    L  l+ +v  FG    KLDiRq +
  gi|1676268   300 QTFLDDL-VKVKSVVDSEYDSLFVDKLDNLILKVKIFGFHFAKLDIRQNA 348

                    eRqtDvlDAittHLeiGsYReWsEeKRqEWLl..aELkGKRPL.lgsDLP
                      +      +        Y   s+  +   L++ aE k  + L++ sDL
  gi|1676268   349 KIHNQFFNELFSENYNLDYQVLSDSEKIKHLVelAEQKSFKELeVNSDLA 398

                    ktEEvkDvldafrvLAELP.iDsFGaYiismataPsDvLAv....ELLqR
                    +  E+ + ++ ++ +    + D+   Yiis a +   +L v +   L  +
  gi|1676268   399 R--ELLETIEVIQYIQQHSgYDAIQRYIISNADSTVSILEVltifKLFNK 446

                    ECgv..kqtLrvvPLFEkLADLeAAPAavekLFsiDWYinridGKqe...
                    +   ++k  + vvPLFE + DL+     ++ L  i  Y   +   q++++
  gi|1676268   447 DIDTnsKIKIEVVPLFETMEDLKNSTQILDELLKIQLYTDNLKAWQNtqt 496

                    vmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvG
                    +m+G+sD  KD G + A W +  A+  + K      +K + F GRGG
  gi|1676268   497 IMLGFSDGTKDGGYFMANWSILEAKRALSKYLSSKSIKPIFFDGRGGPPS 546

                    RGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtA
                    RGGG   L          n  + +t+qG  i   FG  n     L
  gi|1676268   547 RGGGDMFLFYKGLSNVVSNHDVQITIQGQSISSKFGNTNSAQYNLEQILT 596

                    AtLEHGmnPPvsPk..PEWRkLmeemAvvAtEEYRsvvvKE.PRFvEYFR
                      L   +n   + + +P    L++e+     + Y  + +K +P F++Y
  gi|1676268   597 SGLYGKLNLHNAHRlnPTETSLINELGKLSFDTY--INLKNhPQFIDYIT 644

                    lAtPElEYGkmniGsRPaKRkPsG..GiesLRAiPWiFaWtqtRFHLPvW
                      tP      mn+GsRPaKR  s +  ++ LRAiP+  aWtq R  +  +
  gi|1676268   645 EITPLKYISEMNVGSRPAKRNSSDkfKLDDLRAIPYGAAWTQMRQNILAF 694

                    LGvGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiA
                     G+G A    + KD  nl  L+ +Yk     +   D      A+    i
  gi|1676268   695 YGLGTAISTVVTKDNNNLTALQKIYKRSLIIKGIFDNALQSIAQTNFNIT 744

                    aLyDkLLvaEeLkPFGksLRdkYvEtkdlLLkiAGHkD.lLEGDPYLKqr
                        k         F ++L d+ +  k++LL +    ++ L   P
  gi|1676268   745 KHISK---DPKYSAFWQQLFDEHQLAKKYLLAVTEKDEsFLHANPVKERS 791

                    lRLRdsYittLnvfqAYtLKRiR.DPsy.kvtlrPhlsKEyAdEnskkad
                    +++Rd     L ++q Y L  +R+ P++++  l   + K   + n
  gi|1676268   792 IKMRDDITLPLVILQQYALDCLRkNPNHrHKKLLKTIIKKSLAAN----- 836

                    eLvkLnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                      +  n                       qn
  gi|1676268   837 --INAN-----------------------QNSI    844

gi|89892437|gb|ABD79011.1|: domain 1 of 1, from 1 to 472: score -109.6, E = 8.7
                    *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|8989243     -    ---------------------------------------------- -

                    qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|8989243     - ---------------------------------------------- -

                    AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|8989243     - ---------------------------------------------- -

                    FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

  gi|8989243     - ---------------------------------------------- -

                    ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR
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  gi|8989243     - ------------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

  gi|8989243     - ------------------------------------------------- -

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|8989243     - ------------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

  gi|8989243     - ------------------------------------------------- -

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|8989243     - ------------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                            it+ +++G Y +W E+ +q +L+ EL+ +RPL++
  gi|8989243     1 ---------ITRYIGLGDYAQWTEDDKQAFLIRELSSRRPLIPQNWTPSP 41

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                   E +++ld+ +v+A         Y+isma   sDvLAv LL +E gv   +
  gi|8989243    42 ETQEILDTCKVIAQQKQGVIACYVISMARNASDVLAVHLLLKEAGVPYHI 91

                   rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                   +vvPLFE L DL+AA   + +LF + WY+  i+ +q vm+GYsDs KDAG
  gi|8989243    92 PVVPLFETLEDLDAAEKVMTQLFNVGWYRGVINNRQMVMIGYSDSAKDAG 141

