

Resource Summary Report

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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. All 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

Availability: Free, Public

Resource Name: NCBI Viral Genomes

Resource ID: SCR_013789

Record Creation Time: 20220129T080318+0000

Record Last Update: 20260725T190756+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: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 43 mentions in open access literature.

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

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

Smolenschi C, et al. (2025) Comprehensive molecular landscape of anal squamous cell carcinoma: analysis of tissue and liquid biopsies from 1844 patients. *NPJ precision oncology*, 9(1), 404.

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).

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.

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).

Chen X, et al. (2021) Sequencing facility and DNA source associated patterns of virus-mappable 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.

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

Bartoszewicz JM, et al. (2021) Interpretable detection of novel human viruses from genome sequencing data. *NAR genomics and bioinformatics*, 3(1), lqab004.

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.

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

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

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.