

COVID Data Tracker

Maps, charts, and data provided by CDC, updates Mondays and Fridays by 8 p.m. ET

COVID-19 Home >



Effective September 29, 2023, weekly updates to maps, charts, and data provided by CDC for COVID Data Tracker will occur on Fridays by 12 p.m. ET. This change aligns with the timing of CDC's weekly updates for respiratory viruses (<https://www.cdc.gov/respiratory-viruses/index.html>).

United States at a Glance

Collapse

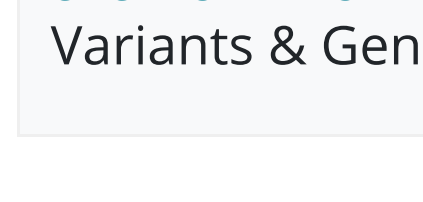
Trend in % Test Positivity



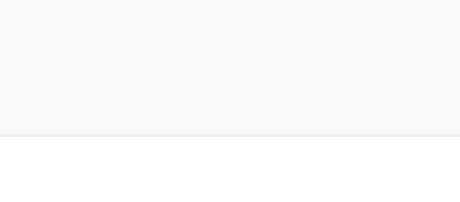
Trend in % Emergency Department Visits



Trend in Hospital Admissions



Trend in % COVID-19 Deaths



Total Hospitalizations
6,422,520

Total Deaths
1,148,691

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Variants & Genomic Surveillance



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Variant Proportions

Monitoring Variant Proportions

SARS-CoV-2, the virus that causes COVID-19, is constantly changing and accumulating mutations in its genetic code over time. New variants of SARS-CoV-2 are expected to continue to emerge. Some variants will emerge and disappear, while others will emerge and continue to spread and may replace previous variants.

To identify and track [SARS-CoV-2 variants](#), CDC uses [genomic surveillance](#). CDC's national genomic surveillance system collects SARS-CoV-2 specimens for sequencing through the National SARS-CoV-2 Strain Surveillance (NS3) program, as well as SARS-CoV-2 sequences generated by commercial or academic laboratories contracted by CDC and state or local public health laboratories. Virus genetic sequences are analyzed and classified as a particular lineage. The proportions of SARS-CoV-2 variants in a population are calculated nationally, by HHS region, and by jurisdiction. The sequences analyzed through CDC's national genomic sequencing and bioinformatics efforts fuel the comprehensive and population-based U.S. surveillance system established to identify and monitor the spread of variants.

Rapid virus genomic sequencing data combined with phenotypic data are further used to determine whether COVID-19 tests, treatments, and vaccines authorized or approved for use in the United States will work against emerging variants.

Types of Variant Proportion Data

CDC provides estimates of variant proportions for two-week periods. These proportions are calculated in two ways: weighted estimates and Nowcast estimates.

Weighted estimates (provided for all two-week periods except the most recent two, two-week periods) are variant proportions that are based on empirical (observed) genomic sequencing data. These estimates are not available for the most recent two-week periods because of the time it takes to generate the sequencing data, including sample collection, specimen treatment, shipping, analysis, and upload into public databases.

Lineages with weighted estimates less than 1% of all circulating variants are combined with their parent lineage. When the weighted estimate of a lineage crosses the 1% threshold and has substitutions in the spike protein that could affect vaccine efficacy, transmission, or severity, it may be separated from its parent lineage and displayed on its own in the variant proportions data.

Nowcast estimates (provided for the most recent two two-week periods when the "Nowcast on" option is selected below) are model-based projections of variant proportions for the most recent two-week periods to enable timely public health action. CDC uses the Nowcast to forecast variant proportions before the weighted estimates are available for a given two-week period.

Projections for an emerging lineage with a high growth rate may have a higher degree of uncertainty (wider predictive interval) when it is just beginning to spread and still has low weighted estimates. Projections may also be biased during times of delayed reporting (e.g., around holidays). CDC performs frequent evaluations of Nowcast to inform performance improvements.

Nowcast estimates for a parent lineage include projected changes in its child lineages until a child lineage's weighted estimate crosses the 1% threshold. Once the weighted estimate crosses the 1% threshold for the two-week period with sequences available, the initial Nowcast projections for the child lineage proportion for the two recent two-week periods may be substantially higher than 1%.

CDC provides updated variant proportions for weighted estimates and Nowcast estimates every other week on Friday.

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HHS Region: Data for the 2-Week Period Ending on:

This shows weighted and Nowcast estimates for the United States. The table and map show estimates for the 2-week period ending on 10/14/2023(Nowcast) if available.

Weighted and Nowcast Estimates in United States for 2-Week Periods in 6/25/2023 – 10/14/2023

Nowcast Estimates in United States for 10/1/2023 – 10/14/2023

Hover over (or tap in mobile) any lineage of interest to see the amount of uncertainty in that lineage's estimate.

