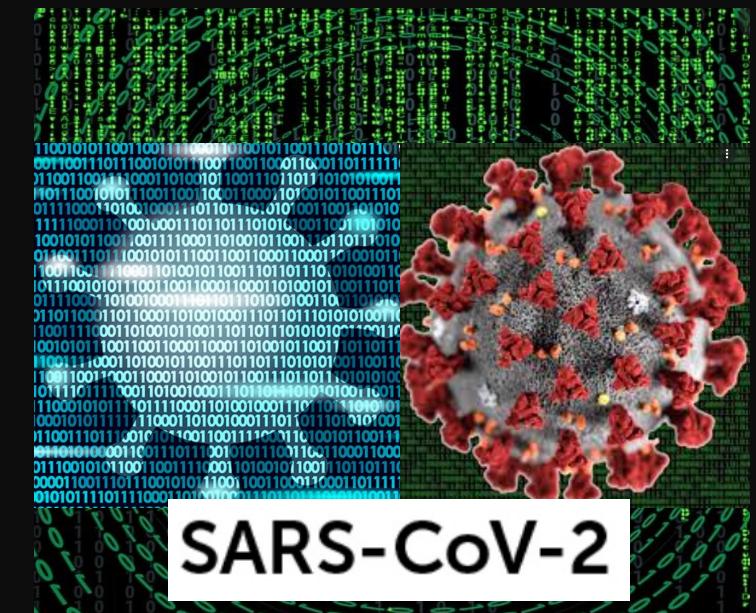


COVID-19 in Africa and Response & A bioinformatics quick guide to analysis of ONT/PacBio/Illumina SARS-CoV-2 reads

Gerald Mboowa



AFRICA CENTER OF EXCELLENCE IN MATERIALS PRODUCT DEVELOPMENT AND NANOTECHNOLOGY (MAPRONANO ACE)

AFRICA CDC
Centres for Disease Control and Prevention
Safeguarding Africa's Health

Teesside University

Tel Aviv University

AFRICAN CENTERS OF EXCELLENCE IN BIOINFORMATICS

ACE

Epidemiology of SARS-CoV-2

Tracking Home

Data Visualizations ▾

Global Map

U.S. Map

Data in Motion

Tracking FAQ



COVID-19 Dashboard by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University (JHU)



Last Updated at (M/D/YYYY)

23/09/2021, 09:21

[Cases](#) | Deaths by
Country/Region/Sovereignty

US

28-Day: 4,182,893 | 48,034
Totals: 42,545,119 | 681,197

India

28-Day: 1,004,891 | 9,685
Totals: 33,563,421 | 446,050

United Kingdom

28-Day: 943,952 | 3,638
Totals: 7,565,758 | 135,961

Iran

28-Day: 680,852 | 14,169
Totals: 5,477,229 | 118,191

Turkey

28-Day: 658,772 | 7,095
Totals: 6,932,423 | 62,307

Brazil

28-Day: 638,030 | 15,671
Totals: 21,283,567 | 592,316

Philippines

28-Day: 534,331 | 4,736
Totals: 2,417,419 | 37,228

Malaysia

28-Day: 524,820 | 0,747

Total Cases
230,090,110Total Deaths
4,719,197Total Vaccine Doses Administered
5,991,295,73728-Day Cases
16,042,28728-Day Deaths
254,81928-Day Vaccine Doses Administered
877,814,323

Esri, FAO, NOAA

Powered by Esri

28-Day

Totals

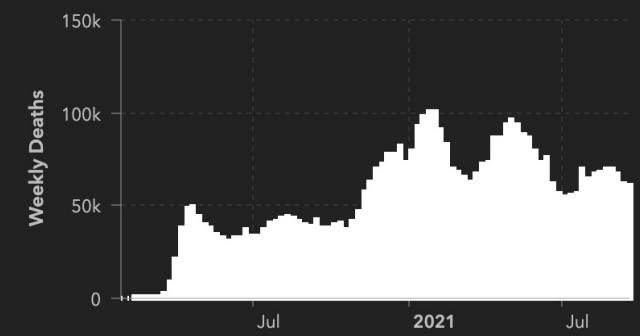
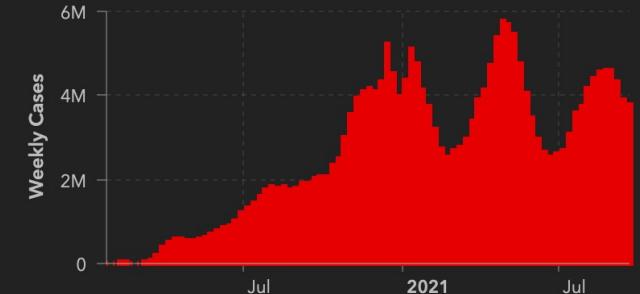
Incidence

Case-Fatality Ratio

Global Vaccinations

US Vaccinations

Terms of Use

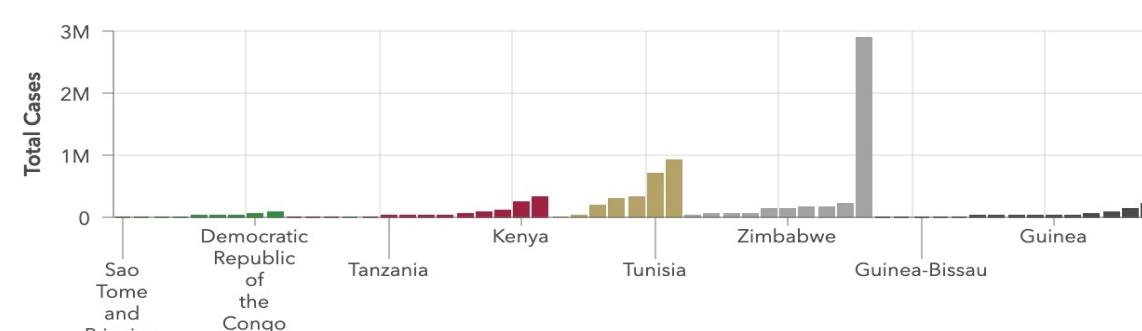
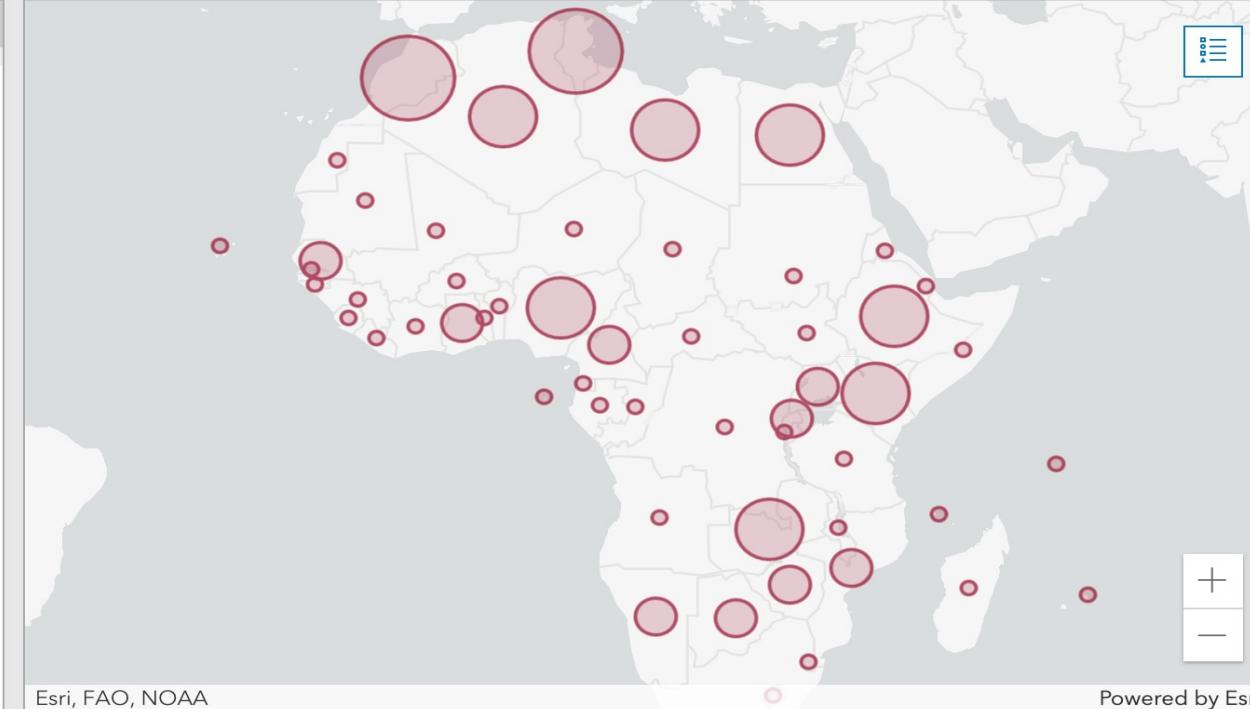


Weekly

Daily



Africa CDC COVID-19 Dashboard

Last update: 23 Sept
2021**Total
8,190,601
Cases****Total
207,594
Deaths****Total
7,552,684
Recoveries****Total
70,739,842
Tests**

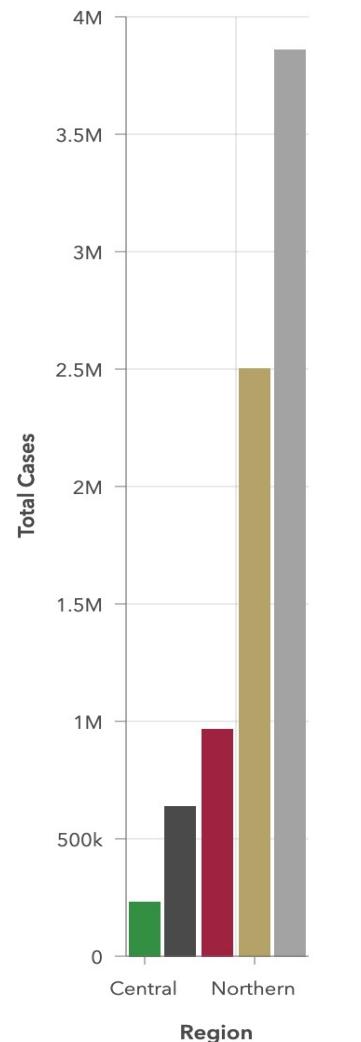
Cases

Deaths

Recoveries

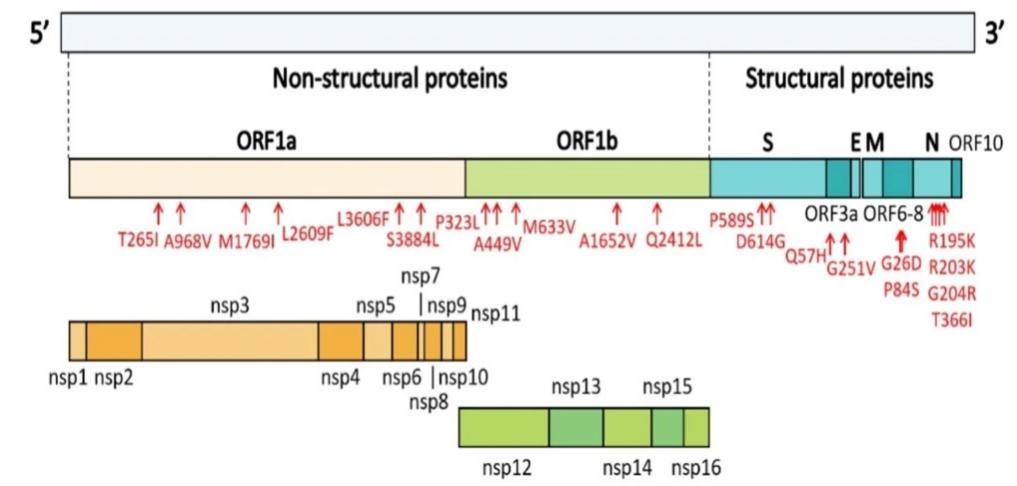
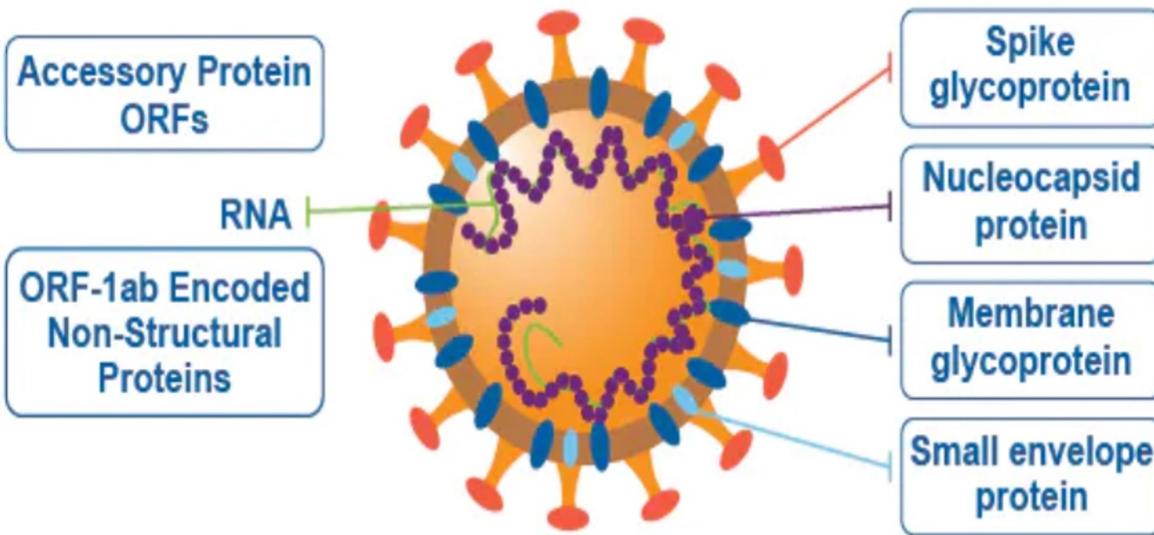
Tests

