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Count: **16 isolates** | GISAID published: **151,446 isolates (673,345 sequences)** | Total isolate count: **291,327 isolates (1,203,950 sequences)**

Basic filters

Predefined search:

Search in: Released files Worksets

Search patterns:

Type	H	N	Lineage	Host	Location
A	3	5		-all-	-all-
B	4	6		Human	Africa
C	5	7		Animal	Antarctica
	6	8		Avian	Asia
	7	9		Chicken	Europe

Additional filters

Collection date (YYYY-MM-DD): From To

Submission date (YYYY-MM-DD): From To

Originating Laboratory:

Submitting Laboratory:

Required Segments: PB2 PB1 PA HA NP NA MP NS HE P3

only complete Min Length

Direct submissions to GISAID Import from public-domain (INSDC)

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FluSurver

Filter Align DNA (NC) Align Proteins (AA)

all PB2 PB1 PA HA NP NA MP NS HE P3

<input type="checkbox"/>	Sequence name	EPI/WSS-Nr	Isolate name	NCBI-Id	Length
<input checked="" type="checkbox"/>	A/Environment/Inner Mongolia/23280/2019__H7N9_HA	EPI1431576	A/Environment/Inner Mongolia/23280/2019		1695
<input checked="" type="checkbox"/>	A/Environment/Inner Mongolia/23280/2019__H7N9_PB2	EPI1431573	A/Environment/Inner Mongolia/23280/2019		2280
<input checked="" type="checkbox"/>	A/Environment/Inner Mongolia/23286/2019__H7N9_HA	EPI1431584	A/Environment/Inner Mongolia/23286/2019		1695
<input checked="" type="checkbox"/>	A/Environment/Inner Mongolia/23286/2019__H7N9_PB2	EPI1431581	A/Environment/Inner Mongolia/23286/2019		2280
<input checked="" type="checkbox"/>	A/Gansu/23276/2019__H7N9_HA	EPI1431600	A/Gansu/23276/2019		1695
<input checked="" type="checkbox"/>	A/Gansu/23276/2019__H7N9_PB2	EPI1431597	A/Gansu/23276/2019		2280
<input checked="" type="checkbox"/>	A/Gansu/23277/2019__H7N9_HA	EPI1431592	A/Gansu/23277/2019		1695
<input checked="" type="checkbox"/>	A/Gansu/23277/2019__H7N9_PB2	EPI1431589	A/Gansu/23277/2019		2280

<< first < prev **1** next > last >>

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H7N9 in 2019



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HA_A/Environment/Inner Mongolia/23280/2019_353995	HA A/Guangdong/17SF003/2016(H7N9) find closest related sequences	96.099	100.000	22	V7I , A27S , R40K , R65K , E89K , I96V , G132R , T134K , E137G , Y143T , S152P , A169T , K181R , I187V , K202R , R279G , K319R , K407E , I431M , L441F , D459N , I540T show in structure
HA_A/Environment/Inner Mongolia/23286/2019_353996	HA A/Guangdong/17SF003/2016(H7N9) find closest related sequences	96.099	100.000	22	V7I , A27S , R40K , R65K , E89K , I96V , G132R , T134K , E137G , Y143T , S152P , A169T , K181R , I187V , K202R , R279G , K319R , K407E , I431M , L441F , D459N , I540T show in structure
HA_A/Gansu/23276/2019_353998	HA A/Guangdong/17SF003/2016(H7N9) find closest related sequences	96.099	100.000	22	V7I , A27S , R40K , R65K , E89K , I96V , G132R , T134K , E137G , Y143X , S152P , A169T , K181R , I187V , K202R , R279G , K319R , K407E , I431M , L441F , D459N , I540T show in structure
HA_A/Gansu/23277/2019_353997	HA A/Guangdong/17SF003/2016(H7N9) find closest related sequences	96.099	100.000	22	V7I , A27S , R40K , R65K , E89K , I96V , G132R , T134K , E137G , Y143T , S152P , A169T , K181R , I187V , K202R , R279G , K319R , K407E , I431M , L441F , D459N , I540T show in structure
PB2_A/Environment/Inner Mongolia/23280/2019_353995	PB2 A/Guangdong/17SF003/2016(H7N9) find closest related sequences	96.179	100.000	29	D9N , K41R , K82N , V109I , V122A , T129I , E188K , E191K , E249G , V292I , M315I , V338I , K340R , P453H , R482K , V511I , K526R , M535L , I560V , M570I , I584V , V588A , I615V , I616V , V640I , I647V , A674V , A684V , R702K show in structure
PB2_A/Environment/Inner Mongolia/23286/2019_353996	PB2 A/Guangdong/17SF003/2016(H7N9) find closest related sequences	96.311	100.000	28	D9N , K82N , V109I , V122A , T129I , E188K , E191K , E249G , V292I , M315I , V338I , K340R , P453H , R482K , V511I , K526R , M535L , I560V , M570I , I584V , V588A , I615V , I616V , V640I , I647V , A674V , A684V , R702K show in structure
PB2_A/Gansu/23276/2019_353998	PB2 A/Guangdong/17SF003/2016(H7N9) find closest related sequences	96.179	100.000	29	D9N , K82N , V109I , V122A , T129I , E188K , E191K , E249G , V292I , M315I , V338I , K340R , P453H , R482K , V511I , K526R , M535L , I560V , M570I , I584V , V588A , I615V , I616V , E627K , V640I , I647V , A674V , A684V , R702K show in structure
PB2_A/Gansu/23277/2019_353997	PB2 A/Guangdong/17SF003/2016(H7N9) find closest related sequences	96.179	100.000	29	D9N , K82N , V109I , V122A , T129I , E188K , E191K , E249G , V292I , M315I , V338I , K340R , P453H , R482K , V511I , K526R , M535L , I560V , M570I , I584V , V588A , I615V , I616V , E627K , V640I , I647V , A674V , A684V , R702K show in structure

