

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: 20260815T182500+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 49 mentions in open access literature.

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

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.

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

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

Sada TS, et al. (2024) Genomic analysis and characterization of lytic bacteriophages that target antimicrobial resistant *Escherichia coli* in Addis Ababa, Ethiopia. *Heliyon*, 10(22), e40342.

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

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).

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

Adeleke IA, et al. (2022) Persistent, and Asymptomatic Viral Infections and Whitefly-Transmitted Viruses Impacting Cantaloupe and Watermelon in Georgia, USA. *Viruses*, 14(6).

Kavalappara SR, et al. (2022) Wild Radish (*Raphanus raphanistrum* L.) Is a Potential Reservoir Host of Cucurbit Chlorotic Yellows Virus. *Viruses*, 14(3).

Sung I, et al. (2022) AutoCoV: tracking the early spread of COVID-19 in terms of the spatial and temporal patterns from embedding space by K-mer based deep learning. *BMC bioinformatics*, 23(Suppl 3), 149.

Lai X, et al. (2022) Comparison of Potato Viromes Between Introduced and Indigenous Varieties. *Frontiers in microbiology*, 13, 809780.

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).

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

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.

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.