



WHO Collaborating Centre
for Reference and
Research on Influenza
VIDRL



KDCA
Korea Disease Control and
Prevention Agency

Uploading sequences to GISAID

—
Clyde Dapat, PhD

WHO Collaborating Centre for Reference
and Research on Influenza



**CENTRE FOR
PATHOGEN
GENOMICS**



A joint venture between The University of Melbourne and The Royal Melbourne Hospital



Objective

- To learn how to upload sequences to GISAID



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Platform Login

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Federal Ministry
of Food
and Agriculture



max planck institut
informatik

GISAID

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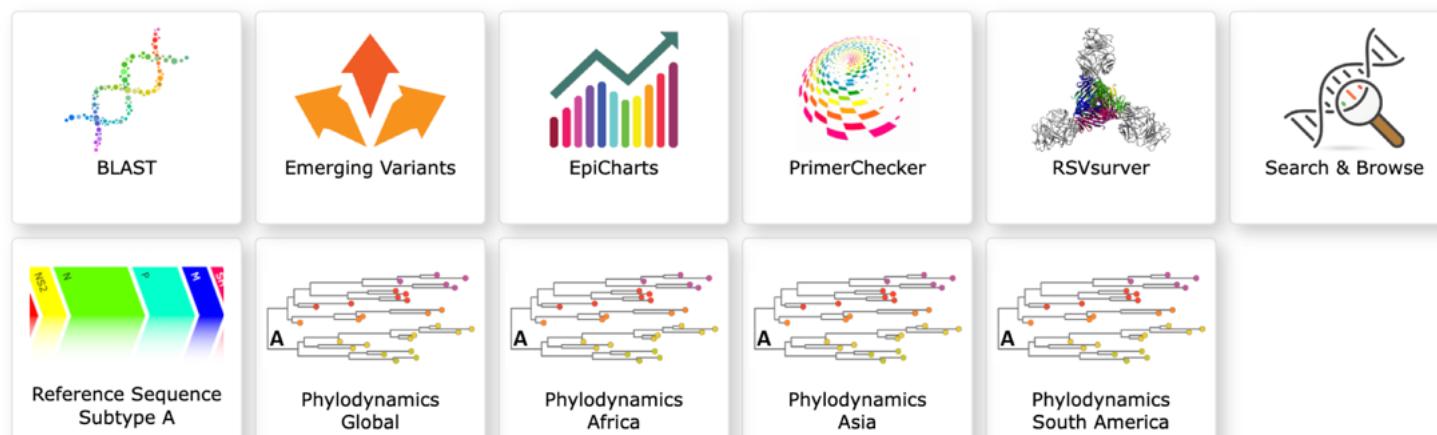
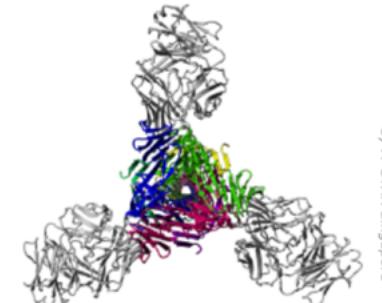
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EpiRSV™ | Search **Upload**

Surveillance of respiratory syncytial virus (RSV)

RSV is one of the main causes of lower respiratory tract infections (LRTI), primarily affecting pediatric populations, older adults and those with chronic co-morbidities. RSV-associated respiratory infections are a major cause of hospital admission and hospital deaths in infants and young children. Many countermeasures against RSV, including vaccines, therapeutics and antibodies are in various stages of development. There is a pressing need to monitor genetic evolution, epidemiology and disease characteristics of RSV, particularly in low and middle-income countries (LMICs).

Global surveillance for RSV, currently built on the Global Influenza Surveillance and Response System (GISRS), will make it possible to further investigate and elucidate knowledge gaps for understanding the transmission of the virus in the world, risk factors for RSV infection and severe disease, but above all, will further describe the genetic background of the virus. Genomic surveillance for RSV will enable predictions on the effectiveness of prophylactic treatments and support countermeasure developments against all circulating viral variants, and is essential for optimal implementation of vaccines to analyze in real-time the impact of interventions on circulating viruses.



