

The GISAID Initiative

Real Time Global Communication in Disease Prevention

Bioinformatics Workshop 26-27 August 2019 Singapore

WHO Global Influenza Programme (GIP)
National Centre for Infectious Diseases (NCID) Singapore
Bioinformatics Institute (BI)
Global Initiative on Sharing All Influenza Data (GISAID)



Database Technical Group



National Centre for
Infectious Diseases



hosted by the
Federal Republic
of Germany

Challenges in 2006-2007

- Access to the latest genetic data for highly pathogenic H5N1 influenza zoonotic infections was often restricted, in part due to the hesitancy by MS to share their information.
- Scientists' reticence to share data pre-publication, out of fear of being scooped¹ delayed sharing.
- Public-domain archives (anonymous access - use of data) offered:
 - no protection of owners' interests (intellectual property rights);
 - limited incentive to share data;
 - no transparency on the use of data;
 - no effective mechanisms to ensure acknowledgement of labs providing viruses or contributing data.

¹ Pearson H. - Competition in biology: It's a scoop! *Nature* 2003; DOI: [10.1038/news031124-9](https://doi.org/10.1038/news031124-9)

GISAID data access and sharing principles

- Data Submitters grant Data Users an irrevocable licence for the use of their data, providing legal certainty for use in research and publications and for the development, testing and dissemination of interventions such vaccines, diagnostics and therapeutics
- Access to the GISAID EpiFlu™ Database is free of charge and open to everyone provided they identify themselves in order to foster collaboration and permit an effective oversight to uphold the enshrined sharing principles
- The guiding principle for those who use the Data in particular in publications is the need to acknowledge the contribution of both the suppliers and the submitters of the data
- Whilst all Data are publicly accessible, Submitters do not forfeit their rights (IPR) to the data they deposit in GISAID

See: [GISAID EpiFlu™ Database Access Agreement](#)

EpiFlu™ Database

- The most complete set of influenza sequences (285K isolates from 1.2 million sequences)
- Includes patient metadata & geographical locations
- Submitters retain rights over their data
- Easy upload of data
- Isolate based entry rather than sequence only
- Isolates can be updated by submitter in real-time
- Automated sequence annotation on upload
- Customized search function outputs
- Customized FASTA headers with sequence downloads
- Metadata can be downloaded in spreadsheet
- Workset function, worksets can be shared amongst users
- Analysis tools

Workflow of EpiFlu™ Database

Data

Sequence data is organized into unique isolates assigned an EPI_ISL Accession (defined by virus name and passage history), and segment EPI Accession metadata fields include: Isolate name, virus type, HA and NA subtype, lineage (B; H1N1), host, collection date, location, patient data i.e.: age, gender, vax status.

Originating Laboratory - collected the specimen (Lab ID)

Submitting Laboratory - sequenced the virus

Upload

Single Upload – using the webpage interface (5-10 min)

Batch Upload – using a macro-enabled excel spreadsheet (necessary fields; time dependent on amount of data; automatic)

Complimented with data from public-domain archives routinely imported

Curation

Checks the correctness of sequence and metadata

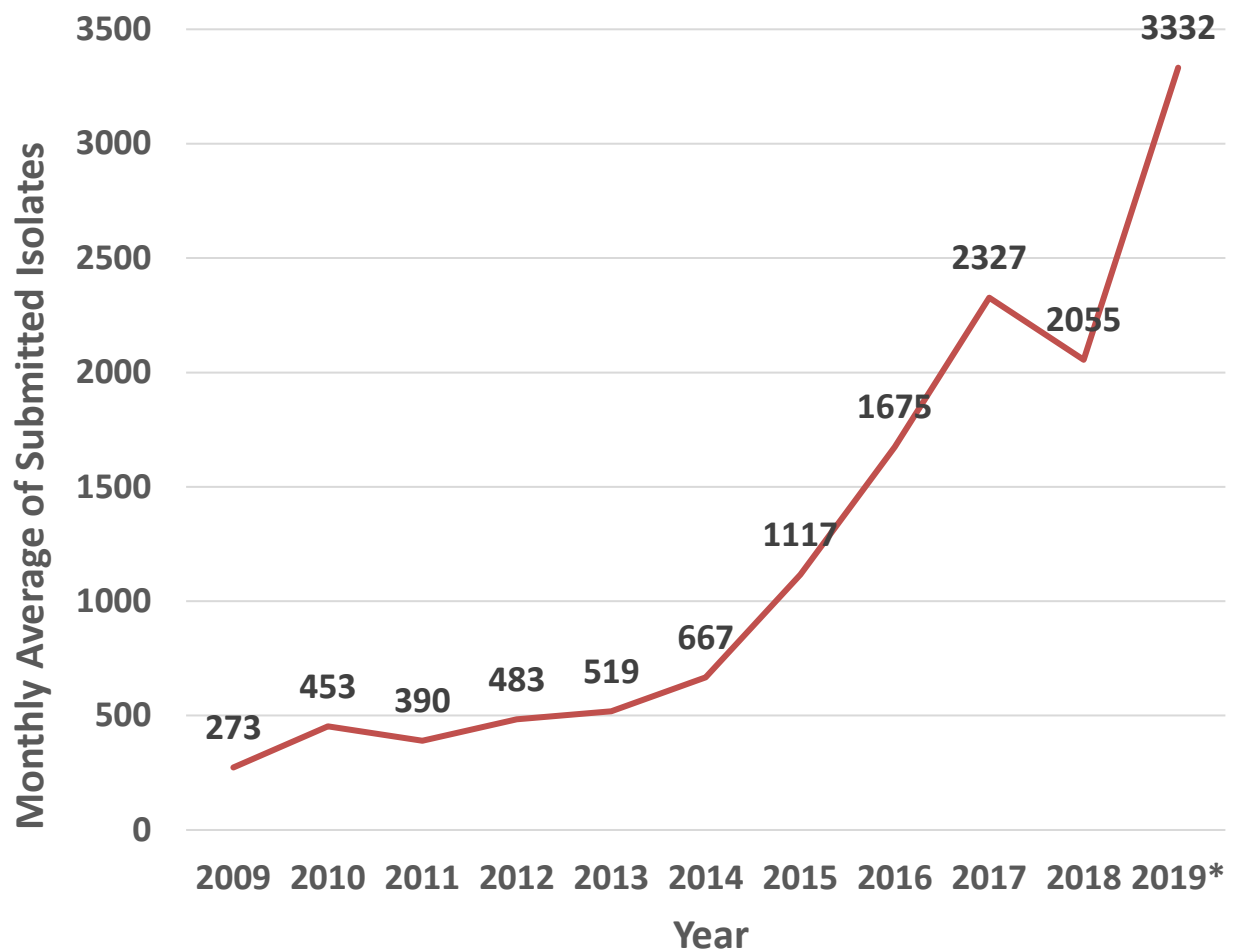
Flags errors

Data to Unreleased Files

Pop-up message – errors, where and what type

Release of corrected data

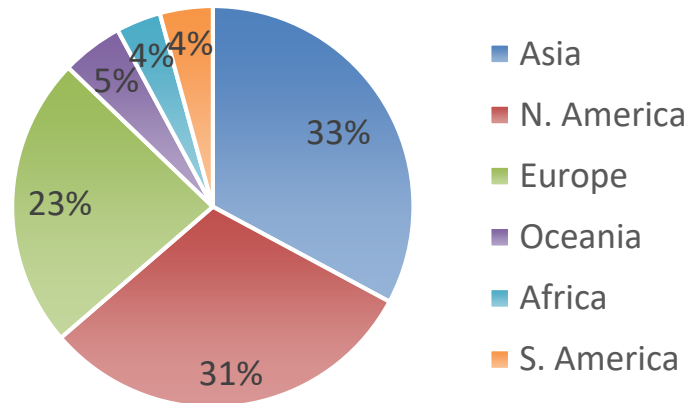
Increase in genetic sequence data published via GISAID



Geographical representativeness

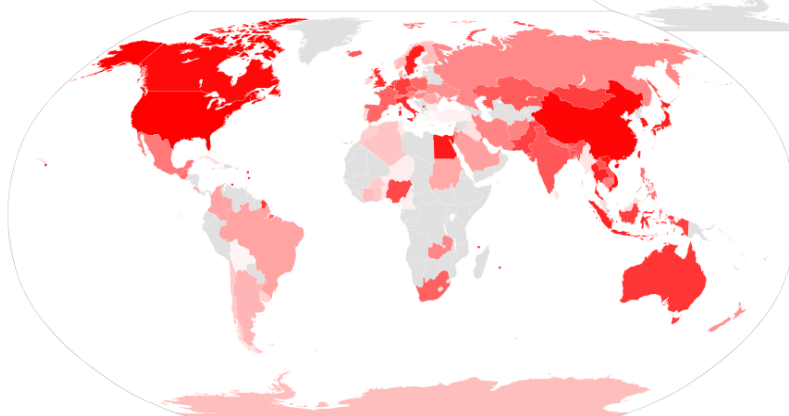
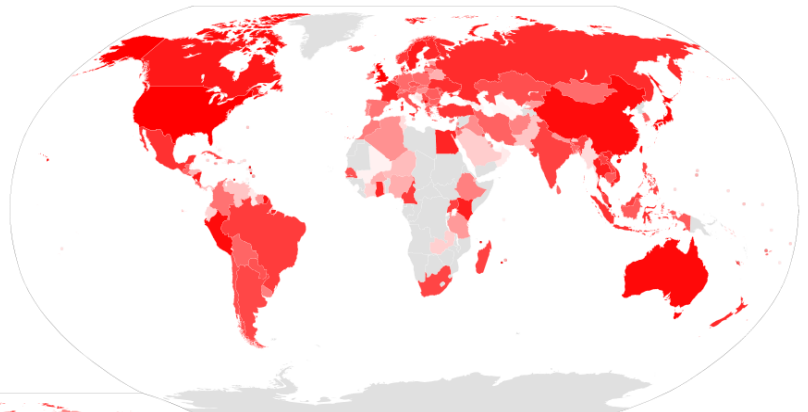
- ~1,2m sequences of ~283,000 influenza viruses (70% human; 30% animal)
- Data from >1,200 labs (incl. all 152 GISRS)
- Contains data from >2,000 influenza viruses with pandemic potential (IVPP)
 - >30,000 animal viruses (H4-H11)
 - Candidate vaccine viruses
- 8,700 active participants
- Human and animal health
- 2017-18: sequence data of ~3,000 viruses (avg) uploaded monthly (70% directly to GISAID)

- Timely submission directly to GISAID: 94% of total within 3 months of collection; 83% (within 6 mo); 81% (within 12 mo); 77% (within 24 mo)



(Hemispheres, Countries, Regions)
(282,481 viruses / 1,175,910 sequences; 9th Aug 2019)

Human-derived
influenza virus



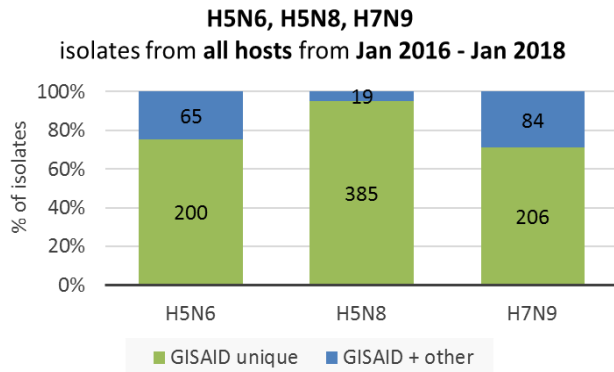
Animal-derived
influenza virus

Data in GISAID from
>1,200 labs worldwide

Countries ranked by number of HA sequences in GISAID, colored by rank percentile from red (most) to white (least), gray (none)

