

Resource Summary Report

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Swiss-PdbViewerDeepViewv4.0

RRID:SCR_013295

Type: Tool

Proper Citation

Swiss-PdbViewerDeepViewv4.0 (RRID:SCR_013295)

Resource Information

URL: <http://spdbv.vital-it.ch>

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Description: First of all, and most importantly, PC and Mac versions have been resynchronized. Support for direct login modelling submissions and result retrieval to/from the SwissModel Workspace Enhanced Import Menu Enhanced user interface with taxonomy support, and new sequence alignment features. New 3D Motif Searching feature Easy access to external user defined scripts directly from the interface Revised Help files accessible from the interface Swiss-PdbViewer (aka DeepView) is an application that provides a user friendly interface allowing to analyze several proteins at the same time. The proteins can be superimposed in order to deduce structural alignments and compare their active sites or any other relevant parts. Amino acid mutations, H-bonds, angles and distances between atoms are easy to obtain thanks to the intuitive graphic and menu interface. Swiss-PdbViewer can also read electron density maps, and provides various tools to build into the density. In addition, various modeling tools are integrated and command files for popular energy minimization packages can be generated. Finally, as a special bonus, POV-Ray scenes can be generated from the current view in order to make stunning ray-traced quality images.

Synonyms: DeepView

Resource Type: software resource

Resource Name: Swiss-PdbViewerDeepViewv4.0

Resource ID: SCR_013295

Alternate IDs: nif-0000-30439

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260725T190751+0000

Ratings and Alerts

No rating or validation information has been found for Swiss-PdbViewerDeepViewv4.0.

No alerts have been found for Swiss-PdbViewerDeepViewv4.0.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 391 mentions in open access literature.

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

Vázquez R, et al. (2025) The New SH3b_T Domain Increases the Structural and Functional Variability Among SH3b-Like CBDs from Staphylococcal Phage Endolysins. Probiotics and antimicrobial proteins, 17(6), 3930.

Ahmed SF, et al. (2025) In silico evaluation of Ocimum sanctum phytochemicals for diabetic foot ulcer therapy through docking, ADMET, DFT, and molecular dynamics. Scientific reports, 15(1), 43092.

Priyodip P, et al. (2024) Characterization of a putative metal-dependent PTP-like phosphatase from Lactobacillus helveticus 2126. International microbiology : the official journal of the Spanish Society for Microbiology, 27(1), 37.

Roy AS, et al. (2024) A computational approach for structural and functional analyses of disease-associated mutations in the human CYLD gene. Genomics & informatics, 22(1), 4.

Benyamini P, et al. (2024) Phylogenetic Tracing of Evolutionarily Conserved Zonula Occludens Toxin Reveals a "High Value" Vaccine Candidate Specific for Treating Multi-Strain Pseudomonas aeruginosa Infections. Toxins, 16(6).

Kong X, et al. (2024) Comparative study of lysine acetylation in Vesicomidae clam Archivesica marissinica and the manila clam Ruditapes philippinarum: adaptation mechanisms in cold seep environments. BMC genomics, 25(1), 1006.

Hasan M, et al. (2024) Pathogenic single nucleotide polymorphisms in RhoA gene: Insights into structural and functional impacts on RhoA-PLD1 interaction through molecular dynamics simulation. Current research in structural biology, 8, 100159.

Tang J, et al. (2024) R229I substitution from oseltamivir induction in HA1 region significantly increased the fitness of a H7N9 virus bearing NA 292K. Emerging microbes & infections, 13(1), 2373314.

Guerra E, et al. (2023) 3D-Informed Targeting of the Trop-2 Signal-Activation Site Drives Selective Cancer Vulnerability. Molecular cancer therapeutics, 22(6), 790.

Benatto VG, et al. (2023) Prospects of ZnS and ZnO as smart semiconductor materials in light-activated antimicrobial coatings for mitigation of severe acute respiratory syndrome coronavirus-2 infection. *Materials today. Communications*, 34, 105192.

Nguyen TH, et al. (2023) Four novel mutations in the androgen receptor gene from Vietnamese patients with androgen insensitivity syndrome. *Genes & genomics*, 45(4), 467.

Poleboyina PK, et al. (2023) Virtual Screening, Molecular Docking, and Dynamic Simulations Revealed TGF- β 1 Potential Inhibitors to Curtail Cervical Cancer Progression. *Applied biochemistry and biotechnology*.

Tamayo-Ordóñez MC, et al. (2023) Non-Structural Proteins (Nsp): A Marker for Detection of Human Coronavirus Families. *Pathogens (Basel, Switzerland)*, 12(9).

Budaya TN, et al. (2023) The Evolution of Polyclonal Antibody from Specific Epitope 47kDA for Detection of Bladder Cancer. *Asian Pacific journal of cancer prevention : APJCP*, 24(9), 3155.

Poleboyina PK, et al. (2022) Screening and Identification of Potential iNOS Inhibitors to Curtail Cervical Cancer Progression: an In Silico Drug Repurposing Approach. *Applied biochemistry and biotechnology*, 194(1), 570.

Schamber MR, et al. (2022) Mechanism of sensitivity modulation in the calcium-sensing receptor via electrostatic tuning. *Nature communications*, 13(1), 2194.

Višnjar T, et al. (2022) Biallelic ATOH1 Gene Variant in Siblings With Pontocerebellar Hypoplasia, Developmental Delay, and Hearing Loss. *Neurology. Genetics*, 8(3), e677.

Hegedus D, et al. (2022) Genetic variation and structural diversity in major seed proteins among and within *Camelina* species. *Planta*, 256(5), 93.

Nappi M, et al. (2022) Gain of function due to increased opening probability by two KCNQ5 pore variants causing developmental and epileptic encephalopathy. *Proceedings of the National Academy of Sciences of the United States of America*, 119(15), e2116887119.

Veerasamy R, et al. (2022) Molecular docking unveils the potential of andrographolide derivatives against COVID-19: an in silico approach. *Journal, genetic engineering & biotechnology*, 20(1), 58.