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.

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Global surveillance for RSV, currently being developed (GISRS), will make it possible to further describe the transmission of the virus in the world, further describe the genetic background of RSV, and on the effectiveness of prophylactic measures against circulating viral variants, and is essential to monitor the impact of interventions on circulating

Single upload | Batch upload | FASTQ *Activate*

BLAST | Emerging Variants | EpiCharts | PrimerChecker | RSVsurver | Search & Browse

Reference Sequence Subtype A | Phydynamics Global | Phydynamics Africa | Phydynamics Asia | Phydynamics South America

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Single Upload

Enter and upload genetic sequence and metadata, available clinical and epidemiological data, geographical as well as species-specific data. Data will be reviewed by a curator prior to release. An email confirmation will be issued upon release.

Virus detail

Virus name*

hRSV/Subtype/Country/Identifier/2021

Accession ID

Subtype*

Passage details/history*

Example: Original, Vero

Sample information

Collection date*

Example: 2020-03-27, 2020-03 (collection in March, specific day unknown), 2020 (collection in 2020, month and day unknown)

Location*

Continent / Country or Territory / Region

Additional location information

Example: Travel history; Residence; Cruise ship; ...

Host*

Example: Human, Environment, Canine, *Manis javanica*, *Rhinolophus affinis*, unknown

Additional host information

Example: Underlying health conditions; other host relevant characteristics

Sampling strategy

Gender*

Example: Male, Female, or unknown

Patient age*

Example: 65, 7 months, or unknown

Patient status*

Submit for Review



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EpiRSV™ | **Search** | **Upload**

Location*

Oceania / Australia / Victoria / Melbourne

Continent / Country or Territory / Region

Additional location information

Example: Travel history; Residence; Cruise ship; ...

Host*

Human

Example: Human, Environment, Canine, *Manis javanica*, *Rhinolophus affinis*, unknown

Additional host information

Example: Underlying health conditions; other host relevant characteristics

Sampling strategy

▼

Gender*

Male

Example: Male, Female, or unknown

Patient age*

38

Example: 65, 7 months, or unknown

Patient status*

unknown

Example: Hospitalized, Released, Live, Deceased, unknown

Specimen source

Nasopharyngeal swab

Example: Sputum, Alveolar lavage fluid, Oropharyngeal swab, Nasopharyngeal swab, Blood, Tracheal swab, Urine, Stool, Cloakal swab, Organ, Feces, Other

Outbreak Detail

Example: Date, Place, Family cluster

Last vaccinated

provide details if applicable

Treatment

Example: Include drug name, dosage

Sequencing technology*

Illumina iSeq

Example: Illumina MiSeq, Sanger, Nanopore MinION, Ion Torrent, etc.

Assembly method

CDC-IRMA

Example: CLC Genomics Workbench 12, Geneious 10.2.4, SPAdes/MEGAHIT v1.2.9, UGENE v. 33, etc.

Coverage

1249x

Example: 70x, 1,000x, 10,000x (average)

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Institute information

Originating lab*

VIC, RCH Molecular Microbiology Dept. (Bio21)

