Resource Summary Report

Generated by NIF on May 20, 2025

Virus Pathogen Resource (ViPR)

RRID:SCR_012983
Type: Tool

Proper Citation

Virus Pathogen Resource (ViPR) (RRID:SCR_012983)

Resource Information

URL: http://www.viprbrc.org/brc/home.do?decorator=vipr

Proper Citation: Virus Pathogen Resource (ViPR) (RRID:SCR_012983)

Description: Provides searchable public repository of genomic, proteomic and other research data for different strains of pathogenic viruses along with suite of tools for analyzing data. Data can be shared, aggregated, analyzed using ViPR tools, and downloaded for local analysis. ViPR is an NIAID-funded resource that support the research of viral pathogens in the NIAID Category A-C Priority Pathogen lists and those causing (re)emerging infectious diseases. It provides a dedicated gateway to SARS-CoV-2 data that integrates data from external sources (GenBank, UniProt, Immune Epitope Database, Protein Data Bank), direct submissions, analysis pipelines and expert curation, and provides a suite of bioinformatics analysis and visualization tools for virology research.

Abbreviations: ViPR

Synonyms: Virus Pathogen Resource, ViPR

Resource Type: software application, data visualization software, service resource, database, data processing software, data or information resource, software resource, storage service resource, data repository

Keywords: flu, gene, bioinformatic, database, diagnostic, genomic, health, human, influenza, pathogen, protein, research, strain, therapeutic, tool, vaccine, virus, visualization, FASEB list

Related Condition: COVID-19

Funding: NIAID

Availability: Restricted

Resource Name: Virus Pathogen Resource (ViPR)

Resource ID: SCR_012983

Alternate IDs: nif-0000-25312, DOI:10.35083, DOI:10.35084, DOI:10.17616/R30P93, DOI:10.25504/FAIRsharing.2qx8n8

Alternate URLs: http://www.viprbrc.org/, https://doi.org/10.17616/r30p93, https://doi.org/10.35083/, https://doi.org/10.35084/, https://dx.doi.org/10.35083/, https://dx.doi.org/10.35084/, https://fairsharing.org/10.25504/FAIRsharing.2qx8n8

License URLs: https://www.viprbrc.org/brc/home.spg?decorator=vipr, http://bit.ly/2umuSBz

Record Creation Time: 20220129T080313+0000

Record Last Update: 20250519T203747+0000

Ratings and Alerts

No rating or validation information has been found for Virus Pathogen Resource (ViPR).

No alerts have been found for Virus Pathogen Resource (ViPR).

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 129 mentions in open access literature.

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

Zhang D, et al. (2025) Enteroviral 3C protease cleaves N4BP1 to impair the host inflammatory response. Journal of virology, 99(1), e0175824.

Dieng I, et al. (2024) The Spatiotemporal Distribution and Molecular Characterization of Circulating Dengue Virus Serotypes/Genotypes in Senegal from 2019 to 2023. Tropical medicine and infectious disease, 9(2).

Orf GS, et al. (2024) The 2023 South Sudanese outbreak of Hepatitis E emphasizes ongoing circulation of genotype 1 in North, Central, and East Africa. Infection, genetics and evolution : journal of molecular epidemiology and evolutionary genetics in infectious diseases, 124, 105667.

Genoveso MJ, et al. (2024) Nuclear reorganization by NPM1-mediated phase separation triggered by adenovirus core protein VII. Microbiology spectrum, 12(10), e0041624.

Amrani N, et al. (2024) CRISPR-Cas9-mediated genome editing delivered by a single AAV9 vector inhibits HSV-1 reactivation in a latent rabbit keratitis model. Molecular therapy. Methods & clinical development, 32(3), 101303.

Manjate F, et al. (2024) Genomic analysis of DS-1-like human rotavirus A strains uncovers genetic relatedness of NSP4 gene with animal strains in Manhiça District, Southern Mozambique. Scientific reports, 14(1), 30705.

Dos Santos Alves RP, et al. (2024) Human coronavirus OC43-elicited CD4+ T cells protect against SARS-CoV-2 in HLA transgenic mice. Nature communications, 15(1), 787.

Vieira CJSP, et al. (2024) Long-term co-circulation of multiple arboviruses in southeast Australia revealed by xeno-monitoring and viral whole-genome sequencing. Virus evolution, 10(1).

Rahman S, et al. (2024) Targeting Yezo Virus Structural Proteins for Multi-Epitope Vaccine Design Using Immunoinformatics Approach. Viruses, 16(9).

Castellano LA, et al. (2024) Dengue virus preferentially uses human and mosquito non-optimal codons. Molecular systems biology, 20(10), 1085.

Moreno A, et al. (2024) Molecular and Serological Detection of Bovine Coronaviruses in Marmots (Marmota marmota) in the Alpine Region. Viruses, 16(4).

da Silva OLT, et al. (2024) Advancing molecular modeling and reverse vaccinology in broad-spectrum yellow fever virus vaccine development. Scientific reports, 14(1), 10842.

Guevara-Barrientos D, et al. (2024) Malivhu: A Comprehensive Bioinformatics Resource for Filtering SARS and MERS Virus Proteins by Their Classification, Family and Species, and Prediction of Their Interactions Against Human Proteins. Bioinformatics and biology insights, 18, 11779322241263671.

Jagtap S, et al. (2023) Evolutionary dynamics of dengue virus in India. PLoS pathogens, 19(4), e1010862.

Tarke A, et al. (2023) Targets and cross-reactivity of human T cell recognition of Common Cold Coronaviruses. bioRxiv : the preprint server for biology.

Agbodzi B, et al. (2023) Whole genome sequencing of outbreak strains from 2017 to 2018 reveals an endemic clade of dengue 1 virus in Cameroon. Emerging microbes & infections, 12(2), 2281352.

Kishimoto M, et al. (2023) Isolation and Characterization of Distinct Rotavirus A in Bat and Rodent Hosts. Journal of virology, 97(1), e0145522.

Bardossy ES, et al. (2023) A conserved Y-shaped RNA structure in the 3'UTR of chikungunya virus genome as a host-specialized element that modulates viral replication and evolution. PLoS pathogens, 19(5), e1011352.

Kim KW, et al. (2023) Universal primers for rift valley fever virus whole-genome sequencing. Scientific reports, 13(1), 18688.

Padane A, et al. (2023) An emerging clade of Chikungunya West African genotype discovered in real-time during 2023 outbreak in Senegal. medRxiv : the preprint server for health sciences.