Bioinformatics Institute - Google Chrome

mendel2.bii.a-star.edu.sg/METHODS/flusurver/beta/tmp/tmp_HA_H7N9_Human_20...

Reference: HA_H7N9_Human_2016_Guangdong17SF003 ([Structure/Model Details](#))

Patient/Sample: HA_A/Gansu/23277/2019_353997

Mutation(s): [V7I](#), [A27S](#), [R40K](#), [R65K](#), [E89K](#), [I96V](#), [G132R](#), [T134K](#), [E137G](#), [Y143T](#), [S152P](#), [A169T](#), [K181R](#), [I187V](#), [K202R](#), [R279G](#), [K319R](#), [K407E](#), [I431M](#), [L441F](#), [D459N](#), [I540T](#)

Wildtype residue only displayed if position is part of available structure.
Hover with mouse over residue to see its position number. Right-click for more options.

FluSurver-JSmol

Spin ON Spin OFF Save IMAGE

[See interactions of position HA 27 in related structures.](#)
[See interactions of position HA 40 in related structures.](#)
[See interactions of position HA 55 in related structures.](#)

E627K

[Right-click here to save/download detailed mutation report table for archiving or import to Excel \(Tab-separated, one mutation per line\)](#)
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environment

human

H7N9 in 2019

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flusurver_result27210_perquery.csv - Excel

Sebastian Maurer-Stroh

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Clipboard Font Alignment Number Styles Cells Editing Ideas

	A	B	C	D	E
1	Query	All Mutations	Red Mutations	Orange Mutations	Reference
2	HA_A/Environment/Inner Mongolia/23280/2019_353998	V7I;A27S;R40K;R65K;E89K;I96V;G132R;T134K;E137G;V143T;S152P;A169T;K181R;I187V;K202R;R279G;K319R;K407E;I431M;L441F;D459N;I540T		T134K;E137G;V143T;S152P;A169T;K202R	HA A/Guangdong/17SF003/2016(H7N9)
3	HA_A/Environment/Inner Mongolia/23286/2019_353997	V7I;A27S;R40K;R65K;E89K;I96V;G132R;T134K;E137G;V143T;S152P;A169T;K181R;I187V;K202R;R279G;K319R;K407E;I431M;L441F;D459N;I540T		T134K;E137G;V143T;S152P;A169T;K202R	HA A/Guangdong/17SF003/2016(H7N9)
4	HA_A/Gansu/23276/2019_353998	V7I;A27S;R40K;R65K;E89K;I96V;G132R;T134K;E137G;V143T;S152P;A169T;K181R;I187V;K202R;R279G;K319R;K407E;I431M;L441F;D459N;I540T		T134K;E137G;S152P;A169T;K202R	HA A/Guangdong/17SF003/2016(H7N9)
5	HA_A/Gansu/23277/2019_353997	V7I;A27S;R40K;R65K;E89K;I96V;G132R;T134K;E137G;V143T;S152P;A169T;K181R;I187V;K202R;R279G;K319R;K407E;I431M;L441F;D459N;I540T		T134K;E137G;V143T;S152P;A169T;K202R	HA A/Guangdong/17SF003/2016(H7N9)
6	PB2_A/Environment/Inner Mongolia/23280/2019_353998	D9N;K41R;K82N;V109I;V122A;T129I;E188K;E191K;E249G;V292I;M315I;V338I;K340R;P453H;R482K;V511I;K526R;M535L;I560V;M570I;I584V;V588A;I540T		D9N;K526R;A674V	PB2 A/Guangdong/17SF003/2016(H7N9)
7	PB2_A/Environment/Inner Mongolia/23286/2019_353997	D9N;K41R;K82N;V109I;V122A;T129I;E188K;E191K;E249G;V292I;M315I;V338I;K340R;P453H;R482K;V511I;K526R;M535L;I560V;M570I;I584V;V588A;I615V		D9N;K526R;A674V	PB2 A/Guangdong/17SF003/2016(H7N9)
8	PB2_A/Gansu/23276/2019_353998	D9N;K82N;V109I;V122A;T129I;E188K;E191K;E249G;V292I;M315I;V338I;K340R;P453H;R482K;V511I;K526R;M535L;I560V;M570I;I584V;V588A;I615V	E627K	D9N;K526R;A674V	PB2 A/Guangdong/17SF003/2016(H7N9)
9	PB2_A/Gansu/23277/2019_353997	D9N;K82N;V109I;V122A;T129I;E188K;E191K;E249G;V292I;M315I;V338I;K340R;P453H;R482K;V511I;K526R;M535L;I560V;M570I;I584V;V588A;I615V	E627K	D9N;K526R;A674V	PB2 A/Guangdong/17SF003/2016(H7N9)
10					

