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 (BII) Global Initiative on Sharing All Influenza Data (GISAID)



Database Technical Group









National Centre for Infectious Diseases







hosted by the Federal Republic of Germany



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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

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)



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

<u>GISAID</u>

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.

GISAID	About us	EpiFlu™ Features	Updates	Collaborations	References		He				
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		Please complete the registration form and help GISAID protect the use of your identity and the user base. You are strongly advised to provide your institutional email address to avoid delays your access credentials. Using webmail addresses for detinification, such as Gmail, Hotmail, Ya QCmail or 126 and 153 Mail, can cause significant delays in receiving your access credentials.									
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Part of the registration page

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Registration FAQ About	GISAID				
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taken). In particular cas	es it may take several days.			City*	
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Title				WHEREAS Freunde von GISAID e.V. ("GISAID") maintains a globa	al database for influenza gene
Desired Legis 105				sequences along with associated data, including virological, clinical, information (if available) for all influenza viruses, including but not i	epidemiological and demographic limited to H5N1 sequences, (the
Contact Information				"GISAID EpiFlu" Database") for the purpose of facilitating the sh such sequences and associated data.	haring, research and investigation of
Use your company or re	search institute's email! Web	emails such as Gmail or Yahoo		NOW, therefore, this Database Access Agreement (the "Agreeme	ent") is entered into by and between
will lead to significant de	elays in processing.			the undersigned ("You") and GISAID.	
Institution*				 Access to the GISAID EpiFlu^m Database, Data. Access to Database and Data, as defined barrin, is commond by this Ac 	o, and use of, the GISAID EpiFlu TH
Department				using the GISAID EpiFlu [™] Database, whether as a provider of	or user of Data, You accept and
Street 1*	L			"Data" means any and all (i) sequence data and other associ	iated data and information contained
Postal code				in the GISAID tpirlu th Database pertaining to influenza virus updates, modifications, improvements, derivatives or other e	ies, (ii) any annotations, corrections, enhancements to any such data
City*				contained in the GISAID EpiFlu ¹¹⁴ Database, and (iii) any safe data or to regulatory approval of vaccines or other therapies	ety information relevant to use of the that embody or utilize the data
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Follow the instructions, and complete the form with accurate information.

Please make sure that you use an institutional email address and <u>not</u> 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 conditons 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 generats. 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 insitutions 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

2008-2018								
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A research study by the University record in the field of influenza, GIS	of Sussex finds that b SAID is contributing to	y developing a successfi global health in at least fi	ve ways: UNIVI	RSITY				
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Searching for isolates in GISAID

EpiFlu[™] Start Page

	© 2008 - 2017 The GISAID Initiative Terms of Use Contact System Requirements
GISAID	
	You are logged in as Naomi Komadina - Jogout
Welcome News	Registered Users EpiFlu ^{IM} FAQ My profile About GISAID
🌏 Browse 👘 Bac	ck to results 🙀 Worksets 🔮 Upload 🛛 📷 Batch Upload 🛛 🛐 Settings 🔜 🚮 Analysis
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Submitting Laboratory	[Argentina, Buenos Airee] Malbran, Instituto Nacional de Enfermedades Infecciosas ANLIS C [Australa, Casurana] Royal Darwin Hospitan Animal Health Laboratory [Australa, Geetong] CSIRO Australian Animal Health Laboratory [Australa, Venna] Medical University Vienna.
Required Segments	
	full genome only complete Min Length
	only GISAID uploaded isolates only INSDC imported isolates
Vaccine specific	. 2007 . 2008 . 2009 . 2010 . 2011 . 2012 . 2013 . 2014 . 2015 . 2016 . 2017
New features	🕐 Help

Select which database you want to search

- Released Files
 - o 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 sequences your search has located

Searching using 'Search patterns' field

Welcome	News	Registered	Users	EpiFlu™	FAQ	My profile	About GISAID		
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Search pattern	is 🔸								

Free text can be used here and different types and subtypes can be seached 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 separted by a space.

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

Registered Users	EpiFlu [™] My profile	
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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.