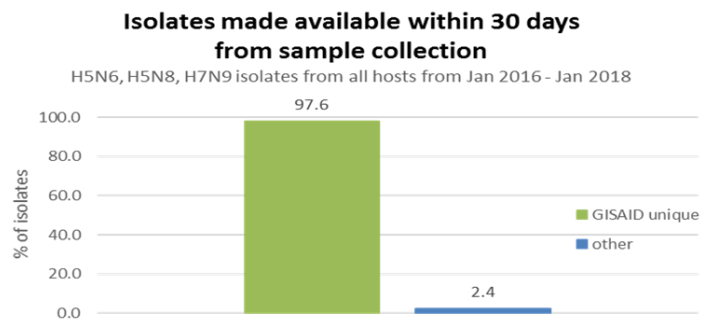
(Analyses compiled by J. Büch (MPII, Germany) & S. Maurer-Stroh (A*STAR BII, Singapore))

Rapid sharing of new avian influenza viruses with pandemic potential via GISAID

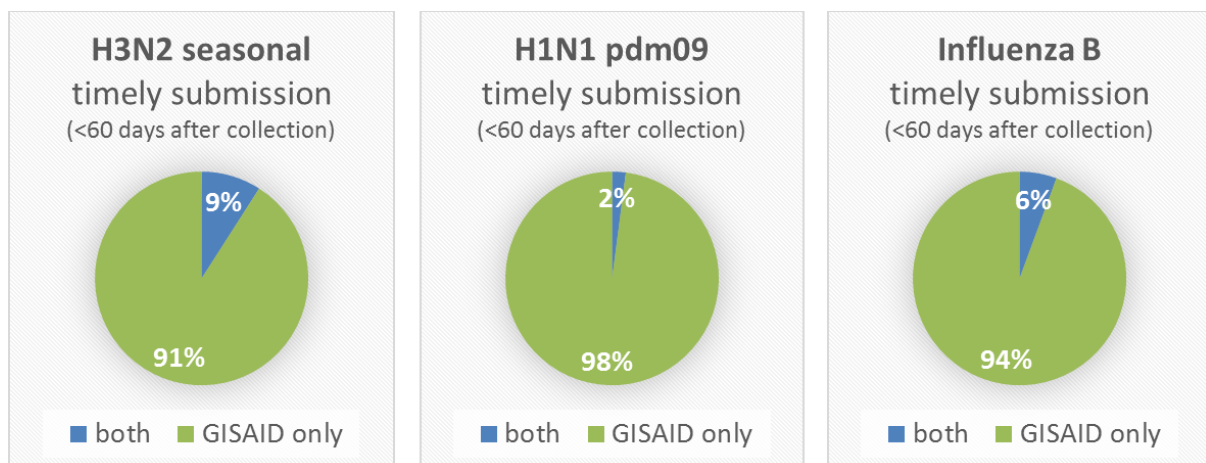


The majority of isolates from new avian influenza subtypes with pandemic potential are **unique to GISAID**.

Timeliness:
98% of the strains submitted within 30 days from sample collection are **unique to GISAID**



Timely submission of data to GISAID-human seasonal viruses

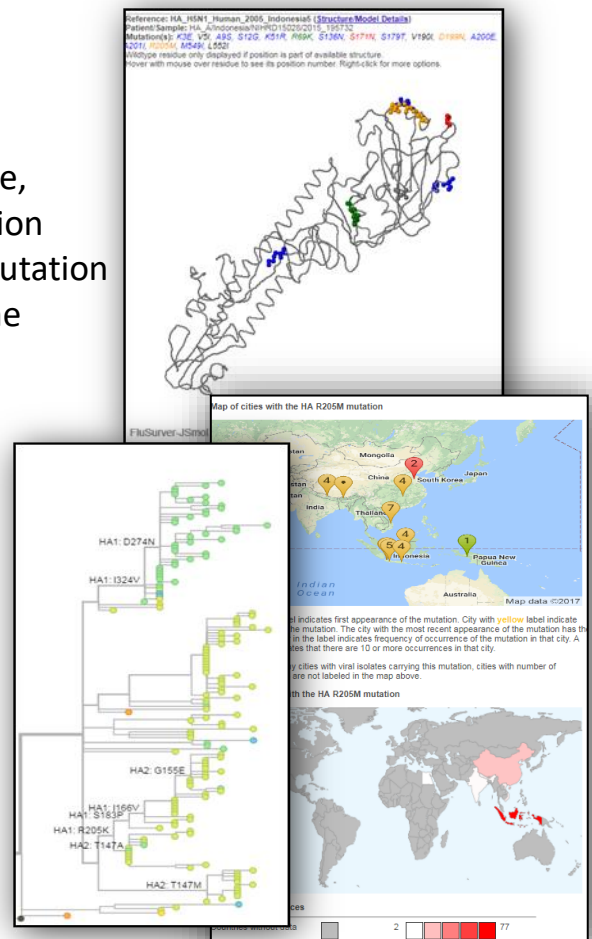


both ... public-domain and GISAID
Proportion of unique sequence information in GISAID

Near real time data analysis

FluSurver: developed at the BII A*STAR, Singapore, assists the identification, analysis and interpretation of mutations in influenza sequences, providing mutation frequencies automatically kept up to date with the latest GISAID data.

Annotated Tree Tool via nextflu: developed at the University of Basel, displays phylogenetic trees, along with alignments of nucleotide and amino acid sequences, showing the emergence of new clades in a temporal & geographical context



Projects

- Global Server Resilience Strategy
- Expansion of Tools and Next Generation Sequencing
- Capacity building through educational program via GISAID's series of workshops, webinars and seminars
- Realization of GISAID scientific retreat and school
- Application of GISAID sharing mechanism to other pathogens

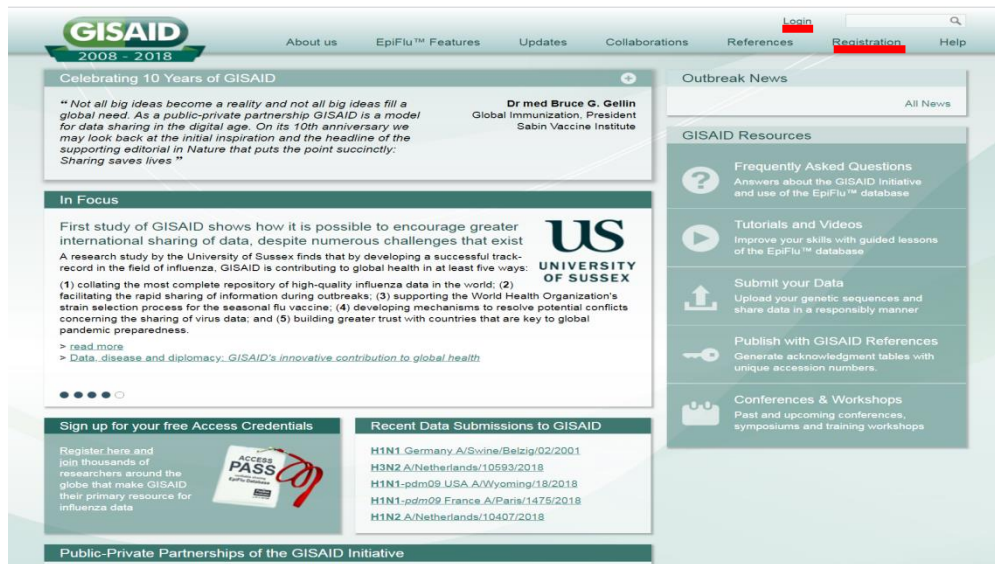
- European Commission PREDEMICS

GISAID

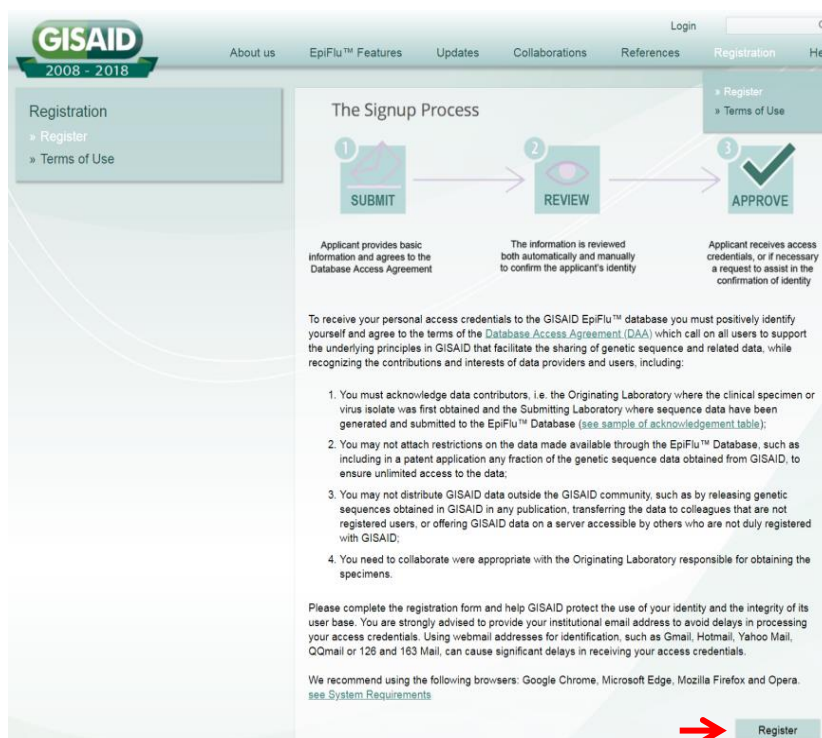
How to Register and obtain Access Credentials

Access the GISAID homepage <https://gisaid.org>

Click the 'Registration' button on the top RHS and select 'Register' in the drop down menu



Be sure to familiarize yourself with the terms of access summarized in the Sign Process screen before you select the 'Register' button at the bottom RHS of the page.



Part of the registration page

The screenshot shows the GISAID registration page. At the top, there is a navigation bar with 'Welcome', 'News', 'Registration', 'FAQ', and 'About GISAID'. Below the navigation bar, there is a section titled 'Registration' with a bullet point: 'Requiring you to make best efforts to collaborate with the Originating Laboratory responsible for obtaining the specimens.' This is followed by instructions for registering and a 'What happens next?' section. The main form is divided into two sections: 'Personal Data' and 'Contact Information'. The 'Personal Data' section includes fields for 'My/His' (radio buttons for Ms and Mr), 'First name*', 'Middle name', 'Last name*', 'Title', and 'Desired Login ID*'. The 'Contact Information' section includes fields for 'Institution*', 'Department', 'Street 1*', 'Postal code', 'City*', 'Location*' (with a dropdown menu for 'Select location'), 'State/province', 'Telephone*', 'Fax', 'Mobile', and 'E-Mail*'. At the bottom of the page, there is a copyright notice: '© 2008 - 2017 | The GISAID Initiative | Terms of Use | Contact | System Requirements'.

