

Instructions to Access to GISAID Database

Step 1: Visit <https://www.gisaid.org/>

The screenshot shows the GISAID homepage. At the top is the GISAID logo and a navigation bar with links: About us, Database Features, Events, Collaborations, References, Registration, and Help. A search bar is located on the right. The main content area is divided into several sections:

- In Focus:** A news article titled "First human case of influenza A/H10N3 virus infection" dated May 28, 2021. It describes a case in Jiangsu Province, China, and mentions the release of the whole genome sequence (A/Jiangsu/428/2021) via the GISAID Initiative. A 3D molecular model of the virus is shown.
- Genomic epidemiology of hCoV-19:** A section featuring a world map and a phylogenetic tree.
- hCoV-19 data sharing via GISAID:** A large green box displaying "4,338,387 genome sequence submissions".
- hCoV-19 Submission Tracking:** Two maps showing global and US submission locations.
- hCoV-19 Tracking of Variants:** A world map with red dots indicating variant locations.
- Enabled by data shared via GISAID:** A section for "Saudi Arabia" showing RT-PCR primer tracking.
- Wisconsin Genomic Dashboard:** A link to a dashboard.
- GISAID Resources:** A link to resources.

Step 2: You need to register before you can login. Your registration information will be reviewed, so it will take a while before you can get access credentials.

The screenshot shows the GISAID registration process page. At the top is the GISAID logo and a navigation bar with links: About us, Database Features, Events, Collaborations, References, Registration, and Help. A search bar is located on the right. The main content area is divided into several sections:

- Registration:** A sidebar with links: » Register and » Terms of Use.
- The Signup Process:** A flowchart with three steps: 1. SUBMIT, 2. REVIEW, and 3. APPROVE.
- Read carefully:** A section with text explaining the registration process and the Database Access Agreement (DAA).
- 1. SUBMIT:** Applicant provides basic information and agrees to the Database Access Agreement.
- 2. REVIEW:** The information is reviewed both automatically and manually to confirm the applicant's identity.
- 3. APPROVE:** Applicant receives access credentials, or if necessary a request to assist in the confirmation of identity.

Read carefully:

To receive your personal access credentials to the GISAID platform you must first positively identify yourself and agree to the terms of the [Database Access Agreement \(DAA\)](#) which call on all users to support the underlying principles in GISAID that facilitate the sharing of genetic sequence and related data, while recognizing the contributions and interests of data providers and users, including:

1. You must acknowledge data contributors, i.e. the Originating Laboratory where the clinical specimen or virus isolate was first obtained and the Submitting Laboratory where sequence data have been generated and submitted to a GISAID Database ([see sample of acknowledgement table](#));
2. You may not attach restrictions on the data made available through a GISAID Database, such as including in a patent application any fraction of the genetic sequence data obtained from GISAID, to ensure unlimited access to the data;

Step 3: After you login in, you will have the options to explore genomic sequences of Flu or CoV. You can select the Tab EpiCoV to investigate SARS CoV sequences.

GISAID

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You are logged in as **Thanh Thi Nguyen** - [logout](#)

Registered Users EpiFlu™ **EpiCoV™** My profile

EpiCoV™ Search Downloads Upload

Pandemic coronavirus causing COVID-19

A previously unknown human coronavirus (hCoV-19) was first detected in late 2019 in patients in the City of Wuhan, who suffered from respiratory illnesses including atypical pneumonia, an illness that has become known as coronavirus disease (COVID-19). The coronavirus originated from an animal host and is closely related to the virus responsible for the Severe Acute Respiratory Syndrome coronavirus (SARS).

