

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 or information resource, data processing software, data repository, data visualization software, database, service resource, software application, software resource, storage service 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: 20260821T194004+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 173 mentions in open access literature.

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

Kaneko M, et al. (2026) Factors contributing to the frequent interspecies transmission of G4P[6] Rotavirus alphagastroenteritidis strains from pigs to humans in Vietnam: molecular epidemiological insights. Microbial genomics, 12(4).

Gallego JC, et al. (2026) Partial nucleotide sequence analysis of the VP6 gene from rotavirus species A, D, and F identified in diarrheic broiler chickens. Brazilian journal of microbiology : [publication of the Brazilian Society for Microbiology], 57(1).

Dutta S, et al. (2026) Prediction of potential NS3-based T cell epitopes of hepatitis C virus by in-silico and in-vitro approach. Scientific reports, 16(1).

Park C, et al. (2026) Development of reference material from Rift Valley fever virus RNA. Virology journal, 23(1).

Wang Y, et al. (2026) Dissecting the evolutionary forces shaping codon usage bias in SFTSV from eastern China: Insights from a previously underrepresented region.

Virulence, 17(1), 2621490.

Zhang X, et al. (2026) scMOVIR: a single-cell multi-omics database for human viral infections and immune responses. *Nucleic acids research*, 54(D1), D871.

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).

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.

Leng C, et al. (2025) Isolation and whole-genome characterization of an emerging G9P[23] porcine rotavirus in Central China. *Frontiers in veterinary science*, 12, 1708098.

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).

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.

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.

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

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.