Resource Summary Report

Generated by dkNET on Apr 27, 2025

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

Funding:

Resource Name: Swiss-PdbViewerDeepViewv4.0

Resource ID: SCR_013295

Alternate IDs: nif-0000-30439

Record Creation Time: 20220129T080315+0000

Record Last Update: 20250420T014640+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 255 mentions in open access literature.

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

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.

Kong X, et al. (2024) Comparative study of lysine acetylation in Vesicomyidae 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.

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.

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.

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-?1 Potential Inhibitors to Curtail Cervical Cancer Progression. Applied biochemistry and biotechnology.

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.

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

Zackria AA, et al. (2022) Computational screening of natural compounds from Salvia plebeia R. Br. for inhibition of SARS-CoV-2 main protease. Vegetos (Bareilly, India), 35(2), 345.

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.

Zhu S, et al. (2022) Adaptively evolved human oral actinomyces-sourced defensins show therapeutic potential. EMBO molecular medicine, 14(2), e14499.

Mun CS, et al. (2022) Multi-targeted molecular docking, pharmacokinetics, and drug-likeness evaluation of coumarin based compounds targeting proteins involved in development of COVID-19. Saudi journal of biological sciences, 29(12), 103458.

Wang H, et al. (2022) Pan-Cancer Transcriptome and Immune Infiltration Analyses Reveal the Oncogenic Role of Far Upstream Element-Binding Protein 1 (FUBP1). Frontiers in molecular biosciences, 9, 794715.

Ahn LY, et al. (2021) An epilepsy-associated ACTL6B variant captures neuronal hyperexcitability in a human induced pluripotent stem cell model. Journal of neuroscience research, 99(1), 110.

Jafary F, et al. (2021) In silico investigation of critical binding pattern in SARS-CoV-2 spike protein with angiotensin-converting enzyme 2. Scientific reports, 11(1), 6927.

González-Faune P, et al. (2021) Computational Study on Temperature Driven Structure-Function Relationship of Polysaccharide Producing Bacterial Glycosyl Transferase Enzyme. Polymers, 13(11).

Cyrus C, et al. (2021) Haemoglobin switching modulator SNPs rs5006884 is associated with increased HbA2 in ?-thalassaemia carriers. Archives of medical science : AMS, 17(4), 1064.

Kumar P, et al. (2021) Immunoinformatics-Based Designing of a Multi-Epitope Chimeric Vaccine From Multi-Domain Outer Surface Antigens of Leptospira. Frontiers in immunology, 12, 735373.