



## COVID-19

# National Genomic Surveillance Dashboard

Updated Mar. 14, 2021

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A new virus variant of SARS-CoV-2 has one or more mutations that differentiate it from predominant variants already circulating among the general population. As the pandemic progresses and new variants of SARS-CoV-2 have emerged, it is critical for the United States and other countries to sequence and analyze virus samples. This sequence data will provide us with real-time information about the genetic diversity, spread, and evolution of the virus to assess the impact on current efforts to control the pandemic, including vaccines. Laboratories in the United States and across the world have generated hundreds of thousands of viral genetic sequences from SARS-CoV-2 positive patient specimens. Through ongoing variant surveillance, CDC can improve our public health response to COVID-19. Since late 2020, CDC's sequencing efforts have increased; even so, considerable gaps exist. CDC is enhancing these efforts by collaborating with state and local public health laboratories and partners, such as the [Association of Public Health Laboratories](#), to increase the number of specimens that are sequenced as part of the National SARS-CoV-2 Strain Surveillance (NS3) program. CDC is also increasing sequencing capacity through contracts with commercial diagnostic laboratories.

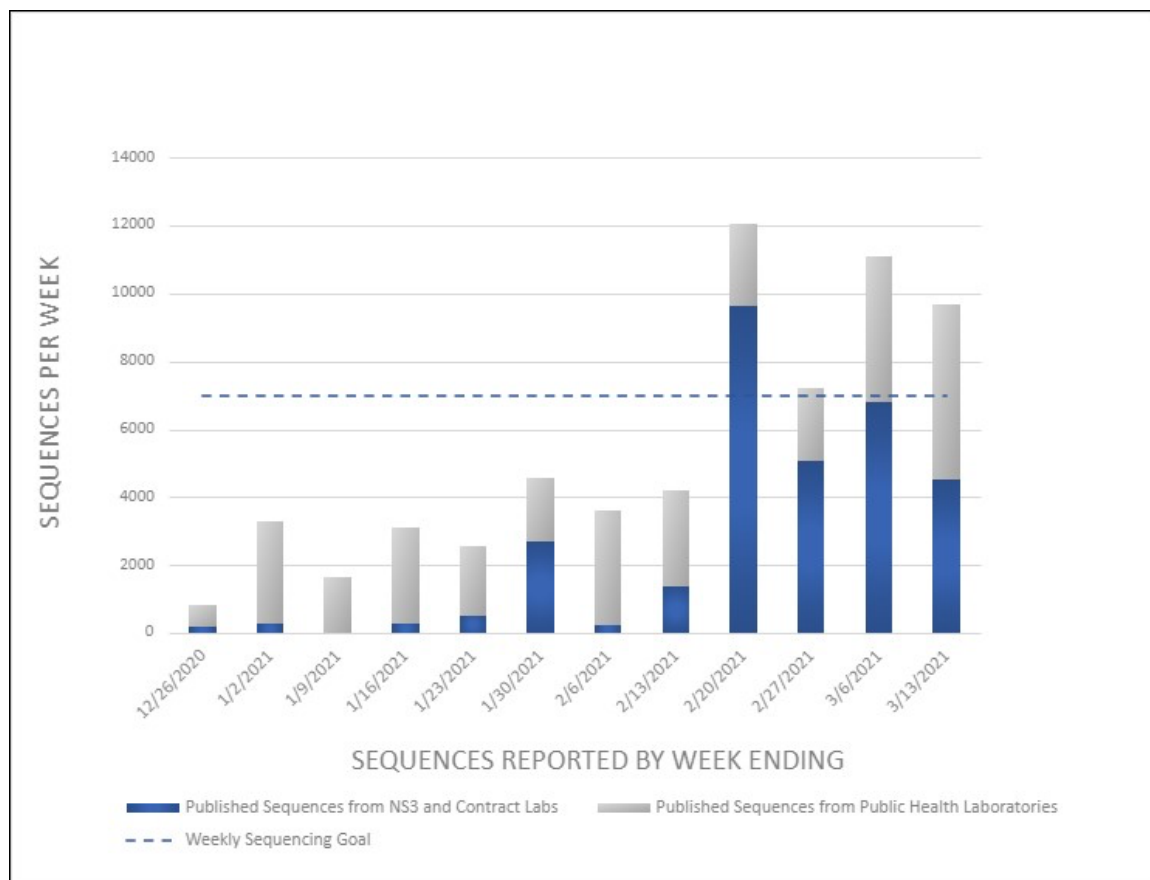
## Variant Information

[US COVID-19 Cases Caused by Variants](#) >[Variant Proportions in the U.S.](#) >[SARS-CoV-2 Variants Surveillance](#) >[SARS-CoV-2 Variants](#) >[How CDC is responding to SARS-CoV-2 variants globally](#) >