Where the clinical specimen or virus isolate was first obtained

Address*

50 Flemington Road Parkville Victoria 3052 Australia

Sample ID given by the originating lab

22170381

Submitting lab*

WHO Collaborating Centre for Reference and Research on Influenza

Where sequence data have been generated and submitted to GISAID

Address*

792 Elizabeth St
3004 Melbourne
Australia

Sample ID given by the Submitting lab

N90004587.1

Authors*

Xiaomin Dong, Steven Edwards, Yi-Mo Deng, Ammar Aziz, Ian Barr

Submitter information

Submitter

Clyde Dapat

Submission date

2023-10-15

Address

792 Elizabeth St
3004 Melbourne
Australia

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originating lab

Submitting lab*

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Address*

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Submitter information

Submitter

Clyde Dapat

Submission date

2023-10-15

Address

792 Elizabeth St
3004 Melbourne
Australia

Sequence

Sequence*

>hRSV/A/Australia/VIC-RCH013/2022
TTGGCTAACCAAAAAATGGGCAAATAAGAATTGATAAGTACCACTAAATTAACTCCTTGTTAGAGATGGCA
GCAACTCATGGAGTATGATAAAAGTTAGATTGCAAAATCTGTTGACAAATGATGAAGTAGCATGTTAAAATAACATGC
TATAGTACAAATTAAACAGTTAACTAATGCTTGGCTAAGGCAGTTACATACATAACATCAAATTGAATGGCATTGTATT
TGTGCATGTTATTACAAGTAGTGTATTGCCCCTAAATAATAATTGTAGTGAATCCAATTTCACAACAATGCCAGTAT
TACAAAATGGAGGTTATATGGGAAATGATGGAATTACACACTGCTCTCAACCTAATGGCTTAATAGATGACAATTGT
GAAATTAAATTCTCCAAAAACTAAGTGATTCAACATGACCAATTATGATCAATTATCTGAATTACTGGATTG
CCTCAATCCATATAATCATATAATCAACTACCAATCAATGCTCAACACCAATTAGTTAAATATAAACTTGACAGA
AGATAAAAATGGGCAAATAAAATCAATTCCGACCCAACCATGGACACAAACACACAATGATACCAACCCACAAAGACT

Upload FASTA from your local computer:

Choose file | No file chosen

Submit for Review





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Batch upload

GISAID

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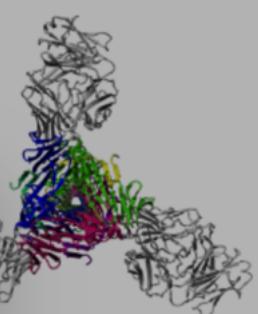
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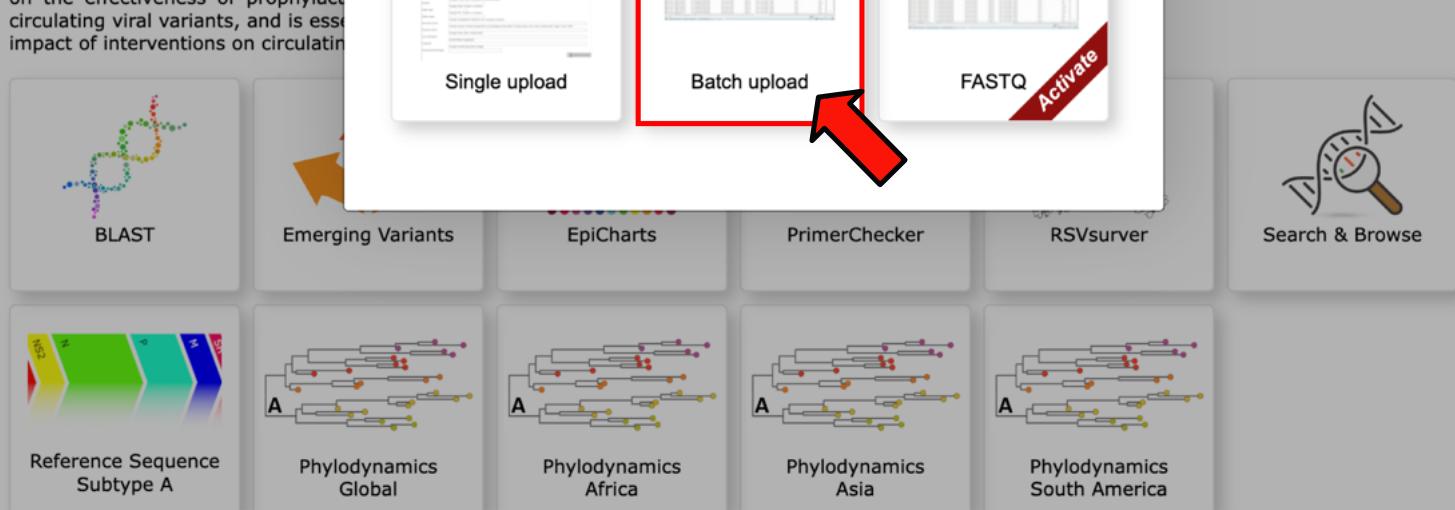
Global surveillance for RSV, currently (GISRS), will make it possible to further describe the genetic background on the effectiveness of prophylactic circulating viral variants, and is essential impact of interventions on circulating