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Searching by subtype ie:-H5N1 viruses

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Count 80	502 isolates	GISAID published	144,591 isolates (531,345 sequenc	es) Total isolate count	268,352 isolates (1,110,977 sequences)
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A total of 8602 isolates have been located

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

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Search can be even further refined by selecting a location

Registered Users	EpiFlu™ My profile		
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Count	778 isolates GISAID publishe	144,591 isolates (631,345 sequen	nces) Total isolate count 268,352 isolates (1,110,977 sequences)
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778 isolates sourced from chicken in Egypt have been located and this can be further refined by selecting a time period

Count	31 isolates	GISAID published	144,591 isolates (631,3	45 sequences) To	otal isolate count	268,352 isolates (1,11	0,977 sequences)
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Additional filters							
Collection date (YYYY-MM-DD)	From	2016-01-01	🤗 To 2016-	12-31	1		

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 which gene 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

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Descriptions Alian Segment 10 ■ 0147730 ■ 07146374 ■ 0714647031 ■ 071464269 ■ 071464269 ■ 071190023 ■ 071290218 ■ 071290023 ■ 071290023 ■ 071290025 ■ 07129025 ■ 07129	Name A/Horosylvania/254(2018 (A/H302) segment 4 (H4) A/Horosylvania/252(2018 (A/H302) segment 4 (H4) A/Baltimeex/P6222(2018 (A/H302) segment 4 (H4) A/Advantas/L4/2017 (H4)H302 (H4)	Score 3208.8 3208.8 3208.8 3208.8 3208.8 3208.8 3208.8 3208.8 3208.8 3208.8	E-Valu Compared and a compa		Andryka 4 proj. Same J2777 Same A78771
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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

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EPI_ISL_280			EPI1073965	1						Alchicken	gA/H5N1			Africa / Egypt	Chicken	Initial import	Other Database Impo	et	Omar, D.M., Marden, N.A., Gaafar, L.M.O., El-Ebrary, E.A., El-Dougdoug, K.A., Othman, B.A., Avafa, A.A., Hussein, H.A.
EPI ISL 327			EP11300988							A/chicken/E	gA/H5N1			Adrica / Egypt	Chickan	Initial import	Other Database Impo	et	Kilany W., Shehata A., Zain El-Abideen M.; Elsayed M.; Ak A. Ande A., Elsharb, O., Hussein M., Parle E.
EPI ISL 3294			EP11307767							Alchicken	a A / H5N1			Adrica / Egypt	Chicken	Initial import	Other Database Impo	et	Azafa A , Elshaziy O , Hassein H , Reda E
EPI_ISL_329			EP11307768	1						A/chicken/E	gA/H5N1			Adrica / Egypt	Chicken	Initial import	Other Database Impo	et	Arafa A.; Elshaziy O.; Hussein H.; Reda E.
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EPI_ISI_243			EP1891872	1						Alchicken	A/HSN1			Adrica / Egypt	Gallus gal	us Initial import	Other Database Impo	et	Hussein, A., Orabi, A., Safeh, A.A., Abu El-Magd, M., Iqbal, M.
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Download Acknowledgement Table for inclusions in Supplementary Material of Publications

We acknowled	ge the author:	s, originating a	and submitting labo	ratories of the sequences from GISAID	<i>'s EpiFlu</i> ™ Database	e on which this research is t	based. The list is detailed below.
All submitters	of data may b	e contacted o	lirectly via the GISA	ID 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 Tarabeley,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/ME1010/2016		Other Database Import	Kilany,W.; Shehata,A.; Zain El-Abideen,M.; Elsayed,M.; Ali,A.
EPI1307766	HA	Egypt	2016-Jan-15	A/chicken/Egypt/CAL9/2016		Other Database Import	Arafa,A.; Elshazly,O.; Hussein,H.; Reda,E.
EPI1307767	HA	Egypt	2016-Jan-23	A/chicken/Egypt/S52/2016		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.; Kandeil,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.; Kandeil, 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.; Kandeil,A.; El-Shesheny,R.; Webby,R.