Starting in November 2020, state health departments and other public health agencies began sending SARS-CoV-2 specimens to CDC for sequencing and further characterization as part of NS3. This system was scaled up to process 750 requested specimens from states and jurisdictions per week beginning January 25, 2021. CDC has also contracted with commercial diagnostic laboratories and obtained commitments to sequence an additional 6,000 samples per week, with plans for further expansion. The SARS-CoV-2 genetic sequence data obtained from these sources, as well as the sequence data generated by state and local public health laboratories and academic partners, inform public health decision-making and is available to scientists globally via publicly accessible databases maintained by the National Center for Biotechnology Information (NCBI) and GISAID.

As laboratories scale up sequencing capacity, CDC is meeting this need by improving our infrastructure and workflow to ensure efficient sequence data submission to public repositories. Next generation sequencing is a multi-step process that involves both laboratory and bioinformatic workflows. The time from sample receipt at CDC to assembled sequence ready for submission into public databases is approximately 10 days. A similar timeline often applies to state, local, academic, and commercial partners. These collaborative sequencing efforts will provide a real-time understanding of what SARS-CoV-2 variants exist in the US.

## Published Sequences from NS3, CDC Sequencing Contracts, and Other CDC Sequencing Efforts



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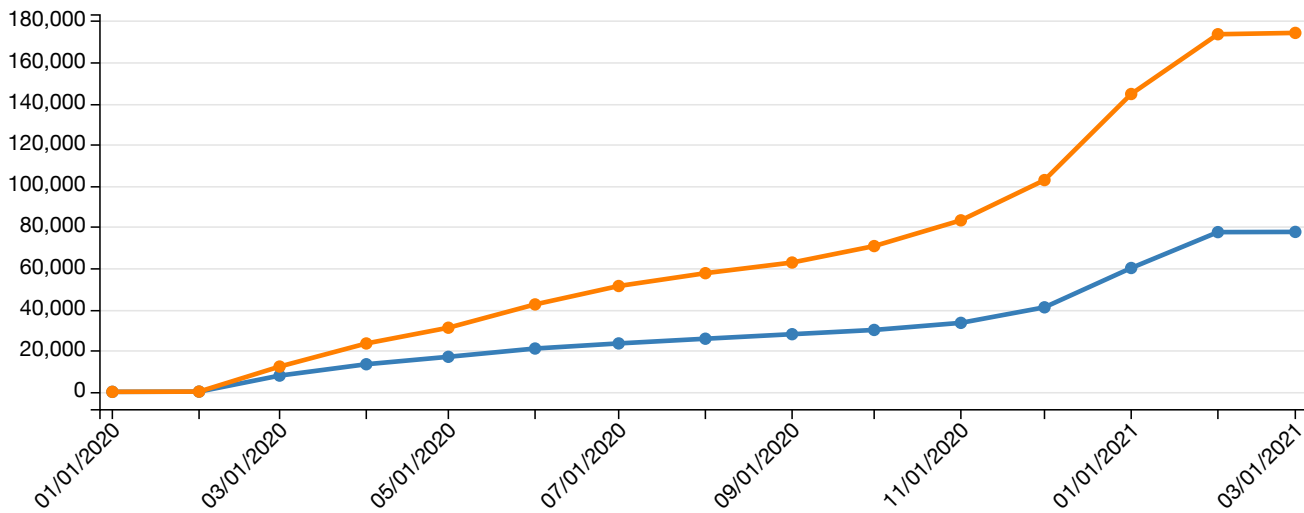
[Download data](#) [CSV - 1 KB]

