

National SARS-Cov-2 Strain Surveillance (NS3) Reporting Dashboard [5 February 2021]

Instructions:

The National SARS-Cov-2 Strain Surveillance (NS3) Reporting dashboard is a web-based reporting site that can be accessed here: <https://amdportal-sams.cdc.gov/>. This is a secure website requiring login via “SAMS Credentials”. You may have existing SAMS credentials that can be used to gain access or you may have recently been invited to create SAMS credentials for access.

Please email eocevent506@cdc.gov if you have any questions related to access.

The website allows you to view and download public SARS-CoV-2 sequence accession numbers and PANGO lineages for specimens submitted by your jurisdiction to CDC for sequencing via the NS3 program. Specimens included in the NS3 Reporting Dashboard were successfully sequenced and accepted by NCBI or GISAID. Specimens submitted to CDC within the last two weeks may not be visible because they are under processing. New results are available in the NS3 Reporting Dashboard on Tuesdays and Fridays of each week. Note: SARS-CoV-2 specimen sequence data that did not pass CDC’s quality control checks or were rejected by NCBI or GISAID are not included at this time.

Secure Access Management Services

https://auth.cdc.gov/siteminderagent/forms/login.fcc?TYPE=335544...

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SEARCH

CDC A-Z INDEX

SAMS
secure access management services

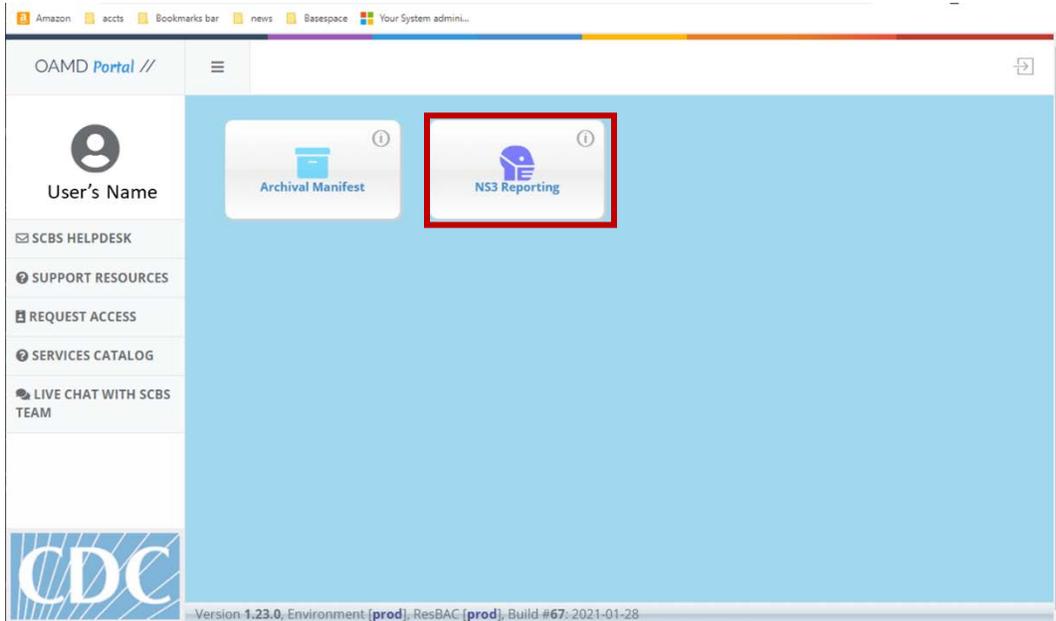
Warning: This warning banner provides privacy and security notices consistent with applicable federal laws, directives, and other federal guidance for accessing this Government system, which includes all devices/storage media attached to this system. This system is provided for Government-authorized use only. Unauthorized or improper use of this system is prohibited and may result in disciplinary action and/or civil and criminal penalties. At any time, and for any lawful Government purpose, the government may monitor, record, and audit your system usage and/or intercept, search and seize any communication or data transiting or stored on this system. Therefore, you have no reasonable expectation of privacy. Any communication or data transiting or stored on this system may be disclosed or used for any lawful Government purpose.