Data can be added to a third party Server for analysis

GISAID	594	2008 - 2018 Terms of Use Contact
Registered Users EpiFlu TM My profile		and the second se
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A/Solomon Isi List of third party servers		EPI_ISL_172994
A/Solomon tal		EPI_ISL_65574
A/Solomon Isl FluSurver (with NE	EXTFLU link)	EPI_ISL_21247
A/Solomon Isl		EPI_ISL_11969
Go back		
Tel Color		
Total: 5 isolates	<- tirst < prev 1 next > tast >>	
Search in results		
Go back 🕐 Help	Copy to Register Tag for INSDC	Download

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

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~	3030010-10	a azver	*3N0_01_4			#P111-103-10	A/Kaman/14/2017			1787
e	610019388					EP11470758	A/Drisbane/02/2010			1745
¢	Go back					ter first -c prov 1	nost > last >		×	Clear list

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



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

Browse 🏾 📲 Back to results 🛛 🎁 Wo	orksets 🎱 Upload 🔯 Bi	atch Upload 🛛 🔊	Settings 🛛 🛃 Ana	alysis	
The main application scenario for FluSurver is to highlight verification of any predicted phenotypes. Importantly, any curated reference sequences used for annotation transfe fruitful and reliable results are current surveillance. H3N2v. Please take a look at the <u>Freque</u>	phenotypically or epidemiologically interest y direct diagnostic use, assumed severity or er of equivalent mutations are mainly comp s sequences with very close relation to ntly Asked Questions and <u>Tutorial</u> if you ar	ting candidate mutations fi recommendation on patie rised of strains that recent o used vaccine strains, i re new to FluSurver. There	or further research and shou int treatment should not be ily infected humans. Therefor including some candidate is also a <u>special note for us</u>	uld ideally be combined v based solely on these co ore, the usage scenari es for avian flu and no sing FluSurver results in	with experimental testing a mputational predictions. O that will give the most vel reassortant swine fl <u>ublications</u> .
EluSurver	Result for comparison with	reference selection: au	torefall Back to Re	ference 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	<u>100.000</u>	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	<u>100.000</u>	2	N206D, T262N show in structure
HA_B/Colorado/06/2017_257735	HA B/Colorado/06/2017 find closest related sequences	99.828	<u>100.000</u>	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/do Right-click here to save/do	ownload detailed mutation report table ownload guery summary report table	e for archiving or import for archiving or import to	to Excel (Tab-separated, Excel (Comma-separate	one mutation per line) ed. one query per line)	
Warning: this reference selection includes	s sequences of strains without co	mplete genomes, e.	g. only HA and NA ava	ailable/included. Th	erefore, hits of othe



Developed by A*STAR Bioinformatics Institute (<u>BII</u>), Singapore Copyright © 2019 BII. All Rights Reserved. FluSurver -

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.



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





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

GISAID	You are logged in as Naomi Komadina - logout
Registered Users	EpiFlu ^M My profile
Browse Bac Count 270538	k to result Worksets Upload Batch Upload S Settings Analysis
Basic filters	
Predefined search	Select Y
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Additional filters	
Collection date (YYYY-MM-DD)	From 🧭 To
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Submitting Laboratory	[Argentina, Buenos Aires] Instituto Nacional Enfermedades Infecciosas C.G.Malbran (Argentina, Buenos Aires] Instituto Nacional de Tecnología Agropecuaria (INTA) [Argentina, Mar del Piata] Instituto Nacional de Epidemiología Juan Hector Jara [Australia, Casuarina] Royal Darwin Hospital [Australia, Geelong] CSIRO Australian Animal Health Laboratory 🗸
Required Segments	PB2 PB1 PA HA NP NA MP NS HE P3
	only complete Min Length
	only GISAID uploaded isolates in only INSDC imported isolates
Vaccine specific	2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019

Select 'Create Workset"

or	kset list				í .
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Τ	💋 nyma3	Pagbajabyn - Nymadawa	47	23-03-2011	08-04-2011
	💋 nyma2	Pagbajabyn - Nymadawa	59	23-03-2011	11-03-2013
	📁 Transfers -H3	Naomi Komadina	10	15-09-2011	16-12-2013
	📁 Transfers - B	Naomi Komadina	7	15-09-2011	03-12-2018
	💋 Transfers	Naomi Komadina	0	08-09-2011	04-12-2015
	C 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	22-08-2011
	📢 Clade Markers	Naomi Komadina	20	24-08-2011	07-04-2017
f 3	a: 55 of 10000 EpiFlu sequences 000 Uploaded sequences Go back	<< first < prev 1 next> last>	~	Dek	ete Create w