Dashboard instructions and other info



Genome of SARS-CoV-2

View Resources by SARS-CoV Target



Genome organization of SARS-CoV-2. Image Credit:
<https://www.biorxiv.org/content/10.1101/2020.12.16.423178v1.full.pdf>

<https://www.novusbio.com/support/sars-cov-research-resources>

Testing for SARS-CoV-2 infection

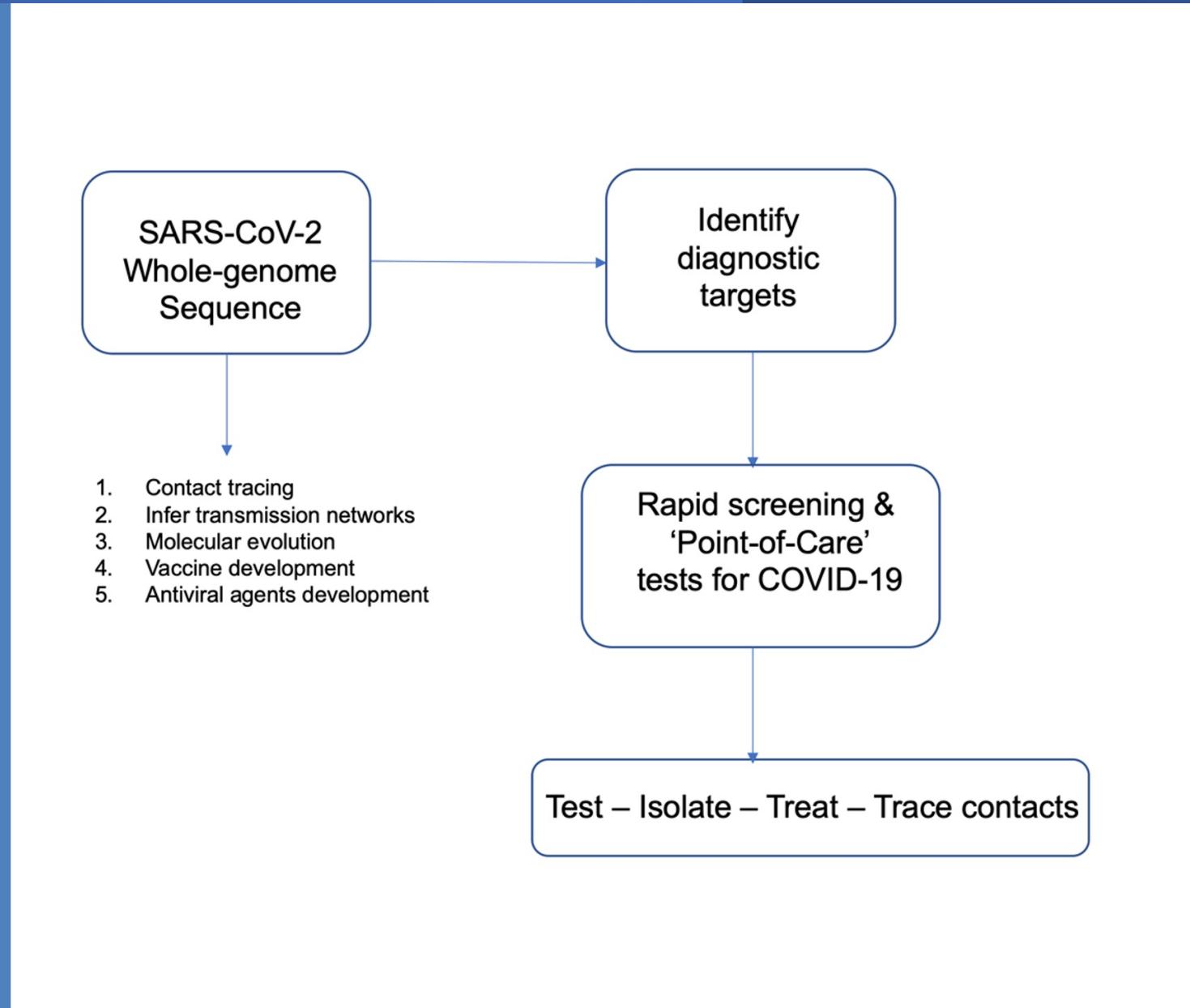
QUICK GUIDE TO COVID-19 TESTING

	MOLECULAR	ANTIGEN	ANTIBODY
ALSO KNOWN AS	PCR, NAAT	Rapid	Serological
SAMPLE NEED	Swab of nasopharynx, nose, or throat; or saliva	Swab of nasopharynx, nose, or throat; or saliva	Blood
WHAT IT TESTS FOR	Presence of virus's genetic material (RNA)	Presence of one or more proteins that are part of the virus	Antibodies produced in response to an infection
WHY YOU WOULD GET THIS TEST	To accurately diagnose or rule out active coronavirus infection	To rapidly diagnose active coronavirus infection, with results in as soon as two hours	To see if you've had coronavirus infection in the past
ACCURACY OF RESULTS	The "gold standard" test that usually doesn't need to be repeated	Positive results are generally accurate. A molecular test may be recommended to confirm a negative result. If an infection is thought to be very unlikely (e.g., no symptoms and no known exposure), a molecular test may also be recommended to confirm a positive.	An antibody test may be negative in the early phases of infection. Additionally, the sensitivity and specificity of antibody tests vary.



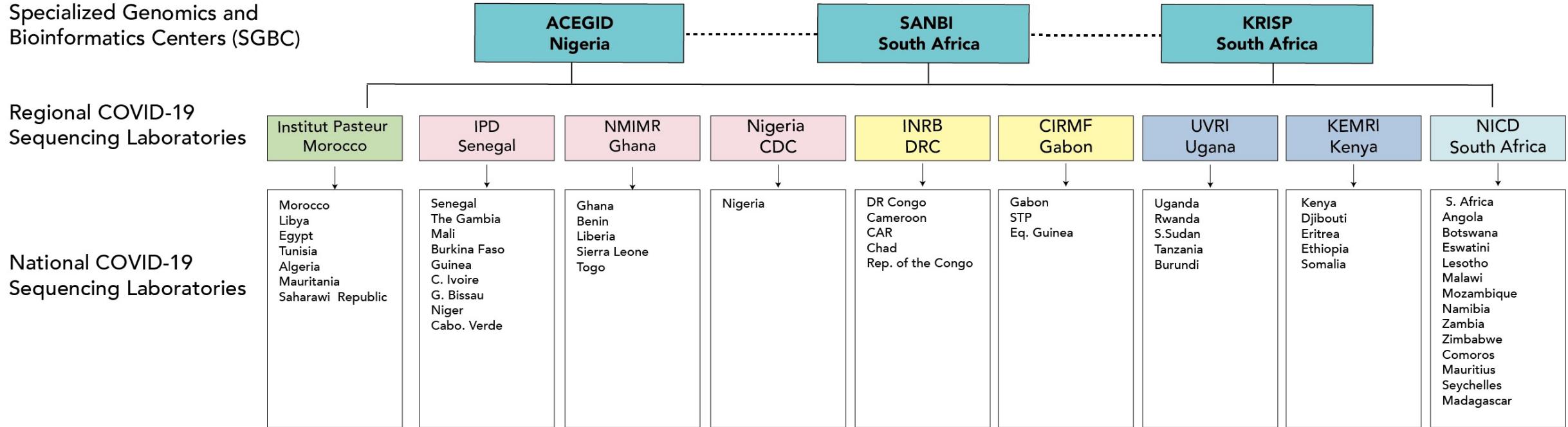
Utility of SARS-CoV-2 whole-genome sequencing

Mboowa G. Current and emerging diagnostic tests available for the novel COVID-19 global pandemic [version 1]. AAS Open Res 2020, 3:8 (doi: 10.12688/aasopenres.13059.1)



SARS-COV-2 SEQUENCING IN AFRICA

Joint Africa CDC and WHO AFRO Sequencing Network for COVID-19 and emerging pathogens



Operationalization of the network

Coordination

Leverage on existing capacity

Access to sequencing

Data sharing

Africa CDC Institute of Pathogen Genomics

Vision: Integration of pathogen genomics and bioinformatics into public health surveillance, outbreak investigations, and improved disease control and prevention in Africa

5 cross-cutting strategic priorities

Enabling mechanisms, policies and guidelines

Enabling and sustainability mechanisms for the integration of genomic-based surveillance in public health systems

Pathogen Genomics & Bioinformatics Network

Building a functional continent-wide pathogen genomics network of laboratories, bioinformatics, data systems and human capacity

Capacity Building

Strengthen sequencing and bioinformatics infrastructure and workforce development

Data Systems

Data architecture, analyses, interpretations, utilization and sharing

Genomic epidemiology

Implementation of public health priority use-cases

Impact:

Rapid and timely response to infectious disease threats in Africa

COVID-19

SARS-CoV-2 genomic surveillance in Africa



Variants	Countries where reported	Sequences of variants
	ALPHA	45
	BETA	41
	DELTA	41
	GAMMA	5
	OTHER	---

43

countries reporting variants

21

countries with genome sequencing capacity

45 493

samples sequenced to date

COVID-19 Statistics in Africa

On average **260** SARS-CoV-2 WGS being added daily from Africa; **3,388** to meet the target (**50,000**)

1.1% of the GISAID SARS-CoV-2 genomes are from Africa

Only **0.5%** of over **8,230,908** million COVID-19 cases in Africa have been sequenced

50 Member States are reporting at least one Variant of Concern

8 weeks is average time from sample collection to submission to GISAID

27 MS on average have routine sequencing capacity

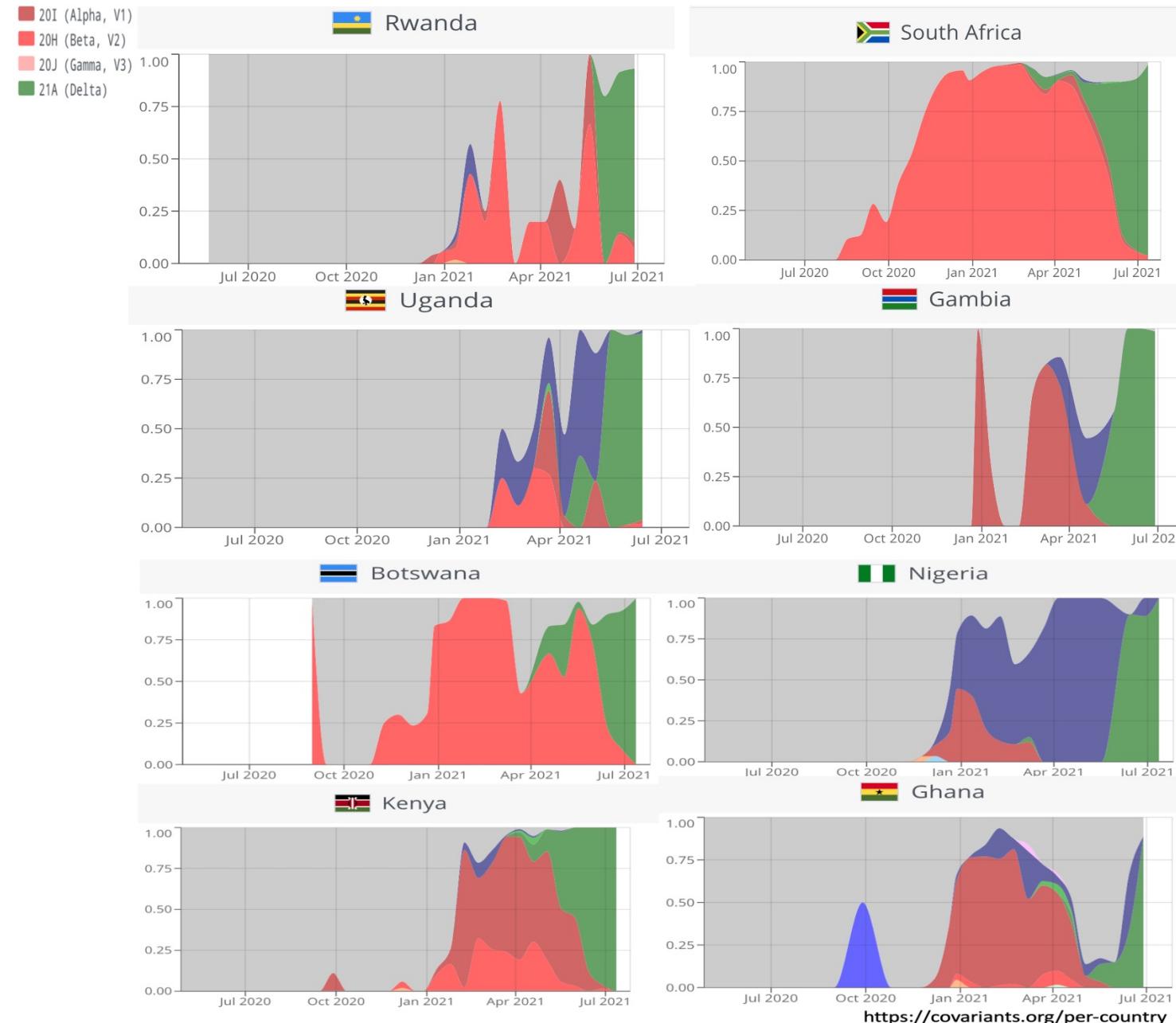
Total SARS-CoV-2 Sequences

46,612

Member States Reporting

39 **45** **41** **6**

BETA **ALPHA** **DELTA** **Gamma**



COVID-19 cases that have been sequenced and submitted in GISAID per month from AU MS since March 2021