                   RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                    ++A W  Y+AqE ++    k G+ L+lFHGRGGt+GRGG P H A+Lsq
  gi|8989243   142 MMAASWAQYRAQEALVNLTEKLGIELTLFHGRGGTIGRGGAPAHAALLSQ 191

                   PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                   PP  ++  lRvt qGE+i f  G   +   +   ++ A LE  + PP  P
  gi|8989243   192 PPRSLKNGLRVTEQGEMIRFKLGLPTVAVETFDLYASAILEANLLPPPEP 241

                   kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                   kPEWR++m+e+  +  + YR vv  +  Fv YFR+AtPE E  k+ +GsR
  gi|8989243   242 KPEWRNIMDELSTISCDIYRGVVRGDKDFVPYFRSATPEQELSKLPLGSR 291

                   PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                   PaKR P GG+esLRAiPWiFaW q R  LP WLG GA  +  i++    +
  gi|8989243   292 PAKRNPNGGVESLRAIPWIFAWMQNRLMLPAWLGAGASIRQIIEQGKGDI 341

                   qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                     ++ m ++WPFF   + +lEmvF K D  +   yD+ Lv  eL+  G++
  gi|8989243   342 --IHKMCENWPFFSTRIGMLEMVFSKSDTWLSQQYDQRLVKKELWYLGEN 389

                   LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                   LR + ++  + +L +    +l+   P++   + LR+ Y   Ln +q   L
  gi|8989243   390 LRKQLEDDIQTVLSLSHQSELMSDLPWIADSIALRNIYTDPLNLLQVELL 439

                   KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                    R R                  En             e+v P +E  L++
  gi|8989243   440 HRFR-----------------EN------------PEQVNPDVEQALMI 459

                   tmKGiAAGmqntG<-*
                   t+ GiAAGm ntG
  gi|8989243   460 TITGIAAGMRNTG    472

gi|159475421|ref|XP_001695817.1|: domain 1 of 1, from 1 to 447: score -117.0, E = 9.3
                   *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|1594754     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|1594754     - ------------------------------------------------- -
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                AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

gi|1594754    - ------------------------------------------------ -

                FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk

gi|1594754    - ------------------------------------------------ -

                ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

gi|1594754    - ------------------------------------------------ -

                RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL

gi|1594754    - ------------------------------------------------ -

                aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

gi|1594754    - ------------------------------------------------ -

                EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv

gi|1594754    - ------------------------------------------------ -

                EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

gi|1594754    - ------------------------------------------------ -

                eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE
                      +DA+tt L++GsY +W E KR  +Ll EL+      g+ L  t
gi|1594754    1 ------MDAVTTYLGLGSYASWDEPKRLAFLLGELQVGAERRGPVL-YTH 43

                EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkqtL
                       +  +       s GaYiisma + sDvLAv LLqRE gv+ +L
gi|1594754   44 ACSRFPPSSLIYPPTHPPSLGAYIISMAKTASDVLAVVLLQRETGVRPAL 93

                rvvPLFEkLADLeAAPAavekLFsiDWYinridGKqevmvGYsDsGKDAG
                rvvPLFE L DL+ AP ++  L   DWY+ +i+G qe m+GYsDsGKDAG
gi|1594754   94 RVVPLFETLDDLHNAPGTMTTLLGNDWYRGHINGVQECMIGYSDSGKDAG 143

                RlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGtvGRGGGPtHLAiLsq
                Rl+AAW LY  qE ++ vA   Gv+LvlFHGRGGtvGRGGGPtH+Ai sq
gi|1594754  144 RLAAAWALYETQEKLVEVAAGCGVRLVLFHGRGGTVGRGGGPTHMAIRSQ 193

                PPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRFtAAtLEHGmnPPvsP
                P  tinG lRvtvqGE+iE+ FGE ++CFr+L  +t A LE  ++PP +P
gi|1594754  194 PSGTINGHLRVTVQGEIIEQQFGEKEVCFRTLDLYTSAVLEAALDPPPAP 243

                kPEWRkLmeemAvvAtEEYRsvvvKEPRFvEYFRlAtPElEYGkmniGsR
                  EWR+Lm  +A    + YRsvv++ P F +YF   t   E G++niGsR
gi|1594754  244 AQEWRDLMSLLATESCDMYRSVVYRTPEFYDYFMQSTAASELGRLNIGSR 293

                PaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLGvGAAFKhAidKDiKnl
                P+ Rk sGGie+LRAiPWiFaWtq R HLPvWLG+G A   AidK    +
gi|1594754  294 PSSRK-SGGIETLRAIPWIFAWTQQRLHLPVWLGIGEALEAAIDKGYGPV 342

                qkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaLyDkLLvaEeLkPFGks
                  L++mY +WPFF  tlDL+Emv AK D  + a y++ Lv   L P G++
gi|1594754  343 --LQDMYANWPFFTSTLDLVEMVLAKADSRLSAFYERTLVDSSLAPLGQR 390

                LRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlRLRdsYittLnvfqAYtL
                LR+  ++        A H D
gi|1594754  391 LRELGQDA-------AEHSDC---------------------------- 404

                KRiRDPsykvtlrPhlsKEyAdEnskkadeLvkLnptervaPGLEDtLiL
                                    +     a++  +  p  +  PG ED   L
gi|1594754  405 --------------------GAQG--DAAGGQHAQPDVHAQPGREDPTAL 432

                tmKGiA..AGmqntG<-*
                 +   A++AG    G
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  gi|1594754   433 ALWRAAqhAGHAEHG    447

gi|224101659|ref|XP_002312371.1|: domain 1 of 1, from 1 to 466: score -121.8, E = 9.7
                  *->siDAqLRlLvPGKvsedekLieYDALLlDkFLDiLqDLHGedLkEav

  gi|2241016     -    ---------------------------------------------- -

                   qECYElsAeYEGKkDtkKLeELGakLtsLdPaDailvAkailHmLnLAnL

  gi|2241016     - ---------------------------------------------- -

                   AEEvelAyRRRikkkkhGDFaDEasAttEsDiEEtlKkLvlklnKsPeEv

  gi|2241016     - ---------------------------------------------- -

                   FeALKnqsvDLvltAHPtqsvRRsLLqKnaRiRnCLaqLsAKDvtveDKk
                    +A    sv L +
  gi|2241016     1 MDAFYARSVCLSF---------------------------------- 13

                   ELDEALHREiqAAFRtDEiRRaqPtPqDEmRaGmsYiHEtvWkGvPKFLR

  gi|2241016     - ---------------------------------------------- -

                   RvDtALKniGinERlPYdvPLikFssWmGGDRDGknPRvtPEvtRDvCLL
                                                  G
  gi|2241016    14 --------------------------------G---------------- 14

                   aRmmAanlYisqvEDLmFElsmWRCndELRvRAEElyrtaardkvvKyYi

  gi|2241016     - ---------------------------------------------- -

                   EFWKqvPPtEPYRviLGdvRDKLYntRERaRHLLAtGiseisEeAvytkv
                    FW qv P
  gi|2241016    15 -FW-QVTP---------------------------------------- 20

                   EeFLEPLELCYksLCeCGDkviADGsLLDlLRqvstFGLsLvKLDiRqEs

  gi|2241016     - ---------------------------------------------- -

                   eRqtDvlDAittHLeiGsYReWsEeKRqEWLlaELkGKRPLlgsDLPktE

  gi|2241016     - ---------------------------------------------- -

                   EvkDvldafrvLAELPiDsFGaYiismataPsDvLAvELLqRECgvkq..
                   +vk+vld+frv AEL +Ds GaY+isma   sDvLAvELLq++  +  ++
  gi|2241016    21 DVKEVLDTFRVAAELGSDSLGAYVISMASNASDVLAVELLQKDARLAVsg 70

                   .........tLrvvPLFEkLADLeAAPAavekLFsiDWYinri....dGK
                   + +++ +++tLrvvPLFE + DL+ A   + kL siDWY  +i +++ G
  gi|2241016    71 elgkpcpggTLRVVPLFETVKDLRGAGLVIRKLLSIDWYSEHIiknhSGH 120

                   qevmvGYsDsGKDAGRlsAAWqLYkAqEEiiKvAKkyGvKLvlFHGRGGt
                   qevmvGYsDsGKDAGR+ AAW LYkAqE+++   K+  +K++lFHGRGG
  gi|2241016   121 QEVMVGYSDSGKDAGRFTAAWELYKAQEDVVAACKDNQIKVTLFHGRGGS 170

                   vGRGGGPtHLAiLsqPPDtinGslRvtvqGEviEfsFGEEnLCFrsLqRF
                   +GRGGGPt LAi sqPP  + G lR t qGE++   FG  +   r L  +
  gi|2241016   171 IGRGGGPTYLAIQSQPPGSVMGTLRSTEQGEMVQAKFGLPHTAVRQLEIY 220

                   tAAtLEHGmnPPvsPkPE.WRkLmeemAvvAtEEYRsvvvKEPRFvEYFR
                   t A L   ++PP  P+ E+WR+Lm+e+  +    YRs v+  P F  YF
  gi|2241016   221 TTAVLLATLKPPERPREEkWRNLMDEISKISCQSYRSTVYENPEFLAYFH 270