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Remove participants Create workse

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™

GISAID	© 2008 - 2019 Terms of Use Privacy Notice Contact 📰 🚟
Registered Users	EpiFlu ^m My profile
Browse Bac	k to results 👘 Worksets 📲 Upload 📷 Batch Upload 👔 Settings 📑 Analysis
Basic filters	
Predefined search	Select Y
Search in	Released files My released files My unreleased files Worksets
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Collection date (YYYY-MM-DD)	From 🧭 To
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Originating Laboratory	(Adphanistan, Kabuji) National Public Health Laboratory (Albania, Tirana) Institute of Public Health (Algeria, Algeria) Institut Pasteur d'Algerie (Argertina, Buenos Aires) CEMIC University Hospital (Argertina, Buenos Aires) CEMIC University Hospital (Argertina, Buenos Aires) CEMIC No. Paste
Submitting Laboratory	[Argentina, Buenos Aires] Instituto Nacional Enfermedades Infecciosas C.G.Maibran [Argentina, Buenos Aires] Instituto Nacional de Tecnología Agropecuaria (INTA) (Argentina, Mar del Flata) Instituto Nacional de Tecnología Metoro Jara [Australia, Casuarina] Royal Darwin Hospital (Australia, Caelong) CSIRO Australian Animal Health Laboratory
Required Segments	PB2 PB1 PA HA NP NA MP NS HE P3
	only complete Min Length
	only GISAID uploaded isolates only INSDC imported isolates
Vaccine specific	2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 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.

Registered Users	FalFlu ^{tte} My nofile
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	Europe North America *
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sample provider	
Submitting lab*	
generator of sequence data	[Australia, North Melbourne] WHO Collaborating Centre for Reference and Research on Influe
Address	UHO Collaborating Centre for Reference and Research on Influenza
	702 511-26445 54
	North Hisbourne, Victoria 3000
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Sample ID given by the	
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In vivo antiviral resist	ance
Phenotype Genotype	Unspecified
Antiviral resistance to	sted by experimental procedures
Adamantanes	Resistant Sensitive Unknown Inconclusive
Oseltamivir	Resistant Sensitive Unknown Inconclusive
Peramivir	Resistant Sensitive Unknown Inconclusive
Zanamivir	Resistant Sensitive Unknown Inconclusive
Other	Resistant Sensitive Unknown Inconclusive
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C OD DACK D Help	

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.

Submitter informatio	n						,			
Submitter:	Komadina,	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	4								
Last modifier:	Komadina,	Naomi								
Last modified:	2019-07-04	4								
edit released	public domain	segment	identifier		length	accession	INSDC	41		
No data found.					Delete segm	ents Release	Tag INSDC Untag II	NSDC		
< Go back 🕐 H	lelp			>	🕻 Cancel 🥡	Copy to	Add new segment	剥 Save		

Add sequence to the following page

Registered Users	EpiFlu [™] My profile
Browse 📒 B	ack to results 🔞 Worksets 🎒 Upload 🛛 🗱 Batch Upload 🛛 🛐 Settings 🛛 🛃 Analysis
Editing sequence	
Sequence identifier:*	Add your unique sequence identifier here
Segment * Sequence: * ₪	select v select PB2 School School Select PB2 School School School School PB1 TitGacActatataGataActataCacAataGacCGAatTGAAGTTACTAATGCTACGATTCTAAGTGTACGGACTTTTGGTCAGAATTGCCAATAGGGACCGCCACAGGCAGTCCTCATCAGATCCTTGA PA1 StataGTGAAAACAATCACAAAATGACCAAATGGACGACCCCAGTGTGACGGCTTTCAAGATAGGAAGCGGACCTTCCAATGGGGACCATGTTTTGTGACGGGCCTTCCAATGGACGAAGGGACCAACGGGACCATGTACCCTTATTG PA1 StatGTCCCCTTAGTGGCACATGGTTGACGGCCTTCAAGTGGACGACTCAATTGCAGGGACCATCCAATGGACAAAGGGAACAAGTGGACAAGGGACAAAGTGGACAAGTGGACAAGTGGAAGAGCCCAACAAGGGAACAATTGACAAGTGGACAAGGGAAGAGCCCAACAAGGGAACAATTGACAAGTGGACAAGGGAATGACCATGGACAAGGGAACAACTTGACCAAGGGAACAATTGACAATGGAAGGACCAAGGGAATAGCTCAAAAGGAACCAAGGGAAGAGCCAAGGGAATTGACAAAGTGGAAGGACAAGCCGGGGACAAGCCAGGGACAAGGCACAGGGAATGACCAATGCAAAGGAAGCCAATGCAAGGAAGAAGCCAATGCAAAGGAAGACCAATTCCAAAATGTAAACAGGAGGCAAGGACAAGCCAAGGAAGAACCAATCCAAGGAAAACCAATGGAAGAGCCAAGGAAGAAGCAATTCAAAAGAAGACTAAGGAAGAAGCAAGC

