

Resource Summary Report

Generated by SPARC SAWG on Jul 31, 2026

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

Defining Citation: [PMID:27899678](#)

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

Availability: Free, Freely available

Resource Name: NCBI Virus

Resource ID: SCR_018253

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260731T043027+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 53 mentions in open access literature.

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

Ehsasatvatan M, et al. (2025) Immunoinformatic design of chimeric multiepitope vaccine for the prevention of human metapneumovirus (hMPV). BMC infectious diseases, 25(1), 964.

Herazo-Álvarez J, et al. (2025) A review of neural networks for metagenomic binning. Briefings in bioinformatics, 26(2).

Wawman D, et al. (2025) A first report of the detection of Avipoxvirus genomic sequences in louse flies (Diptera: Hippoboscidae). Parasitology, 152(5), 522.

Bertacca S, et al. (2025) Oxford nanopore sequencing as a useful tool for investigating the population dynamics of invasive begomoviruses in Sicily. Microbial genomics, 11(11).

Boži? A, et al. (2025) Increased preference for lysine over arginine in spike proteins of SARS-CoV-2 BA.2.86 variant and its daughter lineages. PloS one, 20(4), e0320891.

Liu J, et al. (2025) Characterization, diversity, and biogeochemical potential of soil viruses inhabiting in Yuncheng Salt Lake. Frontiers in microbiology, 16, 1597514.

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

Pan L, et al. (2025) Cross-neutralization ability of anti-MERS-CoV monoclonal antibodies against a variety of merbecoviruses. Frontiers in microbiology, 16, 1593095.

Schneggenburger T, et al. (2025) SKiM: accurately classifying metagenomic ONT reads in limited memory. Bioinformatics (Oxford, England), 41(10).

Su S, et al. (2025) Predicting viral host codon fitness and path shifting through tree-based learning on codon usage biases and genomic characteristics. Scientific reports, 15(1), 12251.

Kandel S, et al. (2025) Phylogenetic analysis of H5N1 influenza viruses isolated from dairy cattle in Texas in December 2024. Journal of virology, 99(8), e0058025.

Johnson ML, et al. (2025) Living Together Apart: Quantitative Perspectives on the Costs and Benefits of a Multipartite Genome Organization in Viruses. Viruses, 17(9).

Nieto EE, et al. (2025) Effects of a novel Paraburkholderia phage IPK on the phenanthrene degradation efficiency of the PAH-degrading strain Paraburkholderia caledonica Bk. Biodegradation, 36(5), 86.

Durnell-Bettis LA, et al. (2025) Mitochondrial targeting by measles virus nucleoprotein modulates viral spread in human airway epithelium. PLoS pathogens, 21(11), e1013713.

Lv JX, et al. (2025) Extensive diversity of unusual microorganisms associated with severe pneumonia in kidney transplant recipients. PLoS pathogens, 21(11), e1013667.

Zhang P, et al. (2025) HCoVDB: a comprehensive database encompassing viral genomes, drug targets, and therapeutics of human coronaviruses. Database : the journal of biological databases and curation, 2025.

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.

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

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.