flusurver_result27210_perquery

[find closest related sequences](#)

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Go back

H7N9 in 2019

Sequence ID	Location	Date	Length	Mutations
HA_A/Environment/Inner Mongolia/23280/2019_353995	A/Shanghai/2/2013(H7N9)	94.821	100,000	32
HA_A/Environment/Inner Mongolia/23286/2019_353996	A/Shanghai/2/2013(H7N9)	94.821	100,000	32
HA_A/Gansu/23276/2019_353998	A/Shanghai/2/2013(H7N9)	94.821	100,000	32
HA_A/Gansu/23277/2019_353997	A/Shanghai/2/2013(H7N9)	94.821	100,000	32
PB2_A/Environment/Inner Mongolia/23280/2019_353995	A/Shanghai/2/2013(H7N9)	97.101	100,000	22
PB2_A/Environment/Inner Mongolia/23286/2019_353996	A/Shanghai/2/2013(H7N9)	97.233	100,000	21
PB2_A/Gansu/23276/2019_353998	A/Shanghai/2/2013(H7N9)	97.365	100,000	20
PB2_A/Gansu/23277/2019_353997	A/Shanghai/2/2013(H7N9)	97.365	100,000	20

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 Right-click here to save/download query summary report table for archiving or import to Excel (Comma-separated, one query per line)

Go back

HA -> A/Shanghai/2/2013 = 32 mutations
 PB2 -> A/Shanghai/2/2013 = 21 mutations

Sequence ID	Location	Date	Length	Mutations
HA_A/Environment/Inner Mongolia/23280/2019_353995	A/Guangdong/17SF003/2016(H7N9)	96.099	100,000	22
HA_A/Environment/Inner Mongolia/23286/2019_353996	A/Guangdong/17SF003/2016(H7N9)	96.099	100,000	22
HA_A/Gansu/23276/2019_353998	A/Guangdong/17SF003/2016(H7N9)	96.099	100,000	22
HA_A/Gansu/23277/2019_353997	A/Guangdong/17SF003/2016(H7N9)	96.099	100,000	22
PB2_A/Environment/Inner Mongolia/23280/2019_353995	A/Guangdong/17SF003/2016(H7N9)	96.179	100,000	29
PB2_A/Environment/Inner Mongolia/23286/2019_353996	A/Guangdong/17SF003/2016(H7N9)	96.311	100,000	28
PB2_A/Gansu/23276/2019_353998	A/Guangdong/17SF003/2016(H7N9)	96.179	100,000	29
PB2_A/Gansu/23277/2019_353997	A/Guangdong/17SF003/2016(H7N9)	96.179	100,000	29

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 Right-click here to save/download query summary report table for archiving or import to Excel (Comma-separated, one query per line)

Go back

HA -> A/Guangdong/17SF003/2016 = 22 mutations
 PB2 -> A/Guangdong/17SF003/2016 = 29 mutations

H7N9 in 2019

https://platform.gisaid.org/epi3/3p/flusurver/entities/MUTA...
platform.gisaid.org/epi3/3p/flusurver/entities/MUTATIONS/H7N9_Hu...