On 10. January 2020, the first virus genomes and associated data were publicly shared via GISAID. The World Health Organization announced on 11. March 2020 the first coronavirus pandemic. As the pandemic progresses, scientists from around the globe are tracking the virus and its genome sequences to ensure optimal virus diagnostic tests, to track and trace the ongoing outbreak and to identify potential intervention options. Several analyses to assist with these efforts are offered here, including sequence alignments, diagnostic primer and probe coordinates, 3D protein models, drug targets, phylogenetic trees and many more.

by A*STAR Singapore

Search

Audacity AudacityInstant BLAST CoVizu® Emerging Variants Official GISAID reference sequence PrimerChecker Spike glycoprotein

Important note: In the GISAID EpiFlu™ Database Access Agreement, you have accepted certain terms and conditions for viewing and using data regarding influenza viruses. To the extent the Database contains data relating to non-influenza viruses, the viewing and use of these data is subject to the same terms and conditions, and by viewing or using such data you agree to be bound by the terms of the GISAID EpiFlu™ Database Access Agreement in respect of such data in the same manner as if they were data relating to influenza viruses.

Step 4: You can select the Tab Search to search for genomic sequences based on different criteria. The sequences recently submitted to the database are shown on top by default.

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EpiCoV™ Search Downloads Upload

Search

Accession ID Virus name ☐ complete ☐ high coverage ☐ low coverage excl ☐ w/Patient status ☐ collection date compl ☐

Location Host

Collection to Submission to

Clade all Lineage Substitutions Variants

<input type="checkbox"/>	Virus name	Passage date	Accession ID	Collection date	Submission date	Length	Host	Location	Originating
<input type="checkbox"/>	hCoV-19/USA/IA-SHL-1886627/2021	Original	EPI_ISL_5324055	2021-10-09	2021-10-19	29,769	Human	North America / U.S.	State Hy
<input type="checkbox"/>	hCoV-19/USA/IA-SHL-1886630/2021	Original	EPI_ISL_5324054	2021-10-09	2021-10-19	29,769	Human	North America / U.S.	State Hy
<input type="checkbox"/>	hCoV-19/USA/IA-SHL-1886631/2021	Original	EPI_ISL_5324053	2021-10-10	2021-10-19	29,769	Human	North America / U.S.	State Hy
<input type="checkbox"/>	hCoV-19/USA/IA-SHL-1886618/2021	Original	EPI_ISL_5324052	2021-10-10	2021-10-19	29,769	Human	North America / U.S.	State Hy
<input type="checkbox"/>	hCoV-19/USA/IA-SHL-1886654/2021	Original	EPI_ISL_5324051	2021-10-09	2021-10-19	29,769	Human	North America / U.S.	State Hy
<input type="checkbox"/>	hCoV-19/USA/IA-SHL-1887632/2021	Original	EPI_ISL_5324050	2021-10-11	2021-10-19	29,769	Human	North America / U.S.	State Hy
<input type="checkbox"/>	hCoV-19/USA/IA-SHL-1886625/2021	Original	EPI_ISL_5324049	2021-10-10	2021-10-19	29,574	Human	North America / U.S.	State Hy
<input type="checkbox"/>	hCoV-19/USA/IA-SHL-1886624/2021	Original	EPI_ISL_5324048	2021-10-10	2021-10-19	29,769	Human	North America / U.S.	State Hy
<input type="checkbox"/>	hCoV-19/USA/IA-SHL-1887638/2021	Original	EPI_ISL_5324047	2021-10-09	2021-10-19	29,769	Human	North America / U.S.	State Hy
<input type="checkbox"/>	hCoV-19/USA/IA-SHL-1887633/2021	Original	EPI_ISL_5324046	2021-10-11	2021-10-19	29,769	Human	North America / U.S.	State Hy
<input type="checkbox"/>	hCoV-19/USA/IA-SHL-1886633/2021	Original	EPI_ISL_5324045	2021-10-11	2021-10-19	29,763	Human	North America / U.S.	State Hy
<input type="checkbox"/>	hCoV-19/USA/IA-SHL-1886655/2021	Original	EPI_ISL_5324044	2021-10-09	2021-10-19	29,769	Human	North America / U.S.	State Hy

Total: 4,447,592 viruses

<< < 1 2 3 4 5 > >>

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Step 5: If you click on any sequence, you will see all details of the virus, such as collection date, location, patient age, etc.

