Resource Summary Report

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

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: 20260801T042717+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 140 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Ikuse T, et al. (2025) Burden of rotavirus and other microorganisms in hospitalized children with acute gastroenteritis in Yangon, Myanmar, before the introduction of rotavirus vaccine. IJID regions, 14, 100589.

Agarwal R, et al. (2025) Identification of immunogenic and cross-reactive chikungunya virus epitopes for CD4+ T cells in chronic chikungunya disease. Nature communications, 16(1), 5756.

Savin TV, et al. (2025) Development and Clinical Validation of a Skin Test for In Vivo Assessment of SARS-CoV-2 Specific T-Cell Immunity. Viruses, 17(9).

Tu Z, et al. (2025) Node role of wild boars in virus circulation among wildlife and domestic animals. Nature communications, 16(1), 8938.

Agarwal R, et al. (2025) Chikungunya virus-specific CD4+ T cells are associated with chronic chikungunya viral arthritic disease in humans. Cell reports. Medicine, 6(5),

102134.

Wei Y, et al. (2025) Genetic and codon usage analyses reveal the evolution of the seoul virus. Frontiers in genetics, 16, 1544577.

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

Koul M, et al. (2025) VITALdb: to select the best viroinformatics tools for a desired virus or application. Briefings in bioinformatics, 26(2).

Wang D, et al. (2025) Amino acid mutations of porcine circovirus type 2 (PCV2) capsid protein increase virus binding to host and evade immune responses: An evaluation of viral evolution. Virulence, 16(1), 2535472.

De Carli A, et al. (2025) Fighting RNA viruses with a gold nanoparticle Cas13d gene-editing armor. Molecular therapy. Nucleic acids, 36(2), 102540.

Houmadi H, et al. (2025) Five-Year (2017-2022) Evolutionary Dynamics of Human Coronavirus OC43 in Southern France Based on Whole Genome Next-Generation Sequencing. Journal of medical virology, 97(12), e70726.

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.

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).

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.

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

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

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

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).