

Resource Summary Report

Generated by PRECISE-TBI on Jul 31, 2026

SAVES

RRID:SCR_018219

Type: Tool

Proper Citation

SAVES (RRID:SCR_018219)

Resource Information

URL: <https://servicesn.mbi.ucla.edu/SAVES/>

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Description: Web server for structure validation in homology modeling. Used to validate of obtained crude models. Structure analysis and validation server.

Synonyms: SAVES v5.0, Structure Analysis and Verification Server

Resource Type: service resource, data access protocol, software resource, web service, production service resource, analysis service resource

Keywords: Structure validation, homology modeling, obtained model, analysis, validation server

Availability: Free, Freely available

Resource Name: SAVES

Resource ID: SCR_018219

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260731T043031+0000

Ratings and Alerts

No rating or validation information has been found for SAVES.

No alerts have been found for SAVES.

Data and Source Information

Usage and Citation Metrics

We found 183 mentions in open access literature.

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

da Silva Dutra M, et al. (2025) Antimicrobial and antiparasitic potential of lupeol: antifungal effect on the *Candida parapsilosis* species complex and nematocidal activity against *Caenorhabditis elegans*. *Journal of medical microbiology*, 74(3).

Patil VS, et al. (2025) Exploring disulfiram mechanisms in renal fibrosis: insights from biological data and computational approaches. *Frontiers in pharmacology*, 16, 1480732.

Qiu J, et al. (2025) Integrated in-silico design and in vivo validation of multi-epitope vaccines for norovirus. *Virology journal*, 22(1), 166.

Cruz-Granados P, et al. (2025) An ultra-rare missense variant in the KIF1B gene linked to autoimmune Menière's disease. *NPJ genomic medicine*, 10(1), 42.

Rani V, et al. (2025) Elucidating the role of pyrabactin-like receptors of finger millet under drought and salinity stress: an insight into in silico, machine learning and molecular approaches. *Frontiers in genetics*, 16, 1598523.

Pham TL, et al. (2025) Phytochemical constituents of *Hydrangea macrophylla* var. *acuminata* leaves and their inhibitory activity against PTP1B and α -glucosidase. *Journal of enzyme inhibition and medicinal chemistry*, 40(1), 2584940.

Nirob MNH, et al. (2025) A multi-epitope vaccine targeting a key virulence factor ClfA: An In-silico approach to combat *Staphylococcus aureus* infections. *PloS one*, 20(10), e0334885.

Heidarinia H, et al. (2025) Design a multi-epitope vaccine candidate against *Acinetobacter baumannii* using advanced computational methods. *AMB Express*, 15(1), 103.

Chansap S, et al. (2025) Development of multi-epitope Cathepsin L driven short peptide vaccine against *Fasciola gigantica*. *Frontiers in veterinary science*, 12, 1547937.

Xu Y, et al. (2025) Enhancing *Bacillus cereus* antibacterial ability through improved cofactor supply. *Microbial cell factories*, 24(1), 52.

Masum MHU, et al. (2025) Revolutionizing Chikungunya Vaccines: mRNA Breakthroughs With Molecular and Immune Simulations. *Bioinformatics and biology insights*, 19, 11779322251324859.

Naderian R, et al. (2025) Rational design of multi-epitope vaccine for Chandipura virus using an immunoinformatics approach. *PloS one*, 20(10), e0335147.

Wang L, et al. (2025) Host cell KRT-18 as a non-redox dependent interactor of *Cryptosporidium parvum* PDI enables parasite infection. *Communications biology*, 8(1),

1840.

Kanwal A, et al. (2025) Computational development of multi-epitope vaccine to induce adaptive immunity against multi-drug resistant *Prevotella intermedia*. BMC infectious diseases, 25(1), 1674.

Aram C, et al. (2025) Development of a candidate mRNA vaccine based on Multi-Peptide targeting VP4 of rotavirus A: an immunoinformatics and molecular dynamics approach. Scientific reports, 15(1), 22610.

Ye Y, et al. (2025) The Identification and Characterization of a Novel Alginate Lyase from *Mesonaria hitae* R32 Exhibiting High Thermal Stability and Potent Antioxidant Oligosaccharide Production. Marine drugs, 23(4).

Akter S, et al. (2025) Comprehensive in silico characterization of nonsynonymous SNPs in the human ezrin (EZR) gene and their role in disease pathogenesis. Biochemistry and biophysics reports, 42, 101972.

Habibie A, et al. (2025) Improving Conformational Stability and Bacterial Membrane Interactions of Antimicrobial Peptides with Amphipathic Helical Structure. Research square.

Al Sharif B, et al. (2025) Genomic and enzymatic insights into α -amylase-producing *Bacillus spizizenii* strains isolated from Isfahan province, Iran. PloS one, 20(12), e0333668.

Monteiro Guedes M, et al. (2025) Repurposing statins for the treatment of larval cestodiasis: in silico evaluation of statin-HMG-CoA reductase interactions and assessment of statin effects on a cestode model. Parasitology, 152(8), 787.