



# Query GISAID with demis\_transaction\_id (/IMS-IDs)



## Intro

- Various submitters asked for their sequences in GISAID
- GISAID contains three IDs
  - Virus name “hCoV-19/USA/AZ-ASU6490/2021”
  - Accession “EPI\_ISL\_2484137”
  - DESH IMS ID “IMS-10334-CVDP-C73D3BB2-105F-4584-B63F-37A84FDCE507”
- Access for Gesundheitsämter et al. only possible with IMS IDs
  - Search in GISAID was initially not possible
  - Alternative: sending out translation tables is not a viable option



## First steps

- Login
- Move to “search”

The screenshot shows the GISAID EpiCoV web interface. At the top, the GISAID logo is on the left, and a copyright notice '© 2020' is on the right. Below the logo is a navigation bar with links: 'Registered Users', 'EpiCoV™', 'EpiCoV™', 'My profile', and 'EpiCoV™'. Below this is a secondary navigation bar with icons and labels: 'EpiCoV™', 'Search' (circled in red), 'Downloads', 'Upload', and 'My Unreleased'. The main section is titled 'Search' and contains several search filters: 'Accession ID' (text input), 'Virus name' (dropdown), 'Location' (dropdown), 'Host' (dropdown), 'Collection' (range input with 'to' and arrows), 'Submission' (range input with 'to' and arrows), 'Clade' (dropdown with 'all' selected), 'Lineage' (dropdown), 'Substitutions?' (dropdown), and 'Variants' (checkbox). At the bottom, there is a table header with columns: 'Virus name', 'Passage de', 'Accession ID', 'Collection dat', and 'Submission C', followed by an information icon.



## Enter IMS IDs

- “Select” (bottom edge of the list)

EPI_ISL_2484103	2021-05-29	2021-06-11	⚠	29.764	Human	North America / U	Arizona S
EPI_ISL_2484102	2021-05-26	2021-06-11	⚠	29.778	Human	North America / U	Arizona S
EPI_ISL_2484101	2021-05-20	2021-06-11	⚠	29.764	Human	North America / U	Arizona S
EPI_ISL_2484100	2021-05-20	2021-06-11	⚠	29.764	Human	North America / U	Arizona S
EPI_ISL_2484099	2021-05-25	2021-06-11	⚠	29.764	Human	North America / U	Arizona S
EPI_ISL_2484098	2021-05-25	2021-06-11	⚠	29.764	Human	North America / U	Arizona S
EPI_ISL_2484097	2021-05-25	2021-06-11	⚠	29.614	Human	North America / U	Arizona S
EPI_ISL_2484096	2021-05-25	2021-06-11	ⓘ	29.766	Human	North America / U	Arizona S
EPI_ISL_2484095	2021-05-25	2021-06-11	⚠	29.765	Human	North America / U	Arizona S

<< < 1 2 3 4 5 > >>

☒ Select ☐ Analysis ☐ Download

By clicking on the link, you have accepted certain terms and conditions for viewing and using data regarding influenza viruses. To the extent that 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 the [Database Access Agreement](#) in respect of such data in the same manner as if they were data relating to influenza viruses.

## Enter IMS IDs

- Activate “sample ID given by the originating lab”
- Enter IMS ID (single/multiple)
- Hit “ok”

**Select combination of entries**

Add any quantity of Sample IDs given by originating lab separated by , ; space or newline, or upload a plain text file.

Browse... No file selected.

