

EpiCoV hCoV-19 bulk upload

Version: 2020-05-01

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 me
- EXCEL extension must remain .xls (not .xlsx). Always save in EXCEL 97 - 2003 Format.
- Provide for every row/virus the filename of the FASTA-File that contains the corresponding sequ
- "FASTA Filename" must match exactly the actual filename without any directory prefixed. ("all_s
- FASTA-Headers in the .FASTA-File must exactly match the values of "Virus name" (e.g. >hCoV
- 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: "YYYYMMMD

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

In the event you experience any difficulties with your upload, please contact us for assistance at [\[link\]](#)
What happens next?

EpiCoV Curators across different timezones will be alerted and review your data. Only if necessa
You will receive an eMail alert informing you that your data has been released.

Column information	
Submitter	mandatory
FASTA filename	mandatory
Virus name	mandatory
Type	mandatory
Passage details/history	mandatory
Collection date	mandatory
Location	mandatory
Additional location information	
Host	mandatory
Additional host information	
Gender	mandatory
Patient age	mandatory
Patient status	mandatory
Specimen source	
Outbreak	
Last vaccinated	
Treatment	

Sequencing technology	mandatory
Assembly method	
Coverage	
Originating lab	mandatory
Address	mandatory
Sample ID given by the sample provider	
Submitting lab	mandatory
Address	mandatory
Sample ID given by the submitting laboratory	
Authors	
<i>Comment</i>	leave empty
<i>Comment icon</i>	leave empty



tadata

ence.

quences.fasta" is OK, "c:/users/meier/docs/all_sequences.fasta" is not)
-19/Netherlands/Gelderland-01/2020)

D_a_descriptive_name_metadata.xls"

d interface

5.1.2e @gisaid.org

ry, will you be contacted, before your data are released

enter your GISAID-Username

the filename that contains the sequence without path (e.g. all_sequences.fasta not c:/users/meier/docs/all_sequence

e.g. hCoV-19/Netherlands/Gelderland-01/2020 (Must be FASTA-Header from the FASTA file all_sequences.fasta)

default must remain "betacoronavirus"

e.g. Original, Vero

Date in the format YYYY or YYYY-MM or YYYY-MM-DD

e.g. Europe / Germany / Bavaria / Munich

e.g. Cruise Ship, Convention, Live animal market

e.g. Human, Environment, Canine, Manis javanica, Rhinolophus affinis, etc

e.g. Patient infected while traveling in

Male, Female, or unknown

e.g. 65 or 7 months, or unknown

e.g. Hospitalized, Released, Live, Deceased, or unknown

e.g. Sputum, Alveolar lavage fluid, Oro-pharyngeal swab, Blood, Tracheal swab, Urine, Stool, Cloakal swab, Organ, F

Date, Location e.g. type of gathering, Family cluster, etc.

provide details if applicable

Include drug name, dosage

e.g. Illumina Miseq, Sanger, Nanopore MinION, Ion Torrent, etc.

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

e.g. 70x, 1,000x, 10,000x (average)

Where the clinical specimen or virus isolate was first obtained

Where sequence data have been generated and submitted to GISAID

a comma separated list of Authors with complete First followed by Last Name

do not use this column

do not use this column

s. fasta)

eces, Other

Submissions

submitter Submitter GISAID username	fn FASTA filename all_sequences.fasta
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[REDACTED]	
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5.1.2e

Submissions

covv_virus_name Virus name	covv_type Type	covv_passage Passage details/history
hCoV-19/Country/Identifier/2020	betacoronavirus.g. Original, Vero	
hCoV-19/Netherlands/NoordHolland/10001/2020	betacoronavirus	Original
hCoV-19/Netherlands/NoordHolland/10002/2020	betacoronavirus	Original
hCoV-19/Netherlands/NoordBrabant/10003/2020	betacoronavirus	Original
hCoV-19/Netherlands/ZuidHolland/10004/2020	betacoronavirus	Original
hCoV-19/Netherlands/ZuidHolland/10005/2020	betacoronavirus	Original
hCoV-19/Netherlands/NoordHolland/10006/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10007/2020	betacoronavirus	Original
hCoV-19/Netherlands/NoordHolland/10008/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10009/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10010/2020	betacoronavirus	Original
hCoV-19/Netherlands/NoordHolland/10011/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10012/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10013/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10014/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10015/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10016/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10017/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10018/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10019/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10020/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10021/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10022/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10023/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10024/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10025/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10026/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10027/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10028/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10029/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10030/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10031/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10032/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10033/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10034/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10035/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10036/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10037/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10038/2020	betacoronavirus	Original
hCoV-19/Netherlands/NoordBrabant/10039/2020	betacoronavirus	Original
hCoV-19/Netherlands/NoordBrabant/10040/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10041/2020	betacoronavirus	Original
hCoV-19/Netherlands/NoordBrabant/10042/2020	betacoronavirus	Original
hCoV-19/Netherlands/NoordHolland/10043/2020	betacoronavirus	Original
hCoV-19/Netherlands/Utrecht/10044/2020	betacoronavirus	Original
hCoV-19/Netherlands/NoordBrabant/10045/2020	betacoronavirus	Original