The screenshot shows the GISAID registration page, specifically the 'Data Access Agreement' section. The section is titled 'Data Access Agreement' and contains the following text: 'GISAID EPIFLU™ DATABASE ACCESS AGREEMENT Effective: March 16, 2011'. Below this, there is a 'WHEREAS' clause and a 'NOW, therefore' clause. The 'NOW, therefore' clause states: 'NOW, therefore, this Database Access Agreement (the "Agreement") is entered into by and between the undersigned ("You") and GISAID.' The 'WHEREAS' clause states: 'WHEREAS Freunde von GISAID e.V. ("GISAID") maintains a global database for influenza gene sequences along with associated data, including virological, clinical, epidemiological and demographic information (if available) for all influenza viruses, including but not limited to H5N1 sequences, (the "GISAID EpiFlu™ Database") for the purpose of facilitating the sharing, research and investigation of such sequences and associated data.' The 'NOW, therefore' clause also states: '1. Access to the GISAID EpiFlu™ Database, Data, Access to, and use of, the GISAID EpiFlu™ Database and Data, as defined herein, is governed by this Agreement. By accessing or otherwise using the GISAID EpiFlu™ Database, whether as a provider or user of Data, You accept and agree to be bound by the terms of this Agreement. For purposes of this Agreement, the term "Data" means any and all (i) sequence data and other associated data and information contained in the GISAID EpiFlu™ Database pertaining to influenza viruses, (ii) any annotations, corrections, updates, modifications, improvements, derivatives or other enhancements to any such data contained in the GISAID EpiFlu™ Database, and (iii) any safety information relevant to use of the data or to regulatory approval of vaccines or other therapies that embody or utilize the data contained in the GISAID EpiFlu™ Database.' The 'License Terms' section states: '2. License Terms: You are hereby granted a non-exclusive, worldwide, royalty-free, non-transferable, and assignable license to access and use the GISAID EpiFlu™ Database and Data.' Below the agreement text, there is a checkbox labeled 'I accept the DAA' and a 'Register' button. At the bottom of the page, there is a copyright notice: '© 2008 - 2018 | Terms of Use | Contact'.

Follow the instructions, and complete the form with accurate information.

Please make sure that you use an institutional email address and not a personal email address, such as Gmail or Yahoo, as this will delay in the issuance of your access credentials

For those without access to an institutional email service, please ensure to provide your mobile phone and the institute's phone number so the registration team can get in touch with you to positively establish your identity. This is necessary to protect the use of your identity, and to uphold the GISAID sharing mechanism and the integrity of its userbase.

Once you have read the conditions of Database Access Agreement (DAA) which outlines the terms of your access to and use of the EpiFlu™ database, you will need to agree to the DAA by ticking the box at the bottom where it states "I accept the DAA" before you select the Register button, to submit your request.

This will be followed by a message asking you to look for an email the system automatically generates. Be sure to look for this email in your inbox, or if need be in your SPAM folder. This email contains a verification link that you are asked to click on, so the GISAID system knows the email address you provided is accurate.

After successful verification of the information you provided, you will on average <12 hours receive an email with your personal access credentials (Username & Password), which are yours to keep even if you should change institutions down the road.

As with any passwords, be sure to change the password to something you can remember. To change the password, logged in first and select the "Settings" tab, see figure at the bottom of Page 9

As a reminder: Never ever share your username or password, as this might cause the loss of your access credentials.

For those of you who are already registered but forgot their username or password, select “Forgot your password or Login?”. This can be found on the front page directly beneath the ‘Login’ button, refer to the first figure of this document.

How to Login

Open the GISAID website

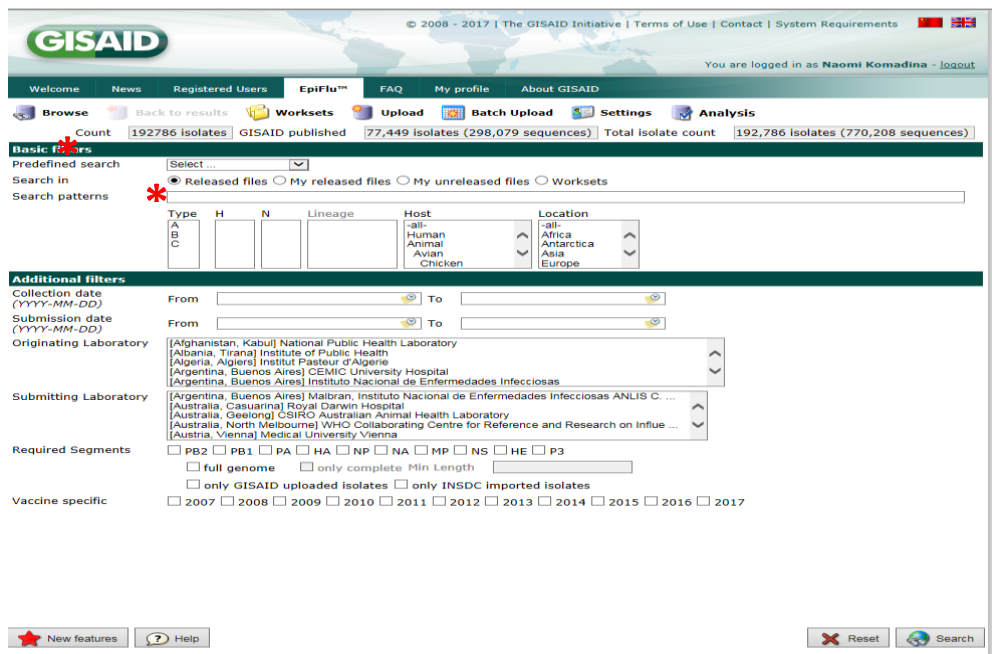
Click the ‘Login’ button on the top RHS and login with your Username and Password on the Login page

The screenshot shows the GISAID website homepage. At the top, there is a navigation bar with links for 'About us', 'EpiFlu™ Features', 'Updates', 'Collaborations', 'References', 'Registration', and 'Help'. A 'Login' button is highlighted in red. Below the navigation bar, there is a section for 'Celebrating 10 Years of GISAID' with a quote from Dr. med Bruce G. Gellin, President of the Sabin Vaccine Institute. To the right, there is a sidebar with 'Outbreak News' and 'GISAID Resources' including 'Frequently Asked Questions', 'Tutorials and Videos', 'Submit your Data', 'Publish with GISAID References', and 'Conferences & Workshops'. The main content area features an 'In Focus' article from the University of Sussex about international data sharing. Below this, there is a 'Sign up for your free Access Credentials' section with an 'ACCESS PASS' graphic, and a 'Recent Data Submissions to GISAID' section listing various influenza virus sequences.

Recent Data Submissions to GISAID
H1N1 Germany A/Swine/Belzig/02/2001
H3N2 A/Netherlands/10593/2018
H1N1-pdm09 USA A/Wyoming/18/2018
H1N1-pdm09 France A/Paris/1475/2018
H1N2 A/Netherlands/10407/2018

Searching for isolates in GISAID

EpiFlu™ Start Page



Select which database you want to search

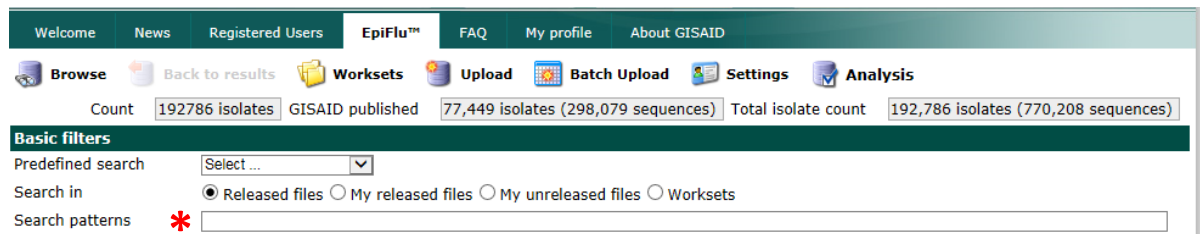
- Released Files
 - This section contains all available sequences in GISAID
- My released files
 - If you have uploaded data to GISAID all your data is contained here and can be searched
- My unreleased files
 - All files which you have uploaded to GISAID but are yet to be released to the main data base are held here. Once checked they can be released & will transfer to 'My released files' and 'Released files'

If you have never uploaded to GISAID only the Released Files databses is available for searching

Multiple search options

Count Button:- gives a running total of how many seqeunces your search has located

Searching using 'Search patterns' field



Free text can be used here and different types and subtypes can be searched for at the same time.

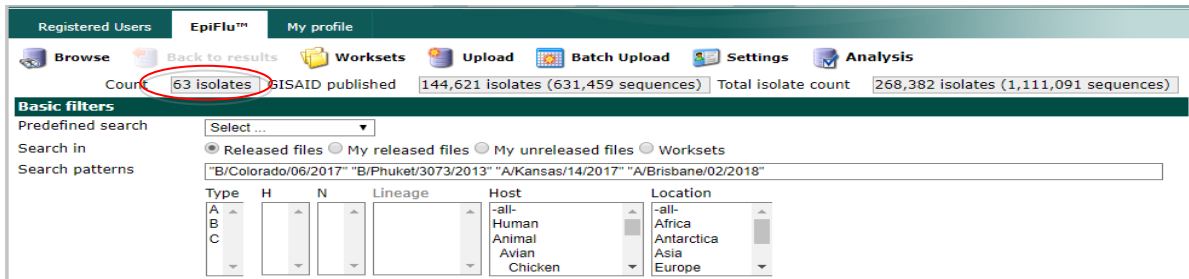
Search here using virus name or ISL_ID or segment number

All virus names must be within inverted commas is "A/Sydney/5/1997"

Search using wild cards ie "A/Hong Kong/27%/2019"

Each name or ID number must also be separated by a space.

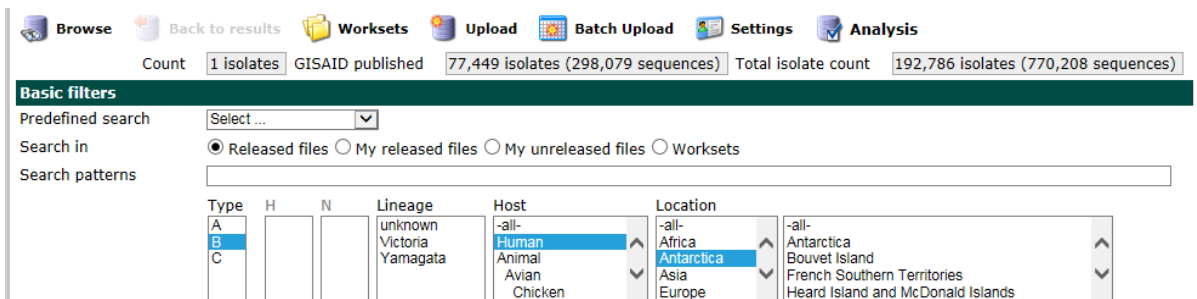
An example of a multi type or subtype search pattern is:-



63 Isolates have been located for these 4 viruses.

If you wish to search for a particular type or subtype from a broad area, such as a continent:-

ie:- Type B viruses from Antarctica, 1 virus found.



Searching by subtype ie:-H5N1 viruses

The screenshot shows the EpiFlu™ interface with the following details:

- Count: 8602 isolates
- GISAID published: 144,591 isolates (631,345 sequences)
- Total isolate count: 268,352 isolates (1,110,977 sequences)
- Basic filters:
 - Predefined search: Select ...
 - Search in: Released files (selected), My released files, My unreleased files, Worksets
 - Search patterns: (empty)
 - Filters: Type (A-C), H (1-5), N (1-5), Lineage, Host (-all-, Human, Animal, Avian, Chicken), Location (-all-, Africa, Antarctica, Asia, Europe)

A total of 8602 isolates have been located

By further refining the search, ie:- chickens, the number of isolates has dropped to 3575.

