

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

Nextstrain

RRID:SCR_018223

Type: Tool

Proper Citation

Nextstrain (RRID:SCR_018223)

Resource Information

URL: <https://nextstrain.org/>

Proper Citation: Nextstrain (RRID:SCR_018223)

Description: Open source project to harness scientific and public health potential of pathogen genome data. Provides continually updated view of publicly available data alongside powerful analytic and visualization tools for use by community. Used to aid epidemiological understanding and improve outbreak response. Open source SARS-CoV-2 genome data and analytic and visualization tools.

Synonyms: nextstrain.org

Resource Type: data or information resource, portal, project portal, data set

Keywords: Pathogen genome data, data, analytic tool, visualization tool, epidemiology, outbreak response

Related Condition: COVID-19

Availability: Free, Freely available

Resource Name: Nextstrain

Resource ID: SCR_018223

Alternate URLs: <https://nextstrain.org/ncov/global>

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260731T043020+0000

Ratings and Alerts

No rating or validation information has been found for Nextstrain.

No alerts have been found for Nextstrain.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 273 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Li L, et al. (2026) Bridging Genomics and Clinical Medicine: RSVrecon Enhances RSV Surveillance With Automated Genotyping and Clinically Important Mutation Reporting. Influenza and other respiratory viruses, 20(1), e70203.

Khare K, et al. (2025) Inter-host diversity associated with age, sex, and menstrual cycle modulates clinical manifestations in DENV-2 patients. iScience, 28(5), 112478.

Feng Z, et al. (2025) Structural and functional insights into the evolution of SARS-CoV-2 KP.3.1.1 spike protein. Cell reports, 44(7), 115941.

Hernandez G, et al. (2025) Dynamic ensembles of SARS-CoV-2 N-protein reveal head-to-head coiled-coil-driven oligomerization and phase separation. Nucleic acids research, 53(11).

Hikmat H, et al. (2025) Implementation of a Multiplex PCR Amplification System Combined With Next-Generation Genome Sequencing to Decipher the Circulation of Human Coronavirus 229E Lineages in Southern France. Journal of medical virology, 97(11), e70653.

Br??ssow H, et al. (2025) The Spread of the Mosquito-Transmitted West Nile Virus in North America and Europe. Microbial biotechnology, 18(3), e70120.

Wu J, et al. (2025) SGV-caller: SARS-CoV-2 genome variation caller. Heliyon, 11(4), e42613.

Ananworanich J, et al. (2025) Safety and Immunogenicity of mRNA-1010, an Investigational Seasonal Influenza Vaccine, in Healthy Adults: Final Results From a Phase 1/2 Randomized Trial. The Journal of infectious diseases, 231(1), e113.

Houmadi H, et al. (2025) Five-Year (2017-2022) Evolutionary Dynamics of Human Coronavirus OC43 in Southern France Based on Whole Genome Next-Generation Sequencing. Journal of medical virology, 97(12), e70726.

Ricaldi JN, et al. (2025) An Advanced Molecular Detection Roadmap for Nonlaboratorians. Emerging infectious diseases, 31(13), 3.

Basile K, et al. (2025) Genomic Evolution of SARS-CoV-2 Variants of Concern Under In Vitro Neutralising Selection Pressure Following Two Doses of the Pfizer-BioNTech BNT162b2 COVID-19 Vaccine. *Viruses*, 17(9).

Dzuvor CKO, et al. (2025) Rational Design of Multiclade Coronavirus Spike Immunodominant Domain Nanoparticles to Elicit Broad Antibody Responses. *bioRxiv : the preprint server for biology*.

Lefebvre A, et al. (2025) Unsupervised detection and fitness estimation of emerging SARS-CoV-2 variants: Application to wastewater samples (ANRS0160). *PLoS computational biology*, 21(12), e1013749.

Ramuth M, et al. (2025) Molecular Evolution of Influenza A Viruses From Mauritius, 2017-2019. *Influenza and other respiratory viruses*, 19(5), e70108.

Di Gioacchino A, et al. (2025) Deciphering the Code of Viral-Host Adaptation Through Maximum-Entropy Nucleotide Bias Models. *Molecular biology and evolution*, 42(6).

Motsa BB, et al. (2025) Variants of the Ebola virus matrix protein VP40 have differential effects on oligomerization and plasma membrane interactions. *The Journal of biological chemistry*, 301(9), 110489.

Shi C, et al. (2025) Phylogenetic and Molecular Evolutionary Insights into Monkeypox Virus Circulation in Shenzhen, China, 2023-2024. *Viruses*, 17(9).

Chiu YT, et al. (2025) SARS-CoV-2 Evolution in Humans Enables Its Transmission to Nonhuman Primates. *Molecular biology and evolution*, 42(11).

Shi J, et al. (2025) Pathogenicity, virological features, and immune evasion of SARS-CoV-2 JN.1-derived variants including JN.1.7, KP.2, KP.3, and KP.3.1.1. *Nature communications*, 16(1), 11002.

Motsa BB, et al. (2024) Minor changes in electrostatics robustly increase VP40 membrane binding, assembly, and budding of Ebola virus matrix protein derived virus-like particles. *bioRxiv : the preprint server for biology*.