Batch upload 

Activate



by A*STAR Singapore



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GISAID RSV Batch Upload

Upload genetic sequence as single FASTA-File and metadata, available clinical and epidemiological data, geographical as well as species-specific data as XLS or CSV. Data will be reviewed by a curator prior to release. An email confirmation will be issued upon release.

Metadata as Excel or
CSV*

max size: 5M No file chosen

Sequences as FASTA*

max size: 32M No file chosen

Report

[Download Instructions and Template](#)

[Contact Curation](#)

[Verify and Submit](#)

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20210611_EpiRSV_BulkUpload_Template.xls [Compatibility Mode]

EpiRSV bulk upload

EpiRSV bulk upload

Version: 2021-06-11

Instructions:

- Enter your data into the sheet "Submissions"
- The mandatory columns are indicated in color.
- Do not change the content of the two first rows (1 & 2)
- Delete, overwrite the examples given in row 3
- Your sequences must be in one single FASTA-File to compliment this spreadsheet with your metadata
- EXCEL extension must remain .xls (not .xlsx). Always save in EXCEL 97 - 2003 Format.
- "FASTA Filename" must match exactly and only the filename that contains the corresponding sequences without any path or directory prefixed.
- FASTA headers (sequence names) in the FASTA-File must exactly match the values of "Virus name" (e.g. hRSV/A/Netherlands/GR-58964/2020)
- Do not change the type of the columns (Collection Date must be formatted as "text" not "date")
- Always use the newest bulk-upload-XLS-Template
- Use "unknown" written in lower case if no value is available
- The user should name the XLS-Sheet as follows prior sending to the curation team: "YYYYMMDD_a_descriptive_name_metadata.xls"

Upload your completed Excel sheet together with the FASTA-File through the Batch Upload interface

In the event you experience any difficulties with your upload, please contact us for assistance at service@gisaid.org

What happens next?

EpiRSV Curators across different timezones will be alerted and review your data. Only if necessary, will you be contacted, before your data are released

You will receive an eMail alert informing you that your data has been released.

Column Information

| | | |
|---------------------------------|-----------|--|
| Submitter | mandatory | enter your GiSAID-username |
| FASTA filename | mandatory | the filename that contains the sequence without path (e.g. all_sequences.fasta not c:\users\meier\docs\all_sequences.fasta) |
| Virus name | mandatory | e.g. hRSV/A/Country/Region/Abbreviation-SampleID/year (must be FASTA-Header from the FASTA file all_sequences.fasta) |
| Subtype | mandatory | e.g. A / B |
| Passage details/history | mandatory | e.g. Original, Viral |
| Collection date | mandatory | Date in the format YYYY-MM-DD or YYYY-MM or YYYY |
| Location | mandatory | e.g. Continent / Country / Province / Subregion / County / City |
| Additional location information | | e.g. Hospital, Nursing home, School, Patient infected while traveling in |
| Host | mandatory | e.g. Human, Laboratory derived |
| Additional host information | | e.g. Underlying diseases, Risk factors |
| Sampling Strategy | | e.g. Sentinel surveillance (IL), Sentinel surveillance (ARI), Sentinel surveillance (SARI), Non-sentinel-surveillance (hospital), Non-sentinel-surveillance (GP), Longitudinal sampling on same patient(s), S gene dropout |
| Gender | mandatory | Male, Female, or unknown |
| Patient age | mandatory | e.g. 65 years or 7 months, or 20 days, unknown |
| Patient status | mandatory | e.g. Hospitalized, Ambulatory, Live, Deceased, unknown |
| Specimen source | | e.g. Nasopharyngeal aspirate, Sputum, Other |
| Outbreak | | Date, Location e.g. type of gathering, Family cluster, etc. |
| Last vaccinated | | provide details if applicable |