The screenshot shows the EpiFlu™ interface with the following details:

- Count: 3575 isolates
- GISAID published: 144,591 isolates (631,345 sequences)
- Total isolate count: 268,352 isolates (1,110,977 sequences)
- Basic filters:
 - Predefined search: Select ...
 - Search in: Released files (selected), My released files, My unreleased files, Worksets
 - Search patterns: (empty)
 - Filters: Type (A-C), H (1-5), N (1-5), Lineage, Host (Chicken selected), Location (-all-, Africa, Antarctica, Asia, Europe)

Search can be even further refined by selecting a location

The screenshot shows the EpiFlu™ interface with the following details:

- Count: 778 isolates
- GISAID published: 144,591 isolates (631,345 sequences)
- Total isolate count: 268,352 isolates (1,110,977 sequences)
- Basic filters:
 - Predefined search: Select ...
 - Search in: Released files (selected), My released files, My unreleased files, Worksets
 - Search patterns: (empty)
 - Filters: Type (A-C), H (1-5), N (1-5), Lineage, Host (Chicken selected), Location (Egypt selected)

778 isolates sourced from chicken in Egypt have been located and this can be further refined by selecting a time period

The screenshot shows the EpiFlu™ interface with the following details:

- Count: 31 isolates
- GISAID published: 144,591 isolates (631,345 sequences)
- Total isolate count: 268,352 isolates (1,110,977 sequences)
- Basic filters:
 - Predefined search: Select ...
 - Search in: Released files (selected), My released files, My unreleased files, Worksets
 - Search patterns: (empty)
 - Filters: Type (A-C), H (1-5), N (1-5), Lineage, Host (Chicken selected), Location (Egypt selected)
- Additional filters:
 - Collection date (YYYY-MM-DD): From 2016-01-01 To 2016-12-31

Egypt had 31 H5N1 isolates from chicken with specimen dates in 2016 submitted to GISAID

This search can be further narrowed by selecting a laboratory who provided the samples, a laboratory which submitted the sequences, a time period when the 2016 were submitted to GISAID and which genes you wish to search for as well as gene length and full genome sets as well.

Searches can be restricted to what was uploaded to GISAID only and therefore is not available on other databases, or those isolates which were uploaded to other databases first then imported to GISAID.

Search parameters are saved and not lost when you move onto another page and can be added to, however if you then wish to search for a different subtype you need to reset the search and start again.

To view sequences, select the Search function at bottom RHS of page and the 34 isolates are displayed

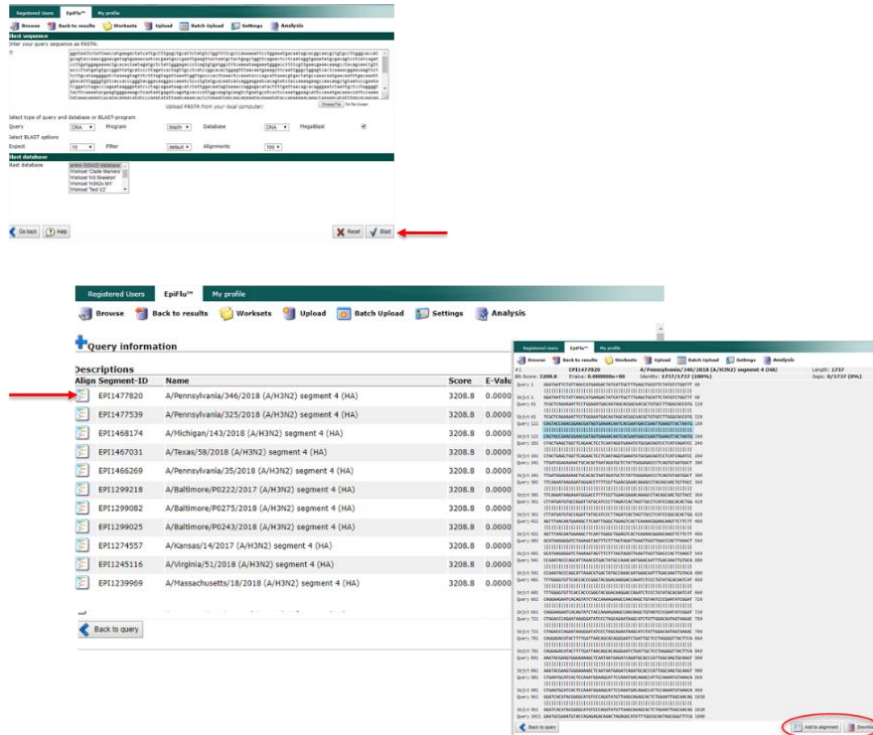
Analysis functions include alignments, BLAST, mutation analysis using [FluSurver](#) & [nextflu](#)

Data downloads include nucleotide and protein sequences, sequence metadata, sequence acknowledgement tables, BLAST results

BLAST function

From search results, click on virus name

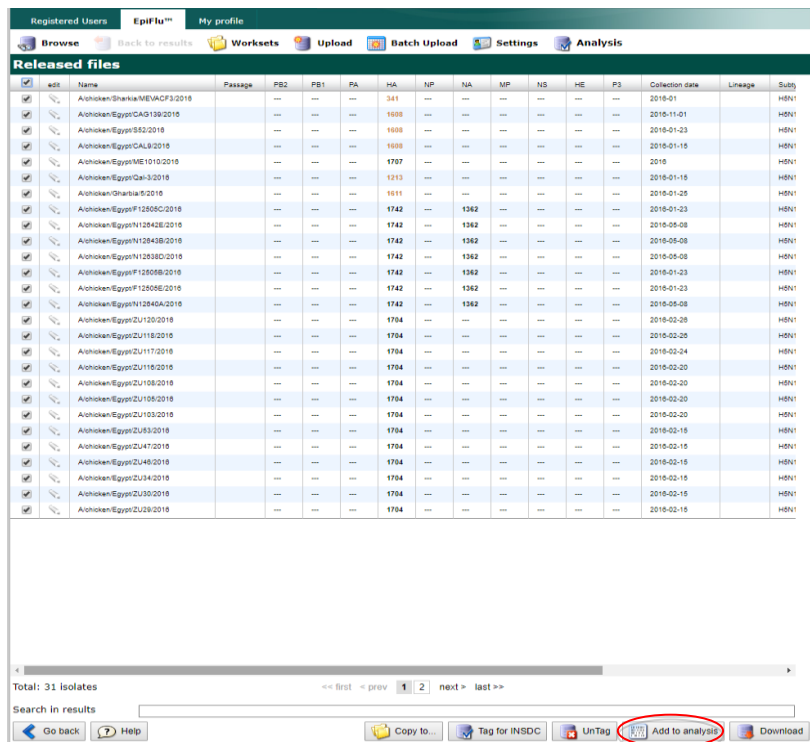
The screenshot displays the EpiFlu™ web interface. At the top, there are navigation tabs: 'Registered Users', 'EpiFlu™', and 'My profile'. Below this is a search bar and a 'Search' button. The main content area is divided into two sections. The left section, titled 'Released files', contains a table with columns for 'Accession #', 'Type', 'Lineage', 'Identifier', 'Length', 'Accession #', and 'Release date'. One row is highlighted with a red circle. The right section, titled 'Search results', shows a list of 34 isolates. A red arrow points to the 'HA' segment of the first isolate. Below this, there are two panels for BLAST analysis. The top panel shows the 'HA' segment with a 'BLAST HA' button and a 'Copy HA to clipboard' button. The bottom panel shows the 'complete CDS' with a 'BLAST gene HA' button and a 'Copy to clipboard' button. Red arrows point to these buttons.



BLAST searches can be carried out against the entire database (Released files) or My released files or any workset that you have created.

Analysis Tools

To add to Analysis, select viruses of interest, then select Add to Analysis Button



The screenshot shows the EpiFlu™ interface with a list of 31 released files. A 'Choose analysis' dialog box is overlaid on the list, showing options for 'Align' and 'Align DNA or Protein', both of which are circled in red. Below the dialog, the 'Add to analysis' button is also circled in red. The interface includes navigation buttons like 'Go back', 'Copy to...', 'Tag for INSDC', 'UnTag', and 'Download'.

Select the gene of interest. Select 'Options' to vary analysis parameter. Select Align segments.

The screenshot shows the 'Filter segments to align' section of the EpiFlu™ interface. The 'Align DNA (NC)' and 'Align Proteins (AA)' options are circled in red. Below this, there is a table of sequences with columns for 'Sequence name', 'EPI_ISL-ID', 'Isolate name', 'NCBI-ID', and 'Length'. The 'Options' button at the bottom right is also circled in red.

Sequence name	EPI_ISL-ID	Isolate name	NCBI-ID	Length
<input checked="" type="checkbox"/> A/ohio/Egypt/F12050C/2018	EPI_ISL1393	A/ohio/Egypt/F12050C/2018	KX558861	1362
<input checked="" type="checkbox"/> A/ohio/Egypt/N12443E/2018	EPI_ISL1394	A/ohio/Egypt/N12443E/2018	KX558862	1362
<input checked="" type="checkbox"/> A/ohio/Egypt/N12443B/2018	EPI_ISL1371	A/ohio/Egypt/N12443B/2018	KX558869	1362

The screenshot shows the 'Options' section of the EpiFlu™ interface. It includes settings for 'Output order', 'Strategy', 'Scoring matrix for amino acid sequences', 'Scoring matrix for nucleotide sequences', 'Gap opening penalty', 'Offset value', 'FASTA Header', and 'Example: from base'. The 'Options' button at the bottom right is circled in red.

Bioinformatics Workshop, Singapore, 26-26 August 2019

https://platform.gisaid.org/epi3/app_entities/entities/msviewer_popup.html?epi3/MSAViewer?sid=PBKJCHOYOGHFUAWYPEOQYXDDFDLITSO&fasta=%2Fepi3%2Fentities%2Ftmp%2Ftmp_2019_06...

Import Sorting Filter Selection Vis elements Color scheme Extras Export Help

ID	Label	130	132	134	136	138	140	142	144	146	148	150	152	154	156	158	160	162	164	166	168	170	172	174	176	178	180	182	184	186	188	190	192																															
1	A/chicken/Egypt/ZU2/2016	I	Q	I	I	P	K	D	S	W	S	D	H	E	A	S	-	G	V	S	S	A	C	P	Y	Q	G	R	S	S	F	F	R	N	V	V	W	L	T	K	K	N	D	A	Y	P	T	I	K	K	S	Y	N	N	T	N	Q	E	D	L	L	V	L	W

Import Sorting Filter Selection Vis elements Color scheme Extras Export Help

- Taylor
- Buried
- Cinema
- Clustal
- Clustal2
- Helix
- Hydrophobicity
- Lesk
- MAE
- Nucleotide**
- Purine
- PID
- Strand
- Turn
- Zappo
- No color

ID	Label	140	142	144	146	148	150	152	154	156	158	160	162	164	166	168	170	172	174	176	178	180	182	184	186	188	190	192																										
1	A/chicken/Egypt/ZU2/2016	D	H	E	A	S	-	G	V	S	S	A	C	P	Y	Q	G	R	S	S	F	F	R	N	V	V	W	L	T	K	K	N	D	A	Y	P	T	I	K	K	S	Y	N	N	T	N	Q	E	D	L	L	V	L	W

To download select isolates of interest by selecting check box next to each sequence of interest, for all select check box above the line, then select download

Registered Users EpiFlu™ My profile

Browse Back to results Worksets Upload Batch Upload Settings Analysis

Released files

<input type="checkbox"/>	edit	Name	Passage	PB2	PB1	PA	HA	NP	NA	MP	NS	HE	P3	Collection date	Lineage	Subty
<input checked="" type="checkbox"/>		A/chicken/Sharkia/MEVACF3/2016	---	---	---	---	141	---	---	---	---	---	---	2016-01		H5N1
<input checked="" type="checkbox"/>		A/chicken/Egypt/CAG139/2016	---	---	---	---	1608	---	---	---	---	---	---	2016-01-01		H5N1

Total: 31 isolates

Search in results

Go back Help Copy to Tag for INSDC UnTag Add to analysis Download

Metadata can be downloaded in an excel sheet or sequences as either DNA or Proteins and an acknowledgment table for inclusion in publication supplementary material

For metadata select “Isolates as XLS”

The screenshot shows a web browser displaying a large data table. The table has columns for isolate ID, date, and various metadata fields. The first few rows are highlighted in blue. The table contains a large amount of data, including isolate IDs, dates, and various metadata fields.