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.

Submitter inform	ation									
Submitter:	Komadina,	Komadina, Naomi								
Address:	WHO Collab 792 Eliza North Melb Australia	WHO Collaborating Centre for Reference and Research on Influenza 792 Elizabeth St North Melbourne, Victoria 3000 Australia								
Submission Date:	Submission Date: 2019-07-04									
Last modifier:	Komadina,	Komadina, Naomi								
Last modified:	2019-07-0	4								
edit release	public domain	segment	identifier		length	accession	INSDC			
🔲 💊 no	no no HA ABCDE 1745 EPI1401159									
Delete segments Release Tag INSDC Untag INSDC										
🔇 Go back 🕐 Help 🕺 😵 Cancel 👘 Copy to										

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



Examples of flagged errors

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Submitter:		Komadina,	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	r:	Komadina,	Naomi								
Last modified	d:	2019-07-04	1								
edit	released	public domain	segment	identifier		length	accession	INSDC			
	no	no	HA	ABCDE Frameshift found in at least one protein.		1743	EPI1491159				
Delete segments Release Tag INSDC Untag INSDC											

Yellow triangle indicates there is an error

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My	My unreleased files																
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		A/Test/1/2019 🔔					1743							2019-07-04		H1	EPĮ

How to release to EPiFlu[™] Database

Submitter informatio	n											
Submitter:	Komadina,	Komadina, Naomi										
Address:	WHO Collab 792 Eliza North Melb Australia	WHO Collaborating Centre for Reference and Research on Influenza 792 Elizabeth St North Melbourne, Victoria 3000 Australia										
Submission Date:	2019-07-04	2019-07-04										
Last modifier:	Komadina,	Komadina, Naomi										
Last modified:	2019-07-04											
edit released	public domain	segment	identifier		length	accession	INSDC					
🖌 💊 no	no HA ABCDE 1745 EPI1491150											
Go back 💽 H	elp			>	Delete segn	nents Release	Tag INSDC Untag INSDC					

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 <u>service@gisaid.org</u> 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



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



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.