Instructions Submissions +

Ready 95%

20210611_EpiRSV_BulkUpload_Template.xls [Compatibility Mode]

A1

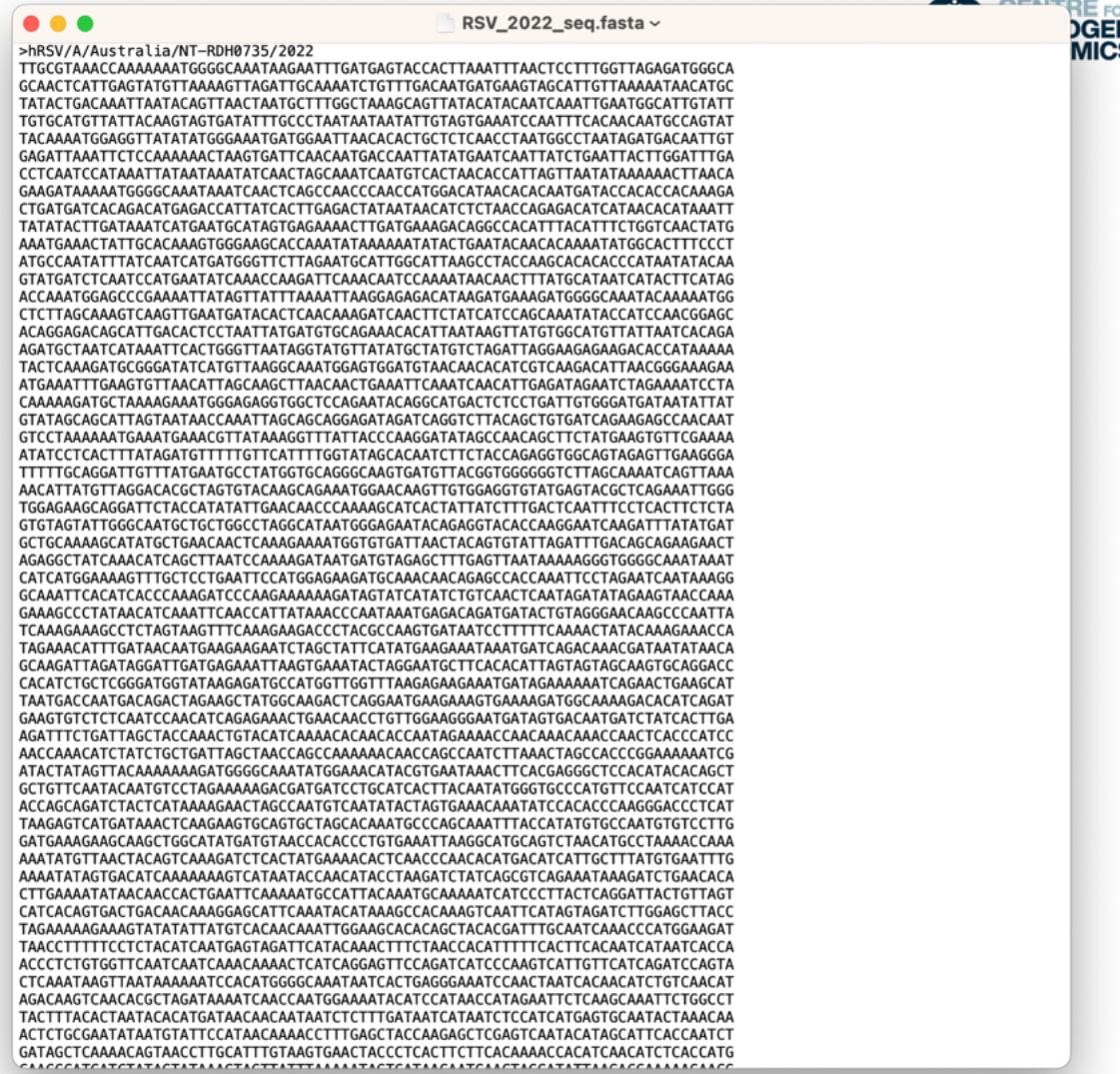
| Submitter | inv_virus_name | inv_subtype | inv_passage | inv_collection_date | inv_location | inv_additional_location | mv_host | mv_additional_info |
|---------------------------------|----------------------------------|-----------------|---------------------|-----------------------|-----------------------------------|---------------------------|-----------|--|
| Subtype | Passage details/history | Collection date | Location | | | Host | Add. | e.g. Cruise Ship, Convention, Live animal e.g. Horse |
| 1 Submitter | 2 inv_virus_name | 3 inv_subtype | 4 inv_passage | 5 inv_collection_date | 6 inv_location | 7 inv_additional_location | 8 mv_host | 9 mv_additional_info |
| GISAID user_all_sequences.fasta | hRSV/A/Netherlands/GR-58964/2021 | e.g. A | e.g. Original, Vero | 2020-03-02 | e.g. Continent / Country / Region | | | |
| 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 |
| 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 |
| 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 |
| 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |
| 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 |