Choose a login option

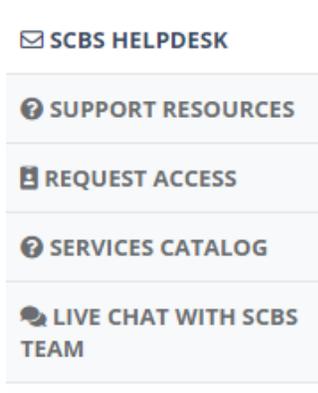
External Partners		HHS Staff	
SAMS Credentials	SAMS Grid Card	AMS Login	AMS One Time Password
			
SAMS Username <input type="text"/>	Click the Login button to sign on with a SAMS Grid Card	How to use AMS	How to use OTP
SAMS Password <input type="password"/>	Login	Login	Login
Forgot Your Password?			
For External Partners who login with <u>only</u> a SAMS issued UserID and Password.	For External Partners who have been issued a SAMS Grid Card.	For all HHS staff including Operating Divisions (CDC, NIH, FDA, etc.)	For all HHS staff including Operating Divisions (CDC, NIH, FDA, etc.) with a One Time Password.

Please email eocevent506@cdc.gov if you have any access-related questions or experience access problems.

After logging in, you will be presented with a screen like below. Note, the number of visible tiles may vary. Please look for the “NS3 Reporting” tile shown below and outlined in red.



Tech support can be obtained by selecting one of the following links on the left side bar:



The “info” link on the NS3 Reporting tile displays the methods text in a popup window.



NS3 Reporting

CDC National SARS-CoV-2 Strain Surveillance Genome Sequencing Report

Thank you for contributing to the National SARS-CoV-2 Strain Surveillance (NS3) program. This data set includes all sequences that passed our workflow QC and were successfully submitted to GenBank and GISAID. Missing

Click on “Open App” or the “NS3 Reporting” tile, for a tabular view of data. The columns can be sorted by clicking on the column header. The data can be downloaded by clicking on the download button

The screenshot shows a web browser window displaying a Metabase query result. The title is "CDC National SARS-CoV-2 Strain Surveillance Genome Sequencing Report (State)". The table has the following columns: specimen_id, genbank, gisaid, pangolin_lineage, state, and virus_name. The first few rows of data are visible. At the bottom of the table, there is a pagination control showing "Rows 1-10 of 22" and a download icon.

specimen_id	genbank	gisaid	pangolin_lineage	state	virus_name
256723	MW406594	EPI_ISL_747142	B.1.2	State	hCoV-19/USA/ST-CDC-2-3693463/2020
558854	MW495942	EPI_ISL_751635	B.1.2	State	hCoV-19/USA/ST-CDC-2-3714099/2020
351375	MW495946	EPI_ISL_751715	B.1.234	State	hCoV-19/USA/ST-CDC-2-3714256/2020
340976	NULL	EPI_ISL_903905	B.1.2	State	hCoV-19/USA/ST-CDC-2-3768699/2020
237123	NULL	EPI_ISL_747141	B.1.234	State	hCoV-19/USA/ST-CDC-2-3693556/2020
537076	MW495947	EPI_ISL_751634	B.1.139	State	hCoV-19/USA/ST-CDC-2-3714098/2020
367136	NULL	EPI_ISL_903829	B.1.2	State	hCoV-19/USA/ST-CDC-2-3769372/2020
357124	NULL	EPI_ISL_903615	B.1.1.119	State	hCoV-19/USA/ST-CDC-2-3768057/2020
341334	NULL	EPI_ISL_903874	B.1.2	State	hCoV-19/USA/ST-CDC-2-3768673/2020
543764	MW495941	EPI_ISL_751737	B.1.2	State	hCoV-19/USA/ST-CDC-2-3714191/2020

FIELD NAME	DESCRIPTION
SPECIMEN_ID	Specimen id provided with submission, key to link data back to local metadata
GENBANK	Genbank accession number (NULL if not available)

GISAID	GISAID accession number (NULL if not available)
PANGOLIN_LINEAGE	Lineage determined by pangolin (subject to change with software updates)
STATE	Submission state
VIRUS_NAME	Name of the virus in the format hCov-19/USA/[2 letter state]-CDC-[unique id]/[Year of collection]

Other important resources for further analysis:

NS3 specific NextStrain build: <https://nextstrain.org/groups/spheres/ncov/NS3>

Nextclade: <https://clades.nextstrain.org/>

Pangolin: <https://pangolin.cog-uk.io/>

<https://cov-lineages.org/>

USHER: <https://genome.ucsc.edu/cgi-bin/hgPhyloPlace>

NCBI: <https://www.ncbi.nlm.nih.gov/sars-cov-2/>

GISAID: <https://gisaid.org>