iSAID (1.1.3) +																
u Commands																
*	$X \sim f_r$	Isolate Id														
e		V W	X I	V 2 A	AB	AC	AD AE	AE A	G AN	AI	AL AK	AL	444	AN	40 4	0
ieg Id (NSI	Seg Id (N Seg Id ()	Seg Id (P Submitting Sample Id	Authors Originatin	g Lab Id Originating S Colle	tior Collection	Collection Date An	tigen (Adamar	t Oseltamiy Zana	mivii Peramiy	ir Other Re	Adamanti Oseltam	h Zanamiv	Peramiy	Other Re	fost Ape Host Ap	se Unit Host
7		10017361 VW10019490	Deng Y-M:	260 A0954288		2019-04-19	Resistan				Sensitive	Sensitive	Sensitive	Sensitive	49 Y	F
7		10018443 VW10019493	Deng, Y-M;	229 F19-017		2019-01-26	Resistan				Sensitive	Sensitive	Sensitive	Sensitive	2 Y	M
		10018452 VW10019498	Deng, Y-M;	229 F19-053(SARI)		2019-02-22	Resistan				Sensitive	Sensitive	Sensitive	Sensitive	46 Y	F
		10018478 VW10019513	Deng, Y-M;	229 F19-109		2019-03-16	Resistan				Sensitive	Sensitive	Sensitive	Sensitive	33 Y	M
		10018576 VW10019515	Deng, Y-M;	208 80191093549		2019-04-19	Resistan				Sensitive	Sensitive	Sensitive	Sensitive	41 Y	
		10019104 VW10019530	Deng, Y-M;	2029 41/361886		2019-04-23	Resistan				Sensitive	Sensitive	Sensitive	Senstre	68 Y	P
		10017936 VW10019366 10017968 MW10019366	Deng, T-M; Deng, Y-M;	1121 /119019400		2019-04-13	Resistan				Sensitive	Canaitian	Canaiting	Sensitive		
		1001/306 97/10013331	Deng Y-M	250 P1013704		2019-04-13	Resistan				Sensitive	Sensitive	Gensitive	Sensitive	1	
		10015538 SI 10021085	Dens Y.M	250 03528117		2019.03.22					Centre	Contraction of	CHILBUIG	04-3074	1 Y	F
		10014753 St 10021087	Dena Y-M	250 03514921		2019.03.01		and Frend		~					1 Y	F
		10014681 SL 10021088	Deng Y-M	260 D3513262		2019-02-26		CROSERY EXCEL		^					45 Y	M
		10016075 SL10019822	Deng, Y-M;	37 19-081-10880		2019-03-22									60 Y	F
		10017602 SL10021242	Deng, Y-M;	129 19EL1057S		2019-04-05		mors occured while	uploading isolate	5					4 Y	M
		10017603 SL10021251	Deng, Y-M;	129 19EL1143Q		2019-04-03									0 Y	7.4
		10017604 SL10021252	Deng, Y-M;	129 19U957275B		2019-04-03			01						72 Y	M
		10016765 SL10021253	Deng, Y-M;	41 8190920021	_	2019-04-02	_		UK.					-	nγ	F
		10020808 VW10021439	Deng, Y-M;	330 19CF0198	Connection		_							×	13 Y	M
		10020825 VW10021443	Deng, Y-M;	330 19VR0377											28 Y	M
		10020381 VW10021089	Deng, Y-M;	260 P1015491	_			Integra	iting Isola	tes				strve	13 Y	F
		10020632 VW10021030	Deng, Y-M;	128 551959727				-	-					itive	55 Y	E
		10020620 VW10020703	Deng, Y-M	128 551959348	_									the	55 Y	
		10020143 10110020105	Deng V.M.	2020 447262227										all ve	20 T	E
		10010852 \00/10020523	Deng Y-M	1138 10124997		2019.06.23					Sanaking	Sanzitian	Gampiting	Canadian	3.M	
		10018295 VW10020214	Dana Y-M	250 03554550		2019-05-04					Sansting	Sansitive	Sansitiva	Sensitive	15 Y	M
		10019344 VW10020218	Dens Y.M	181 199152502		2019.05.03					Sensitive	Sensitive	Sensitive	Sensitive	37 Y	M
		10019689 VW10020221	Deng Y-M;	141 190522306		2019-05-21					Sensitive	Sensitive	Sensitive	Sensitive	7 Y	2.4
		10018491 VW10019951	Deng Y-M;	229 F19-171		2019-04-08					Sensitive	Sensitive	Sensitive	Sensitive	28 Y	F
		10018494 VW10019953	Deng, Y-M;	229 F19-187		2019-04-16					Sensitive	Sensitive	Sensitive	Sensitive	20 Y	F
		10019098 VW10019954	Deng, Y-M;	37 19-120-12327		2019-04-30					Sensitive	Sensitive	Sensitive	Sensitive	61 Y	F
		10018141 VW10019727	Deng, Y-M;	132 1127191X		2019-04-06					Sensitive	Sensitive	Sensitive	Sensitive	5 Y	M
		10018147 VW10019729	Deng, Y-M;	132 11171038		2019-03-30					Sensitive	Sensitive	Sensitive	Sensitive	4 Y	F
		10014101 VW10019814	Deng Y-M	37 19-039-10801		2019-02-08									56 Y	
		10011906 VW10019976	Deng, Y-M;	260 D3484969		2019-01-09									61 Y	M
		10016864 VW10019815	Deng, Y-M;	1138 1907/317		2019-04-01									14	M
0018953.8	N10018953.5	10016866 VW10018177		1138 19079038		2019-04-02	Resistan				Sensitive	Sensitive	Sensitive	Senstre	6 Y	-
0018354.0	N10018354.5	10016660 VVV100161/9		1136 19963136		2019-04-07	Poesistan				Sensitive	Sensitive	Sensitive	Sensitive	10 1	M
10018955.8	N10018961.5	10017364 97710018185		216 DL 10469	2019	2015-04-13	Resistan				Sensitive	Sansitian	Sensitive	Sensitive	0.1	
10018968.8	N10018968.5	10017269 V/V10018171		181 192114613	2010	2019-03-20	Resistan				Sensitive	Sensitive	Sensitive	Sensitive	57 Y	м
10018975.8	N10018975.5	10016897 VW10017287		181 190018567		2019-02-19	Resistan				Sensitive	Sensitive	Securities	Sensitive	3 Y	M
0017555.8	N10017555.5	10016762 \0\10017283	Deep Y-M	41 1190810059		2019.03.22	Resistan				Sensitive	Sansitive	Rensition	Sensitive	30 Y	F
0017222 0	110017555 5	10016763 10017283	Dana V M	41 0100010000		2010 02 22	Decistor				Canadian	Canadian	Canadian	Concilion	TAY	-
0047077.0	10017000.0	10010763 07010017204	Deny, Fred,	6130610134		2019-03-22	Resistan				Sensitive	OPINISTING	Omistive	Omethie	C T	-
8.\devr.wi	N1001/00/.5	10016911 VW1001/290	Ueng, t-M	101 191020536		2019-02-27	Resistan				Sensitive	Sensitive	Sensitive	Sensitive	20 Y	P
0017558.8	N10017558.5	10016914 VW10017292	Deng, Y-M	181 19p079820		2019-02-28	Resistan				Sensitive	Sensitive	Sensitive	Sensitive	19 Y	M
0017559.8	N10017559.5	10016928 VW10017294	Deng, Y-M;	181 19n026113		2019-03-19	Resistan				Sensitive	Sensitive	Sensitive	Sensitive	27 Y	F
10017560.8	N10017560.5	10016729 VW10017295	Deng, Y-M;	41 8190720276		2019-03-13	Resistan				Sensitive	Sensitive	Sensitive	Sensitive	45 Y	M
	21400477774 F	400407777 144440447007	Change of the	0000 007300000			-				-		-	-		E
10017561.8	N10017561.5	10010555 97910017296	Deng, T-M,	2029 417304042		2019-03-06	Resistan				Sensitive	Sensitive	Sensitive	Sensitive	66 Y	-