Instructions Submissions +

Ready 95%

The screenshot shows an Excel spreadsheet titled "RSV_2022_metadata.xls [Compatibility Mode]" in a Mac-style window. The spreadsheet contains data from row 1 to 34, with columns A through H. The columns represent various metadata fields: Submitter, fn, rsv_virus_name, rsv_subtype, rsv_passage, rsv_collection_date, rsv_location, and rsv_add_location. The data shows multiple entries for different RSV isolates, primarily from Australia, with collection dates ranging from 2022-06-05 to 2022-09-28.

| | A | B | C | D | E | F | G | H |
|----|-----------|--------------------|----------------------------------|-------------|----------------------------|---------------------|---|------------------|
| 1 | submitter | fn | rsv_virus_name | rsv_subtype | rsv_passage | rsv_collection_date | rsv_location | rsv_add_location |
| 2 | Submitter | FASTA filename | Virus name | Subtype | Passage of Collection date | Location | Additional location information | |
| 3 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/NT-RDH0108/2022 | B | Original | 2022-07-27 | Oceania / Australia / Northern Territory / Darwin | |
| 4 | Clyde | RSV_2022_seq.fasta | hRSV/A/Australia/VIC-RCH019/2022 | A | Original | 2022-06-05 | Oceania / Australia / Victoria / Melbourne | |
| 5 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/VIC-RCH036/2022 | B | Original | 2022-06-12 | Oceania / Australia / Victoria / Melbourne | |
| 6 | Clyde | RSV_2022_seq.fasta | hRSV/A/Australia/VIC-RCH037/2022 | A | Original | 2022-06-12 | Oceania / Australia / Victoria / Melbourne | |
| 7 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/VIC-RCH057/2022 | B | Original | 2022-06-19 | Oceania / Australia / Victoria / Melbourne | |
| 8 | Clyde | RSV_2022_seq.fasta | hRSV/A/Australia/VIC-RCH063/2022 | A | Original | 2022-06-19 | Oceania / Australia / Victoria / Melbourne | |
| 9 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/VIC-RCH088/2022 | B | Original | 2022-06-25 | Oceania / Australia / Victoria / Melbourne | |
| 10 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/VIC-RCH089/2022 | B | Original | 2022-06-27 | Oceania / Australia / Victoria / Melbourne | |
| 11 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/VIC-RCH099/2022 | B | Original | 2022-07-03 | Oceania / Australia / Victoria / Melbourne | |
| 12 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/VIC-RCH101/2022 | B | Original | 2022-07-04 | Oceania / Australia / Victoria / Melbourne | |
| 13 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/VIC-RCH121/2022 | B | Original | 2022-07-10 | Oceania / Australia / Victoria / Melbourne | |
| 14 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/VIC-RCH127/2022 | B | Original | 2022-07-10 | Oceania / Australia / Victoria / Melbourne | |
| 15 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/VIC-RCH129/2022 | B | Original | 2022-07-10 | Oceania / Australia / Victoria / Melbourne | |
| 16 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/NT-RDH0142/2022 | B | Original | 2022-08-04 | Oceania / Australia / Northern Territory / Darwin | |
| 17 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/NT-RDH0164/2022 | B | Original | 2022-08-14 | Oceania / Australia / Northern Territory / Darwin | |
| 18 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/NT-RDH0287/2022 | B | Original | 2022-08-27 | Oceania / Australia / Northern Territory / Darwin | |
| 19 | Clyde | RSV_2022_seq.fasta | hRSV/A/Australia/NT-RDH0295/2022 | A | Original | 2022-08-27 | Oceania / Australia / Northern Territory / Darwin | |