Month 2021	* Total new COVID-19 cases per month from MS	# Total new SARS- CoV-2 sequences per month from MS	# AU Member States sharing sequences
March	328,285	2,362	27
April	333,840	3,036	23
May	300,981	3,894	29
June	673,297	6,401	24
July	1,216,102	7,157	34
August	1,045,835	5,331	21
Sept	494,346	8,305	33

Proportion of COVID-19 cases that have been sequenced and submitted in GISAID per continent



Continent	COVID19Cases	SequencedGenomes	SequencesGISAID
South America	37,213,429	67,833	0.2%
Asia	72,442,394	223,801	0.3%
Africa	8,087,508	39,745	0.5% 
North America	50,121,308	1,096,429	2.2%
Europe	56,624,753	1,977,500	3.5%
Oceania	183,974	30,801	16.7%



<https://www.worldometers.info/coronavirus/>



<https://www.gisaid.org/>

Analysis solutions for SARS-CoV-2 sequences

- Instrument onboard bioinformatics platforms for SARS-CoV-2 sequence analysis
- Online Open access Bioinformatics resources for SARS-CoV-2 sequence analysis
- National Public Health Institutes (NPHIs) bioinformatics resources for SARS-CoV-2 sequence analysis

Illumina SARS-CoV-2 NGS Data Toolkit

Novel Pathogen Detection



DRAGEN
Metagenomics App

Detection and Surveillance



DRAGEN RNA
Pathogen Detection
App



DRAGEN COVID
Lineage App

Sharing and Collaboration



SRA Import App



GISAID
Submission App

The Illumina SARS-CoV-2 NGS Data Toolkit is available on BaseSpace Sequence Hub.

Open-source bioinformatic platforms for analysis of SARS-CoV-2 genomes from NGS sequencing data

- SARS-CoV-2 RECoVERY
- Stanford Coronavirus Antiviral & Resistance Database (CoVDB) (<https://covdb.stanford.edu/>)
- Galaxy server
- GEAR: Genome analysis server
- poreCov (nanopore)

Analysis function comparison of SARS-CoV-2 online resources

Functions or features		2019nCoVR	NCBI SARS-CoV-2 resources	UCSC SARS-CoV-2 browser	Genome detective	NMDC	VIC
Genome sequences	Sequence comparison	√	√	√		√	
	Gene annotation	√				√	
	Variant identification	√			√		
	Phylogenetic tree	√			√	√	
NGS raw reads	<i>De novo</i> assembly	√			√		√
	Variant identification	√					
	Variant annotation	√		√			
Open access	Do not need login	√	√	√	√	√	√

*: 2019nCoVR: 2019 Novel Coronavirus Resource; NCBI: National Center for Biotechnology Information; UCSC: University of California, Santa Cruz; NMDC: National Microbiology Data Center; VIC: Virus Identification Cloud.

De Sabato, Luca, et al. "SARS-CoV-2 RECoVERY: a multi-platform open-source bioinformatic pipeline for the automatic construction and analysis of SARS-CoV-2 genomes from NGS sequencing data." *bioRxiv* (2021).

National Public Health Institutes (NPHIs) bioinformatics resources for SARS-CoV-2 sequence analysis

- COVID-19 Genomics UK (COG-UK)'s Cloud Infrastructure for Microbial Bioinformatics (CLIMB)
- Canadian VirusSeq Data Portal
- European COVID-19 Data Portal | ELIXIR
- US CDC EDGE COVID-19
- AusTrakka (Australia)
- BIG Sub - National Genomics Data Center | China (<https://ngdc.cncb.ac.cn/ncov/>)

Cloud-based solutions for bioinformatic data storage and analysis: DaaS, Data as a Service; IaaS, Infrastructure as a Service; PaaS, Platform as a Service; SaaS, Software as a Service |Amazon | Google Cloud Platform | Microsoft Azure | Terra Bioinformatics Platform

- QIAGEN CLC Genomics Workbench
- Genome Detective
- BioMérieux Episeq SARS-CoV-2 genomic software
- COVIDomic platform
- EzCOVID19

Download sequence data files using **SRA Toolkit** `fastq-dump -I --split-files SRR15571394 --gzip`



SRA - Now available on the cloud

Sequence Read Archive (SRA) data, available through multiple cloud providers and NCBI servers, is the largest publicly available repository of high throughput sequencing data. The archive accepts data from all branches of life as well as metagenomic and environmental surveys. SRA stores raw sequencing data and alignment information to enhance reproducibility and facilitate new discoveries through data analysis.

Sequence assembly

<https://github.com/rrwick/Unicycler>

Illumina-only assembly:

```
unicycler -1 short_reads_1.fastq.gz -2 short_reads_2.fastq.gz -o output_dir
```

Long-read-only assembly:

```
unicycler -l long_reads_high_depth.fastq.gz -o output_dir
```

Hybrid assembly:

```
unicycler -1 short_reads_1.fastq.gz -2 short_reads_2.fastq.gz -l long_reads.fastq.gz -o output_dir
```

← → C pangolin.cog-uk.io

 Reset entries Upload another file

File name	Sequence name	Lineage
ANALYSED (Click tick icon for more info)	1 sequence	
✓ assembly.fasta	1 length=29721 depth=1.00x	AY.30 

ncbi.nlm.nih.gov/sra/?term=ERR4914338

NCBI Resources How To Sign in to NCBI

SRA SRA ERR4914338 Search Help

Create alert Advanced

COVID-19 Information

Public health information (CDC) | Research information (NIH) | SARS-CoV-2 data (NCBI) | Prevention and treatment information (HHS) | Español

Full Send to:

ERX4781101: MinION sequencing
1 OXFORD_NANOPORE (MinION) run: 105,173 spots, 53.6M bases, 46.4Mb downloads

Design: hCoV-19 ONT reads obtained following the Artic protocol

Submitted by: NVRL

Study: Interinstitutional effort to sequence SARS-CoV-2 circulating genomes in Ireland during the Covid-19 global pandemic.
[PRJEB40277](#) • [ERP123896](#) • All experiments • All runs
[show Abstract](#)

Sample: hCov-19 ONT reads obtained following the Artic v3 protocol
[SAMEA7686042](#) • [ERS5442574](#) • All experiments • All runs
Organism: Severe acute respiratory syndrome coronavirus 2

Library:
Name: 75IRL94334
Instrument: MinION
Strategy: AMPLICON
Source: GENOMIC
Selection: unspecified
Layout: SINGLE
Construction protocol: Artic protocol version 3

Runs: 1 run, 105,173 spots, 53.6M bases, [46.4Mb](#)

Run	# of Spots	# of Bases	Size	Published
ERR4914338	105,173	53.6M	46.4Mb	2020-12-06

ID: 12599863

Related information

BioProject
BioSample
Taxonomy

Search details

ERR4914338[All Fields]

Search See more...

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SRA

SRA

Advanced

Search

Help



COVID-19 Information

[Public health information \(CDC\)](#) | [Research information \(NIH\)](#) | [SARS-CoV-2 data \(NCBI\)](#) | [Prevention and treatment information \(HHS\)](#) | [Español](#)

Full ▾

Send to: ▾

Related information

BioProject

BioSample

Taxonomy

Recent activity

[Turn Off](#) [Clear](#)

Your browsing activity is empty.

SRX11869109: Amplicon-Seq of SARS-CoV-2

1 ILLUMINA (Illumina MiSeq) run: 359,991 spots, 153.1M bases, 68.5Mb downloads

Design: Illumina DNA Prep Kit**Submitted by:** AFRIMS**Study:** Coding-Complete Genome Sequences of Alpha and Delta SARS-CoV-2 variants from Kamphaeng Phet Province, Thailand from May to July 2021[PRJNA757144](#) • [SRP333803](#) • [All experiments](#) • [All runs](#)
[show Abstract](#)**Sample:**[SAMN20934643](#) • [SRS9881227](#) • [All experiments](#) • [All runs](#)*Organism:* Severe acute respiratory syndrome coronavirus 2**Library:***Name:* AFRIMS-COV2228*Instrument:* Illumina MiSeq*Strategy:* WGS*Source:* VIRAL RNA*Selection:* RT-PCR*Layout:* PAIRED**Runs:** 1 run, 359,991 spots, 153.1M bases, [68.5Mb](#)

Run	# of Spots	# of Bases	Size	Published
SRR15571394	359,991	153.1M	68.5Mb	2021-08-23

ID: 15786886

ncbi.nlm.nih.gov/sra/SRX12230737[accn]

NCBI Resources How To

SRA SRA Advanced Search Help

COVID-19 Information

[Public health information \(CDC\)](#) | [Research information \(NIH\)](#) | [SARS-CoV-2 data \(NCBI\)](#) | [Prevention and treatment information \(HHS\)](#) | [Español](#)

SRX12230737: Other Sequencing of Severe acute respiratory syndrome coronavirus 2
1 PACBIO_SMRT (Sequel II) run: 6,998 spots, 5.1M bases, 2.1Mb downloads

External Id: LC0250009
Submitted by: CDC-OAMD

Study: SARS-CoV-2 Genome sequencing and assembly - LabCorp
[PRJNA716984](#) • [SRP325386](#) • [All experiments](#) • [All runs](#)
[show Abstract](#)

Sample: CDC Sars CoV2 Sequencing Baseline Constellation
[SAMN21478406](#) • [SRS10206474](#) • [All experiments](#) • [All runs](#)
Organism: Severe acute respiratory syndrome coronavirus 2

Library:
Name: SARS-CoV-2/Human/USA/TX-CDC-LC0250009/2021
Instrument: Sequel II
Strategy: AMPLICON
Source: VIRAL RNA
Selection: RT-PCR
Layout: PAIRED
Construction protocol: Freed primers

Runs: 1 run, 6,998 spots, 5.1M bases, [2.1Mb](#)

Run	# of Spots	# of Bases	Size	Published
SRR15940510	6,998	5.1M	2.1Mb	2021-09-17

Send to: Related information

BioProject

BioSample

Taxonomy

Recent activity

Turn Off Clear

Your browsing activity is empty.

So what do we do with all this sequence data?

PACBIO®



Oxford
NANOPORE
Technologies

PacBio Sequel II



illumina®



Benchtop

Production-Scale



@edge-covid19.edgebioinformatics.org

Gerald



HOME Analytics

about EDGE COVID-19

load Files

in EDGE COVID-19

t EDGE COVID-19

ports

jects

Input Your Sample

EDGE requires sequence data files in **FASTQ** format. EDGE accepts both paired-end and single-end sequence data files. [User Guide](#)

Input Raw Reads

Project/Run Name

#

Description

(optional)

Input Source

READS / FASTQ

NCBI SRA

Platform

Nanopore

Illumina

PacBio

Sequencing Reads:

Pair-1 FASTQ File

PublicData/SRR13530301.1.fastq.gz



Pair-2 FASTQ File

PublicData/SRR13530301.2.fastq.gz



and/or

Single-end FASTQ File

absolute file path/select file



| additional options |

A screenshot of a web browser window showing the Austrakka portal at portal.austrakka.net.au. The browser interface includes a back button, forward button, refresh button, address bar, and various icons for file operations and settings.

The Austrakka logo is visible in the top left corner of the page. The logo features a green hexagonal shape with internal lines forming a cube-like structure, surrounded by small green and black dots connected by lines, resembling a molecular or network diagram.

The main content area contains three descriptive text blocks:

- Combining Genomics & Epidemiological Data**
- Promoting Data Sharing Across Public Health Labs**
- Ensuring Better Health Outcomes for Australians**

Below these descriptions is the large Austrakka logo with the tagline "Real-time pathogen genomics surveillance".



SARS-CoV-2 Sequence Reads (NGS) Analysis

SARS-CoV-2 Sequence Reads of each SARS-CoV-2 gene, Spike, RdRP, nsp1-10 (include PLpro and 3CLpro), nsp13-16, ORF3a, E, M, ORF6, ORF7a, ORF8, N and ORF10, can be submitted in the form of [codon frequency](#).

We provide a pipeline for directly aligning FASTQ files and generating CodFreq tables from the MINIMAP2 alignments. To use this pipeline, just add the .fastq or .fastq.gz files to the below input form. By clicking the "Analyze" button, the pipeline will automatically start the FASTQ pipeline, upload your FASTQ files to our server. Once the pipeline is finished, buttons for downloading the CodFreq tables or directly running the analysis will appear.

For submitted FASTQ files, please note that these files will be stored for two weeks for quality control purposes in the event that questions arise regarding the manner in which the codon frequency file is produced.

Input mutations

Input sequences

Input sequence reads

Upload file(s):

[Choose File](#)

No file chosen

[Load Example Data](#)

Drag and drop CodFreq files

Output options



HTML



Printable HTML



Sequences and spreadsheets (FASTA/CSV)

Reset

Analyze

Convert FASTQ

[Browse](#)

covdb.stanford.edu/sierra/sars2/by-reads/



Stanford University
CORONAVIRUS ANTIVIRAL & RESISTANCE DATABASE
A Stanford HIVDB team website. Last updated on 9/19/2021, 11:08:54 PM.