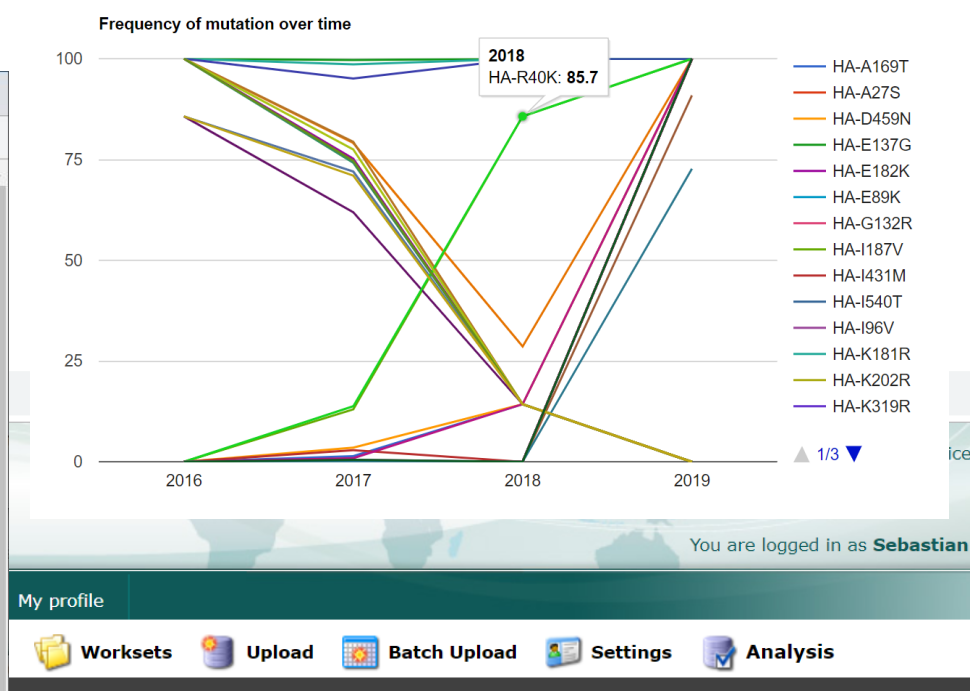
Map of cities with the HA R40K mutation

The city with **red** label indicates first appearance of the mutation. City with **blue** label indicate later appearance of the mutation. The city with the most recent appearance of the mutation has the **green** label. Number in the label indicates frequency of occurrence of the mutation in that city. Click on the city marker to show the frequency of mutations found in the city.

Map of countries with the HA R40K mutation

Number of occurrences

Countries without data: [Grey square] 3 [White square] [Light red square] [Red square] 94



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to highlight phenotypically or epidemiologically interesting candidate mutations for further research and should ideally be combined with...
trantly, any direct diagnostic use, assumed severity or recommendation on patient treatment should not be based solely on these compu...
ation transfer of equivalent mutations are mainly comprised of strains that recently infected humans. Therefore, the usage scenario the...
surveillance sequences with very close relation to used vaccine strains, including some candidates for avian flu and novel...
the **Frequency** X

HA R40K

Key to alternative position numbering:

39	FluSurver numbering (absolute as in 2009 H1N1 pandemic)
HA1 32	Classical H3N2 strain numbering
HA1 22	Classical H1N1 strain numbering

Chosen reference: HA_H7N9_Human_2016_Guangdong17SF003
Position in reference: 40
AA in reference: R
AA in query: K

Mutation HA R40K already occurred 104 times (15.81% of all samples with HA sequence) in 6 countries. The first strain with this mutation, collected in January 2017, was A/duck/Japan/AQ-HE29-22/2017/-1. The mutation most recently occurred in strain A/Environment/Inner Mongolia/23286/2019, collected in April 2019. (see map)
[See detailed global statistics for this position](#)

As seen in resolved structures of proteins from related strains, the HA position equivalent to your mutation is involved in:
- viral oligomerization interfaces
- binding small ligand(s)
[See all interactions for this position](#)

[PubMed search for this mutation \(including alternative numbering\)](#)

HA_39_1HGD_A_32 - Google Chrome

mendel2.bii.a-star.edu.sg/METHODS/flusurver/beta/INTERACTIONS/HA/39/...

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Description:
The mutation position (red atoms) corresponds to position 32 on viral chain A (yellow backbone) and is within 5 Å from oligomeric subunit chain D (blue backbone).

Legend:
White backbone: other chains found in the structure

[See all 475 interactions for this position](#)

JSmol