Resource Summary Report

Generated by NIF on Apr 18, 2025

VIPERdb

RRID:SCR_002853
Type: Tool

Proper Citation

VIPERdb (RRID:SCR_002853)

Resource Information

URL: http://viperdb.scripps.edu/

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Description: Database for icosahedral virus capsid structures. The emphasis of the resource is on providing data from structural and computational analyses on these systems, as well as high quality renderings for visual exploration. In addition, all virus capsids are placed in a single icosahedral orientation convention, facilitating comparison between different structures. The web site includes powerful search utilities , links to other relevant databases, background information on virus capsid structure, and useful database interface tools. It is an information source for the analysis of high resolution virus structures. VIPERdb is a one-stop site dedicated to helping users around the world examine the many icosahedral virus structures contained within the Protein Data Bank (PDB) by providing them with an easy to use database containing current data and a variety of analytical tools. Sponsors: VIPERdb is funded by the NIH.

Synonyms: Virus Particle ExploreR

Resource Type: database, data or information resource

Defining Citation: PMID:33313778, PMID:30265627

Keywords: exploration, analysis, capsid, computational, convention, database, icosahedral, structural, structure, system, virus, visual, bio.tools, FASEB list

Funding:

Resource Name: VIPERdb

Resource ID: SCR_002853

Alternate IDs: nif-0000-25311, nif-0000-03630, biotools:viperdb, SCR_007970

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

Record Creation Time: 20220129T080215+0000

Record Last Update: 20250418T055006+0000

Ratings and Alerts

No rating or validation information has been found for VIPERdb.

No alerts have been found for VIPERdb.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 55 mentions in open access literature.

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

Toyooka R, et al. (2024) Explicit description of viral capsid subunit shapes by unfolding dihedrons. Communications biology, 7(1), 1509.

Joshi PU, et al. (2024) Design Rules for the Sequestration of Viruses into Polypeptide Complex Coacervates. Biomacromolecules, 25(2), 741.

Li L, et al. (2024) Dissecting positive selection events and immunological drives during the evolution of adeno-associated virus lineages. PLoS pathogens, 20(6), e1012260.

Martin GM, et al. (2023) Affinity-matured homotypic interactions induce spectrum of PfCSP structures that influence protection from malaria infection. Nature communications, 14(1), 4546.

Heldt CL, et al. (2023) Empty and Full AAV Capsid Charge and Hydrophobicity Differences Measured with Single-Particle AFM. Langmuir : the ACS journal of surfaces and colloids, 39(16), 5641.

Dishlers A, et al. (2023) PreS1 Containing HBc VLPs for the Development of a Combined Therapeutic/Prophylactic Hepatitis B Vaccine. Microorganisms, 11(4).

Ritsch M, et al. (2023) Navigating the Landscape: A Comprehensive Review of Current Virus Databases. Viruses, 15(9).

Switalski K, et al. (2022) Direct measurement of Stokes-Einstein diffusion of Cowpea mosaic virus with 19 µs-resolved XPCS. Journal of synchrotron radiation, 29(Pt 6), 1429.

El Andari J, et al. (2022) Semirational bioengineering of AAV vectors with increased potency and specificity for systemic gene therapy of muscle disorders. Science advances, 8(38), eabn4704.

Villa TG, et al. (2021) Animal and human RNA viruses: genetic variability and ability to overcome vaccines. Archives of microbiology, 203(2), 443.

Mattenberger F, et al. (2021) Globally defining the effects of mutations in a picornavirus capsid. eLife, 10.

Mattenberger F, et al. (2021) Increased RNA virus population diversity improves adaptability. Scientific reports, 11(1), 6824.

Montiel-Garcia D, et al. (2021) VIPERdb v3.0: a structure-based data analytics platform for viral capsids. Nucleic acids research, 49(D1), D809.

Coulibaly F, et al. (2021) virusMED: your travel guide to the virus world. IUCrJ, 8(Pt 6), 857.

Havlik LP, et al. (2021) Receptor Switching in Newly Evolved Adeno-associated Viruses. Journal of virology, 95(19), e0058721.

Real-Hohn A, et al. (2020) nanoDSF: In vitro Label-Free Method to Monitor Picornavirus Uncoating and Test Compounds Affecting Particle Stability. Frontiers in microbiology, 11, 1442.

Havlik LP, et al. (2020) Coevolution of Adeno-associated Virus Capsid Antigenicity and Tropism through a Structure-Guided Approach. Journal of virology, 94(19).

Wu R, et al. (2020) Rapid prediction of crucial hotspot interactions for icosahedral viral capsid self-assembly by energy landscape atlasing validated by mutagenesis. PLoS computational biology, 16(10), e1008357.

Hildebrandt E, et al. (2020) Evolution of dependoparvoviruses across geological timescales-implications for design of AAV-based gene therapy vectors. Virus evolution, 6(2), veaa043.

Mietzsch M, et al. (2020) Structural Characterization of Cuta- and Tusavirus: Insight into Protoparvoviruses Capsid Morphology. Viruses, 12(6).