### NS3, CDC Sequencing Contracts and Other CDC Sequencing Efforts

#### Weekly Published Sequences

The bars in this graph represent the number of SARS-CoV-2 sequences available in public repositories each week since December 2020. The blue bars show sequences published to public repositories by NS3, CDC sequencing contracts and other CDC sequencing efforts. The light gray bars show the sequences published to public repositories by state and local public health laboratories. The blue dotted line represents CDC's current weekly sequencing goal. The published sequences are reported by week ending date. These numbers do not include academic contracts or all public health laboratory sequences that have been published. Sequences generated by CDC and contract laboratories are available to inform public health actions before they are published. Delays in processing data may impact displayed results. Weekly totals reflect date of submission and may change over time as sequences are published in databases.

# U.S. Sequences Available in Public Repositories\*



US Sequences in NCBI  US Sequences submitted to GISAID [Reset](#)

This line chart captures the cumulative number of published SARS-CoV-2 sequences by collection date from laboratories in states and territories across the US from January 2020 to the present. The blue line represents US sequences available in NCBI, the National Center for Biotechnology Information, and the orange represents sequences available in GISAID, a global initiative that maintains a repository of virus sequence data.

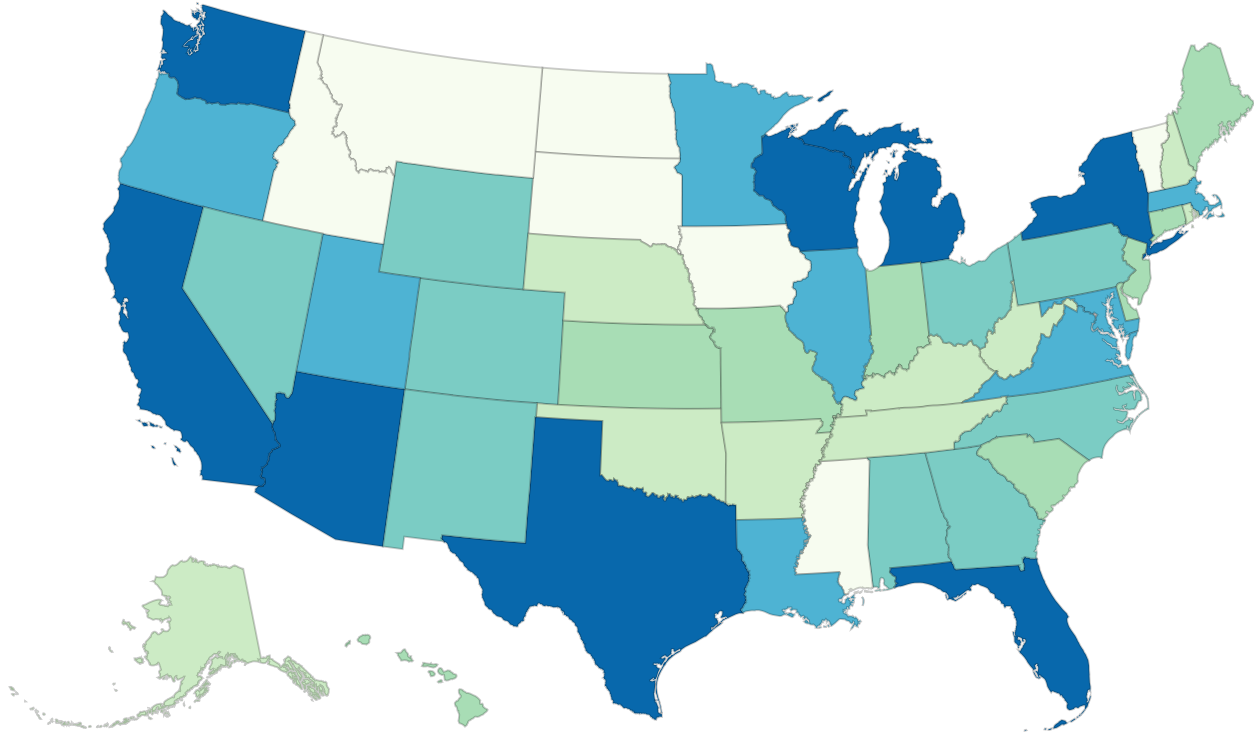
Data Table -

	01/01/2020	02/01/2020	03/01/2020	04/01/2020	05/01/2020	06/01/2020	07/01/2020
<b>US Sequences in NCBI</b>	19	121	7894	13408	17016	21033	21033
<b>US Sequences submitted to GISAID</b>	17	134	12281	23487	31128	42435	42435

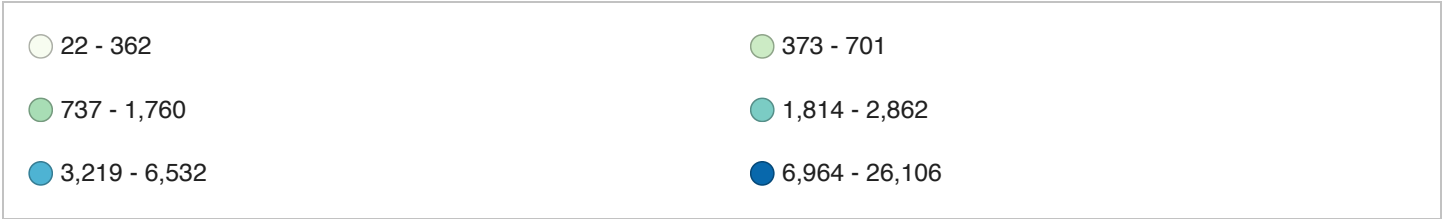
[Scroll for additional info](#)

[Download Table Data \(csv\)](#)

**Total Sequences Submitted Publicly Available\***



Territories **PR** **VI**



Data Table	
Location	Total SARS-CoV-2 S...
Alabama	2,031
Alaska	701
Arizona	6,964
Arkansas	381
California	25,822
Colorado	1,992
Connecticut	1,760
Delaware	778
Florida	7,534
Georgia	2,316