HOME RESISTANCE ANALYSIS PROGRAM DRUGS TRIALS CITATION SUPPORT COVDB

SARS-CoV-2 Sequence Reads (NGS) Analysis

SARS-CoV-2 Sequence Reads of each SARS-CoV-2 gene, Spike, RdRP, nsp1-10 (include PLpro and 3CLpro), nsp13-16, ORF3a, E, M, ORF6, ORF7a, ORF8, N and ORF10, can be submitted in the form of [codon frequency tables \(CodFreq files\)](#).

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Input mutations Input sequences **Input sequence reads**

Upload file(s): No file chosen

Drag and drop CodFreq files

Output options

HTML Printable HTML Sequences and spreadsheets (FASTA/CSV)

Convert FASTQ => CodFreq Files

<https://covdb.stanford.edu/sierra/sars2/by-reads/>

SARS-CoV-2 Sequence Reads (NGS) Analysis

SARS-CoV-2 Sequence Reads of each SARS-CoV-2 gene, Spike, RdRP, nsp1-10 (include PLpro and 3CLpro), nsp13-16, ORF3a, E, M, ORF6, ORF7a, ORF8, N and ORF10, can be submitted in the form of [codon frequency tables \(CodFreq files\)](#).

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Input mutations Input sequences **Input sequence reads**

Upload file(s): No file chosen [Load Example Data](#)

Drag and drop CodFreq files

Output options

HTML Printable HTML Sequences and spreadsheets (FASTA/CSV)

Convert FASTQ => CodFreq Files

FASTQ format

Name: ✖

✖

1 file:



SARS-CoV-2 Sequence Reads (NGS) Analysis

SARS-CoV-2 Sequence Reads of each SARS-CoV-2 gene, Spike, RdRP, nsp1-10 (include PLpro and 3CLpro), nsp13-16, ORF3a, E, M, ORF6, ORF7a, ORF8, N and ORF10, can be submitted in the form of [codon frequency tables \(CodFreq files\)](#).

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For submitted FASTQ files, please note that these files will be stored for two weeks for quality control purposes in the event that questions arise regarding the manner in which the codon frequency file is produced.

Input mutations Input sequences **Input sequence reads**

Upload file(s): [Choose File](#) No file chosen [Load Example Data](#)

Drag and drop CodFreq files

Output options

HTML Printable HTML Sequences and spreadsheets (FASTA/CSV)

Reset Analyze

Convert FASTQ => CodFreq Files

Browse files

Name: SRR15571394 [Edit](#)

SRR15571394_1.fastq.gz [Delete](#)

SRR15571394_2.fastq.gz [Delete](#)

2 files: [Start process](#) Reset



SARS-CoV-2 Sequence Reads (NGS) Analysis

SARS-CoV-2 Sequence Reads of each SARS-CoV-2 gene, Spike, RdRP, nsp1-10 (include PLpro and 3CLpro), nsp13-16, ORF3a, E, M, ORF6, ORF7a, ORF8, N and ORF10, can be submitted in the form of [codon frequency tables \(CodFreq files\)](#).

We provide a pipeline for directly aligning FASTQ files and generating CodFreq tables from the MINIMAP2 alignments. To use this pipeline, just add the .fastq or .fastq.gz files to the below input form. By clicking the "Start process" button, the program will automatically start the FASTQ pipeline, upload your FASTQ files to our server. Once the pipeline is finished, buttons for downloading the CodFreq tables or directly running the analysis will appear.

For submitted FASTQ files, please note that these files will be stored for two weeks for quality control purposes in the event that questions arise regarding the manner in which the codon frequency file is produced.

Input mutations Input sequences Input sequence reads

Upload file(s):

No file chosen

[Load Example Data](#)

Drag and drop CodFreq files

Output options

HTML Printable HTML Sequences and spreadsheets (FASTA/CSV)

Reset

Analyze

Creating task...

Retrieving uploading credential...

Uploading ERR4914338_1.fastq.gz... (27,197,440/43,079,272)



SARS-CoV-2 NGS Pipeline

SARS-CoV-2 NGS Pipeline **converts FASTQ files into codon frequency tables (CodFreq files)**. The pipeline first aligns FASTQ files using MINIMAP2. It then extracts codon frequency tables from the output SAM fil

Creating task...

Triggering parallel task runners, this may take 1-2 minutes...

Aligning ERR4914338_1 with Wuhan-Hu-1::NC_045512.2 using Minimap2, this may take 1-2 minutes...

Minimal example of a CodFreq file:

gene position totalReads codon reads

S	1	1247	ATG	1226
S	1	1247	ATT	9
S	1	1247	CTG	4
S	1	1247	AGG	3
S	1	1247	TTG	3
S	1	1247	TTT	2
S	2	1248	TTT	1241
S	2	1248	TGT	3
S	2	1248	GTT	1
S	2	1248	TAT	1
S	2	1248	TTA	1
S	2	1248	TTG	1



SARS-CoV-2 NGS Pipeline

SARS-CoV-2 NGS Pipeline **converts FASTQ files into codon frequency tables (CodFreq files)**. The pipeline first aligns FASTQ files using MINIMAP2. It then extracts codon frequency tables from the output SAM files.

Creating task...
Triggering parallel task runners, this may take 1-2 minutes...
Aligning SRR15571394 with Wuhan-Hu-1::NC_045512.2 using Minimap2, this may take 1-2 minutes...
Processing file(s) SRR15571394_1.fastq.gz, SRR15571394_2.fastq.gz... (711,373/711,373)
Task finished.

1 CodFreq file:

[Download](#)

[Analyze](#)

Minimal example of a CodFreq file:

gene	position	totalReads	codon	reads
S	1	1247	ATG	1226
S	1	1247	ATT	9
S	1	1247	CTG	4
S	1	1247	AGG	3
S	1	1247	TTG	3
S	1	1247	TTT	2
S	2	1248	TTT	1241
S	2	1248	TGT	3
S	2	1248	GTT	1
S	2	1248	TAT	1
S	2	1248	TTA	1
S	2	1248	TTG	1

[←](#) [→](#) [⟳](#) covdb.stanford.edu/sierra/sars2/ngs2codfreq/?task=f7879c9a-4837-4043-add6-11b798076043 [☆](#) [☰](#)

 Stanford University
CORONAVIRUS ANTIVIRAL & RESISTANCE DATABASE
A Stanford HIVDB team website. Last updated on 9/19/2021, 11:08:54 PM.

HOME RESISTANCE ANALYSIS PROGRAM DRUGS TRIALS CITATION SUPPORT COVDB

SARS-CoV-2 NGS Pipeline

SARS-CoV-2 NGS Pipeline **converts FASTQ files into codon frequency tables (CodFreq files)**. The pipeline first aligns FASTQ files using MINIMAP2. It then extracts codon frequency tables from the output SAM files.

Creating task...

Triggering parallel task runners, this may take 1-2 minutes...

Aligning ERR4914338_1 with Wuhan-Hu-1::NC_045512.2 using Minimap2, this may take 1-2 minutes...

Processing file(s) ERR4914338_1.fastq.gz... (105,173/105,173)

Task finished.

1 CodFreq file:

[Download](#)

[Analyze](#)

Minimal example of a CodFreq file:

gene	position	totalReads	codon	reads
S	1	1247	ATG	1226
S	1	1247	ATT	9
S	1	1247	CTG	4
S	1	1247	AGG	3
S	1	1247	TTG	3
S	1	1247	TTT	2
S	2	1248	TTT	1241
S	2	1248	TGT	3
S	2	1248	GTT	1
S	2	1248	TAT	1
S	2	1248	TTA	1
S	2	1248	TTG	1

→ ↗ covdb.stanford.edu/sierra/sars2/by-reads/report/

Stanford University
CORONAVIRUS ANTI VIRAL & RESISTANCE DATABASE

A Stanford HIVDB team website. Last updated on 9/19/2021, 11:08:54 PM.

HOME RESISTANCE ANALYSIS PROGRAM DRUGS TRIALS CITATION

[CodFreq File](#)

1. SRR15571394

«

1

»

This submission contains 1 sequences.

1. SRR15571394

Sequence summary

Sequence includes following genes:

nsp1 • nsp2 • PLpro • nsp4 • 3CLpro • nsp6 • nsp7 • nsp8 • nsp9 • nsp10 • RdRP • nsp13 • nsp14 • nsp15 • nsp16
• Spike • ORF3a • E • M • ORF6 • ORF7a • ORF7b • ORF8 • N • ORF10

Median read depth:

4,815

PANGO lineage:

B.1.617.2 (Prob=1.0; pangolin: 3.1.11; pangoLEARN: 2021-08-24)

Spike Variant:

Delta (0.03%)

Outbreak.info:

B.1.617.2 (n=522,766)

Nucleotide mixture threshold:

≤0.05% (actual: 0.014%)

Mutation detection threshold:

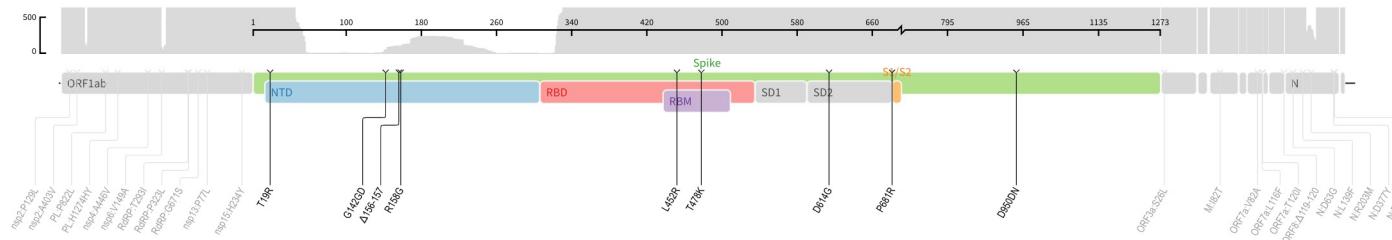
≥10% (actual: ≥13%)

Read depth threshold by codon:

≥10

[Consensus sequence](#)

Sequence quality assessment



[CodFreq File](#)

1. ERR5159276_1

«

1

»

This submission contains 1 sequences.

1. ERR5159276_1

Sequence summary

Sequence includes following genes:

- nsp1 • nsp2 • PLpro • nsp4 • 3CLpro • nsp6 • nsp7 • nsp8 • nsp9 • nsp10 • RdRP • nsp13 • nsp14 • nsp15 • nsp16 • Spike • ORF3a • E • M • ORF6
- ORF7a • ORF7b • ORF8 • N • ORF10

[Consensus sequence](#)

Median read depth:

4,801

PANGO lineage:

B.1.222 (Prob=1.0; pangolin: 3.1.11; pangoLEARN: 2021-08-24)

Outbreak.info:

B.1.222 (n=580)

Nucleotide mixture threshold:

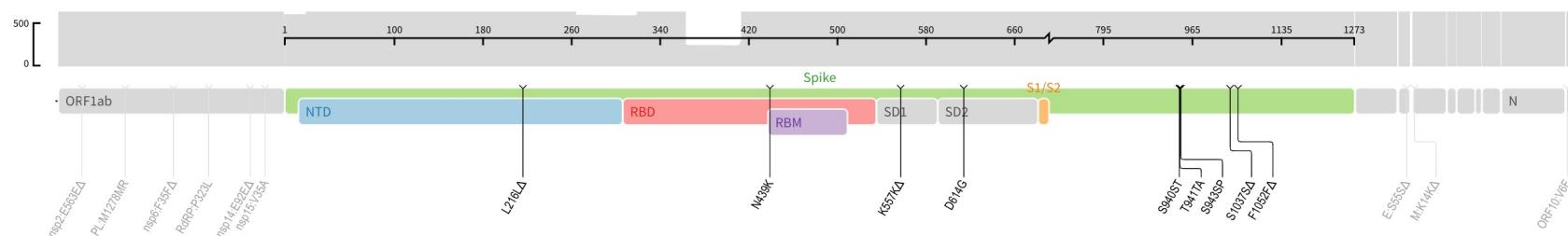
(actual: 0.048%)

Mutation detection threshold:

(actual: ≥26%)

Read depth threshold by codon:

Sequence quality assessment



Mutation list

[CodFreq File](#)

1. ERR5159276_1

1

This submission contains 1 sequences.

Mutation list

nsp2: E563E Δ E: 60%, Δ: 30% cov=5,574

PLpro: M1278MR M: 50%, R: 40% cov=7,038

nsp6: F35F Δ F: 36%, Δ: 30% cov=3,280RdRP: P323L Δ 82% cov=4,695nsp14: E92E Δ E: 59%, Δ: 32% cov=14,514nsp15: V35A Δ 91% cov=2,683Spike: L216L Δ L: 54%, Δ: 38% • N439K Δ 73% cov=6,014 • K557K Δ K: 63%, Δ: 26% • D614G Δ 83% cov=5,397 • S940ST Δ S: 52%, T: 37% cov=3,828• T941TA Δ T: 54%, A: 40% • S943SP Δ S: 47%, P: 47% • S1037S Δ S: 55%, Δ: 32% • F1052F Δ F: 62%, Δ: 26% cov=3,831 cov=4,337 cov=2,825 cov=6,084E: S55S Δ S: 45%, Δ: 38% cov=3,423M: K14K Δ K: 52%, Δ: 30% cov=7,296ORF10: V6F Δ 74% cov=6,623

Mutation comments

Last updated on Aug 30, 2021

• RdRP:P323L

The RdRP mutation P323L (Orf1b:P314L) emerged in the same virus containing D614G. It has now reached a global prevalence of 95%, which is slightly lower than that of D614G (98%). Its impact on RdRp function has not been well studied.