Virus detail

Virus name:

hCoV-19/USA/IA-SHL-1886618/2021

Accession ID:

EPI_ISL_5324052

Type:

betacoronavirus

Clade:

GK

Pango Lineage:

AY.4 (Pango v.3.1.14 2021-09-28), Delta (B.1.617.2-like) (Scorpio)

AA Substitutions:

Spike D614G, Spike D950N, Spike E156G, Spike F157del, Spike L452R, Spike P681R, Spike Q675H, Spike R158del, Spike T19R, Spike T478K, M182T, N D63G, N D377Y, N G215C, N R203M, NS3 S26L, NS7a T120I, NS7a V82A, NS7b T40I, NSP3 A488S, NSP3 P1228L, NSP3 P1469S, NSP4 A92V, NSP4 T492I, NSP4 V167L, NSP6 T77A, NSP12 G671S, NSP12 P323L, NSP13 P77L, NSP14 A323S, NSP14 A394V

Variant:

VOC Delta GK/478K.V1 (B.1.617.2+AY.x) first detected in India

Passage details/history:

Original

Sample information

Collection date:

2021-10-10

Location:

North America / USA / Iowa

Host:

Human

Additional location information:

Gender:

unknown

Patient age:

20

Patient status:

unknown

Specimen source:

Nasopharyngeal swab

Additional host information:

Sampling strategy:

Baseline surveillance

Outbreak:

Last vaccinated:

Treatment:

Sequencing technology:

Clear Labs Clear Dx

Assembly method:

Coverage:

890x

Comment:

Stretches of NNNs (1.91% of overall sequence). Gap of 13 nucleotides when compared to the reference WIV04 sequence.

Institute information

Originating lab:

State Hygienic Laboratory at the University of Iowa

Back

Contact Submitter

Metadata

FASTA

Step 6: Using Search criteria, e.g., if I select the Location Oceania/Australia, I will see the total number of sequences available in this location is 34,748. And the latest sequences are appearing in the screen:

Registered UsersEpiFlu™EpiCoV™My profile

EpiCoV™

Search

Downloads

Upload

Search

Accession ID

Virus name

Location

Collection

Clade

Lineage

Substitutions

Length

Host

Location

Originating

complete

high coverage

low coverage excl

w/Patient status

collection date compl

Reset

Fulltext

	Virus name	Passage de	Accession ID	Collection da	Submission L	Length	Host	Location	Originating
<input type="checkbox"/>	hCoV-19/Australia/TAS000298/2021	Original	EPI_ISL_5115217	2021	2021-10-14	29,804	Human	Oceania / Austr	Royal Hc
<input type="checkbox"/>	hCoV-19/Australia/NSW-RPAH-1799/2021	Original	EPI_ISL_5095146	2021-10-09	2021-10-13	29,701	Human	Oceania / Austr	New Soc
<input type="checkbox"/>	hCoV-19/Australia/NSW-RPAH-1798/2021	Original	EPI_ISL_5095145	2021-09-09	2021-10-13	29,684	Human	Oceania / Austr	New Soc
<input type="checkbox"/>	hCoV-19/Australia/NSW-RPAH-1797/2021	Original	EPI_ISL_5095144	2021-09-09	2021-10-13	29,675	Human	Oceania / Austr	New Soc
<input type="checkbox"/>	hCoV-19/Australia/NSW-RPAH-1795/2021	Original	EPI_ISL_5095143	2021-10-06	2021-10-13	29,684	Human	Oceania / Austr	New Soc
<input type="checkbox"/>	hCoV-19/Australia/NSW-RPAH-1788/2021	Original	EPI_ISL_5095142	2021-09-09	2021-10-13	29,675	Human	Oceania / Austr	New Soc
<input type="checkbox"/>	hCoV-19/Australia/NSW-RPAH-1787/2021	Original	EPI_ISL_5095141	2021-09-09	2021-10-13	29,701	Human	Oceania / Austr	New Soc
<input type="checkbox"/>	hCoV-19/Australia/NSW-RPAH-1786/2021	Original	EPI_ISL_5095140	2021-09-09	2021-10-13	29,684	Human	Oceania / Austr	New Soc
<input type="checkbox"/>	hCoV-19/Australia/NSW-RPAH-1785/2021	Original	EPI_ISL_5095139	2021-09-09	2021-10-13	29,684	Human	Oceania / Austr	New Soc
<input type="checkbox"/>	hCoV-19/Australia/NSW-RPAH-1784/2021	Original	EPI_ISL_5095138	2021-09-09	2021-10-13	29,684	Human	Oceania / Austr	New Soc
<input type="checkbox"/>	hCoV-19/Australia/NSW-RPAH-1783/2021	Original	EPI_ISL_5095137	2021-09-09	2021-10-13	29,701	Human	Oceania / Austr	New Soc
<input type="checkbox"/>	hCoV-19/Australia/WA824/2021	Original	EPI_ISL_5054910	2021-10-03	2021-10-12	29,396	Human	Oceania / Austr	PathWes