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

			10010147 V VV 10013723 Delig, T-IVI,
			10014101 VW10019814 Deng, Y-M;
			10011906 VW10019976 Deng, Y-M;
			10016864 VW10019815 Deng, Y-M;
N10018953.3	N10018951N10018953.8	N10018953.5	10016866 VW10018177
N10018954.3	N10018954N10018954.8	N10018954.5	10016880 VW10018179
N10018955.3	N1001895(N10018955.8	Mine update segme	at already exists with different sequence: • ERI ISL 265160 / NS
N10018961.3	N1001896 ⁻ N10018961.8	Nito update, segine	10017310 VW10010037
N10018968.3	N1001896(N10018968.8	N10018968.5	10017269 VW10018171
N10018975.3	N1001897(N10018975.8	N10018975.5	10016897 VW10017287
N10017555.3	N1001755{N10017555.8	N10017555.5	10016762 VW10017283 Deng, Y-M;
N140047555 2	NI4004755(NI40047555 0	N140047556 5	10010702 \00017094 Deee \000

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/South Australia/8/2019		Yamagata	MDCK2	Australia	South Austral
365163 HAND Update for isolate 365164		Yamagata	MDCK2	Australia	Northern Terri
365164 HA. LFT14 D/ Victoria/305/2013		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



🕐 Help

🙎 Change password 🛛 🛃 Save

nextflu

https://gisaid.org/nextflu



