Resource Summary Report

Generated by NIF on May 19, 2025

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 set, data or information resource, portal, project portal

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

Related Condition: COVID-19

Funding:

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: 20250517T060355+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 254 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Shan KJ, et al. (2024) Molecular Evolution of Protein Sequences and Codon Usage in Monkeypox Viruses. Genomics, proteomics & bioinformatics, 22(1).

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.

Ruiz F, et al. (2024) Delineating the functional activity of antibodies with cross-reactivity to SARS-CoV-2, SARS-CoV-1 and related sarbecoviruses. PLoS pathogens, 20(10), e1012650.

Fan S, et al. (2024) Assessment of the antigenic evolution of a clade 6B.1 human H1N1pdm influenza virus revealed differences between ferret and human convalescent sera. EBioMedicine, 101, 105013.

Huang C, et al. (2024) Ubiquitination of NS1 Confers Differential Adaptation of Zika Virus in Mammalian Hosts and Mosquito Vectors. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(39), e2408024.

Feng Z, et al. (2024) Structural and Functional Insights into the Evolution of SARS-CoV-2 KP.3.1.1 Spike Protein. bioRxiv : the preprint server for biology.

Wagner EK, et al. (2024) High-throughput specificity profiling of antibody libraries using ribosome display and microfluidics. Cell reports methods, 4(12), 100934.

Aguilar-Martinez SL, et al. (2024) Genomic and Phylogenetic Characterisation of SARS-CoV-

2 Genomes Isolated in Patients from Lambayeque Region, Peru. Tropical medicine and infectious disease, 9(2).

Motsa BB, et al. (2024) Minor electrostatic changes robustly increase VP40 membrane binding, assembly, and budding of Ebola virus matrix protein derived virus-like particles. The Journal of biological chemistry, 300(5), 107213.

Branda F, et al. (2024) A One Health Platform for Future Epidemic Preparedness. Infectious disease reports, 16(2), 281.

Ling-Hu T, et al. (2024) Integration of individualized and population-level molecular epidemiology data to model COVID-19 outcomes. Cell reports. Medicine, 5(1), 101361.

Li Z, et al. (2024) Molecular epidemiology and population immunity of SARS-CoV-2 in Guangdong (2022-2023) following a pivotal shift in the pandemic. Nature communications, 15(1), 7033.

Deng J, et al. (2024) Natural evidence of coronaviral 2'-O-methyltransferase activity affecting viral pathogenesis via improved substrate RNA binding. Signal transduction and targeted therapy, 9(1), 140.

Gigante CM, et al. (2024) Notes from the Field: Mpox Cluster Caused by Tecovirimat-Resistant Monkeypox Virus - Five States, October 2023-February 2024. MMWR. Morbidity and mortality weekly report, 73(40), 903.

Muehleman D, et al. (2024) Using SARS-CoV-2 Sequencing Data to Identify Reinfection Cases in the Global Emerging Infections Surveillance Program, United States. Emerging infectious diseases, 30(14), 53.

Loes AN, et al. (2024) High-throughput sequencing-based neutralization assay reveals how repeated vaccinations impact titers to recent human H1N1 influenza strains. bioRxiv : the preprint server for biology.

Narkhede Y, et al. (2024) Computational and experimental identification of keystone interactions in Ebola virus matrix protein VP40 dimer formation. Protein science : a publication of the Protein Society, 33(5), e4978.

Zhang X, et al. (2024) SARS-CoV-2 Evolution: Immune Dynamics, Omicron Specificity, and Predictive Modeling in Vaccinated Populations. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(40), e2402639.

Raisinghani N, et al. (2024) AlphaFold2 Modeling and Molecular Dynamics Simulations of the Conformational Ensembles for the SARS-CoV-2 Spike Omicron JN.1, KP.2 and KP.3 Variants: Mutational Profiling of Binding Energetics Reveals Epistatic Drivers of the ACE2 Affinity and Escape Hotspots of Antibody Resistance. Viruses, 16(9).

Liu Y, et al. (2024) Lineage-specific pathogenicity, immune evasion, and virological features of SARS-CoV-2 BA.2.86/JN.1 and EG.5.1/HK.3. Nature communications, 15(1), 8728.