

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Swiss-PdbViewerDeepViewv4.0

RRID:SCR_013295

Type: Tool

Proper Citation

Swiss-PdbViewerDeepViewv4.0 (RRID:SCR_013295)

Resource Information

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

Proper Citation: Swiss-PdbViewerDeepViewv4.0 (RRID:SCR_013295)

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: 20260905T132734+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 413 mentions in open access literature.

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

Le DM, et al. (2026) Distinct Associations of GTF2I, TP53, and NOTCH1 Variants with Indolent and Aggressive Thymic Epithelial Tumors in Vietnamese Patients. *Genes*, 17(5).

Ahmed SF, et al. (2025) In silico identification of promising PD-L1 inhibitors from selected indian medicinal plants for treatment of triple negative breast cancer. *PloS one*, 20(7), e0327475.

Rehman K, et al. (2025) Exploring the Therapeutic Potential of Virtual Screened Novel HER2 Inhibitors via QSAR, Molecular Docking and Dynamics Simulations. *Dose-response : a publication of International Hormesis Society*, 23(4), 15593258251394191.

Hossain MA, et al. (2025) In silico identification of bilobetin and ginsenoside as dual CK2 and ULK2 inhibitors targeting triple-negative breast cancer. *Scientific reports*, 16(1), 3461.

Wang J, et al. (2025) Adaptive mutations in HA of avian H9N2 influenza viruses facilitate their transmission to swine. *Veterinary research*, 57(1), 3.

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.

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.

Singh SP, et al. (2025) A synergistic herbal formulation targeting *Malassezia furfur* and *Staphylococcus epidermidis* for effective dandruff management. *Frontiers in microbiology*, 16, 1654658.

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.

Nguyen TT, et al. (2024) The First Genetic Characterization of the SPRN Gene in Pekin Ducks (*Anas platyrhynchos domesticus*). *Animals : an open access journal from MDPI*, 14(11).

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.

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.

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.

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*.

Choudhary S, et al. (2023) Molecular modeling, simulation and docking of Rv1250 protein from *Mycobacterium tuberculosis*. *Frontiers in bioinformatics*, 3, 1125479.