• N439K

N439K is an ACE2-binding site RBD mutation reported to increase ACE2 affinity^{[1][2][3]}. It causes high-level resistance to imdevimab^{[4][5]} and reduces binding to tixagevimab^[6]. Viruses containing N439K usually retain full susceptibility to convalescent plasma^{[7][8][3]}.

• D614G

D614G began increasing in prevalence in late February 2020 and within several months rose to a global prevalence approximating 100%^[9]. Virus clones containing D614G produce higher levels of replication in primary human airway cells and in the upper respiratory tracts of hamsters^{[10][11][12]}. D614G disrupts one or more interprotomer contacts resulting in a greater likelihood that one or more of the three RBDs are in an open versus closed position^{[13][14]}. D614G may also be responsible for increasing the number of spike proteins per virion^{[15][16]} and increasing the rate of S1/S2 cleavage^[17]. In some studies, viruses with D614G have been slightly more susceptible to neutralization by mAbs, convalescent plasma, and plasma from vaccinated persons^{[18][14]} while in other studies they were slightly more resistant to neutralization^{[10][19]}.

 Hide all reference footnotes

[CodFreq File](#)

1. ERR4914338_1

1

This submission contains 1 sequences.

1. ERR4914338_1

Sequence summary

Sequence includes following genes:

- nsp1 • nsp2 • PLpro • nsp4 • 3CLpro • nsp6 • nsp7 • nsp8 • nsp9 • nsp10 • RdRP • nsp13 • nsp14 • nsp15 • nsp16 • Spike • ORF3a • E • M • ORF6
- ORF7a • ORF7b • ORF8 • N • ORF10

[Consensus sequence](#)

Median read depth:

1,202

PANGO lineage:

B.1.177.54 (Prob=1.0; pangolin: 3.1.11; pangoLEARN: 2021-08-24)

Outbreak.info:

[B.1.177.54 \(n=1,621\)](#)

Nucleotide mixture threshold:

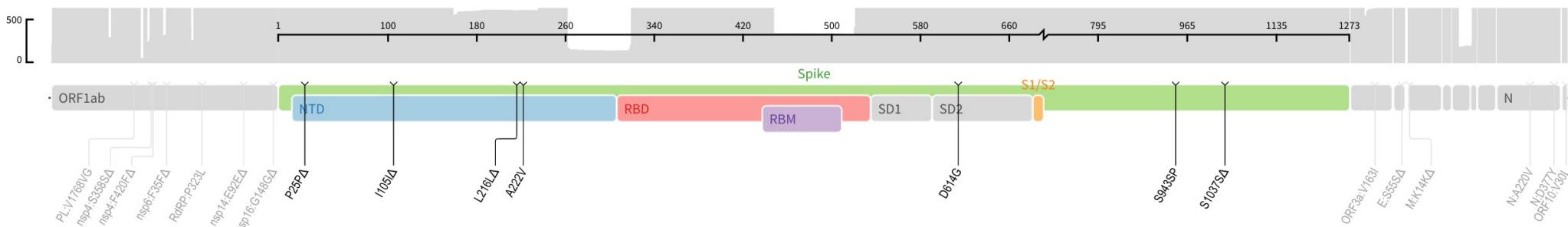
 (actual: 0.048%)

Mutation detection threshold:

 (actual: ≥24%)

Read depth threshold by codon:

Sequence quality assessment



Sequence summary

Sequence includes following genes:

nsp1 • nsp2 • PLpro • nsp4 • 3CLpro • nsp6 • nsp7 • nsp8 • nsp9 • nsp10 • RdRP • nsp13 • nsp14 • nsp15 • nsp16 • Spike • ORF3a • E • M • ORF6 • ORF7a
• ORF7b • ORF8 • N • ORF10

Median read depth:

4,815

PANGO lineage:

B.1.617.2 (Prob=1.0; pangolin: 3.1.11; pangoLEARN: 2021-08-24)

Spike Variant:

Delta (0.03%)

- EPI_ISL_4416353: Romania (2021); Delta (0.03%); best match
- EPI_ISL_2513528: United Kingdom (2021); Delta (0.03%)
- EPI_ISL_2568065: United Kingdom (2021); Delta (0.03%)
- EPI_ISL_4295481: United States (2021); Delta (0.03%)
- EPI_ISL_4176350: United States (2021); Delta (0.03%)
- EPI_ISL_3298531: Ireland (2021); Delta (0.03%)
- EPI_ISL_4416231: Canada (2021); Delta (0.03%)
- EPI_ISL_4349086: Japan (2021); Delta (0.05%)
- EPI_ISL_4415033: Norway (2021); Delta (0.05%)
- EPI_ISL_4409160: Canada (2021); Delta (0.05%)

Outbreak.info:

B.1.617.2 (n=530,988)

Nucleotide mixture threshold:

≤0.05% (actual: 0.014%)

Mutation detection threshold:

≥10% (actual: ≥13%)

Read depth threshold by codon:

≥10

[Consensus sequence](#)

[Download FASTA](#)

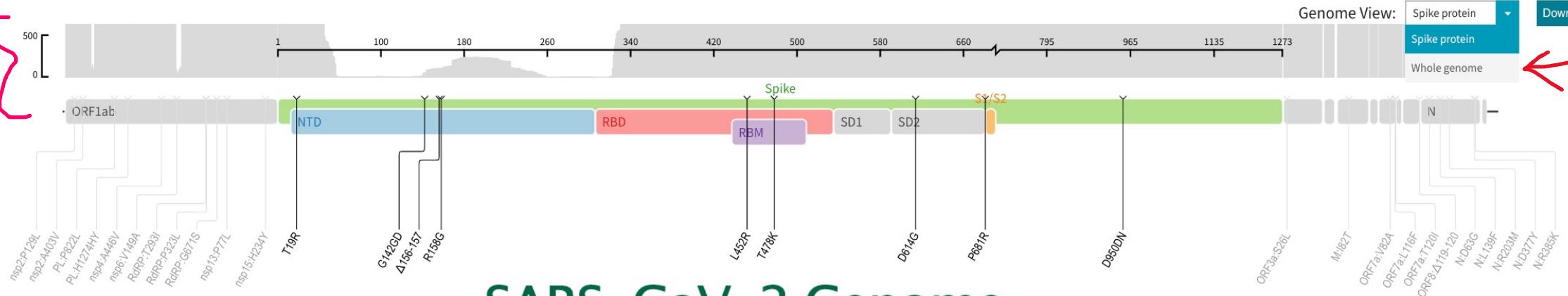
GISAID

gisaid.org

Viral Genome Annotation

Sequence quality assessment

Depth of coverage



GISAID submission requirement
Single upload

```
>SRR15571394 cdreads: 10; cutoff: 0.1; mixrate: 0.0005
ATTAAGGTTATACCTCCCAGGTAAACAAACCAACCAACTTCGAATCTCTTGTAGATCTGTTCTCTAAAACGAACTTAAAATCTGTGCGCTGTCACTCGGCTGCAT
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TGCAAGCCGATCATCAGCACATCTAGAGTTTGCCGGGTGACCGAAAAGGTAAAGATGGAGAGCCTGTCCTGGTTCAACGAGAAAACACACGTCCAACTCAG
TTTGCCCTGTTTACAGGTTCGCGACGTGCTCGTACGTGGTTGGAGACTCCGTGGAGGGTCTTACAGAGGCACGTCAACATCTAAAGATGGCACTTGTGGCT
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http://www.bioinformatics.org/sms2/combine_fasta.html
```