                   lAtPElEYGkmniGsRPaKRkPsGGiesLRAiPWiFaWtqtRFHLPvWLG
                    AtP  E G +niGsRP++Rk s Gi  LRAiPW+FaWtqtRF LP WLG
  gi|2241016   271 EATPQAELGFLNIGSRPTRRKSSTGIGHLRAIPWVFAWTQTRFVLPAWLG 320

                   vGAAFKhAidKDiKnlqkLkEmYkeWPFFRvtlDLlEmvFAKGDPGiAaL
                   vGA  K   +K     q Lk mYkeWPFF  t+DL+Emv  K D  iA
  gi|2241016   321 VGAGLKGVCEKGHT--QDLKAMYKEWPFFQSTIDLIEMVLGKADVPIAKH 368
```

```
                    yDkLLvaEe.LkPFGksLRdkYvEtkdlLLkiAGHkDlLEGDPYLKqrlR
                    yD++Lv++ + +  G  LR +   t++++L + GH  l E    L+  +
  gi|2241016   369 YDEVLVSDKsRRELGAALRRELLTTEKFVLVVSGHERLSENNRSLRRLIE 418

                    LRdsYittLnvfqAYtLKRiRDPsykvtlrPhlsKEyAdEnskkadeLvk
                     R +Y+  +n++q   LKR+R                d++
  gi|2241016   419 SRLPYLNPINMLQVEILKRLR----------------SDDD--------- 443

                    LnptervaPGLEDtLiLtmKGiAAGmqntG<-*
                     n        L D L++t+ GiAAGm ntG
  gi|2241016   444 -N------HKLRDALLITINGIAAGMRNTG    466