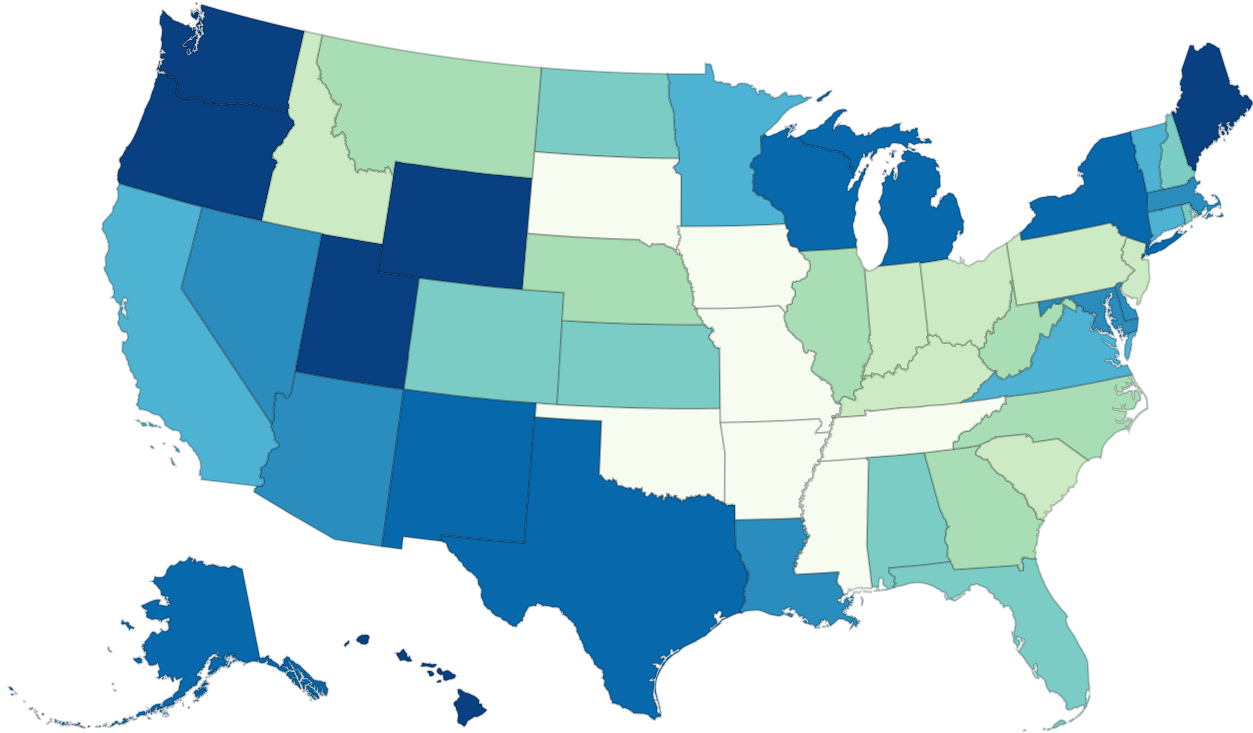
<input checked="" type="radio"/> Hawaii	941
<input type="radio"/> Idaho	362
<input checked="" type="radio"/> Illinois	3,219
<input checked="" type="radio"/> Indiana	1,070
<input type="radio"/> Iowa	286
<input checked="" type="radio"/> Kansas	900
<input checked="" type="radio"/> Kentucky	603
<input checked="" type="radio"/> Louisiana	3,596
<input checked="" type="radio"/> Maine	1,591
<input checked="" type="radio"/> Maryland	3,324
<input checked="" type="radio"/> Massachusetts	4,979
<input checked="" type="radio"/> Michigan	8,033
<input checked="" type="radio"/> Minnesota	3,501
<input type="radio"/> Mississippi	351
<input checked="" type="radio"/> Missouri	737
<input type="radio"/> Montana	227
<input checked="" type="radio"/> Nebraska	456
<input checked="" type="radio"/> Nevada	2,411
<input checked="" type="radio"/> New Hampshire	455
<input checked="" type="radio"/> New Jersey	1,330
<input checked="" type="radio"/> New Mexico	2,862
<input checked="" type="radio"/> New York	17,148
<input checked="" type="radio"/> North Carolina	2,581
<input type="radio"/> North Dakota	347
<input checked="" type="radio"/> Ohio	1,814
<input checked="" type="radio"/> Oklahoma	375
<input checked="" type="radio"/> Oregon	3,388
<input checked="" type="radio"/> Pennsylvania	1,937
<input type="radio"/> Puerto Rico	282
<input checked="" type="radio"/> Rhode Island	537
<input checked="" type="radio"/> South Carolina	1,026
<input type="radio"/> South Dakota	112
<input checked="" type="radio"/> Tennessee	507

● Texas	26,106
● Utah	6,532
○ Vermont	124
○ Virgin Islands	22
● Virginia	3,725
● Washington	10,540
● West Virginia	373
● Wisconsin	7,397
● Wyoming	2,561

