

Resource Summary Report

Generated by [NIF](#) on Jul 31, 2026

ViralZone

RRID:SCR_006563

Type: Tool

Proper Citation

ViralZone (RRID:SCR_006563)

Resource Information

URL: <http://viralzone.expasy.org/>

Proper Citation: ViralZone (RRID:SCR_006563)

Description: ViralZone is a SIB Swiss Institute of Bioinformatics web-resource for all viral genus and families, providing general molecular and epidemiological information, along with virion and genome figures. Each virus or family page gives an easy access to UniProtKB/Swiss-Prot viral protein entries. ViralZone project is handled by the virus program of SwissProt group. Proteins popups were developed in collaboration with Prof. Christian von Mering and Andrea Franceschini, Bioinformatics Group, Institute of Molecular Life Sciences, University of Zurich, Winterthurerstrasse 190, CH-8057 Zurich, Switzerland, funded in part by the SIB Swiss Institute of bioinformatics. All pictures in ViralZone are copyright of the SIB Swiss Institute of Bioinformatics.

Abbreviations: ViralZone

Synonyms: Viral Zone

Resource Type: data or information resource, database

Defining Citation: [PMID:20947564](#)

Keywords: dna virus, rna virus, virus, dna, rna, genomic, proteomic, sequence, reference strain, image, virion, retro-transcribing virus, genome, bibliographic, bio.tools

Funding: Swiss Institute of Bioinformatics

Resource Name: ViralZone

Resource ID: SCR_006563

Alternate IDs: biotools:viralzone, r3d100013314, nlx_144372

Alternate URLs: <https://bio.tools/viralzone>, <https://doi.org/10.17616/R31NJMRM>

Old URLs: <http://www.expasy.org/viralzone/>

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260729T044137+0000

Ratings and Alerts

No rating or validation information has been found for ViralZone.

No alerts have been found for ViralZone.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 128 mentions in open access literature.

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

Brüssow H, et al. (2025) The Spread of the Mosquito-Transmitted West Nile Virus in North America and Europe. Microbial biotechnology, 18(3), e70120.

Worp N, et al. (2025) Unveiling the global urban virome through wastewater metagenomics. Nature communications, 16(1), 10707.

Birling MC, et al. (2025) Genome engineering with Cas9 and AAV repair templates, successes and pitfalls. Mammalian genome : official journal of the International Mammalian Genome Society, 36(2), 376.

da Silva MK, et al. (2025) Immunoinformatic profiling of parvovirus B19 VP1/VP2 epitopes: relevance to surgical transfusion safety. International journal of surgery (London, England), 111(9), 6030.

Brüssow H, et al. (2025) Monkeypox Virus: WHO's Second Public Health Emergency of International Concern Within 2 Years. Microbial biotechnology, 18(4), e70142.

Ahmad F, et al. (2025) An exploratory binding study of molnupiravir efficacy against emerging Omicron SARS-CoV-2 variants. Scientific reports, 15(1), 36549.

Gaertner NF, et al. (2025) A SUMO interacting motif in the replication initiator protein of tomato yellow leaf curl virus is required for viral replication. Journal of virology, 99(12), e0128625.

Ofer D, et al. (2025) Protein Language Models Expose Viral Immune Mimicry. Viruses, 17(9).

Ford CE, et al. (2024) Five Species of Wild Freshwater Sport Fish in Wisconsin, USA, Reveal Highly Diverse Viromes. *Pathogens* (Basel, Switzerland), 13(2).

Wang Y, et al. (2024) Unveiling bat-borne viruses: a comprehensive classification and analysis of virome evolution. *Microbiome*, 12(1), 235.

Zhu D, et al. (2024) Adaptive expression of phage auxiliary metabolic genes in paddy soils and their contribution toward global carbon sequestration. *Proceedings of the National Academy of Sciences of the United States of America*, 121(49), e2419798121.

Messias TS, et al. (2024) Potential of Viruses as Environmental Etiological Factors for Non-Syndromic Orofacial Clefts. *Viruses*, 16(4).

Sarvmeili J, et al. (2024) Immunoinformatics design of a structural proteins driven multi-epitope candidate vaccine against different SARS-CoV-2 variants based on fynomer. *Scientific reports*, 14(1), 10297.

De Castro E, et al. (2024) ViralZone 2024 provides higher-resolution images and advanced virus-specific resources. *Nucleic acids research*, 52(D1), D817.

Leng F, et al. (2024) DVsc: An Automated Framework for Efficiently Detecting Viral Infection from Single-cell Transcriptomics Data. *Genomics, proteomics & bioinformatics*, 22(2).

Chen G, et al. (2024) RNAVirHost: a machine learning-based method for predicting hosts of RNA viruses through viral genomes. *GigaScience*, 13.

Tonelli A, et al. (2024) Identifying life-history patterns along the fast-slow continuum of mammalian viral carriers. *Royal Society open science*, 11(7), 231512.

Istvan P, et al. (2024) Exploring the gut DNA virome in fecal immunochemical test stool samples reveals associations with lifestyle in a large population-based study. *Nature communications*, 15(1), 1791.

Zárate A, et al. (2024) VirDetect-AI: a residual and convolutional neural network-based metagenomic tool for eukaryotic viral protein identification. *Briefings in bioinformatics*, 26(1).

Wei Y, et al. (2024) Advances of computational methods enhance the development of multi-epitope vaccines. *Briefings in bioinformatics*, 26(1).