GISAID submission requirement

Batch upload



Fasta to multi-Fasta

```
TTACACCACTGTTGTCAGACTATTGAAGTGAATAGTTAGTGGTATTAAAACCTACTGACAATGTATACATTAAAATGCAAGACATTGTGGAAGAAGCTAAAAG
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```

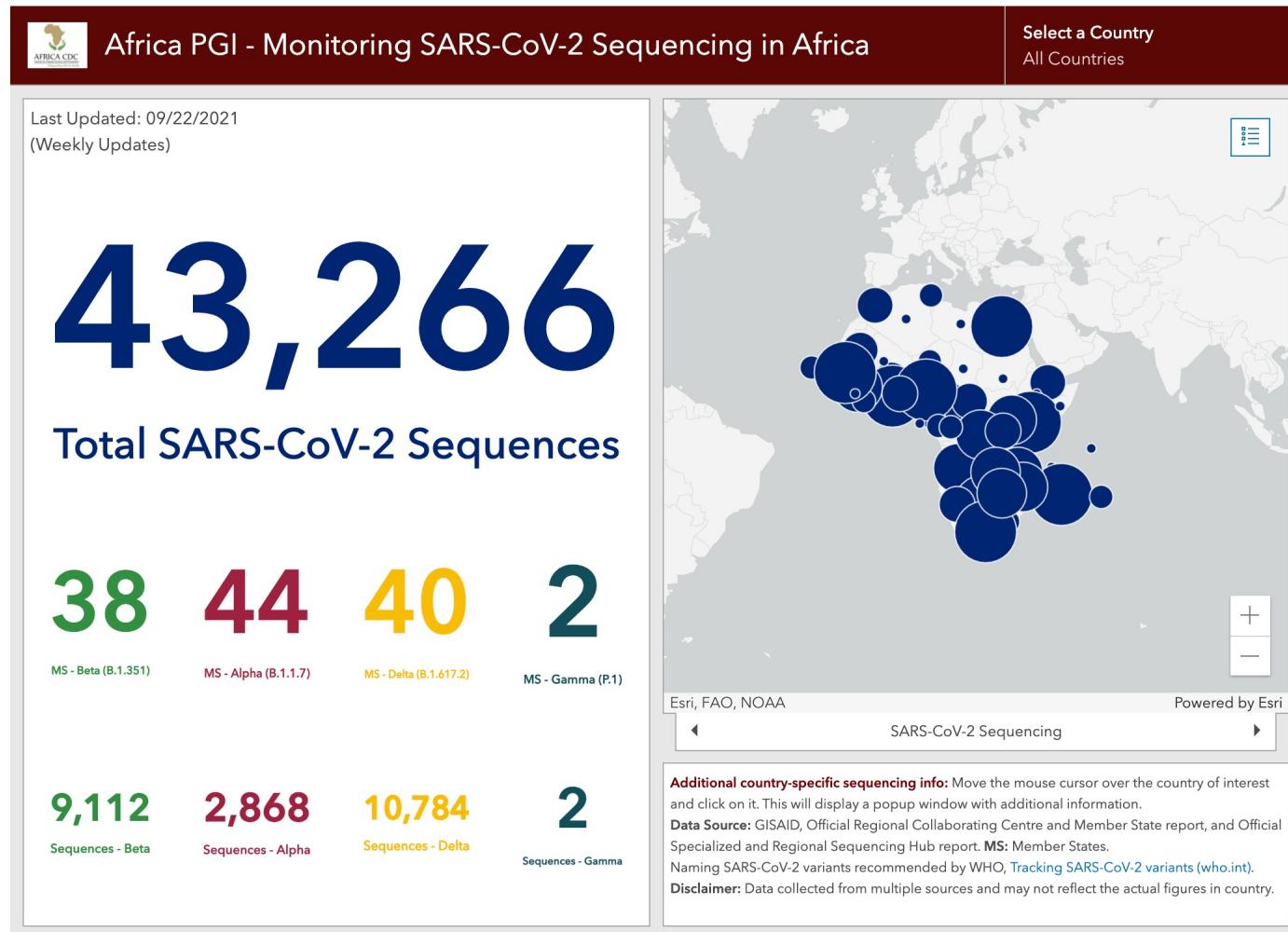
SARS-CoV-2 Variants of Concern and Variants of Interest, updated 31 May 2021

Variants of Concern

A SARS-CoV-2 variant that meets the definition of a VOI (see below) and, through a comparative assessment, has been demonstrated to be associated with one or more of the following changes at a degree of global public health significance:

- Increase in transmissibility or detrimental change in COVID-19 epidemiology; or
- Increase in virulence or change in clinical disease presentation; or
- Decrease in effectiveness of public health and social measures or available diagnostics, vaccines, therapeutics.

WHO label	Pango lineage	GISAID clade/variant	Nextstrain clade	Earliest documented samples	Date of designation
Alpha	B.1.1.7	GRY (formerly GR/501Y.V1)	20I/S:501Y.V1	United Kingdom, Sep-2020	18-Dec-2020
Beta	B.1.351	GH/501Y.V2	20H/S:501Y.V2	South Africa, May-2020	18-Dec-2020
Gamma	P.1	GR/501Y.V3	20J/S:501Y.V3	Brazil, Nov-2020	11-Jan-2021
Delta	B.1.617.2	G/452R.V3	21A/S:478K	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021



COVID-19 Statistics in Africa

On average **244** SARS-CoV-2 WGS being added daily from Africa; **7,059** to meet the target (**50,000**)

1.2% of the GISAID SARS-CoV-2 genomes are from Africa

Only **0.5%** of over **8,134,511** million COVID-19 cases in Africa have been sequenced

48 Member States are reporting at least one Variant of Concern

8 weeks is average time from sample collection to submission to GISAID

26 MS on average have routine sequencing capacity

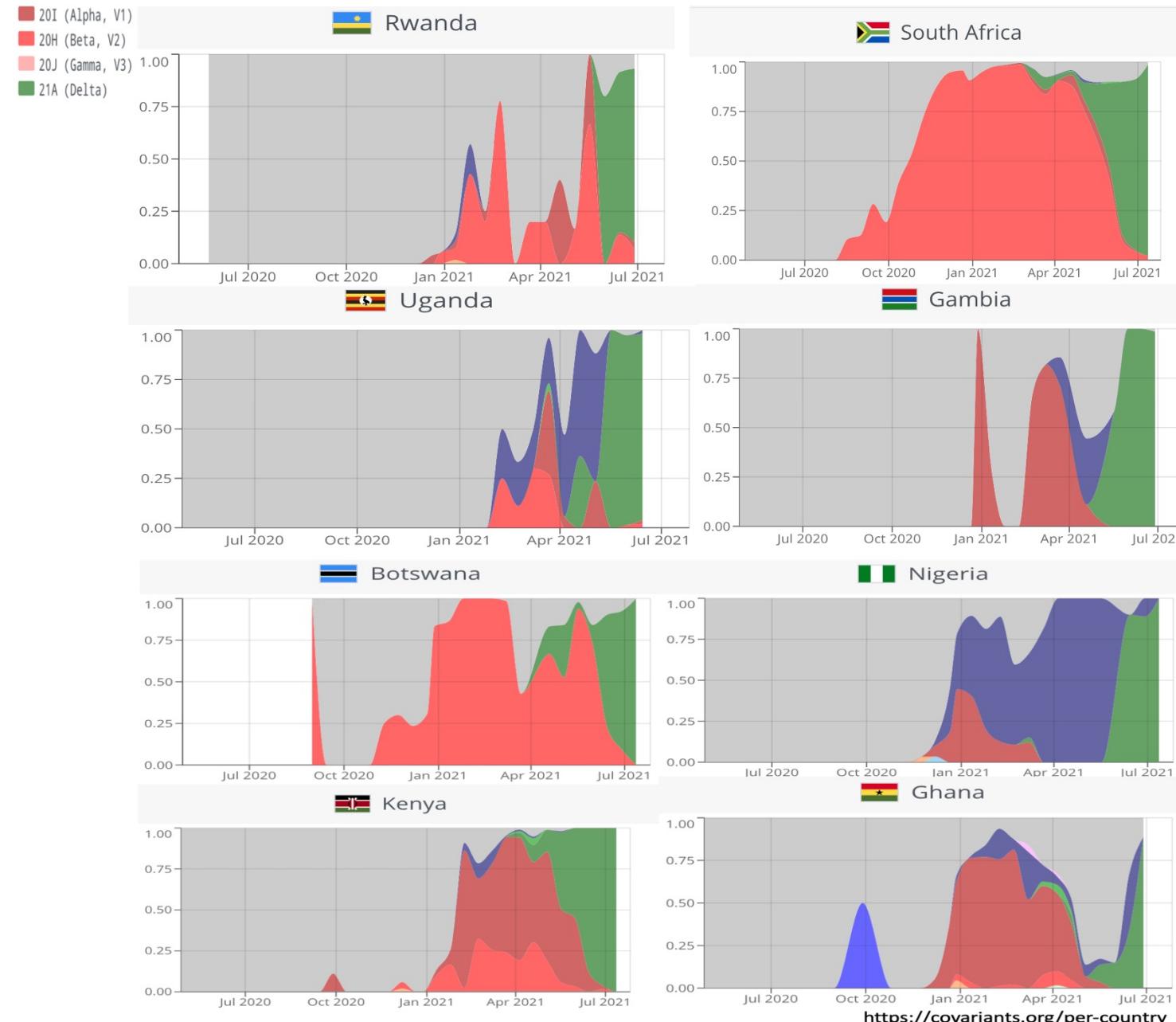
Total SARS-CoV-2 Sequences

42,941

Member States Reporting

43 **37** **38** **2**

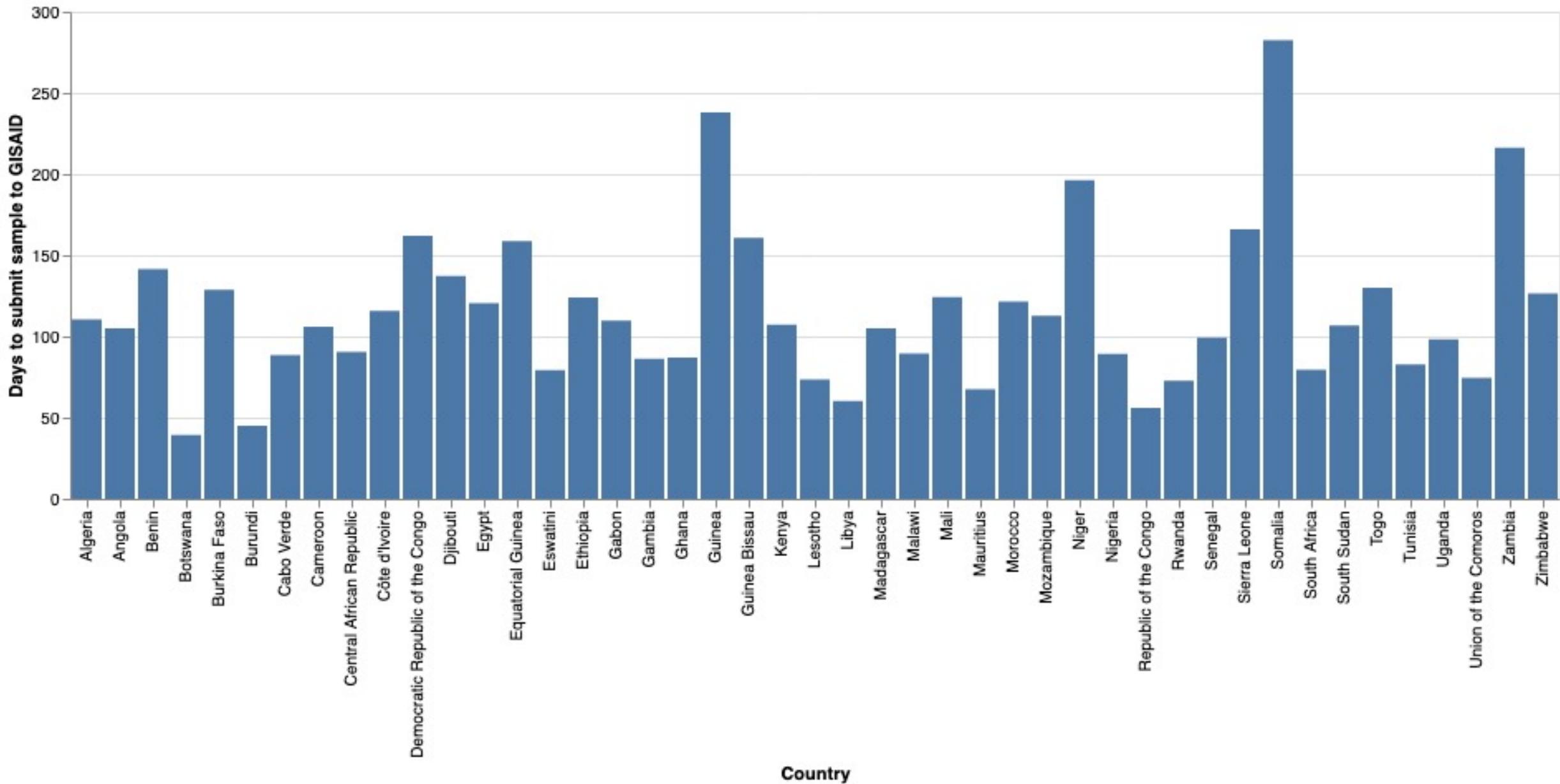
BETA **ALPHA** **DELTA** **Gamma**



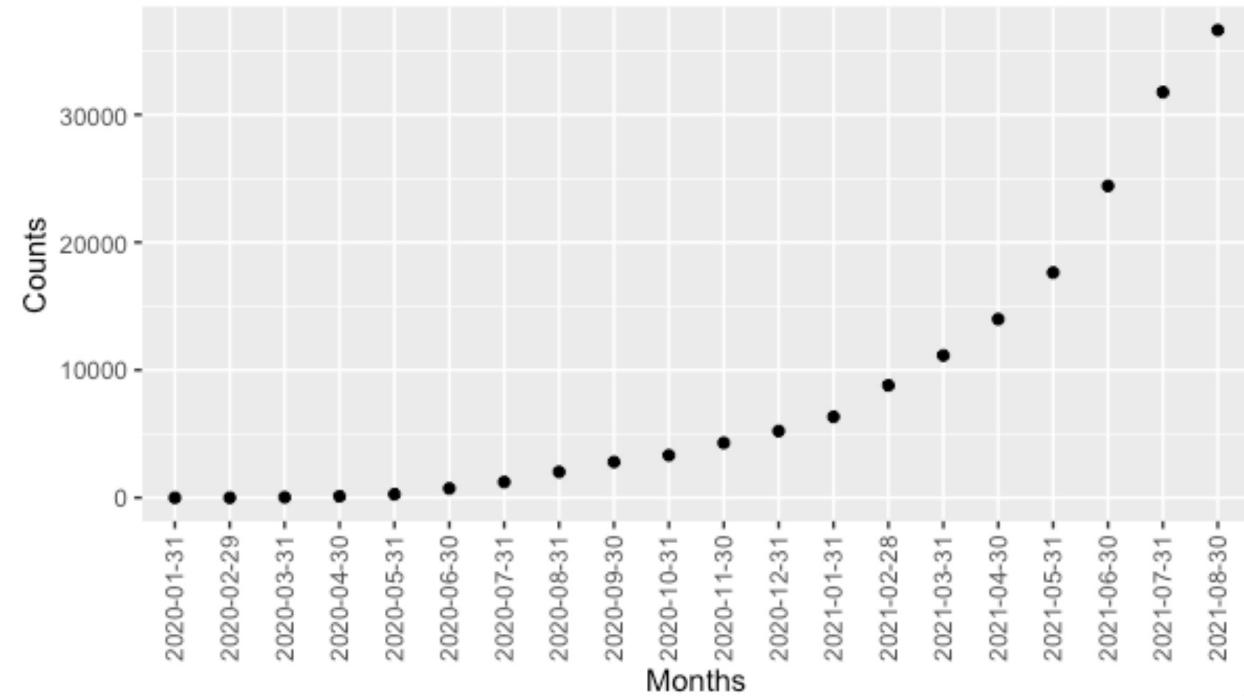
COVID-19 cases that have been sequenced and submitted in GISAID per month from AU MS since March 2021

Month 2021	* Total new COVID-19 cases per month	# Total new SARS- CoV-2 sequences per month	# AU Member States sharing sequences
March	328,285	2,362	27
April	333,840	3,036	23
May	300,981	3,894	29
June	673,297	6,401	24
July	1,216,102	7,157	34
August	1,045,835	5,331	21
Sept	377,225	5,864	17

Average days for African countries to submit data to GISAID. Data extracted as of 20th August 2021

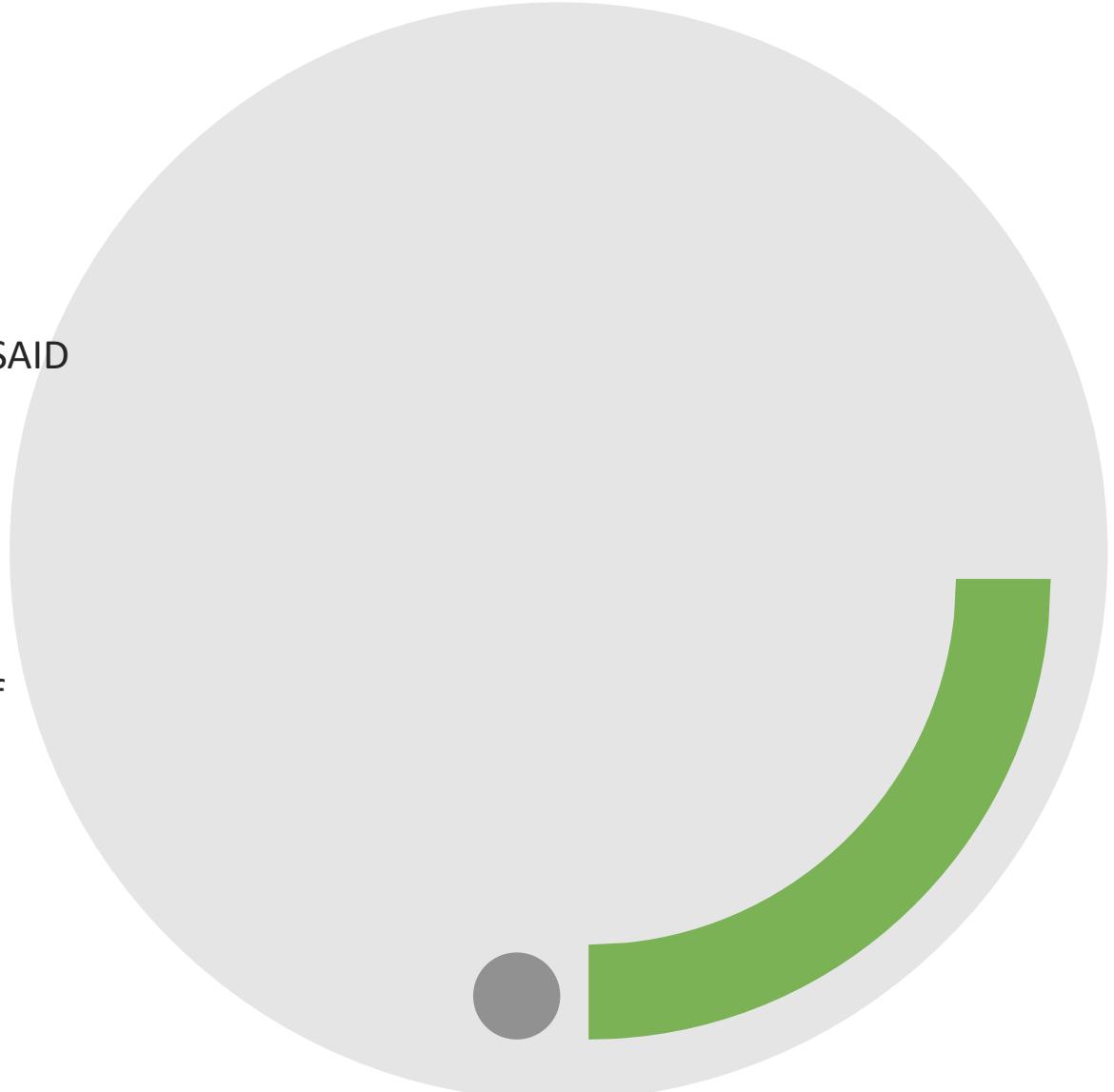


SARS-CoV-2 genomes shared on GISAID from Africa



Challenges | Opportunities

- Sampling, representativeness and generalizability
- Bioinformatics expertise – Training/workshops
- Delays in sequencing and sharing SARS-CoV-2 genomes via GISAID
- NGS reagents supply chain disruptions
- Sample referral costs (\$23/Sample)
- South America, Asia and Africa have each sequenced <1.0% of their SARS-CoV-2 cases
- Federated database management system
- WGS cost is \$100/Sample





The next phase of SARS-CoV-2 surveillance: real-time molecular epidemiology

Bas B. Oude Munnink^{ID}, Nathalie Worp, David F. Nieuwenhuijse^{ID}, Reina S. Sikkema, Bart Haagmans^{ID}, Ron A. M. Fouchier^{ID} and Marion Koopmans^{ID} 

The current coronavirus disease 2019 (COVID-19) pandemic is the first to apply whole-genome sequencing near to real time, with over 2 million severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) whole-genome sequences generated and shared through the GISAID platform. This genomic resource informed public health decision-making throughout the pandemic; it also allowed detection of mutations that might affect virulence, pathogenesis, host range or immune escape as well as the effectiveness of SARS-CoV-2 diagnostics and therapeutics. However, genotype-to-phenotype predictions cannot be performed at the rapid pace of genomic sequencing. To prepare for the next phase of the pandemic, a systematic approach is needed to link global genomic surveillance and timely assessment of the phenotypic characteristics of novel variants, which will support the development and updating of diagnostics, vaccines, therapeutics and nonpharmaceutical interventions. This Review summarizes the current knowledge on key viral mutations and variants and looks to the next phase of surveillance of the evolving pandemic.

- Received: 26 May 2021; Accepted: 20 July 2021;
- Published online: 09 September 2021

Proportion of COVID-19 cases that have been sequenced and submitted in GISAID per continent



Continent	COVID19Cases	SequencedGenomes	SequencesGISAID
South America	37,213,429	67,833	0.2%
Asia	72,442,394	223,801	0.3%
Africa	8,087,508	39,745	0.5% 
North America	50,121,308	1,096,429	2.2%
Europe	56,624,753	1,977,500	3.5%
Oceania	183,974	30,801	16.7%



<https://www.worldometers.info/coronavirus/>



<https://www.gisaid.org/>

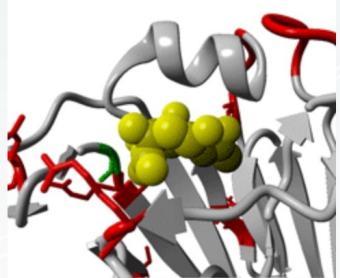
Data Access & Sharing

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In Focus

First human case of influenza A/H10N3 virus infection

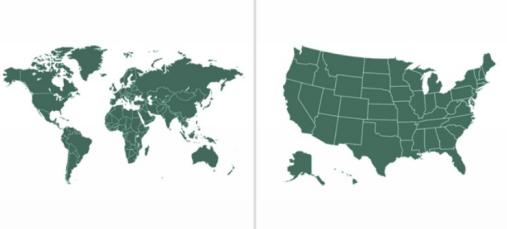
On May 28, 2021 a resident of the City of Zhenjiang in Jiangsu Province, China, was diagnosed with an influenza A/H10N3 virus infection. This is the first human case of infection with a low pathogenic avian influenza virus of this subtype. How the person was infected is unclear. There is no evidence that the virus spreads easily between humans. A/H10 influenza viruses are abundant in wild birds globally, and occasionally transmit to poultry.



The whole genome sequence of the virus, A/Jiangsu/428/2021, was released rapidly via the GISAID Initiative by the Jiangsu Provincial Center for Disease Control and Prevention in Nanjing (EPI_ISL_2379892).

[> read more](#)

hCoV-19 Submission Tracking



hCoV-19 Tracking of Variants



Public-Private Partnerships of the GISAID Initiative

The GISAID Initiative involves public-private-partnerships between the Initiative's administrative arm Freunde of GISAID e.V., a registered non-profit association, and governments of the [Federal Republic of Germany](#), the official host of the GISAID platform, [Singapore](#) and the [United States of America](#), with support from private and corporate philanthropy.



Genomic epidemiology of hCoV-19

Showing 119 of 119 genomes sampled between Dec 2019 and Feb 2020.

Phylogeny Country ▾

NETZLAYOUT

Transmissions

RESET ZOOM

hCoV-19 data sharing via GISAID

3,742,934
submissions

Enabled by data shared via GISAID

Fully interactive platform to explore and monitor variants of SARS-CoV-2

CoVerage

Helmholtz Centre for Infection Research

GISAID Resources

Free Access Credentials

Register here and join thousands of researchers around the globe.

Frequently Asked Questions

Answers about the GISAID Initiative



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information and agrees to the
Database Access Agreement

done automatically and manually
to confirm the applicant's identity

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;
3. You may not distribute GISAID data outside the GISAID community, such as by releasing genetic sequences obtained in GISAID in any publication, transferring the data to colleagues that are not registered users, or offering GISAID data on a server accessible by others who are not duly registered with GISAID;
4. You need to collaborate where appropriate with the Originating Laboratory responsible for obtaining the specimens.

Please complete the registration form and help GISAID protect the use of your identity and the integrity of its user base.

To avoid losing your priority in line for access credentials, you are strongly advised to properly complete the registration form. Incomplete or misspelled names or numbers require additional work for the reviewer, thereby potentially delaying other registration request.

Using webmail addresses for your identification, such as Gmail, Hotmail, Yahoo Mail, QQmail or 126 and 163 Mail, are likely to lower your priority or cause significant delays in reviewing your request. You are encouraged to provide your institutional email address to expedite this process.

We recommend using the following browsers: [Google Chrome](#), [Mozilla Firefox](#)

Register



Registration

Platform Login

Username

gmboowa

Password

Login

[Forgot your password or username?](#)



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Search



Back to results



Worksets



Upload



Batch Upload



Settings



Analysis

Count

342,558 viruses