Histogram of all scores:
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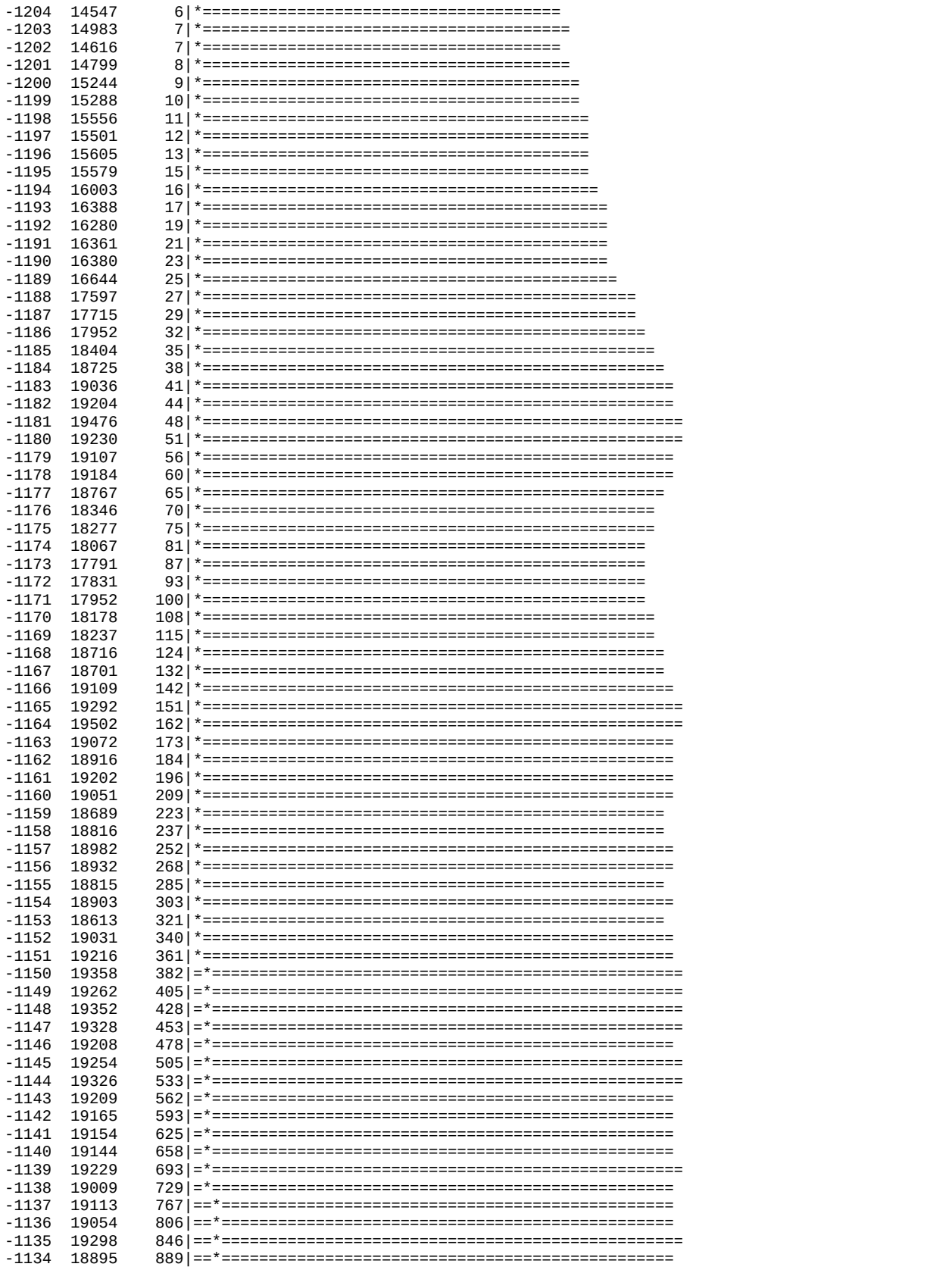
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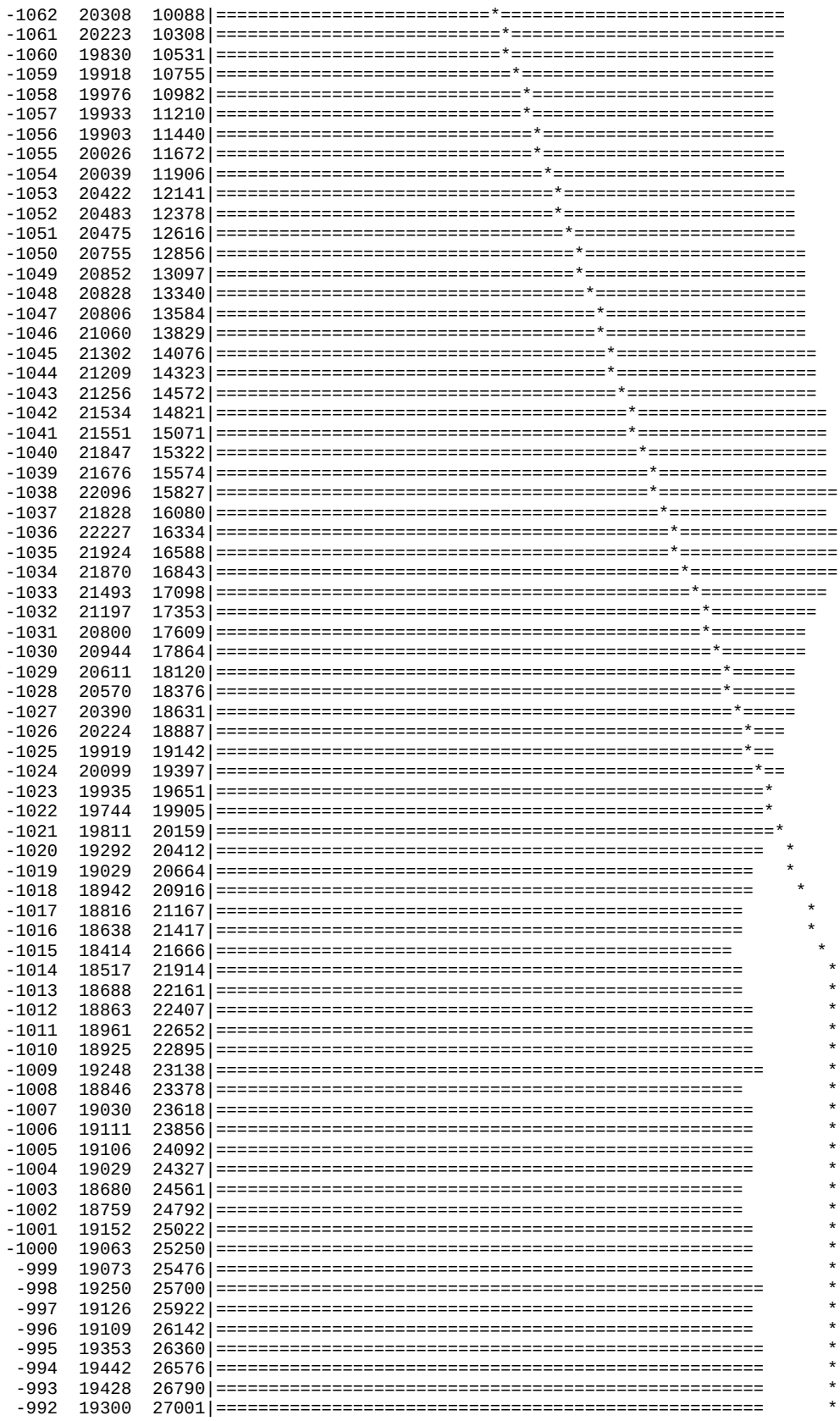
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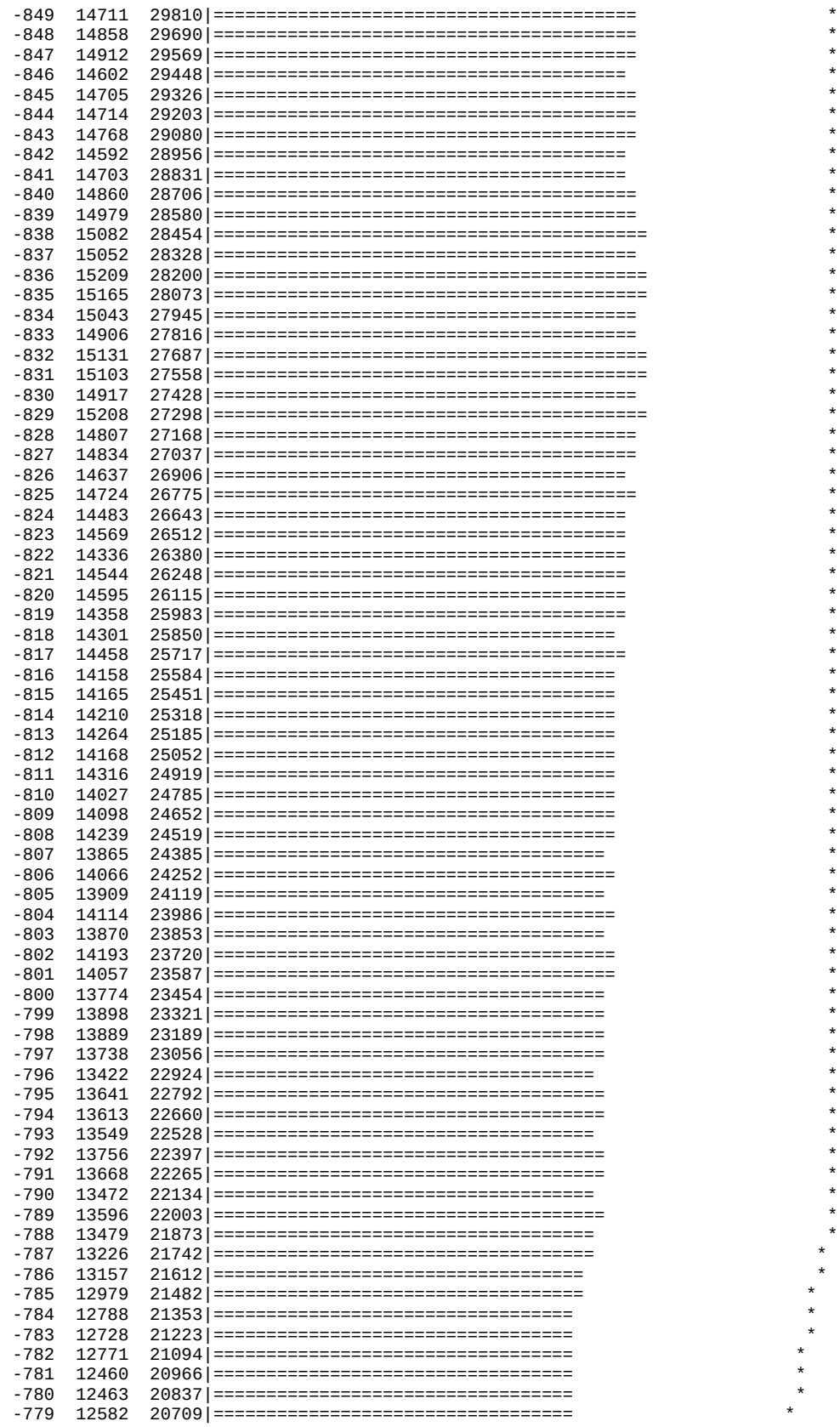
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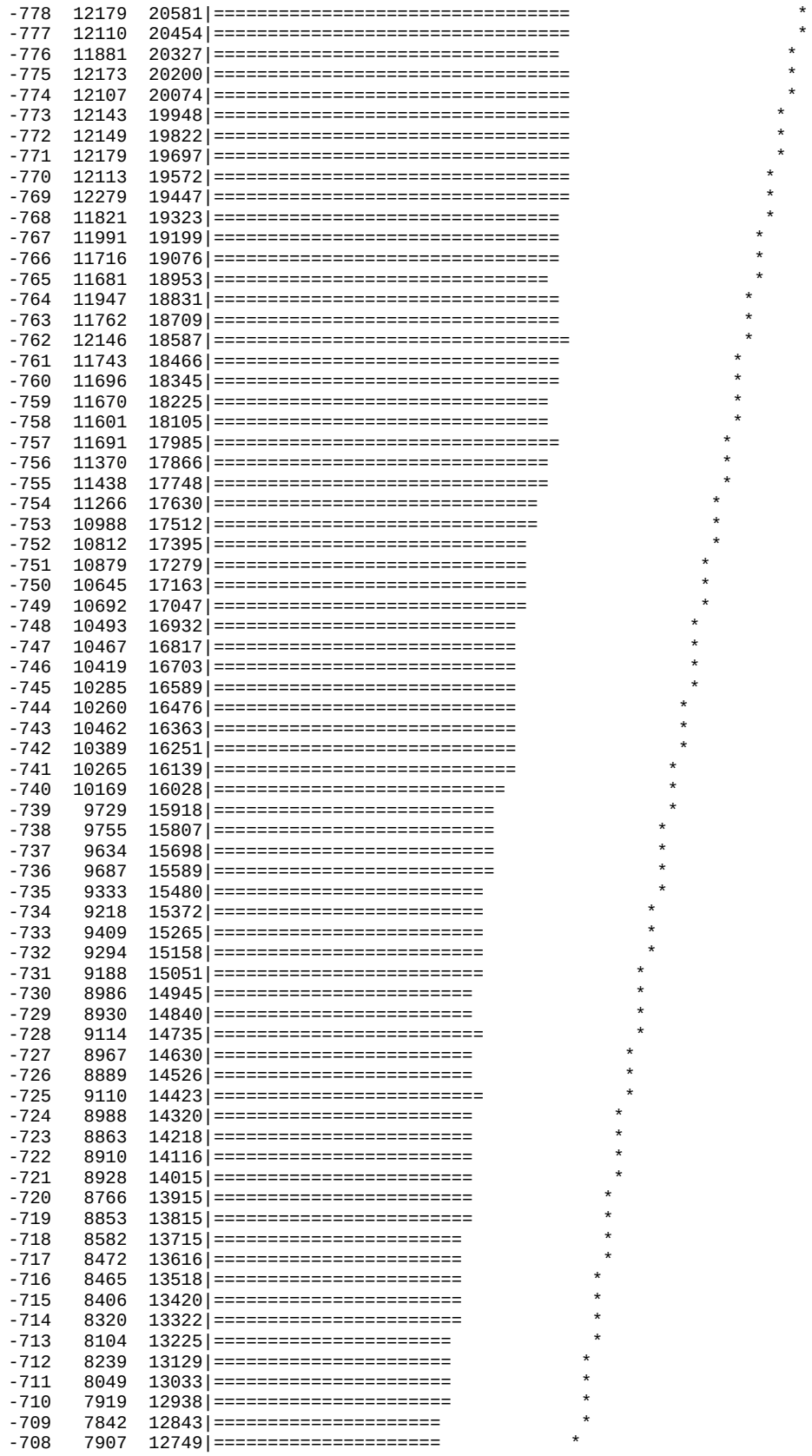
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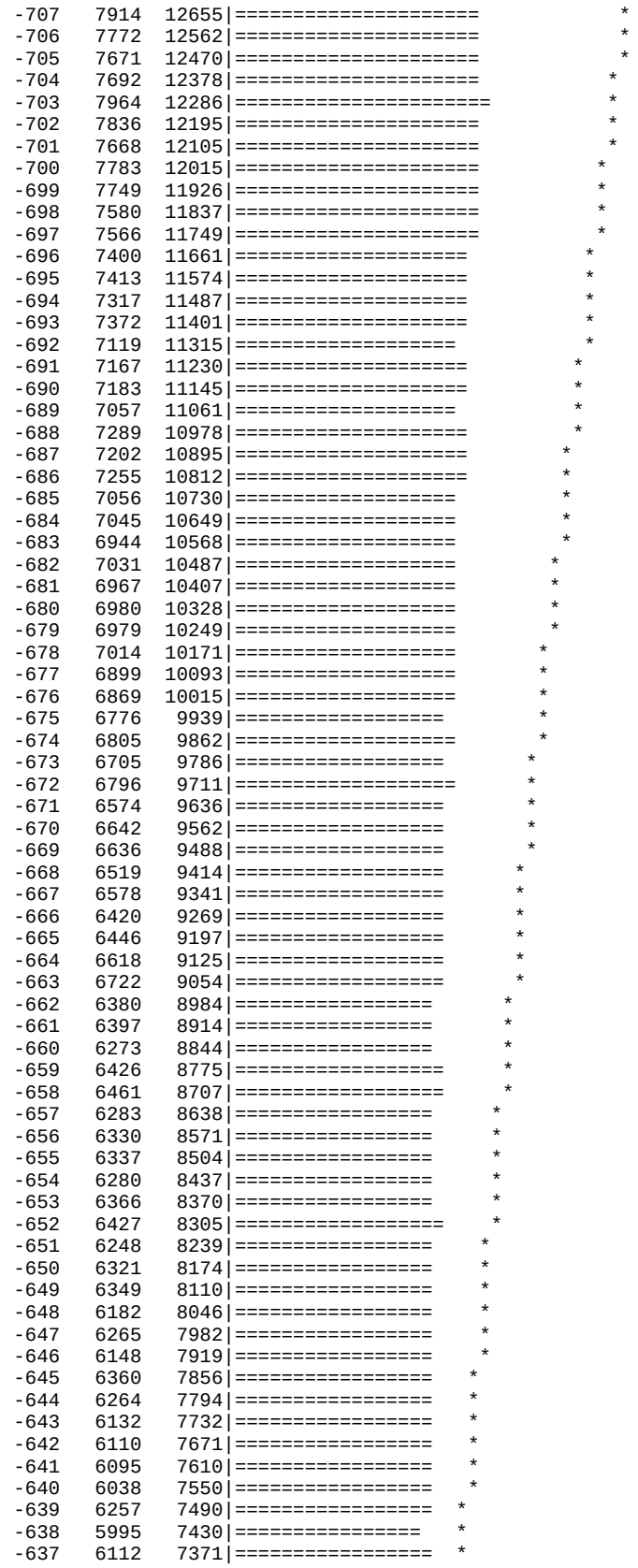
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-638 5995 7430
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-522   7957   2845|=======*==============
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-495   6353   2261|=====*==========
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-493   6015   2223|=====*==========