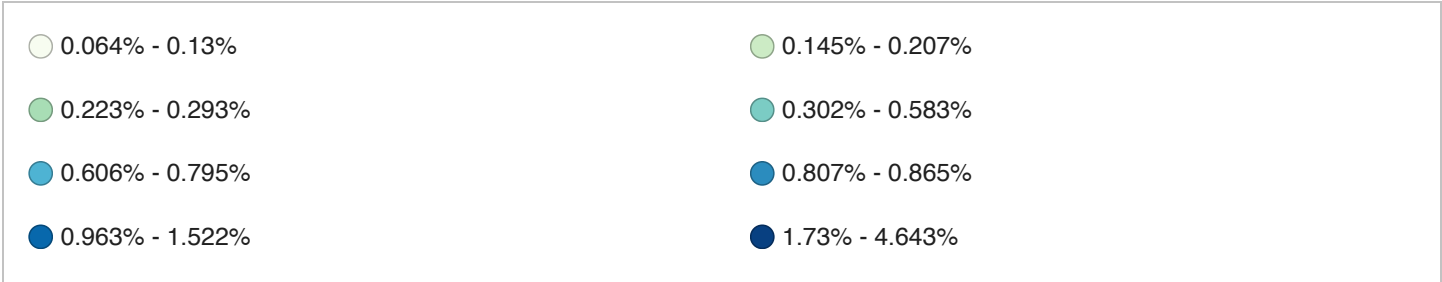
[Download Data \(CSV\)](#)

The map shows the cumulative number of SARS-CoV-2 sequences by state that have are publicly available from January 2020 to the present.

Percentage of Cumulative Cases Sequenced (%)\*



Territories **PR** **VI**



Data Table	
Location	Cumulative Cases S...
Alabama	0.404%
Alaska	1.213%
Arizona	0.837%
Arkansas	0.117%
California	0.734%
Colorado	0.451%
Connecticut	0.606%
Delaware	0.865%
Florida	0.39%



● Georgia	0.224%
● Hawaii	3.45%
● Idaho	0.207%
● Illinois	0.267%
● Indiana	0.159%
○ Iowa	0.084%
● Kansas	0.302%
● Kentucky	0.145%
● Louisiana	0.824%
● Maine	3.396%
● Maryland	0.847%
● Massachusetts	0.865%
● Michigan	1.202%
● Minnesota	0.707%
○ Mississippi	0.117%
○ Missouri	0.13%
● Montana	0.224%
● Nebraska	0.223%
● Nevada	0.807%
● New Hampshire	0.583%
● New Jersey	0.16%
● New Mexico	1.522%
● New York	0.99%
● North Carolina	0.293%
● North Dakota	0.344%
● Ohio	0.184%
○ Oklahoma	0.087%
● Oregon	2.13%
● Pennsylvania	0.201%
● Puerto Rico	0.275%
● Rhode Island	0.411%
● South Carolina	0.194%
○ South Dakota	0.098%

 Tennessee	0.064%
 Texas	0.963%
 Utah	1.73%
 Vermont	0.746%
 Virgin Islands	0.795%
 Virginia	0.628%
 Washington	3.024%
 West Virginia	0.277%
 Wisconsin	1.184%
 Wyoming	4.643%

[Download Data \(CSV\)](#)

The map shows the percentage of SARS-CoV-2-positive cases by state that have been sequenced and published in public repositories from Jan 2020 to the present.

\*Numbers will be updated every Sunday by 7:00 pm.

## Related Resources

[Emerging SARS-CoV-2 Variants](#)

[New Variants of the Virus that Causes COVID-19](#)

[Cases, Data, and Surveillance](#)

Last Updated Mar. 14, 2021

Content source: [National Center for Immunization and Respiratory Diseases \(NCIRD\), Division of Viral Diseases](#)