GISAID published

189,015 viruses (879,581 sequences)

Total count

342,558 viruses (1,480,050 sequences)

Basic filters

Predefined search

Select ...

Search in

 Released files Worksets

Search patterns

Type	H	N	Lineage	Host	Location
A				-all-	-all-
B				Human	Africa
C				Animal	Antarctica
				Avian	Asia
				Chicken	Europe
				Curlew	North America
				Duck	Oceania
				Eagle	South America
				Falcon	
				Goose	

Additional filters

Collection date
(YYYY-MM-DD)

From

To

Submission date

From

To

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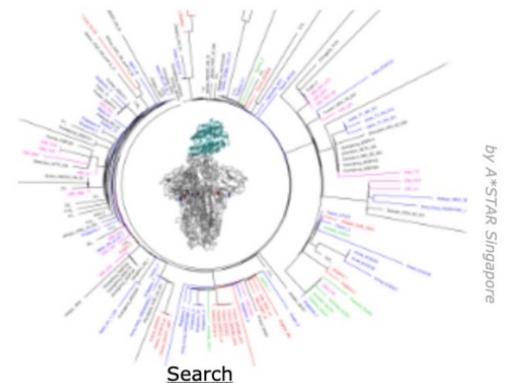
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EpiCoV™ **Search**

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.



[Search](#)

 Audacity	 AudacityInstant	 BLAST	 CoVizue	 Emerging Variants	 Official GISAID reference sequence
 PrimerChecker	 Spike glycoprotein mutation surveillance				

Search										
Accession ID	<input type="text"/>		Virus name	<input type="text"/>		<input type="checkbox"/> complete <small>?</small>	<input type="checkbox"/> high coverage <small>?</small>			
Location	<input type="text"/> Europe / United Kingdom <small>▼</small>		Host	<input type="text"/>		<input type="checkbox"/> low coverage excl <small>?</small>	<input type="checkbox"/> w/Patient status <small>?</small>			
Collection	<input type="text"/> <small>▼</small> to <small>▼</small> <input type="text"/>		Submission	2021-09-01 <small>▼</small>	<input type="text"/> <small>▼</small> to <small>▼</small> <input type="text"/>	<input type="checkbox"/> collection date compl <small>?</small>				
Clade	<input type="text"/> all <small>▼</small>	Lineage	<input type="text"/> <small>▼</small>	Substitutions <small>?</small>	<input type="text"/> <small>▼</small>	Variants	VOC Delta GK/478K.V1 <small>▼</small>	Reset	Fulltext <small>▲</small>	
	Virus name	Passage de	Accession ID	Collection da	Submission D	<small>i</small>	Length	Host	Location	Originating
<input type="checkbox"/>	hCoV-19/E									Lighthou
<input type="checkbox"/>	hCoV-19/W									Lighthou
<input type="checkbox"/>	hCoV-19/W									Lighthou
<input type="checkbox"/>	hCoV-19/W									Lighthou
<input type="checkbox"/>	hCoV-19/W									Lighthou
<input type="checkbox"/>	hCoV-19/W									Lighthou
<input type="checkbox"/>	hCoV-19/W									Lighthou
<input type="checkbox"/>	hCoV-19/E									Lighthou
<input type="checkbox"/>	hCoV-19/W									Lighthou
<input type="checkbox"/>	hCoV-19/W									Lighthou
<input type="checkbox"/>	hCoV-19/W									Lighthou
<input type="checkbox"/>	hCoV-19/England/NEWC-1EA7AC0/2021	Original	EPI_ISL_4503078	2021-09-16	2021-09-25	<small>i</small>	29,769	Human	Europe / United K	Integrate
<input type="checkbox"/>	hCoV-19/Wales/ALDP-1EA8740/2021	Original	EPI_ISL_4503077	2021-09-16	2021-09-25	<small>i</small>	29,760	Human	Europe / United K	Lighthou
<input type="checkbox"/>	hCoV-19/Wales/ALDP-1EA884D/2021	Original	EPI_ISL_4503076	2021-09-15	2021-09-25	<small>!</small>	29,705	Human	Europe / United K	Lighthou
<input type="checkbox"/>	hCoV-19/Wales/ALDP-1EA89B3/2021	Original	EPI_ISL_4503075	2021-09-13	2021-09-25	<small>i</small>	29,769	Human	Europe / United K	Lighthou
<input type="checkbox"/>	hCoV-19/Wales/ALDP-1EA8A56/2021	Original	EPI_ISL_4503074	2021-09-15	2021-09-25	<small>i</small>	29,769	Human	Europe / United K	Lighthou

Single upload

Batch upload

GISAID submission requirement

Single upload

GISAID

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EpiCoV™ Search Downloads Upload

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* hCoV-19/Country/Identifier/2021

Accession ID

Type betacoronavirus

Passage details/history* Example: Original, Vero

Sample information

Collection date* Example: 2021-03-27, 2021-03 (collection in March, specific day unknown), 2021 (collection in 2021, month and day unknown)

Location* Continent / Country or Territory / Region

Additional location information Travel history; Residence; Cruise ship; ...

Host* Human, Environment, Canis lupus.

Additional host information Example: Underlying health conditions; other host relevant characteristics

Outbreak Detail Example: Date, Place, Family cluster

Sampling strategy Baseline surveillance; Active surveillance; Clinical trial; ...

Gender* Male, Female, or unknown

Patient age* Example: 65, 7 months, or unknown

Patient status* Hospitalized, Released, Live, Dec

Specimen source Sewage, Sputum, Alveolar lavage fluid, Oropharyngeal swab, Mid-Turbinate swab, Nasopharyngeal swab, Blood, Tracheal swab, Urine, Stool, Ci

Last vaccinated provide details if applicable

Treatment Example: Include drug name, dosage

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

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

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

Institute information

Originating lab* Where the clinical specimen or virus isolate was first obtained

Address*

Sample ID given by the originating lab

GISAID submission requirement

Batch upload

AGAACAC

epicov.org/epi3/frontend#32636b

GISAID

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EpiCoV™ Search Downloads Upload

GISAID hCoV-19 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*

Sequences as FASTA*

max size: 5M Choose file No file chosen

Sequences as FASTA*

max size: 32M Choose file No file chosen

Confirmation options (Default) Notify me about ALL DETECTED FRAMESHIFTS in this submission for reconfirmation of affected sequences

Report Upload XLS/CSV and FASTA.

[Download Instructions and Template](#)

[Contact Curator](#) [Verify and Submit](#)

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.

1 EpiCoV hCoV-19 bulk upload

2 Version: 2021-02-24

3 Instructions:

- 4 - Enter your data into the sheet "Submissions"
- 5 - The mandatory columns are indicated in color.
- 6 - Do not change the content of the two first rows (1 & 2)
- 7 - Delete, overwrite the examples given in row 3
- 8 - your sequences must be in one single FASTA-File to compliment this spreadsheet with your metadata
- 9 - EXCEL extension must remain .xls (not .xlsx). Always save in EXCEL 97 - 2003 Format.
- 10 - Provide for every row/virus the filename of the FASTA-File that contains the corresponding sequence.
- 11 - "FASTA Filename" must match exactly the actual filename without any directory prefixed. ("all_sequences.fasta" is OK, "c:/users/meier/docs/all_sequences.fasta" is not)
- 12 - FASTA-Headers in the .FASTA-File must exactly match the values of "Virus name" (e.g. >hCoV-19/Netherlands/Gelderland-01/2020)
- 13 - Do not change the type of the columns (Collection Date must be formatted as "text" not "date")
- 14 - Always use the newest bulk-upload-XLS-Template
- 15 - Use "unknown" written in lower case if no value is available
- 16 - The user should name the XLS-Sheet as follows prior sending to the curation team: "YYYYMMDD_a_descriptive_name_metadata.xls"
- 17 **Upload your completed Excel sheet together with the FASTA-File through the Batch Upload interface**
- 18 In the event you experience any difficulties with your upload, please contact us for assistance at hCoV-19@gisaid.org
- 19 What happens next?
- 20 EpiCoV Curators across different timezones will be alerted and review your data. Only if necessary, will you be contacted, before your data are released
- 21 You will receive an eMail alert informing you that your data has been released.

22

23

24 Column information		
25 Submitter	mandatory	enter your GISAID-Username
26 FASTA filename	mandatory	the filename that contains the sequence without path (e.g. all_sequences.fasta not c:/users/meier/docs/all_sequences.fasta)
27 Virus name	mandatory	e.g. hCoV-19/Netherlands/Gelderland-01/2020 (Must be FASTA-Header from the FASTA file all_sequences.fasta)
28 Type	mandatory	default must remain "betacoronavirus"
29 Passage details/history	mandatory	e.g. Original, Vero
30 Collection date	mandatory	Date in the format YYYY or YYYY-MM or YYYY-MM-DD
31 Location	mandatory	e.g. Europe / Germany / Bavaria / Munich
32 Additional location information		e.g. Cruise Ship, Convention, Live animal market
33 Host	mandatory	e.g. Human, Environment, Canine, Manis javanica, Rhinolophus affinis, etc
34 Additional host information		e.g. Patient infected while traveling in
Sampling Strategy		e.g. Sentinel surveillance (IL), Sentinel surveillance (ARI), Sentinel surveillance (SARI), Non-sentinel-surveillance (hospital), Non-sentinel-surveillance (GP network), Longitudinal sampling on same patient(s), S gene dropout
35 Gender	mandatory	Male, Female, or unknown
36 Patient age	mandatory	e.g. 65 or 7 months, or unknown
