

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 phylogenetic tree and a world map showing the spread of the virus.
- hCoV-19 data sharing via GISAID:** A large green box displaying "4,338,387 genome sequence submissions".
- hCoV-19 Submission Tracking:** Two world maps showing 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 can will have the options to explore genomic sequences of Flu or CoV. You can select the Tab EpiCoV to investigate SARS CoV.

GISAID

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

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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 most recently deposited to the database are shown on top in default.

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Search

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

Location to Host to Submission to

Clade 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/MN-UNDGC-G2021_85_78/	Original	EPI_ISL_5172559	2021-03-31	2021-10-15	29,763	Human	North America / U	Altru Hei
<input type="checkbox"/>	hCoV-19/USA/MN-UNDGC-G2021_85_77/	Original	EPI_ISL_5172553	2021-03-31	2021-10-15	29,782	Human	North America / U	Altru Hei
<input type="checkbox"/>	hCoV-19/USA/MN-UNDGC-G2021_85_63/	Original	EPI_ISL_5172545	2021-03-29	2021-10-15	29,763	Human	North America / U	Altru Hei
<input type="checkbox"/>	hCoV-19/USA/MN-UNDGC-G2021_85_48/	Original	EPI_ISL_5172538	2021-03-26	2021-10-15	29,749	Human	North America / U	Altru Hei
<input type="checkbox"/>	hCoV-19/USA/MN-UNDGC-G2021_85_45/	Original	EPI_ISL_5172530	2021-03-26	2021-10-15	29,782	Human	North America / U	Altru Hei
<input type="checkbox"/>	hCoV-19/USA/MN-UNDGC-G2021_85_41/	Original	EPI_ISL_5172525	2021-03-25	2021-10-15	29,763	Human	North America / U	Altru Hei
<input type="checkbox"/>	hCoV-19/USA/MN-UNDGC-G2021_65redo	Original	EPI_ISL_5172516	2021-03-29	2021-10-15	29,837	Human	North America / U	Altru Hei
<input type="checkbox"/>	hCoV-19/USA/MN-UNDGC-G2021_65redo	Original	EPI_ISL_5172510	2021-03-26	2021-10-15	29,837	Human	North America / U	Altru Hei
<input type="checkbox"/>	hCoV-19/USA/MN-UNDGC-G2021_65redo	Original	EPI_ISL_5172508	2021-03-25	2021-10-15	29,837	Human	North America / U	Altru Hei
<input type="checkbox"/>	hCoV-19/USA/MN-UNDGC-G2021_65redo	Original	EPI_ISL_5172500	2021-03-25	2021-10-15	29,837	Human	North America / U	Altru Hei
<input type="checkbox"/>	hCoV-19/USA/MN-UNDGC-G2021_65redo	Original	EPI_ISL_5172495	2021-03-22	2021-10-15	29,837	Human	North America / U	Altru Hei
<input type="checkbox"/>	hCoV-19/USA/MN-UNDGC-G2021_65redo	Original	EPI_ISL_5172486	2021-03-22	2021-10-15	29,357	Human	North America / U	Altru Hei

Total: 4,339,299 viruses

<< 1 2 3 4 5 >>

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Step 5: For example, if I select the Location Oceania/Australia, I will see the total number of sequences available so far in this location is 34,748. And the latest sequences are appearing in the screen:

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EpiCoV™ Search Downloads Upload

Search

Accession ID Virus name ☐ complete ☐ high coverage ☐
 Location Host ☐ low coverage excl ☐ w/Patient status ☐
 Collection to Submission to ☐ collection date compl ☐
 Clade 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/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 Sou
<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 Sou
<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 Sou
<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 Sou
<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 Sou
<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 Sou
<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 Sou
<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 Sou
<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 Sou
<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 Sou
<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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Step 6: You can select the checkboxes corresponding to the sequences you want to download. For example, I selected 5 sequences and hit the Download button:

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EpiCoV™ Search Downloads Upload

Search


Accession ID Virus name ☐ complete ☐ high coverage ☐
 Location Host ☐ low coverage excl ☐ w/Patient status ☐
 Collection to Submission to ☐ collection date compl ☐
 Clade Lineage Substitutions Variants