To download sequences, select genes of interest

Select other information of interest, these choices remain saved for other downloads

Select date format, this remains saved for other downloads

Make sure the ‘Replace spaces with underscores in FASTA header’ box has been ticked, this remains saved

The screenshot shows a web browser displaying a download form. The form has several sections: 'Format', 'DNA', 'FASTA Header', 'Date format', and 'Example for copied segment'. The 'Format' section has radio buttons for 'Isolates as XLS', 'Sequences (DNA) as FASTA', 'Sequences (proteins) as FASTA', and 'Acknowledgment table'. The 'DNA' section has checkboxes for 'all', 'PB2', 'PB1', 'PA', 'HA', 'NP', 'NA', 'MP', 'NS', 'HE', and 'P3'. The 'FASTA Header' section has a text input field for 'Isolate name' and a dropdown menu for 'Isolate name', 'Isolate ID', 'Type', 'Passage details/history', and 'Lineage'. The 'Date format' section has a dropdown menu for 'MON-DD-YYYY (FEB-28-2009)'. The 'Example for copied segment' section has a text area with a FASTA header and sequence. The 'Example for uploaded segment' section has a text area with a FASTA header and sequence.

For DNA or protein sequence data select either 'sequences as (DNA) FASTA' or sequences (proteins) as FASTA.

Sequences are downloaded in a FASTA file, which can then be used in a number of analysis programs

The screenshot shows the GISAID download interface. Under 'Format', 'Sequences (DNA) as FASTA' is selected. Under 'DNA', 'all' is selected. The 'FASTA Header' section shows 'Isolate name' and 'Segment' as headers. The 'Date format' is set to 'MON-DD-YYYY (FEB-28-2009)'. The 'Example for copied segment' shows a FASTA entry for 'A/Chick/Egypt/ZU/2016'. The 'Example for uploaded segment' shows a similar entry with a different isolate name. Below the interface, a Notepad window titled 'gisaid_epiflu_sequence (10).fasta' displays the downloaded FASTA file content, which includes headers like 'A/Chick/Egypt/ZU/2016' and corresponding DNA sequence blocks.

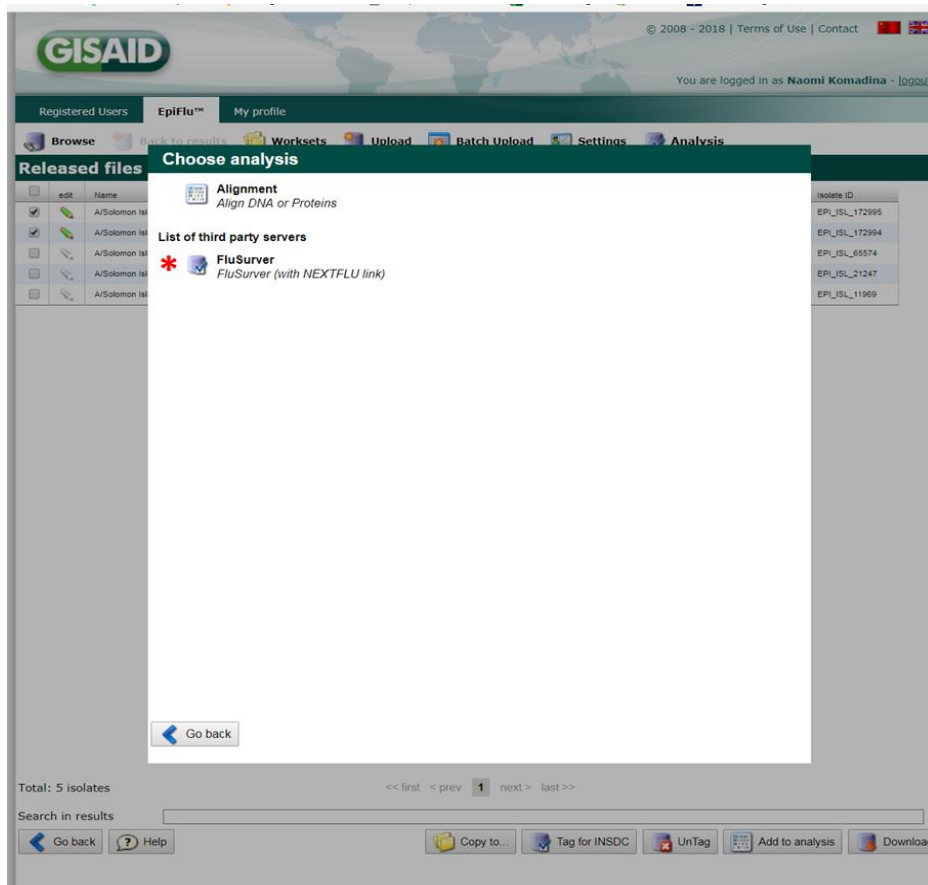
Download Acknowledgement Table for inclusions in Supplementary Material of Publications

We acknowledge the authors, originating and submitting laboratories of the sequences from GISAID's EpiFlu™ Database on which this research is based. The list is detailed below.

All submitters of data may be contacted directly via the GISAID website www.gisaid.org

Segment ID	Segment	Country	Collection date	Isolate name	Originating Lab	Submitting Lab	Authors
EPI1035127	HA	Egypt	2016-Jan-25	A/chicken/Gharbia/5/2016	Other Database Import	Zanaty A.; Saleh M.; El Shehedy M.; El Tarabehy M.; Abdel Fatah S.; Selim A.	
EPI1073965	HA	Egypt	2016-Jan-15	A/chicken/Egypt/Qal-3/2016	Other Database Import	Omar D.M.; Marden N.A.; Gaafar L.M.O.; El-Ebiary E.A.; El-DougDoug K.A.; Othman B.A.; Arafa A.A.; Hussein H.A.	
EPI1300988	HA	Egypt	2016-Sep-01	A/chicken/Egypt/ME10/10/2016	Other Database Import	Kilany W.; Shehata A.; Zain El-Abideen M.; Elsayed M.; Ali A.	
EPI1307766	HA	Egypt	2016-Jan-15	A/chicken/Egypt/CAL 9/2016	Other Database Import	Arafa A.; Elshazly O.; Hussein H.; Reda E.	
EPI1307767	HA	Egypt	2016-Jan-23	A/chicken/Egypt/SS2/2016	Other Database Import	Arafa A.; Elshazly O.; Hussein H.; Reda E.	
EPI1307768	HA	Egypt	2016-Nov-01	A/chicken/Egypt/CAG139/2016	Other Database Import	Arafa A.; Elshazly O.; Hussein H.; Reda E.	
EPI1308276	HA	Egypt	2016-Jan-01	A/chicken/Sharkia/MEVACF3/2016	Other Database Import	Shehata A.A.; Ali A.; Kilany W.H.; Sedik M.; Elbestawy A.; Zain El-Abideen M.A.; Elsayed M.	
EPI891870	HA	Egypt	2016-Feb-15	A/chicken/Egypt/ZU2/2016	Other Database Import	Hussein A.; Orabi A.; Saleh A.A.; Abu El-Magd M.; Iqbal M.	
EPI891871	HA	Egypt	2016-Feb-15	A/chicken/Egypt/ZU3/2016	Other Database Import	Hussein A.; Orabi A.; Saleh A.A.; Abu El-Magd M.; Iqbal M.	
EPI891872	HA	Egypt	2016-Feb-15	A/chicken/Egypt/ZU28/2016	Other Database Import	Hussein A.; Orabi A.; Saleh A.A.; Abu El-Magd M.; Iqbal M.	
EPI953352	HA	Egypt	2016-May-08	A/chicken/Egypt/N12643B/2016	Other Database Import	Rubrum A.; Jeevan T.; Kayali G.; Ali M.A.; Kandell A.; El-Shesheny R.; Webby R.	
EPI953354	HA	Egypt	2016-May-08	A/chicken/Egypt/N12642E/2016	Other Database Import	Rubrum A.; Jeevan T.; Kayali G.; Ali M.A.; Kandell A.; El-Shesheny R.; Webby R.	
EPI953368	HA	Egypt	2016-Jan-23	A/chicken/Egypt/F12505C/2016	Other Database Import	Rubrum A.; Jeevan T.; Kayali G.; Ali M.A.; Kandell A.; El-Shesheny R.; Webby R.	

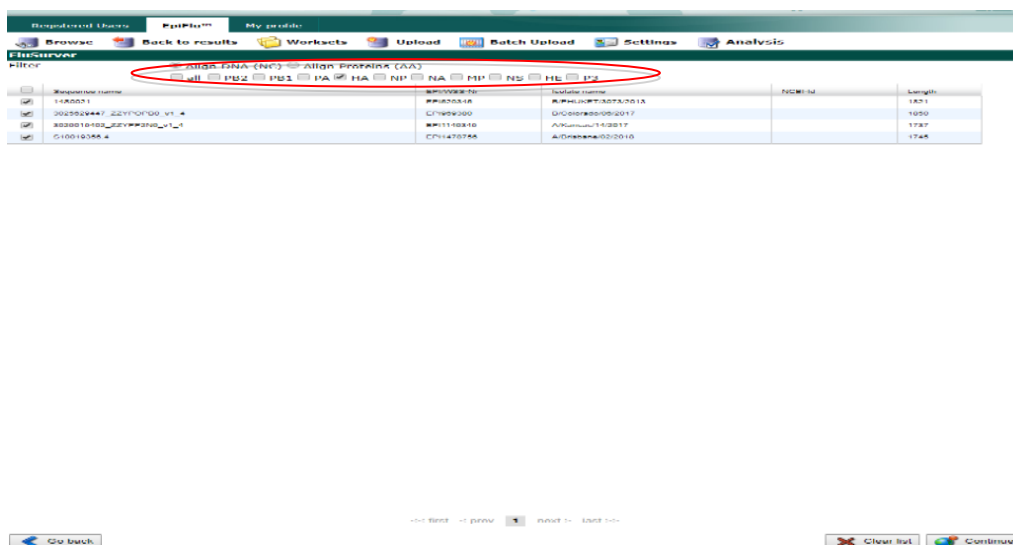
Data can be added to a third party Server for analysis



FluSurver compares your sequences of interest and summarises amino acid changes to a reference strain.

Can be used to for sites which are known to have amino acid changes associated with neuraminidase inhibition activity

To add data for analysis in FluSurver, check the box for the gene of interest



Select continue and the genes of interest are inserted into the FluSurver program

Registered Users EpiFlu™ My profile

Browse Back to results Worksets Upload Batch Upload Settings Analysis

Important usage notes:
 The main application scenario for FluSurver is to highlight phenotypically or epidemiologically interesting candidate mutations for further research and should ideally be combined with experimental testing and verification of any predicted phenotypes. Importantly, any direct diagnostic use, assumed severity or recommendation on patient treatment should not be based solely on these computational predictions. Our curated reference sequences used for annotation transfer of equivalent mutations are mainly comprised of strains that recently infected humans. Therefore, the **usage scenario that will give the most fruitful and reliable results are current surveillance sequences with very close relation to used vaccine strains, including some candidates for avian flu (including the recent H7N9 and avian H5N8/H5N6, for GISAID users only!) and novel reassortant swine flu H3N2v.** Please take a look at the [Frequently Asked Questions](#) and [Tutorial](#) if you are new to FluSurver. You could also look at this [NA example analysis walkthrough](#) and the [GISAID access preview poster](#).


Note for H7N9 analysis: A tutorial with example analysis and interpretation is available [here](#).

