Resource Summary Report

Generated by RRID on May 23, 2025

NCBI Viral Genomes

RRID:SCR_013789 Type: Tool

Proper Citation

NCBI Viral Genomes (RRID:SCR_013789)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/genome/viruses/

Proper Citation: NCBI Viral Genomes (RRID:SCR_013789)

Description: A database which provides viral and viroid genome sequence data and resource tools. Al viral genomes are downloadable and a complete RefSeq release of viral and viroid genome sequences are available.

Synonyms: Viral Genomes

Resource Type: information resource

Keywords: database, viral genome sequence, viroid genome sequence

Funding:

Availability: Free, Public

Resource Name: NCBI Viral Genomes

Resource ID: SCR_013789

Record Creation Time: 20220129T080318+0000

Record Last Update: 20250519T203817+0000

Ratings and Alerts

No rating or validation information has been found for NCBI Viral Genomes.

No alerts have been found for NCBI Viral Genomes.

Data and Source Information

Source: <u>SciCrunch Registry</u>

Usage and Citation Metrics

We found 42 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>RRID</u>.

Mughal F, et al. (2025) Evolution of intrinsic disorder in the structural domains of viral and cellular proteomes. Scientific reports, 15(1), 2878.

Kim BJ, et al. (2024) Whole-genome demography of COVID-19 virus during its pandemic period and on "panvalent" vaccine design. Scientific reports, 14(1), 17752.

Liu G, et al. (2024) VirusPredictor: XGBoost-based software to predict virus-related sequences in human data. Bioinformatics (Oxford, England), 40(4).

Li Q, et al. (2024) Detection and discovery of plant viruses in Disporopsis through high-throughput sequencing. Frontiers in microbiology, 15, 1434554.

Ritsch M, et al. (2023) Navigating the Landscape: A Comprehensive Review of Current Virus Databases. Viruses, 15(9).

Lin CY, et al. (2023) Identifying the Gut Virome of Diaphorina citri from Florida Groves. Insects, 14(2).

Xiao H, et al. (2023) Molecular and Metagenomic Analyses Reveal High Prevalence and Complexity of Viral Infections in French-American Hybrids and North American Grapes. Viruses, 15(9).

Zaragoza-Solas A, et al. (2022) Long-Read Metagenomics Improves the Recovery of Viral Diversity from Complex Natural Marine Samples. mSystems, 7(3), e0019222.

Wang X, et al. (2022) First Detection and Genome Characterization of a New RNA Virus, Hibiscus Betacarmovirus, and a New DNA Virus, Hibiscus Soymovirus, Naturally Infecting Hibiscus spp. in Hawaii. Viruses, 15(1).

Kavalappara SR, et al. (2021) High Throughput Sequencing-Aided Survey Reveals Widespread Mixed Infections of Whitefly-Transmitted Viruses in Cucurbits in Georgia, USA. Viruses, 13(6). Sidharthan VK, et al. (2021) Discovery of putative novel viruses in the transcriptomes of endangered plant species native to India and China. Gene, 786, 145626.

Bartoszewicz JM, et al. (2021) Interpretable detection of novel human viruses from genome sequencing data. NAR genomics and bioinformatics, 3(1), Iqab004.

Johnston S, et al. (2021) AAV ablates neurogenesis in the adult murine hippocampus. eLife, 10.

Chen X, et al. (2021) Sequencing facility and DNA source associated patterns of virusmappable reads in whole-genome sequencing data. Genomics, 113(1 Pt 2), 1189.

Kang J, et al. (2021) Zooming on dynamics of marine microbial communities in the phycosphere of Akashiwo sanguinea (Dinophyta) blooms. Molecular ecology, 30(1), 207.

Brito AF, et al. (2020) The evolution of protein domain repertoires: Shedding light on the origins of the Herpesviridae family. Virus evolution, 6(1), veaa001.

Gulyaeva AA, et al. (2020) LAMPA, LArge Multidomain Protein Annotator, and its application to RNA virus polyproteins. Bioinformatics (Oxford, England), 36(9), 2731.

Mwatuni FM, et al. (2020) Occurrence, genetic diversity, and recombination of maize lethal necrosis disease-causing viruses in Kenya. Virus research, 286, 198081.

Sidharthan VK, et al. (2020) Robust Virome Profiling and Whole Genome Reconstruction of Viruses and Viroids Enabled by Use of Available mRNA and sRNA-Seq Datasets in Grapevine (Vitis vinifera L.). Frontiers in microbiology, 11, 1232.

Chang T, et al. (2020) First Report of a Mesonivirus and Its Derived Small RNAs in an Aphid Species Aphis citricidus (Hemiptera: Aphididae), Implying Viral Infection Activity. Journal of insect science (Online), 20(2).