<input type="checkbox"/>	Virus name	Passage date	Accession ID	Collection date	Submission date	Length	Host	Location	Originating
<input checked="" 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 Sou
<input checked="" 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 Sou
<input checked="" 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 Sou
<input checked="" 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 Sou
<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 Sou
<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 Sou
<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 Sou
<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 Sou
<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 Sou
<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 Sou
<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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Step 7: 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 ">":

 gisaid_hcov-19_2021_10_15_12 - Notepad

File Edit Format View Help

>hCoV-19/Australia/NSW-RPAH-1787/2021|EPI_ISL_5095141|2021-09-09

```
AGATCTGTTCTCTAAACGAACCTTAAATCTGTGTGGCTGTCACCTCGGCTGCATGCTTAGTGCACTCACGCAGTATAATT
AATAACTAATTACTGTCGTTGACAGGACACGAGTAACCTCGTCTATCTTCTGCAGGCTGCTTACGGTTTCGTCCGTTTTGC
AGCCGATCATCAGCACATCTAGGTTTTGTCCGGGTGTGACCGAAAGGTAAGATGGAGAGCCTTGTCCCTGGTTTTCAACGA
GAAAACACACGTCCTCAACTCAGTTTGCCTGTTTTACAGGTTTCGCGACGTGCTCGTACGTGGCTTTGGAGACTCCGTGGAGG
AGGTCTTATCAGAGGCACGTCAACATCTTAAAGATGGCACTTGTGGCTTAGTAGAAGTTGAAAAAGGCGTTTTGCCTCAA
CTTGAACAGCCCTATGTGTTTCATCAACGTTTCGGATGCTCGAAGTGCACCTCATGGTCATGTTATGGTTGAGCTGGTAGC
AGAACTCGAAGGCATTACGTACGGTCGTAGTGGTGAGACACTTGGTGTCTTGTCCCTCATGTGGGCGAAATACCAAGTGG
CTTACCGCAAGGTTCTTCTTCGTAAGAACGGTAATAAAGGAGCTGGTGGCCATAGTTACGGCGCCGATCTAAAGTCATTT
GACTTAGGCGACGAGCTTGGCACTGATCCTTATGAAGATTTTCAAGAAAACTGGAACACTAAACATAGCAGTGGTGTAC
CCGTGAAGTTCATGCGTGAGCTTAAACGGAGGGGCATACACTCGCTATGTCGATAACAACTTCTGTGGCCCTGATGGCTACC
CTCTTGAGTGCATTAAAGACCTTCTAGCACGTGCTGGTAAAGCTTCATGCACCTTGTCCGAACAACTGGACTTTATTGAC
ACTAAGAGGGGTGTATACTGCTGCCGTGAACATGAGCATGAAATTGCTTGGTACACGGAACGTTCTGAAAAGAGCTATGA
ATTGCAGACACCTTTTGAATTAATTTGGCAAAGAAATTTGACACCTTCAATGGGGAATGTCCAAATTTTGTATTTCCCT
TAAATTCATAATCAAGACTATTCAACCAAGGGTTGAAAAGAAAAAGCTTGATGGCTTTATGGGTAGAATTCGATCTGTC
TATCCAGTTGCGTCACCAAATGAATGCAACCAATGTGCCTTTCAACTCTCATGAAGTGTGATCATTGTGGTGAACTTC
ATGGCAGACGGGCGATTTTGTAAAGCCACTTGCGAATTTTGTGGCACTGAGAATTTGACTAAAGAAGGTGCCACTACTT
GTGGTTACTTACCCCAAAATGCTGTTGTTAAATTTATTGTCCAGCATGTCACAATTCAGAAGTAGGACCTGAGCATAGT
CTTGCCGAATACCATAATGAATCTGGCTTGAAAACCATTTCTCGTAAGGGTGGTCGCACTATTGCCCTTGGAGGCTGTGT
GTTCTCTTATGTTGGTTGCCATAACAAGTGTGCCTATTGGGTTCCACGTGCTAGCGCTAACATAGGTTGTAACCATACAG
GTGTTGTTGGAGAAGGTTCCGAAGGTCTTAATGACAACCTTCTTGAAATACTCCAAAAAGAGAAAGTCAACATCAATATT
GTTGGTGACTTTAACTTAATGAAGAGATCGCCATTATTTGGCATCTTTTCTGCTTCCACAAGTGCTTTTGTGGAAAC
TGTGAAAGGTTTTGGATTATAAAGCATTCAAACAAATTTGTTGAATCCTGTGGTAATTTTAAAGTTACAAAAGGAAAAGCTA
AAAAAGGTGCCTGGAATATTGGTGAACAGAAATCAATACTGAGTCCTCTTTATGCATTTGCATCAGAGGCTGCTCGTGT
GTACGATCAATTTTCTCCGCACTCTTGAAACTGCTCAAAATCTGTGCGTGTTTTACAGAAGGCCGCTATAACAATACT
AGATGGAATTTACAGATTACTGAGACTCATTGATGCTATGATGTTTACATCTGATTTGGCTACTAACAATCTAGTTG
TAATGGCTACATTACAGGTGGTGTGTTGAGTTGACTTCGAGTGGCTAACTAACATCTTTGGCACTGTTTATGAAAAA
CTCAAAACCCGTCCTTGATTGGCTTGAAGATAAGTTTAAAGGAAGGTGTAGAGTTTCTTAGAGACGGTTGGGAAATTGTTAA
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