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-481   3551   2006|=====*====
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-477   2969   1939|=====*==
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-473   2494   1873|====*==
-472   2178   1857|====*=
-471   2091   1842|====*=
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-468   1808   1795|====*
-467   1531   1779|====*
-466   1529   1764|====*
-465   1371   1749|====*
-464   1210   1734|====*
-463   1212   1719|====*
-462   1094   1705|=== *
-461   1026   1690|=== *
-460    963   1676|=== *
-459    915   1661|=== *
-458    820   1647|=== *
-457    777   1633|=== *
-456    763   1619|=== *
-455    652   1605|==  *
-454    621   1591|==  *
-453    581   1578|==  *
-452    582   1564|==  *
-451    422   1551|==  *
-450    456   1538|==  *
-449    432   1524|==  *
-448    350   1511|=   *
-447    338   1498|=  *
-446    301   1486|=  *
-445    313   1473|=  *
-444    256   1460|=  *
-443    276   1448|=  *
-442    207   1435|=  *
-441    218   1423|=  *
-440    225   1411|=  *
-439    163   1399|=  *
-438    170   1387|=  *
-437    144   1375|=  *
-436    132   1363|=  *
-435    131   1351|=  *
-434    126   1340|=  *
-433     93   1328|=  *
-432     93   1317|=  *
-431     74   1305|=  *
-430     58   1294|=  *
-429     58   1283|=  *
-428     51   1272|=  *
-427     60   1261|=  *
-426     46   1250|=  *
-425     34   1240|=  *
-424     37   1229|=  *
```

```
 -423     19   1218|=  *
 -422     22   1208|=  *
 -421     18   1197|=  *
 -420     15   1187|=  *
 -419      9   1177|=  *
 -418     14   1167|=  *
 -417     10   1157|=  *
 -416      4   1147|=  *
 -415      7   1137|=  *
 -414      6   1127|= *
 -413      5   1118|= *
 -412      1   1108|= *
 -411      3   1098|= *
 -410      2   1089|= *
 -409      0   1080|  *
 -408      1   1070|= *
 -407      1   1061|= *
 -406      1   1052|= *
>-405   1482      -|====


% Statistical details of theoretical EVD fit:
              mu =  -918.6488
          lambda =     0.0087
chi-sq statistic = 569175936.0000
  P(chi-square)  =          0

Total sequences searched: 10818955

Whole sequence top hits:
tophits_s report:
     Total hits:           1400
     Satisfying E cutoff:  1344
     Total memory:         329K

Domain top hits:
tophits_s report:
     Total hits:           1400
     Satisfying E cutoff:  1400
     Total memory:         4667K
```