Loaded protein sequences of your selected isolates for FluSurver analysis:

```
>HA_B/Colorado/06/2017_257735
MKAIIVLVVVSTSSADRICTGITSNSPHVVKATQGEVNVTVGIPLTTPTKSHFANKGTETRGKLCPKLNCTDLVALGRPKCTGKIP SARVSI LHEVRPVTS
GCFFIHDRTIKIQLPNLIRGVEHRLSTHWNINAEAGAPGGPKYIGTSGSCPNITNGNGFFATAMAVPDKNKATNPLTIEVYVCTEGEDQITVNGFHSNDETQM
AKLYGDSKPKFTSSAINGVTHYVSIQGFPMQTEGGLPQSGRIVDVYVWQKSGKGTITVQRGILLPQVNCASGRSKVIGKSLPIGEADCLHEKYVGLNKSXP
YYTGEHAKAIGNCPWIKPLKLANGTKYRPPAKLLKERGFAGIAGLEGGHEGMIAGHGYTSHGAGHVAADLKSTQEAINKITKLNLSLELVKMLQRLSG
AIDELHNEILELDEKVDLRAADTSSQELAVLLSNEGIINSEDEHLALERLKKMLGPSAVEIGNGCFETKHKCNQTKLCKAAGTFDAGEFSLPTFDSLNIATA
SLNDDGLDNHTILLVYSTAASSLAVTLMIATFVYVWYVSRDWSVCSICL
>HA_A/Kansas/14/2017_292575
MKTIIALSCLLCLVFAQIPGNDINSTATLCLGHAVPMTIVKTIITNDRIEVTNATELVQNSSIGEICDOPHQILDGENCTLIDALLGDPQCDFQNKWDLFVERN
KAYSINCPYDPVYASLRSLVASSGLTEFNWESFNMAQVTVQGTSSSICIRGSKSFFSRLNWLTHLNSKYPALNWHTPMIEQFDKLYIIVGWHHPGTDKQDLSLYAQS
```

Please select the reference strain(s) to compare to:
 Automatic detection of closest reference (larger selection of strains, not always full genomes. NOT SUITED to judge reassortment) *

Analyze with FluSurver



Select Analyse with FluSurver, can also select which reference strain you wish to compare to

Registered Users EpiFlu™ My profile

Browse Back to results Worksets Upload Batch Upload Settings Analysis

The main application scenario for FluSurver is to highlight phenotypically or epidemiologically interesting candidate mutations for further research and should ideally be combined with experimental testing and verification of any predicted phenotypes. Importantly, any direct diagnostic use, assumed severity or recommendation on patient treatment should not be based solely on these computational predictions. Our curated reference sequences used for annotation transfer of equivalent mutations are mainly comprised of strains that recently infected humans. Therefore, the usage scenario that will give the most fruitful and reliable results are current surveillance sequences with very close relation to used vaccine strains, including some candidates for avian flu and novel reassortant swine flu H3N2v. Please take a look at the [Frequently Asked Questions](#) and [Tutorial](#) if you are new to FluSurver. There is also a [special note for using FluSurver results in publications](#).



FluSurver Result for comparison with reference selection: autorefall Back to Reference Selection

Query	Best reference hit	% AA identity	% length coverage	# mutations	List of mutations
HA_A/Brisbane/02/2018_362099 Show in NEXTFLU tree	HA A/Brisbane/02/2018(H1N1) find closest related sequences	100.000	100.000	0	no mutations
HA_A/Kansas/14/2017_292575 Show in NEXTFLU tree	HA A/Kansas/14/2017(H3N2) find closest related sequences	99.647	100.000	2	N206D_T262N show in structure
HA_B/Colorado/06/2017_257735	HA B/Colorado/06/2017 find closest related sequences	99.828	100.000	1	T210N show in structure
HA_B/PHUKET/3073/2013_161843	HA B/Phuket/3073/2013 find closest related sequences	99.829	100.000	1	D211N show in structure

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

Warning: this reference selection includes sequences of strains without complete genomes, e.g. only HA and NA available/included. Therefore, hits of other segments to different reference strains do not represent reassortments. Please see also [this help section](#) regarding reassortments.

Back to Reference Selection

Developed by A*STAR Bioinformatics Institute (BI), Singapore
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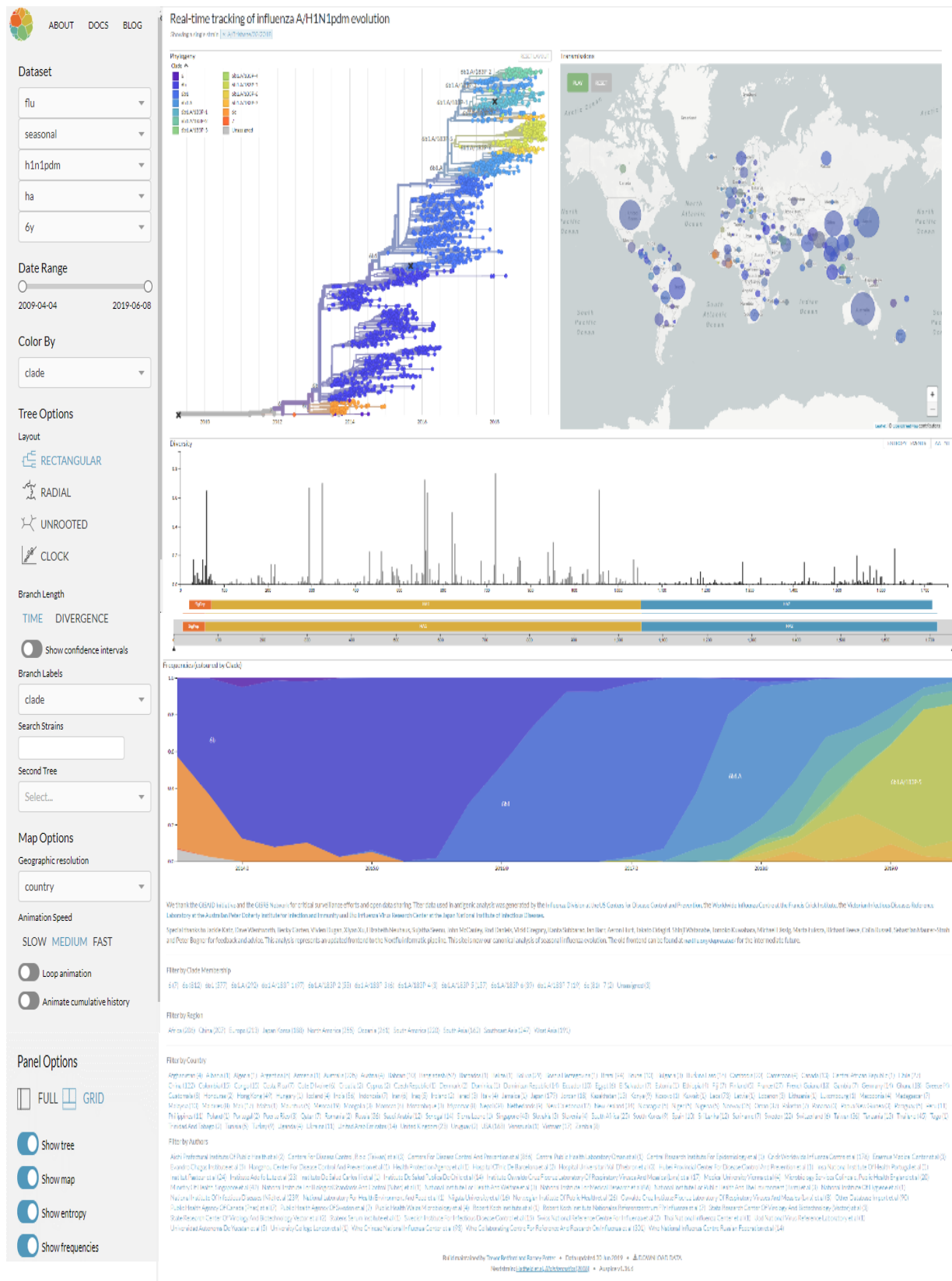
Click on the underlined fields to find information, view the structure in 3D and to see a list of important sites related to drug resistance.

The screenshot displays the EpiFlu™ FluSurfer web interface. At the top, there is a navigation bar with options like 'Registered Users', 'EpiFlu™', and 'My profile'. Below this, there are tabs for 'Browse', 'Back to results', 'Worksets', 'Upload', 'Batch Upload', 'Settings', and 'Analysis'. The main content area shows a search result for 'HA_A/Brisbane/02/2018_362099'. The search table lists the query, best reference hit, % AA identity, % length coverage, # mutations, and list of mutations. A red arrow points to the 'Show in NEXTFLU tree' link. To the left, there is a 3D protein structure of the HA protein. Below the search table, there is a 'Real-time tracking of influenza A/H1N1pdm evolution' plot. A red arrow points to the 'Phylogenetic context of this mutation at NEXTFLU' link in the pop-up window.

Phylogenetic context of mutation in nextflu

Select 'Show in nextflu' to see virus in phylogenetic tree

The screenshot displays the EpiFlu™ FluSurfer web interface. At the top, there is a navigation bar with options like 'Registered Users', 'EpiFlu™', and 'My profile'. Below this, there are tabs for 'Browse', 'Back to results', 'Worksets', 'Upload', 'Batch Upload', 'Settings', and 'Analysis'. The main content area shows a search result for 'HA_A/Brisbane/02/2018_362099'. The search table lists the query, best reference hit, % AA identity, % length coverage, # mutations, and list of mutations. A red arrow points to the 'Show in NEXTFLU tree' link. To the left, there is a 3D protein structure of the HA protein. Below the search table, there is a 'Real-time tracking of influenza A/H1N1pdm evolution' plot. A red arrow points to the 'Phylogenetic context of this mutation at NEXTFLU' link in the pop-up window.



How to Create Work-sets

Work-sets can be shared between both Institute colleagues or between colleagues in other Institutes within the country or internationally.

Useful for storing frequently used datasets and inter-institution collaborative work. Up to 10,000 sequences can be stored in the Workset folder.

On front page click on the Worksets option

The screenshot shows the GISAID EpiFlu™ web interface. The user is logged in as Naomi Komadina. The navigation bar includes 'Browse', 'Back to results', 'Worksets' (highlighted with a red circle), 'Upload', 'Batch Upload', 'Settings', and 'Analysis'. Below the navigation bar, there are statistics for 'Count' (270538 isolates), 'GISAID published' (146,777 isolates (648,409 sequences)), and 'Total isolate count' (270,538 isolates (1,128,041 sequences)). The 'Basic filters' section includes a 'Predefined search' dropdown, a 'Search in' radio button menu (with 'Released files' selected), and a 'Search patterns' input field. Below this are dropdown menus for 'Type', 'Host', and 'Location'. The 'Additional filters' section includes date range filters for 'Collection date' and 'Submission date', a list of 'Originating Laboratory' and 'Submitting Laboratory' options, 'Required Segments' checkboxes (PB2, PB1, PA, HA, NP, NA, MP, NS, HE, P3), and 'Vaccine specific' checkboxes for years from 2007 to 2019.

Select 'Create Workset'

The screenshot shows the 'Workset list' page in the GISAID EpiFlu™ interface. It features a table with columns for 'Workset name', 'Owner', '# Segments', 'Created', and 'Last modified'. The table lists several worksets, including 'nyma3', 'nyma2', 'Transfers -H3', 'Transfers - B', 'Transfers', 'Test V2', 'H3N2v M1', 'H3 Skeleton', and 'Clade Markers'. Below the table, there is a quota notice: 'Quota: 55 of 10000 EpiFlu sequences' and '0 of 300 Uploaded sequences'. Navigation controls include '<< first', '< prev', '1', 'next >', and 'last >>'. At the bottom, there are buttons for 'Go back', 'Help', 'Delete', and 'Create workset'. A red arrow points to the 'Create workset' button.