| 20 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/NT-RDH0329/2022 | B | Original | 2022-08-26 | Oceania / Australia / Northern Territory / Darwin | |
| 21 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/NT-RDH0338/2022 | B | Original | 2022-09-02 | Oceania / Australia / Northern Territory / Darwin | |
| 22 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/NT-RDH0425/2022 | B | Original | 2022-09-08 | Oceania / Australia / Northern Territory / Darwin | |
| 23 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/NT-RDH0438/2022 | B | Original | 2022-09-07 | Oceania / Australia / Northern Territory / Darwin | |
| 24 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/NT-RDH0449/2022 | B | Original | 2022-09-08 | Oceania / Australia / Northern Territory / Darwin | |
| 25 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/NT-RDH0464/2022 | B | Original | 2022-08-24 | Oceania / Australia / Northern Territory / Darwin | |
| 26 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/NT-RDH0468/2022 | B | Original | 2022-09-13 | Oceania / Australia / Northern Territory / Darwin | |
| 27 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/NT-RDH0514/2022 | B | Original | 2022-09-15 | Oceania / Australia / Northern Territory / Darwin | |
| 28 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/NT-RDH0528/2022 | B | Original | 2022-09-15 | Oceania / Australia / Northern Territory / Darwin | |
| 29 | Clyde | RSV_2022_seq.fasta | hRSV/A/Australia/NT-RDH0531/2022 | A | Original | 2022-09-15 | Oceania / Australia / Northern Territory / Darwin | |
| 30 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/NT-RDH0532/2022 | B | Original | 2022-09-15 | Oceania / Australia / Northern Territory / Darwin | |
| 31 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/NT-RDH0595/2022 | B | Original | 2022-09-27 | Oceania / Australia / Northern Territory / Darwin | |
| 32 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/NT-RDH0607/2022 | B | Original | 2022-09-29 | Oceania / Australia / Northern Territory / Darwin | |
| 33 | Clyde | RSV_2022_seq.fasta | hRSV/A/Australia/NT-RDH0613/2022 | A | Original | 2022-09-30 | Oceania / Australia / Northern Territory / Darwin | |
| 34 | Clyde | RSV_2022_seq.fasta | hRSV/B/Australia/NT-RDH0614/2022 | B | Original | 2022-09-28 | Oceania / Australia / Northern Territory / Darwin | |



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GISAID RSV Batch Upload

Upload genetic sequence as single FASTA-File and metadata, available clinical and epidemiological data, geographical as well as species-specific data as XLS or CSV. Data will be reviewed by a curator prior to release. An email confirmation will be issued upon release.

Metadata as Excel or CSV*



[RSV_2022_metadata.xls \(81.5 kbytes\)](#)

max size: 5M

[Choose file](#)

No file chosen

Sequences as FASTA*



[RSV_2022_seq.fasta \(1.04 MB\)](#)

max size: 32M

[Choose file](#)

No file chosen

Report

[Upload XLS/CSV and FASTA.](#)

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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.





World Health
Organization
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WHO Collaborating Centre
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THANK YOU

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KDCA

Korea Disease Control and
Prevention Agency



A joint venture between The University of Melbourne and The Royal Melbourne Hospital