Total: 34,748 viruses

<<

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1

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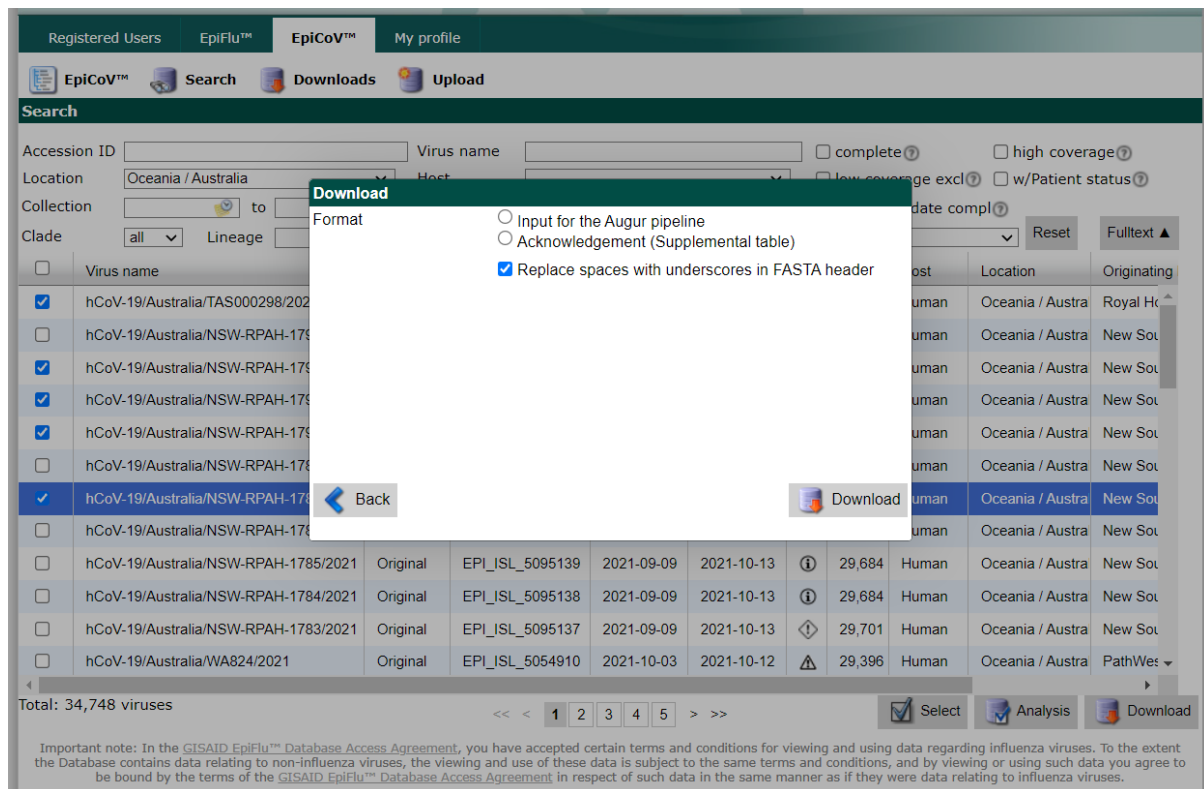
Select

Analysis

Download

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Step 7: You can select the checkboxes corresponding to the sequences you want to download. For example, I selected 5 sequences and hit the Download button:



Step 8: After downloading, you will obtain a FASTA file containing the genomic sequences of the 5 viruses you selected. Each sequence is separated with others by its header, starting with symbol ">":