Weighted Estimates: Variant proportions based on reported genomic sequencing results

Nowcast: Model-based projected estimates of variant proportions

% Viral Lineages Among Infections

Collection date, two-week period ending

7/6/23 7/20/23 8/6/23 8/19/23 9/2/23 9/16/23

EG.5 XBB.1.5

EG.5 XBB.1.5

EG.5 XBB.1.5

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EG.5 XBB.1.5

EG.5 XBB.1.5

WHO label Lineage # %Total 95%PI

Omicron EG.5 23.6% 21.2-26.3%

HV.1 19.5% 16.8-22.6%

FL.1.5.1 13.5% 10.8-16.7%

XBB.1.16.6 10.3% 9.1-11.8%

HK.3 4.9% 3.6-6.7%

XBB.2.3 4.1% 3.4-4.9%

XBB.1.16.11 3.1% 2.5-3.8%

XBB.1.16 2.8% 2.4-3.3%

XBB.1.16.1 2.2% 1.7-2.7%

XBB.1.16.15 1.8% 1.3-2.4%

HF.1 0.3% 0.1-0.8%

GK.1.1 1.6% 1.2-2.4%

XBB.1.4 1.4% 1.2-1.7%

GE.1 1.4% 1.0-1.9%

XBB.1.5.70 1.2% 0.8-1.8%

GK.2 0.9% 0.7-1.2%

XBB.1.5 0.9% 0.7-1.0%

EG.6.1 0.8% 0.6-1.2%

XBB.1.9.1 0.8% 0.6-1.0%

XBB.1.5.2.2 0.8% 0.4-0.8%

XBB.1.5.68 0.6% 0.3-0.8%

XBB.1.9.2 0.5% 0.4-0.7%

XBB.1.42.2 0.5% 0.3-0.8%

BA.2 0.3% 0.1-0.8%

XBB.1.5.10 0.3% 0.2-0.4%

CH.1.1 0.2% 0.1-0.3%

XBB.2.3.8 0.2% 0.1-0.3%

XBB.1.5.59 0.1% 0.1-0.2%

FD.1.1 0.1% 0.1-0.1%

FE.1.1 0.1% 0.0-0.1%

XBB.1.5.1 0.0% 0.0-0.0%

EU.1.1 0.0% 0.0-0.0%

B.1.1.529 0.0% 0.0-0.0%

BQ.1 0.0% 0.0-0.0%

FD.2 0.0% 0.0-0.0%

Other* 0.0% 0.0-0.1%

Regional proportions from specimens collected in the 2-week period ending on 10/14/2023(Nowcast).

US Territories not shown are included in HHS regions: PR, VI - Region 2; AS, FM, GU, MH, MP, PW - Region 9

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Lineages called using pangolin v4.3.1, pangolin-data v1.22 and usher v0.6.2.

Updated October 13, 2023

Download Data

The diagram below shows how the [Pango lineages](#) on COVID Data Tracker are related to each other. For a full list of the current Pango lineages see https://cov-lineages.org/lineage_list.html.

CDC monitors SARS CoV-2 viruses from every lineage, but COVID Data Tracker only includes the lineages whose weighted estimates are above 1%. Some lineages have key differences in spike protein sequence that may reduce the effectiveness of some treatments or increase the virus's ability to spread. These lineages may be separated from their parent lineage on COVID Data Tracker when their biweekly proportion reaches more than 1%.

Origin Strain

BA.1.529

BA.1

BA.2.75

BA.4

BA.4.6

BA.5.2.6

BF.7

BQ.1.1

CH.1.1

BA.2.75.2

BN.1

XBB.1.5

XBB.1.5.70

XBB.1.9.1

XBB.1.9.2

XBB.1.16

XBB.1.16.1

XBB.1.16.6

XBB.1.16.15

FE.1.1

XBB.1.42.2

GE.1

XBB.2.3.8

FL.1.5.1

XBB.1.5.68

XBB.1.5.70

EG.5

EG.6.1

XBB.1.16.1

XBB.1.16.6

XBB.1.16.15

HF.1

GK.1.1

HK.3

FL.1.5.1

XBB.1.5.70

EG.5

EG.6.1

XBB.1.16.1

XBB.1.16.6

XBB.1.16.15

FE.1.1

XBB.1.42.2

GE.1

XBB.2.3.8

FL.1.5.1

XBB.1.5.68

XBB.1.5.70

EG.5

EG.6.1

XBB.1.16.1

XBB.1.16.6

XBB.1.16.15

HF.1

GK.1.1

HK.3

FL.1.5.1

XBB.1.5.70

EG.5

EG.6.1

XBB.1.16.1

XBB.1.16.6

XBB.1.16.15

HF.1

GK.1.1

HK.3

FL.1.5.1

XBB.1.5.70

EG.5

EG.6.1

XBB.1.16.1

XBB.1.16.6

XBB.1.16.15

HF.1

GK.1.1

HK.3

FL.1.5.1

XBB.1.5.70

EG.5

EG.6.1

XBB.1.16.1

XBB.1.16.6

XBB.1.16.15

HF.1

GK.1.1

HK.3

FL.1.5.1

XBB.1.5.70

EG.5

EG.6.1

XBB.1.16.1

XBB.1.16.6

XBB.1.16.15

HF.1

GK.1.1

HK.3

FL.1.5.1

XBB.1.5.70

EG.5

EG.6.1

XBB.1.16.1

XBB.1.16.6

XBB.1.16.15

HF.1

GK.1.1

HK.3

FL.1.5.1

XBB.1.5.70

EG.5

EG.6.1

XBB.1.16.1

XBB.1.16.6

XBB.1.16.15

HF.1

GK.1.1

HK.3

FL.1.5.1

XBB.1.5.7