Resource Summary Report

Generated by dkNET on May 19, 2025

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: database, data or information resource

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, nlx_144372

Alternate URLs: https://bio.tools/viralzone

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

Record Creation Time: 20220129T080236+0000

Record Last Update: 20250517T055751+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 117 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.

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

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

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

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.

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

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

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).

Peters D, et al. (2024) The plant virus transmissions database. The Journal of general virology, 105(3).

Tan CCS, et al. (2024) The evolutionary drivers and correlates of viral host jumps. Nature ecology & evolution, 8(5), 960.

Sun Y, et al. (2024) GateView: A Multi-Omics Platform for Gene Feature Analysis of Virus Receptors within Human Normal Tissues and Tumors. Biomolecules, 14(5).

Waman VP, et al. (2024) Predicting human and viral protein variants affecting COVID-19 susceptibility and repurposing therapeutics. Scientific reports, 14(1), 14208.

Deng A, et al. (2024) Synoptic Variation Drives Genetic Diversity and Transmission Mode of Airborne DNA Viruses in Urban Space. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(46), e2404512.

Nie W, et al. (2024) Advances in phage-host interaction prediction: in silico method enhances the development of phage therapies. Briefings in bioinformatics, 25(3).

Nomburg J, et al. (2024) Birth of protein folds and functions in the virome. Nature, 633(8030), 710.

Zhang S, et al. (2024) Conserved untranslated regions of multipartite viruses: Natural markers of novel viral genomic components and tags of viral evolution. Virus evolution, 10(1), veae004.

Valero-Rello A, et al. (2024) Cellular receptors for mammalian viruses. PLoS pathogens, 20(2), e1012021.

Harrigan WL, et al. (2024) Improvements in viral gene annotation using large language models and soft alignments. BMC bioinformatics, 25(1), 165.

Pertics BZ, et al. (2023) Characterization of a Lytic Bacteriophage and Demonstration of Its Combined Lytic Effect with a K2 Depolymerase on the Hypervirulent Klebsiella pneumoniae Strain 52145. Microorganisms, 11(3).