☐ Accession Numbers
 ☒ Sample ID given by originating lab

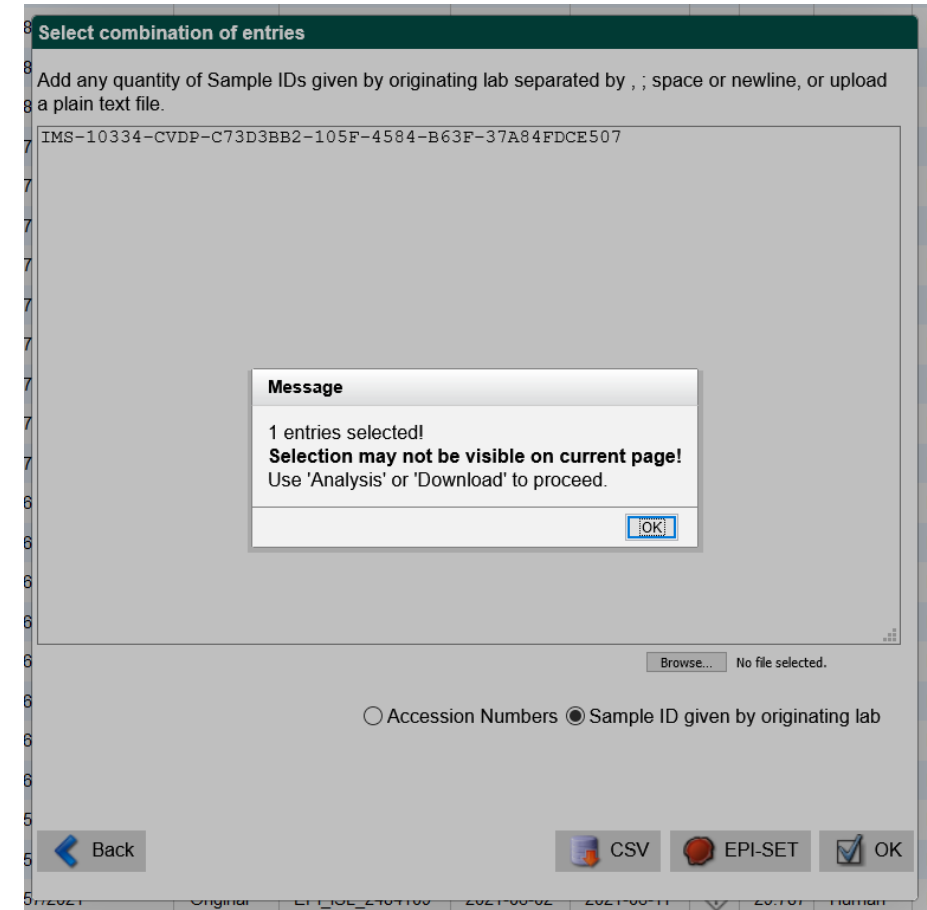
← Back

CSV
 EPI-SET
 OK



## Select samples

- Samples will get selected, but this will not be visible if samples are not on the first page





## Select samples

- Samples will get selected, but this will not be visible if samples are not on the first page
  - Selected sample may be on subsequent pages of the list  
-> only empty boxes visible

**Select combination of entries**

Add any quantity of Sample IDs given in a plain text file.

TMS-10334-CVDP-C73D3BB2-105E

**Message**

1 entries s  
**Selection**  
Use 'Analy

[Back](#)




Clade all Lineage




<input type="checkbox"/>	Virus name
<input type="checkbox"/>	hCoV-19/USA/AZ-ASU6490/2021
<input type="checkbox"/>	hCoV-19/USA/AZ-ASU6489/2021
<input type="checkbox"/>	hCoV-19/USA/AZ-ASU6488/2021
<input type="checkbox"/>	hCoV-19/USA/AZ-ASU6487/2021
<input type="checkbox"/>	hCoV-19/USA/AZ-ASU6486/2021
<input type="checkbox"/>	hCoV-19/USA/AZ-ASU6485/2021
<input type="checkbox"/>	hCoV-19/USA/AZ-ASU6484/2021
<input type="checkbox"/>	hCoV-19/USA/AZ-ASU6483/2021
<input type="checkbox"/>	hCoV-19/USA/AZ-ASU6482/2021
<input type="checkbox"/>	hCoV-19/USA/AZ-ASU6479/2021
<input type="checkbox"/>	hCoV-19/USA/AZ-ASU6478/2021
<input type="checkbox"/>	hCoV-19/USA/AZ-ASU6477/2021
<input type="checkbox"/>	hCoV-19/USA/AZ-ASU6475/2021
<input type="checkbox"/>	hCoV-19/USA/AZ-ASU6474/2021
<input type="checkbox"/>	hCoV-19/USA/AZ-ASU6473/2021



## Retrieve information

- “Download” information  
(bottom edge of the list)

06-11		29.614	Human	North America / U	Arizona S
06-11		29.766	Human	North America / U	Arizona S
06-11		29.765	Human	North America / U	Arizona S

 Select  Analysis  Download

nditions for viewing and using data regarding influenza viruses. To the  
object to the same terms and conditions, and by viewing or using such





## Retrieve information

- Select data to download
- “Download” information
- A large file format with all compiled info is under construction

A screenshot of a web application interface. At the top, there is a table with columns: 'Original', 'EPI\_ISL\_2484126', '2021-06-02', '2021-06-11', an information icon, '29.764', and 'Human'. Below this, a 'Download' modal window is open. The modal has a title bar 'Download' and a 'Format' section with the following options: 

- ☒ Sequences (FASTA)
- ☐ Patient status metadata
- ☐ Sequencing technology metadata
- ☐ Dates and Location
- ☐ Input for the Augur pipeline
- ☐ Acknowledgement (Supplemental table)

At the bottom of the modal, there are two buttons: 'Back' with a left arrow icon and 'Download' with a download icon. Below the modal, another table is partially visible with columns: 'Original', 'EPI\_ISL\_2484114', '2021-05-27', '2021-06-11', a download icon, '29.765', and 'Human'.