Workset name	Owner	# Segments	Created	Last modified
nyma3	Pagbajabyn - Nymadava	47	23-03-2011	09-04-2011
nyma2	Pagbajabyn - Nymadava	59	23-03-2011	11-03-2013
Transfers -H3	Naomi Komadina	10	15-09-2011	18-12-2013
Transfers - B	Naomi Komadina	7	15-09-2011	03-12-2018
Transfers	Naomi Komadina	0	08-09-2011	04-12-2015
Test V2	Naomi Komadina	18	17-07-2017	17-07-2017
H3N2v M1	Naomi Komadina	0	15-02-2019	15-02-2019
H3 Skeleton	Naomi Komadina	0	14-04-2011	22-06-2011
Clade Markers	Naomi Komadina	20	24-08-2011	07-04-2017

Registered Users | EpiFlu™ | My profile

Browse | Back to results | Worksets | Upload | Batch Upload | Settings | Analysis

Create new workset

Name*

Description

Owner

Add participant

- A K M Muraduzzaman (Monash University)
- Amy Tran (Monash University)
- Andrew Pattison (Monash University)
- Ayisha Rumana Hameed (Monash University)
- Celeste Michelle Donato (Monash University)
- Charmaine To (Monash University)
- Chen Li (Monash University)
- Clemente I Montero (Quest Diagnostics Incorporated)
- Colleen M Ryan Smith (Montgomery County Maryland Government)
- Don Teng (Monash University)
- ... more than 10 matches found ...

Go back | Help | Remove participants | Create workset

Name the workset and add a description if you wish.

To invite collaborators, begin typing in a name and select the name of your collaborator.

Only registered GISAID users can be selected.

The person who created the workset is the owner and can add or delete collaborators or delete the entire workset.

Collaborators can add sequences to the workset.

Sequences can be uploaded to the workset from your PC

Uploading sequences to GISAID.

Sequences can be uploaded using the Single Upload or the Batch Upload function.

A single upload must be performed before the Batch Upload sheet is used. This creates your “My unreleased files” folder.

When you login to EpiFlu™ to upload data, your details as the submitter are automatically entered.

GISAID users are able to contact isolate submitters by using the ‘Contact Submitter’ function at the bottom of the Isolate information page. Your email is hidden from view and not visible to those who contact you through this button.

Duplicates Isolates i.e. Have the same name, the same collection date and the same passage will not be uploaded.

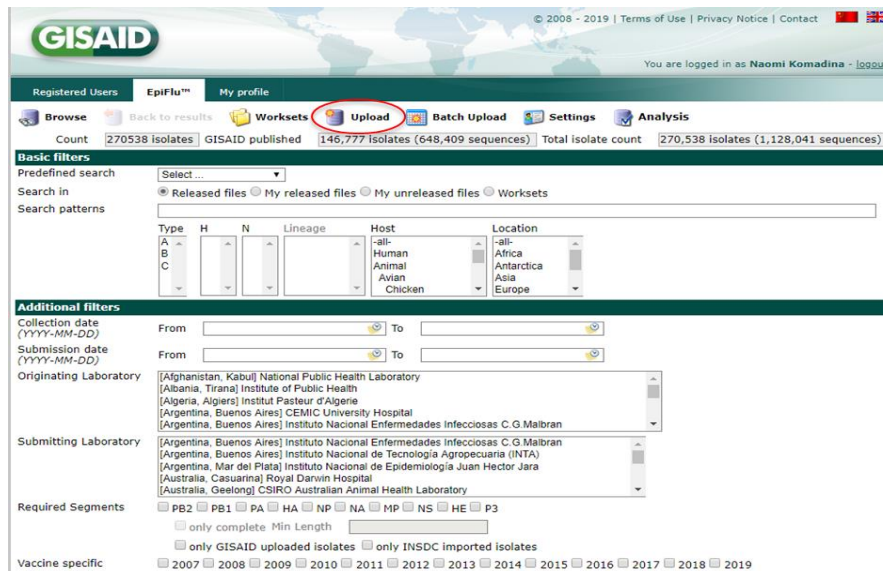
Isolate data is added in only once, sequences are attached to the isolate

Your isolates will be flagged with a green pencil on the LHS of search results.

The green pencil is the 'edit' function allowing you to add further gene sequences & metadata.

Single Uploads

Use this function if you are uploading a very small number of isolates to EpiFlu™



The screenshot shows the GISAID EpiFlu™ web interface. At the top, there is a navigation bar with 'Registered Users', 'EpiFlu™', and 'My profile'. Below this is a secondary navigation bar with buttons for 'Browse', 'Back to results', 'Worksets', 'Upload', 'Batch Upload', 'Settings', and 'Analysis'. The 'Upload' button is circled in red. Below the navigation bar, there is a status bar showing 'Count 270538 isolates', 'GISAID published 146,777 Isolates (648,409 sequences)', and 'Total isolate count 270,538 Isolates (1,128,041 sequences)'. The main content area is divided into 'Basic filters' and 'Additional filters'. The 'Basic filters' section includes a 'Predefined search' dropdown, a 'Search in' dropdown (with 'Released files' selected), and a 'Search patterns' input field. Below these are dropdown menus for 'Type' (A, B, C), 'Host' (Human, Animal, Avian, Chicken), and 'Location' (Africa, Antarctica, Asia, Europe). The 'Additional filters' section includes 'Collection date' and 'Submission date' (both with 'From' and 'To' date pickers), 'Originating Laboratory' and 'Submitting Laboratory' (both with dropdown menus), 'Required Segments' (checkboxes for PB2, PB1, PA, HA, NP, NA, MP, NS, HE, P3), and 'Vaccine specific' (checkboxes for years 2007-2019).

Click on the upload button

The Isolate ID is automatically generated

Begin filling out the form, use the drop down menus where available.

Fill in as much information that you have. Metadata is valuable to researchers.

Fields that have * are mandatory.

When you select a region i.e. Africa a second menu opens up for Country selection

In Institute information, select the region & country then open the 'Originating Lab' filed and a list of laboratories in that country opens, select the correct submitting laboratory.

You will notice that your Institute details as the submitter have been already filled in.

Once you have completed all the Isolate information, select the save button at the bottom RHS.

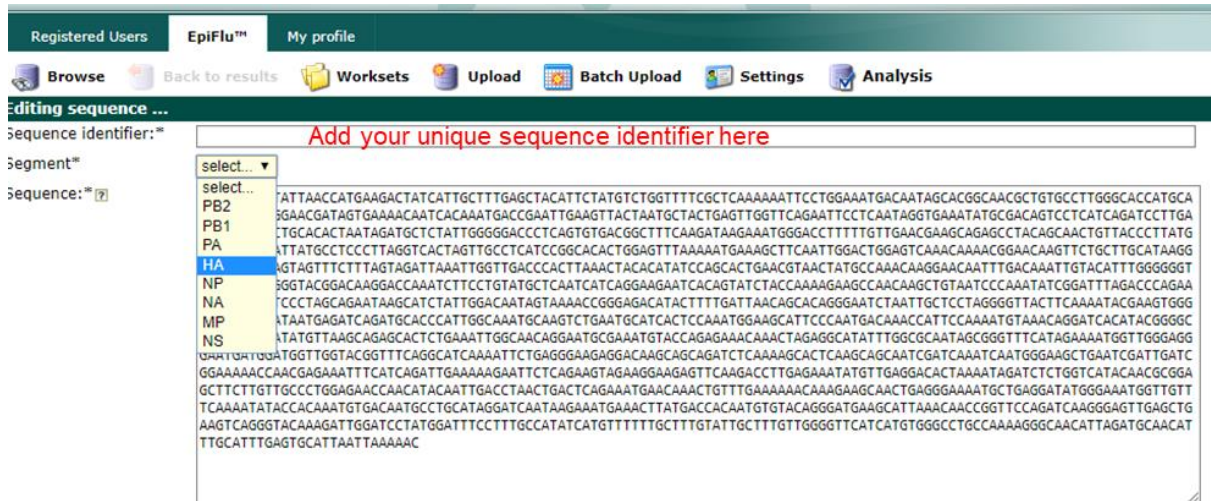
If any mandatory information has been missed it will be flagged and must be filled in before you can move to the next section.

This page creates the 'Isolate information' to which sequences can be added to.

Once the isolate has been saved, this panel appears at the bottom of the “Isolate information”

Select the “Add new segment” button at the bottom of the RHS to add sequences to the isolate.

Add sequence to the following page



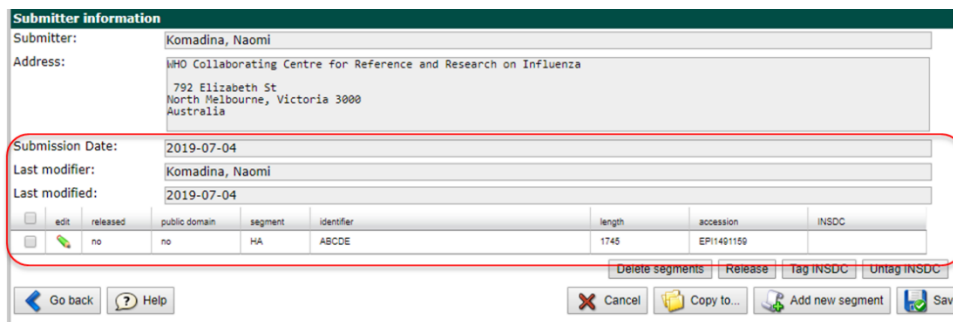
Add your ID in the Sequence identifier field

Select the segment you are adding, then paste in the sequence and select “Save’ at the bottom RHS.

If you have selected HA and pasted in the NA sequence this will be flagged as an error which needs to be fixed.

If there is an error in the sequence which places a stop codon in the wrong place, this is also flagged and can be amended immediately.

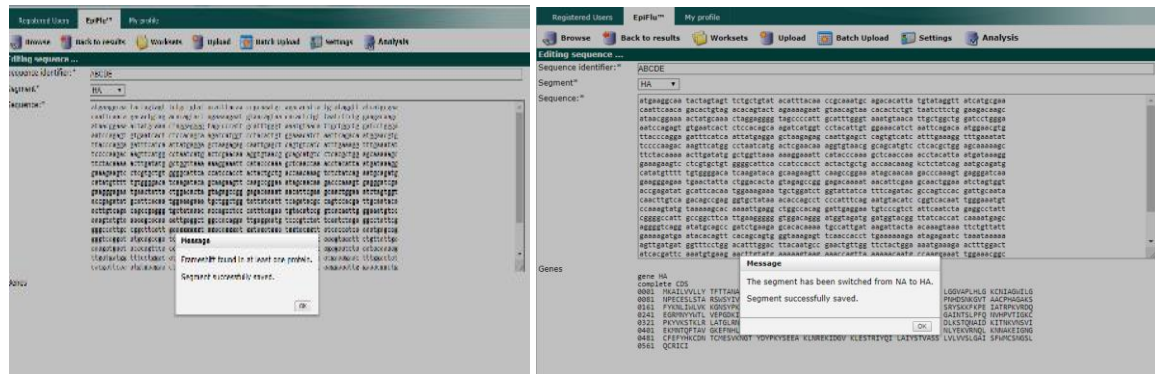
Once saved the Isolate page reopens ready to add a new segment. The bottom of the page now has the segments available added as well as the upload date and the date it was last amended.



A correct sequence appears as below. The Isolate page has correct data, with correct sequence and needs to be released to become publicly accessible to registered users of GISAID.



