

Resource Summary Report

Generated by [dkNET](#) on Aug 7, 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: portal, project portal, data set, data or information resource

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: 20260807T042918+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 342 mentions in open access literature.

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

Carranza C, et al. (2026) Diversity and clinical correlations of SARS-CoV-2 variant during the introduction of the Delta variant in Guatemala. *Access microbiology*, 8(3).

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.

Korsun N, et al. (2026) Viral pathogens in the etiology of acute respiratory infections in Bulgaria during the 2024-2025 season and genetic diversity of circulating influenza viruses. *Frontiers in microbiology*, 17, 1785399.

Ogrzewalska M, et al. (2026) Genomic analysis of high pathogenicity avian influenza viruses from Antarctica reveals multiple introductions from South America. *Nature communications*, 17(1).

Monamele CG, et al. (2026) Genome characterization of the SARS-CoV-2 omicron in Cameroon. *BMC infectious diseases*, 26(1).

Seo HY, et al. (2026) A transferable SARS-CoV-2 IRES module enables dual translation initiation for enhanced antigen expression in COVID-19 mRNA vaccines. *Molecular therapy*. *Nucleic acids*, 37(2), 102886.

Haddox HK, et al. (2026) Clonal interference and changing selective pressures shape the escape of SARS-CoV-2 from hundreds of antibodies. *Virus evolution*, 12(1), veaf104.

Matalatala AM, et al. (2026) Imported SARS-CoV-2 Infections at N'djili International Airport in Kinshasa, Democratic Republic of Congo: An Epidemiological and Genomic Analysis. *Influenza and other respiratory viruses*, 20(5), e70259.

Neher RA, et al. (2026) Nomenclature for Tracking of Genetic Variation of Seasonal Influenza Viruses. *Influenza and other respiratory viruses*, 20(2), e70230.

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.

Lim MS, et al. (2025) Rapid and Multiplex Diagnosis of Malaria Using Chelex-100 Extraction and LAMP-MS Assay. *Bio-protocol*, 15(13), e5375.

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.

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.

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).

Alshahrani M, et al. (2025) Multiscale Modeling and Dynamic Mutational Profiling of Binding Energetics and Immune Escape for Class I Antibodies with SARS-CoV-2 Spike Protein: Dissecting Mechanisms of High Resistance to Viral Escape Against Emerging Variants. *Viruses*, 17(8).

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.

Feng Z, et al. (2025) A highly divergent cryptic SARS-CoV-2 lineage exhibits strong receptor binding and immune evasion. *medRxiv : the preprint server for health sciences*.