

National SARS-CoV-2 Strain Surveillance (NS3) Frequently Asked Questions

Why is CDC organizing this?

There are multiple goals for routinely sequencing and characterizing clinical specimens that are positive for SARS-CoV-2 as part of the public health response to the COVID-19 pandemic. These can broadly be grouped into two primary objectives:

1. **Population-level molecular epidemiology/virus monitoring:** By routinely acquiring sequences and associated metadata from a subset of COVID-19 cases, CDC aims to monitor the spread of viral lineages across time and within populations.
2. **Virus characterization:** By routinely collecting standardized epidemiologic and clinical data, and linking these with associated virus sequences, sequencing can be a valuable tool to identify viral variants that might have different transmissibility, pathogenicity, clinical outcomes, or vaccine and treatment resistance.

What are we asking from state public health labs?

For NS3, we request all state laboratories provide on a weekly basis: laboratory confirmed, deidentified, diagnostic specimens (with Ct values ≤ 28) and standardized metadata on a representative selection of COVID-19 cases. We are seeking specimens **collected within the 7 days prior to shipment** representing a variety of demographic and clinical characteristics and geographic locations. The selection of a diverse set of specimens will help ensure that a representative set of sequences is generated for national monitoring.

For enhanced surveillance activities, which started in January 2021, we request all state laboratories provide additional specimens, for a defined, specified period of time (short-term, interim), to specifically address contemporary SARS-CoV-2 variants of interest. Variants of interest are identified through genomic analysis of circulating viruses. Criteria for selecting variants of interest for submission are outlined in Appendix 3, Section 2, which will be continually updated with changes communicated through updates to the guidance and through APHL.

What is our commitment to you?

For NS3, CDC will deposit sequence results into public repositories in a timely manner and provide routine national level analyses to monitor trends in transmission of the virus in the United States.

For enhanced surveillance activities, which started in January 2021, CDC will provide results more rapidly and follow up directly with the state or territorial epidemiologist in the event of unexpected or unusual observations (e.g., sequence confirmation of a variant of concern). Such sequence data will not be made available publicly until communication with the relevant jurisdictional partners have occurred. CDC will serve as an available resource for questions or further technical guidance on use of SARS-CoV-2 genomic data.

How many specimens should I send and how often?

For NS3, we are requesting that states submit specimens every week and that you select specimens collected within 7 days of the shipment date. We are asking each state to submit a minimum of 5 specimens every week, plus additional specimens based on population size (see Appendix 2).

For enhanced surveillance activities, which started in January 2021, we are requesting additional specimens that are suspect variants of concern. Each state can submit up to twenty specimens from cases representing potential emerging variants or vaccine breakthrough cases as outlined in the criteria described in Appendix 3. Given the need to rapidly characterize new viral lineages as they emerge, these requests will often be short-term, and will be opened and closed through updated versions of the NS3 guidance documents and disseminated via communications with APHL.

How should I select specimens to send?

For NS3, we are asking states to select a diverse set of specimens that represent multiple geographic locations not associated with a single outbreak event and, if possible, varying demographic characteristics and clinical outcomes. It is important that all specimens have a relatively low Ct value (≤ 28) and have been stored properly (for more information, see <https://www.cdc.gov/coronavirus/2019-ncov/lab/guidelines-clinical-specimens.html>).

For enhanced surveillance activities, please see Appendix 3.

How do I send those specimens?

Please see Appendix 1, for detailed specimen submission information. Please ship specimens on **every Monday** (or bi-weekly), in 1.0–2.0 mL O-ring screw cap centrifuge tubes. If this date is an observed holiday, please ship on the next available business day (Tuesday through Thursday). Include a printed specimen manifest. Ship overnight on dry ice using your usual courier, such as FedEx or UPS, to the following address:

ATTN: STATT Lab: Unit 66 TRL
Centers for Disease Control and Prevention
1600 Clifton Road, NE
Atlanta, Georgia, 30333
Telephone: 404-639-3931
Email: sarsseqshipping@cdc.gov

Where will the sequence data be deposited?

Once genomic sequences are obtained and assessed for quality, the consensus sequence data will be uploaded and released into GenBank and GISAID with a minimum set of metadata. Raw sequence reads will be deposited into the Sequence Read Archive (SRA) at a later date, once quality assurances have been met and any human reads have been removed. The following metadata information will be included in all sequence data submissions: specimen type, collection date, gender, age, and geolocation information including state. Race will not be reported to these public databases. Sequences will be named according to their geographical location, as per established conventions (e.g., SARS-CoV-2/human/USA/XX (state acronym)-CDC-xxxxxxx (unique identifier)/2021). CDC is included in the name to reference that it was sequenced at CDC and not by the state public health laboratory or other entity. Note that NCBI and GISAID require slightly different naming conventions:

ICTV (NCBI) SARS-CoV-2/host/location/isolate/date
SARS-CoV-2/human/USA/XX-CDC-xxxxxxx2021

GISAID hCoV-19/location/isolate/date
hCoV-19/USA/XX-CDC-xxxxxxx2021

Where will NS3 results be reported?

Summarized results will be available through the NS3 Reporting Dashboard in the CDC Secure Access Management System located at: <https://amdportal-sams.cdc.gov/>. Users can login with the “SAMS Credentials” option. For access to the SAMS system and OAMD Portal please contact eocevent506@cdc.gov. A guidance document for the reporting system can be found [here](#).