Resource Summary Report

Generated by NIF on May 8, 2025

NCBI Virus

RRID:SCR_018253
Type: Tool

Proper Citation

NCBI Virus (RRID:SCR_018253)

Resource Information

URL: https://www.ncbi.nlm.nih.gov/labs/virus/vssi

Proper Citation: NCBI Virus (RRID:SCR_018253)

Description: Community portal for viral sequence data from RefSeq, GenBank and other NCBI repositories. Integrative, value added resource designed to support retrieval, display and analysis of curated collection of virus sequences and large sequence datasets. Used to increase usability of data archived in GenBank and other NCBI repositories.

Synonyms: National Center for Biotechnology Information Virus

Resource Type: portal, web service, software resource, data or information resource, data access protocol, topical portal

Defining Citation: PMID:27899678

Keywords: Viral sequence data, viral data retrival, viral data analysis, viral data display, curated virus sequence, data set

Funding:

Availability: Free, Freely available

Resource Name: NCBI Virus

Resource ID: SCR_018253

Record Creation Time: 20220129T080339+0000

Record Last Update: 20250507T061323+0000

Ratings and Alerts

No rating or validation information has been found for NCBI Virus.

No alerts have been found for NCBI Virus.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 38 mentions in open access literature.

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

Dodd GK, et al. (2025) In silico functional analysis of the human, chimpanzee, and gorilla MHC-A repertoires. Immunogenetics, 77(1), 12.

Baker SJC, et al. (2024) Chronic COVID-19 infection in an immunosuppressed patient shows changes in lineage over time: a case report. Virology journal, 21(1), 8.

Acúrcio RC, et al. (2024) Intranasal Multiepitope PD-L1-siRNA-Based Nanovaccine: The Next-Gen COVID-19 Immunotherapy. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(40), e2404159.

Ogando-Rivas E, et al. (2024) Expanded specific T cells to hypomutated regions of the SARS-CoV-2 using mRNA electroporated antigen-presenting cells. Molecular therapy. Methods & clinical development, 32(1), 101192.

Ma E, et al. (2024) A predictive language model for SARS-CoV-2 evolution. Signal transduction and targeted therapy, 9(1), 353.

O'Leary NA, et al. (2024) Exploring and retrieving sequence and metadata for species across the tree of life with NCBI Datasets. Scientific data, 11(1), 732.

Peters D, et al. (2024) The plant virus transmissions database. The Journal of general virology, 105(3).

Liu Z, et al. (2024) Variation and evolution analysis of SARS-CoV-2 using self-game sequence optimization. Frontiers in microbiology, 15, 1485748.

Sekaran K, et al. (2023) A systematic review of artificial intelligence-based COVID-19 modeling on multimodal genetic information. Progress in biophysics and molecular biology, 179, 1.

Su Y, et al. (2023) Identification and genomic analysis of temperate Halomonas

bacteriophage vB_HmeY_H4907 from the surface sediment of the Mariana Trench at a depth of 8,900 m. Microbiology spectrum, 11(5), e0191223.

Lubin JH, et al. (2023) A comprehensive survey of coronaviral main protease active site diversity in 3D: Identifying and analyzing drug discovery targets in search of broad specificity inhibitors for the next coronavirus pandemic. bioRxiv : the preprint server for biology.

Chabi-Jesus C, et al. (2023) Citrus Bright Spot Virus: A New Dichorhavirus, Transmitted by Brevipalpus azores, Causing Citrus Leprosis Disease in Brazil. Plants (Basel, Switzerland), 12(6).

Popov IV, et al. (2023) Detection of coronaviruses in insectivorous bats of Fore-Caucasus, 2021. Scientific reports, 13(1), 2306.

Giovanetti M, et al. (2023) Monitoring Monkeypox: Safeguarding Global Health through Rapid Response and Global Surveillance. Pathogens (Basel, Switzerland), 12(9).

Li H, et al. (2023) Global genomic diversity and conservation of SARS-CoV-2 since the COVID-19 outbreak. Microbiology spectrum, 11(6), e0282623.

Abrahamian P, et al. (2023) Coding-complete genome sequence of an isolate of papaya virus E in tomato. Microbiology resource announcements, 12(9), e0034423.

Holtz A, et al. (2023) Integrating full and partial genome sequences to decipher the global spread of canine rabies virus. Nature communications, 14(1), 4247.

Gómez M, et al. (2023) Characterizing viral species in mosquitoes (Culicidae) in the Colombian Orinoco: insights from a preliminary metagenomic study. Scientific reports, 13(1), 22081.

Guruprasad K, et al. (2022) Mutations in human SARS-CoV-2 spike proteins, potential drug binding and epitope sites for COVID-19 therapeutics development. Current research in structural biology, 4, 41.

Rout RK, et al. (2022) Feature-extraction and analysis based on spatial distribution of amino acids for SARS-CoV-2 Protein sequences. Computers in biology and medicine, 141, 105024.