

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 7, 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, data or information resource, portal, software resource, topical portal, web service

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: 20260905T133009+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 76 mentions in open access literature.

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

Kamitaki N, et al. (2026) The DNA virome varies with human genes and environments. *Nature*, 653(8116), 1099.

Escalante C, et al. (2026) Metatranscriptomics analysis reveals the cotton virome in the southern United States. *Scientific reports*, 16(1).

Kant P, et al. (2026) On the Low Abundance of Antibiotic Resistance Genes in Bacteriophage Genomes and Their Random Acquisition via Specialized Transduction. *Genome biology and evolution*, 18(5).

Möller SR, et al. (2026) Viral and Host Factors Involved in Host Gain and Host Loss by Tomato Leaf Curl Begomoviruses in Tomato and Cucumbers. *Molecular plant pathology*, 27(3), e70202.

Ma L-L, et al. (2026) Near-complete genome sequence of a rhabdovirus identified from the rice pest *Stenchaetothrips biformis*. *Microbiology resource announcements*, 15(6), e0000126.

Hawkins TÉ, et al. (2026) An Evolutionary Distinct Nipah Virus N-Glycosylation Site Provides Stability for Receptor Engagement. *Molecular & cellular proteomics : MCP*, 25(4), 101531.

Maia C, et al. (2026) Catching up with old friends: a 2-year survey of phlebotomine sand fly-borne phleboviruses presence in southern Portugal. *Parasites & vectors*, 19(1).

Daodu RO, et al. (2026) Lassa virus live tracking and lineage assignment: how nextstrain can enhance surveillance and public health in Africa and beyond. *Emerging microbes & infections*, 15(1), 2640699.

Wang H, et al. (2026) Genetic insights into hepatitis E virus through environmental surveillance in Europe. *One health (Amsterdam, Netherlands)*, 22, 101302.

Guerra-Assunção JA, et al. (2026) Extensive evolution and T cell escape by SARS-CoV-2 in a 2.5-year persistent infection of an immunocompromised host. *iScience*, 29(3), 114917.

Chew JJ, et al. (2026) Genus- and host-associated codon usage bias patterns in coronavirus spike genes. *PloS one*, 21(6), e0351693.

Pan Y, et al. (2026) Analysis of Epidemiological and Molecular Characteristics of Bocavirus in Guangzhou. *Viruses*, 18(6).

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

Mitsuwan W, et al. (2025) Multidrug Resistance, Biofilm-Forming Ability, and Molecular Characterization of *Vibrio* Species Isolated from Foods in Thailand. *Antibiotics* (Basel, Switzerland), 14(3).

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

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.

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).

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.

Liu J, et al. (2025) TempSnap-Trace: A temporal snapshot-based framework for haplotype network tracing. *Biosafety and health*, 7(6), 403.