Examples of flagged errors



Submitter information

Submitter: Komadina, Naomi
 Address: WHO Collaborating Centre for Reference and Research on Influenza
 792 Elizabeth St
 North Melbourne, Victoria 3000
 Australia
 Submission Date: 2019-07-04
 Last modifier: Komadina, Naomi
 Last modified: 2019-07-04

<input type="checkbox"/>	edit	released	public domain	segment	identifier	length	accession	INSDC
<input type="checkbox"/>		no	no	HA	ABCDE <i>Frameshift found in at least one protein.</i>	1743	EPI1491159	

Buttons: Delete segments, Release, Tag INSDC, Untag INSDC, Go back, Help, Cancel, Copy to..., Add new segment, Save

Yellow triangle indicates there is an error

Registered Users | EpiFlu™ | My profile

Browse | Back to results | Worksets | Upload | Batch Upload | Settings | Analysis

My unreleased files

<input type="checkbox"/>	edit	Name	Passage	PB2	PB1	PA	HA	NP	NA	MP	NS	HE	P3	Collection date	Lineage	Subtype	Isol
<input type="checkbox"/>		A/Tsai/1/2019		---	---	---	1743	---	---	---	---	---	---	2019-07-04		H1	EPI

How to release to EpiFlu™ Database

Submitter information

Submitter: Komadina, Naomi
 Address: WHO Collaborating Centre for Reference and Research on Influenza
 792 Elizabeth St
 North Melbourne, Victoria 3000
 Australia
 Submission Date: 2019-07-04
 Last modifier: Komadina, Naomi
 Last modified: 2019-07-04

<input checked="" type="checkbox"/>	edit	released	public domain	segment	identifier	length	accession	INSDC
<input checked="" type="checkbox"/>		no	no	HA	ABCDE	1745	EPI1491159	

Buttons: Delete segments, Release, Tag INSDC, Untag INSDC, Go back, Help, Cancel, Copy to..., Add new segment, Save

Bioinformatics Workshop, Singapore, 26-26 August 2019

Select the tick box on LH, either for each virus or for all, select the Release button on the RHS.

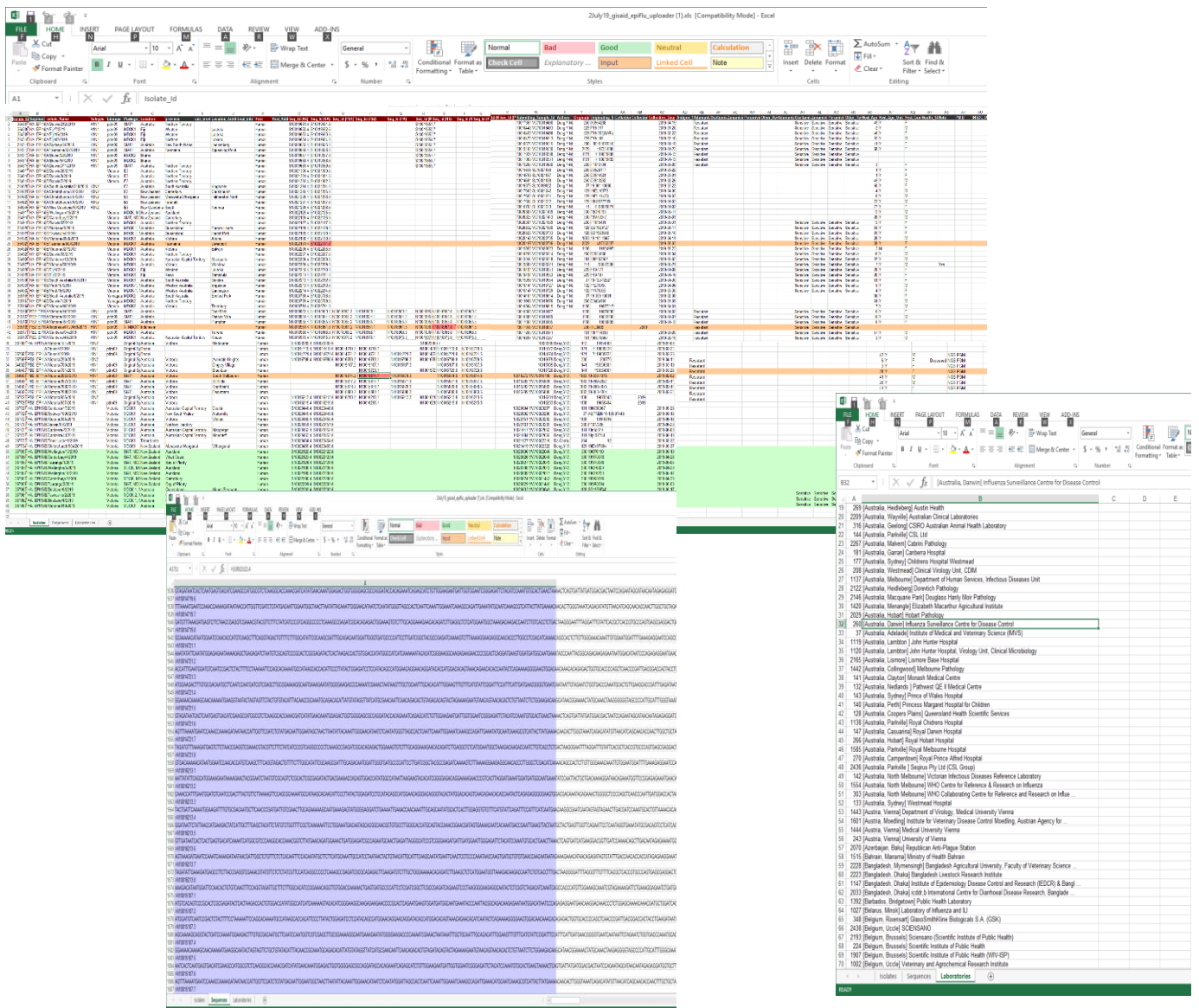
Isolates disappear from 'My unreleased files' and are transferred to both the 'Released files' and 'My released files'

If an isolate has been released and you find that there is a problem with the isolate it can be removed from the Released Files back to My unreleased files by contacting service@gisaid.org and requesting that the isolate be 'unreleased', supply the name & the EPI_ISL number of the isolate in question.

Batch Uploads

To use the Batch Upload Sheet, select Batch upload sheet, accept the T&Cs then download the sheet.

When the sheet opens up



Fill out the information for each isolate per line as per the example above. The first 2 columns will remain blank until they data has been uploaded when the EPI-ISL numbers will have been inserted.

All fields with a red coloured header are mandatory and must be completed

Fields with a grey header are optional, however filling out as many fields as you have information allows for better research opportunities

Hover over the red triangle in each field for pop-up with information of the format and data required, see examples below

The first screenshot shows a table with columns: Isolate Name, Mandatory, Location, Prov. It lists isolates like P114 A/Darwin/21/2019 and P114 A/Fiji/16/2019.

The second screenshot shows a table with columns: Subtype, Mandatory, Location. It lists subtypes like H1N1 and pdm09.

The third screenshot shows a table with columns: Collector, Collection Date, Mandatory. It lists collectors like S and collection dates like 2015-04-15.

Laboratory number for Originating laboratory are available in Alphabetical order by selecting Tab marked “Laboratories”

Adding the Unique Originating Laboratory number to The Field named “Originating_Lab_ID” autofills the information on the Isolate page

To add sequences click on Tab marked “Sequences”

Paste in FASTA file, the page turns purple when the sequences have been pasted in

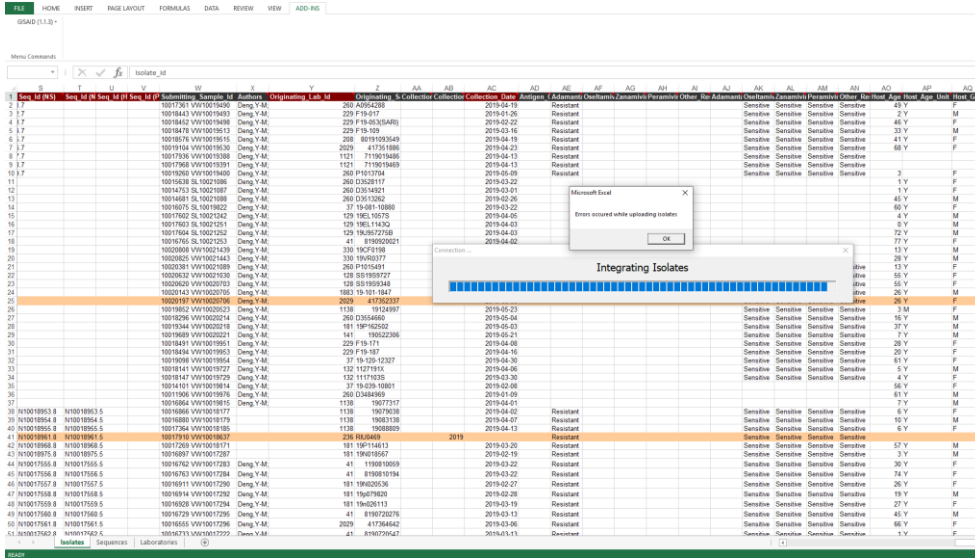
Once completed, select the “Add-Ins” tab at the top of the page, the GISAID menu at the top of the LHS of the page drops down.

Select “Batch upload isolates” in the drop down menu and the GISAID Login feature opens up.

Enter you Login and password details and select the Login button

The screenshot shows an Excel spreadsheet with the 'ADD-INS' tab selected. A dropdown menu is open showing 'Batch upload isolates'. A GISAID login dialog box is overlaid on the spreadsheet, asking for a login and password.

If the isolates have been successfully uploaded, a message indicating that the ere has been a succesful upload, if there has been an error the message below is received.



Isolates which have the error are flagged in orange, the field with the error is flagged in red

					10010141 VV10019729	Deng Y-M
					10014101 VV10019814	Deng Y-M
					10011906 VV10019976	Deng Y-M
					10016864 VV10019815	Deng Y-M
N10018953.3	N1001895:N10018953.8	N10018953.5		10016866 VV10018177		
N10018954.3	N1001895:N10018954.8	N10018954.5		10016880 VV10018179		
N10018955.3	N1001895:N10018955.8	N10018955.5				
N10018961.3	N1001896:N10018961.8	N10018961.5	No update, segment already exists with different sequence: : EPI_ISL_365169 / NS			
N10018968.3	N1001896:N10018968.8	N10018968.5		10017269 VV10018171		
N10018975.3	N1001897:N10018975.8	N10018975.5		10016897 VV10017287		
N10017555.3	N1001755:N10017555.8	N10017555.5		10016762 VV10017283	Deng Y-M	
N10017556.3	N1001756:N10017556.8	N10017556.5		10016763 VV10017284	Deng Y-M	

Click on the red triangle in the cell top RHS and an error message appears. In the example the message relates to the fact that particular segment was not updated, this message can occur if you have uploaded a segment then re-use the same Batch-Upload sheet to add further segments.

If the sequence is missing then that is flagged in the error message.

If you are re-using a Batch Upload sheet to add extra information or sequence to incomplete data sets you will see the message below for isolates that have not been updated.

364932	HA: EPI14 B/Perth/16/2019		Victoria	MDCK-1	Australia	Western Aust
365165	HA: EPI14 B/Australia/8/2019		Yamagata	MDCK2	Australia	South Austral
365163	HA: EPI14 B/Victoria/305/2019		Yamagata	MDCK2	Australia	Northern Terri
365164	HA: EPI14 B/Victoria/950/2019		Victoria	MDCK2	Australia	Victoria
365166	PB2: EPI1 A/Victoria/940/2019	H1N1	pdm09	SIAT1	Australia	
365167	PB2: EPI1 A/Victoria/950/2019	H1N1	pdm09	SIAT1	Australia	
365168	PB2: EPI1 A/Victoria/957/2019	H1N1	pdm09	SIAT1	Australia	

When you login and to batch upload a sheet and receive a message ‘You have no internet connection’ save the Batch Upload sheet, close it, then re-open the sheet, select ‘Enable Content’ in the yellow security warning, select Yes for making the file a ‘Trusted document’, select OK in the GISAID Batch Upload box, then proceed with selecting Add-Ins & uploading to GISAID as above.

Once all the isolates have been uploaded, open you “Unreleased files”, check that all is OK, then release the data to the EpiFlu™ database as for a single upload.

Settings

Select the Settings button to change your settings for viewing search returns and passwords

Settings can be changed any time, saved then return to what you were working on

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Personal settings User permissions

Modify your personal settings

Result columns	Available columns	Displayed columns
	Isolate ID Location Host Submission date Submitting Lab Submitter Name Originating Lab	Subtype Passage Segments Collection date Lineage

? Help

Change password Save

nextflu

<https://gisaid.org/nextflu>