37 Patient status	mandatory	e.g. Hospitalized, Released, Live, Deceased, or unknown
38 Specimen source		e.g. Sputum, Alveolar lavage fluid, Oro-pharyngeal swab, Blood, Tracheal swab, Urine, Stool, Cloakal swab, Organ, Feces, Other
39 Outbreak		Date, Location e.g. type of gathering, Family cluster, etc.
40 Last vaccinated		provide details if applicable
41 Treatment		Include drug name, dosage
42 Sequencing technology	mandatory	e.g. Illumina MiSeq, Sanger, Nanopore MinION, Ion Torrent, etc.
43 Assembly method		e.g. CLC Genomics Workbench 12, Geneious 10.2.4, SPAdes/MEGAHIT v1.2.9, UGENE v. 33, etc.
44 Coverage		e.g. 70x, 1,000x, 10,000x (average)
45 Originating lab	mandatory	Where the clinical specimen or virus isolate was first obtained
46 Address	mandatory	
47 Sample ID given by the originating laboratory		
48 Submitting lab	mandatory	Where sequence data have been generated and submitted to GISAID
49 Address	mandatory	
50 Sample ID given by the submitting laboratory		
51 Authors	mandatory	a comma separated list of Authors with complete First followed by Last Name
52 Comment	leave empty	do not use this column
53 Comment icon	leave empty	do not use this column
54		
55		
56		
57		
58		
59		



GISAID submissions require metadata for each sample.

The screenshot shows a GISAID submission page with the following details:

Host: Human
Additional location information:
Gender: Male
Patient age: 45
Patient status: unknown
Specimen source: Nasopharyngeal and oropharyngeal swab
Additional host information:
Sampling strategy:
Outbreak:
Last vaccinated:
Treatment:
Sequencing technology: Nanopore MinION
Assembly method: artic-network/fieldbioinformatics
Coverage:
Comment: ⓘ NS8_Q27stop results in 78.5% truncation of the protein sequence. Gap of 19 nucleotides when compared to the reference sequence.

Institute information

Originating lab: Laboratoire Professeur Daniel GAHOUMA (LPDG)
Address: Libreville, Gabon
Sample ID given by the originating laboratory: LPDG0442

Submitting lab: Centre de Recherches Médicales de Lambaréne (CERMEL)
Address: B.P.242 Lambaréne, Gabon
Sample ID given by the submitting laboratory: LPDG0442

Authors: Gedéon Prince Manouana, Moustapha Nzamba Maloum, Rodrigue Bikangui, Samira Zoa Assoumou, Sam O'neilla Oye Bingono, Georgelin Nguema Ondo, Kevine Zang Ella, Ayong More, Emilio Skarwan, Sandrine Zeh Nfor, Davy Leger Mouangala, Ludovic Mewono, Rodrigue Mintsa Nguema, Elvyre Mbongo-Nkama, Noé Patrick Mbondoukwe, Guy Stéphane Padzys, Srinivas reddy Pallerla, Jean Bernard Lekana-Douki, Steffen Borrmann, Thirumalaisamy P. Velavan, Bertrand Leill, Joël-Fleury Djoba Siawaya and Ayola Akim Adegnika

Submitter information

Submitter: Manouana, Gedéon Prince
Submission Date: 2021-07-29
Address:

Back

Navigating through GISAID

epicov.org/epi3/frontend#4d2629

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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 Submission to collection date compl
Clade Substitutions Variants

Collection da	Submission d	Length	Host	Location	Originating lab	Submitting lab
2021-07-14	2021-08-02	29,782	Human	Africa / Botswana	Botswana Harvard	Botswana Harvard
R23B85_BHP_A						
2021-07-14	2021-08-02	29,782	Human	Africa / Botswana	Botswana Harvard	Botswana Harvard
R23B84_BHP_A						
2021-07-14	2021-08-02	29,782	Human	Africa / Botswana	Botswana Harvard	Botswana Harvard
R23B81_BHP_A						
2021-07-14	2021-08-02	29,782	Human	Africa / Botswana	Botswana Harvard	Botswana Harvard
R23B77_BHP_A						
2021-07-14	2021-08-02	29,782	Human	Africa / Botswana	Botswana Harvard	Botswana Harvard
R23B71_BHP_00						
2021-07-09	2021-08-02	29,782	Human	Africa / Botswana	Botswana Harvard	Botswana Harvard
R23B70_BHP_00						
2021-07-09	2021-08-02	29,782	Human	Africa / Botswana	Botswana Harvard	Botswana Harvard
R23B69_BHP_00						
2021-07-09	2021-08-02	29,782	Human	Africa / Botswana	Botswana Harvard	Botswana Harvard
R23B67_BHP_00						
2021-07-09	2021-08-02	29,782	Human	Africa / Botswana	Botswana Harvard	Botswana Harvard
R23B65_BHP_00						
2021-07-09	2021-08-02	29,782	Human	Africa / Botswana	Botswana Harvard	Botswana Harvard
R23B64_BHP_00						
2021-07-09	2021-08-02	29,782	Human	Africa / Botswana	Botswana Harvard	Botswana Harvard
R23B63_BHP_00						
2021-07-09	2021-08-02	29,782	Human	Africa / Botswana	Botswana Harvard	Botswana Harvard
R23B62_BHP_00						
2021-07-09	2021-08-02	29,782	Human	Africa / Botswana	Botswana Harvard	Botswana Harvard
R23B61_BHP_00						
2021-07-09	2021-08-02	29,782	Human	Africa / Botswana	Botswana Harvard	Botswana Harvard
R23B60_BHP_00						
2021-07-09	2021-08-02	29,782	Human	Africa / Botswana	Botswana Harvard	Botswana Harvard
R23B59_BHP_00						
2021-07-09	2021-08-02	29,782	Human	Africa / Botswana	Botswana Harvard	Botswana Harvard
R23B55_BHP_00						
2021-07-09	2021-08-02	29,782	Human	Africa / Botswana	Botswana Harvard	Botswana Harvard
R23B17_BHP_nr						
2021-07-09	2021-08-02	29,782	Human	Africa / Botswana	Botswana Harvard	Botswana Harvard
Total: 31,844						

<< < 1 2 3 4 5 > >> Select Analysis Download

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Search

Accession ID	<input type="text"/>	Virus name	<input type="text"/>	<input type="checkbox"/> complete <small>?</small>	<input type="checkbox"/> high coverage <small>?</small>
Location	<input type="text"/> Africa / Gabon	Host	<input type="text"/>	<input type="checkbox"/> low coverage excl <small>?</small>	<input type="checkbox"/> w/Patient status <small>?</small>
Collection	<input type="text"/>	Submission	<input type="text"/>	<input type="checkbox"/> collection date compl <small>?</small>	
Clade	<input type="text"/> all	Lineage	<input type="text"/>	Substitutions <small>?</small>	Variants <small>?</small>

<input type="checkbox"/> Virus name	Passage de	Accession ID	Collection da	Submission d	<small>i</small>
<input type="checkbox"/> hCoV-19/Gabon/LPDG0442/2021	Original	EPI_ISL_3129932	2021-02-24	2021-07-29	<small>i</small>
<input type="checkbox"/> hCoV-19/Gabon/LPDG0439/2021	Original	EPI_ISL_3129931	2021-02-24	2021-07-29	
<input type="checkbox"/> hCoV-19/Gabon/LPDG0413/2021	Original	EPI_ISL_3129930	2021-03-06	2021-07-29	<small>i</small>
<input type="checkbox"/> hCoV-19/Gabon/LPDG0410/2021	Original	EPI_ISL_3129929	2021-04-04	2021-07-29	<small>w</small>
<input type="checkbox"/> hCoV-19/Gabon/LPDG0405/2021	Original	EPI_ISL_3129580	2021-03-29	2021-07-29	<small>!</small>
<input type="checkbox"/> hCoV-19/Gabon/LPDG0403/2021	Original	EPI_ISL_3129045	2021-03-28	2021-07-29	<small>w</small>
<input type="checkbox"/> hCoV-19/Gabon/LPDG0390/2021	Original	EPI_ISL_3128833	2021-03-22	2021-07-29	<small>!</small>
<input type="checkbox"/> hCoV-19/Gabon/LPDG0388/2021	Original	EPI_ISL_3128793	2021-03-19	2021-07-29	<small>!</small>
<input type="checkbox"/> hCoV-19/Gabon/CHUMEII19/2020	Original	EPI_ISL_2758406	2020-12	2021-06-24	<small>i</small>
<input type="checkbox"/> hCoV-19/Gabon/236LPDG/2020	Original	EPI_ISL_2758405	2020-12	2021-06-24	<small>i</small>
<input type="checkbox"/> hCoV-19/Gabon/157LPDG/2021	Original	EPI_ISL_2758404	2021-01	2021-06-24	<small>i</small>
<input type="checkbox"/> hCoV-19/Gabon/148LPDG/2021	Original	EPI_ISL_2758403	2021-01	2021-06-24	<small>i</small>
<input type="checkbox"/> hCoV-19/Gabon/132LPDG/2020	Original	EPI_ISL_2758402	2020-12	2021-06-24	<small>i</small>
<input type="checkbox"/> hCoV-19/Gabon/119LPDG/2020	Original	EPI_ISL_2758401	2020-12	2021-06-24	<small>i</small>
<input type="checkbox"/> hCoV-19/Gabon/CERMEL-CC0499/2021	Original	EPI_ISL_2442384	2021-04-26	2021-06-07	<small>!</small>
<input type="checkbox"/> hCoV-19/Gabon/CERMEL-CC0433/2021	Original	EPI_ISL_2442383	2021-04-20	2021-06-07	<small>w</small>
<input type="checkbox"/> hCoV-19/Gabon/CERMEL-DD0036/2021	Original	EPI_ISL_2442383	2021-05-08	2021-06-07	<small>!</small>

VOC Alpha 202012/01 GRY (B.1.1.7) first detected in the UK
 VOC Beta GH/501Y.V2 (B.1.351+B.1.351.2+B.1.351.3) first detected in South Africa
 VOC Gamma GR/501Y.V3 (P.1+P.1.1+P.1.2) first detected in Brazil/Japan
 VOC Delta G/478K.V1 (B.1.617.2+AY.1+AY.2+AY.3) first detected in India
 VOI Zeta GR/484K.V2 (P.2) first detected in Brazil
 VOI Eta G/484K.V3 (B.1.525) first detected in UK/Nigeria
 VOI Iota GH/253G.V1 (B.1.526) first detected in USA/New York
 VOI Kappa G/452R.V3 (B.1.617.1) first detected in India
 VOI Lambda GR/452Q.V1 (C.37) first detected in Peru

Total: 219 viruses

<< < 1 2 3 4 5 > >>

 Select Analysis Download

RESOURCES

<https://www.cdc.gov/amd/training/covid-toolkit/>



THANK YOU



LEARN MORE AT

africacdc.org/covid-19

Safeguarding Africa's Health