Submissions

covv_collection_date Collection date	covv_location Location	covv_add_location Additional location information	covv_host Host
2020-03-02	e.g. Continent / Country / Region	e.g. Cruise Ship, Convention, Live	e.g. Human
2020/02/27	Europe/Netherlands		Human
2020/02/28	Europe/Netherlands		Human
2020/02/28	Europe/Netherlands		Human
2020/02/28	Europe/Netherlands		Human
2020/02/28	Europe/Netherlands		Human
2020/03/03	Europe/Netherlands		Human
2020/03/05	Europe/Netherlands		Human
2020/03/06	Europe/Netherlands		Human
2020/03/11	Europe/Netherlands		Human
2020/03/13	Europe/Netherlands		Human
2020/03/14	Europe/Netherlands		Human
2020/03/14	Europe/Netherlands		Human
2020/03/16	Europe/Netherlands		Human
2020/03/16	Europe/Netherlands		Human
2020/03/16	Europe/Netherlands		Human
2020/03/18	Europe/Netherlands		Human
2020/03/23	Europe/Netherlands		Human
2020/03/23	Europe/Netherlands		Human
unknown	Europe/Netherlands		Human
2020/03/24	Europe/Netherlands		Human
2020/03/25	Europe/Netherlands		Human
2020/03/23	Europe/Netherlands		Human
2020/03/26	Europe/Netherlands		Human
2020/03/26	Europe/Netherlands		Human
2020/03/27	Europe/Netherlands		Human
2020/04/01	Europe/Netherlands		Human
2020/04/02	Europe/Netherlands		Human
2020/04/01	Europe/Netherlands		Human
2020/04/03	Europe/Netherlands		Human
2020/04/04	Europe/Netherlands		Human
2020/04/04	Europe/Netherlands		Human
2020/04/04	Europe/Netherlands		Human
2020/04/11	Europe/Netherlands		Human
2020/04/22	Europe/Netherlands		Human
2020/04/22	Europe/Netherlands		Human
2020/03/10	Europe/Netherlands		Human
2020/03/11	Europe/Netherlands		Human
2020/03/12	Europe/Netherlands		Human
2020/03/16	Europe/Netherlands		Human
2020/03/20	Europe/Netherlands		Human
2020/03/24	Europe/Netherlands		Human
2020/03/25	Europe/Netherlands		Human
2020/03/27	Europe/Netherlands		Human
2020/03/31	Europe/Netherlands		Human
2020/04/07	Europe/Netherlands		Human

Submissions

covv_add_host_info	covv_gender	covv_patient_age	covv_patient_status	covv_specimen
Additional host information	Gender	Patient age	Patient status	Specimen source
e.g. Patient infected while traveling, e.g. Male, Female, 65 or 70 years old, e.g. Hospitalized, e.g. Sputum, Alveolar				
	unknown	44	unknown	
	Male	47	unknown	
	Female	57	unknown	
	Female	23	unknown	
	Female	23	unknown	
	Male	48	unknown	
	Male	29	unknown	
	Female	50	unknown	
	Male	50	unknown	
	Male	47	unknown	
	Male	77	unknown	
	Female	57	unknown	
	Female	28	unknown	
	Male	33	unknown	
	Male	89	unknown	
	Female	40	unknown	
	Male	85	unknown	
	Female	88	unknown	
	Male	93	unknown	
	Female	99	unknown	
	Male	51	unknown	
	Female	87	unknown	
	Male	89	unknown	
	Female	91	unknown	
	Female	77	unknown	
	Female	44	unknown	
	Male	83	unknown	
	Female	89	unknown	
	Female	63	unknown	
	Male	78	unknown	
	Female	71	unknown	
	Male	92	unknown	
	Female	89	unknown	
	Male	82	unknown	
	Male	85	unknown	
	Male	68	unknown	
	Female	48	unknown	
	Male	50	unknown	
	Female	44	unknown	
	Male	85	unknown	
	Female	81	unknown	
	Female	66	unknown	
	Male	50	unknown	
	Female	74	unknown	
	Female	31	unknown	

Submissions

[illegible]

Submissions

cow_assembly_method

Assembly method

e.g. CLC Genomics Workbench 12, Geneious 10.2.4, SPAdes/MEGAHIT v1.2.9, UGENE v. 33

Submissions

cow_provider_sample_id

Sample ID given by the sample provider

Submissions

cow_subm_lab

Submitting lab

Where sequence data have been generated and submitted to GISAID

[illegible]

covv_subm_sample_id

Sample ID given by the submitting laboratory

Page 10

Submissions

cow_authors

Authors

e.g. Jane Doe, John Doe

[illegible]

Submissions

cow_comment

Comment

comment_type

Comment Icon

[illegible]