

Resource Summary Report

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

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: 20260912T195858+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 219 mentions in open access literature.

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

Zhang L, et al. (2027) Discovery of leucine analogues of tyrocidines and tryptocidines from *Brevibacillus brevis* B011 through genome mining and in vitro biosynthesis. *Synthetic and systems biotechnology*, 15, 58.

Hakim MS, et al. (2026) Reverse vaccinology-based design of a universal multiepitope vaccine against chikungunya virus: Phylogenetic and immunoinformatics approaches. *Scientific reports*, 16(1).

Inan D, et al. (2026) AI fragmentation-based optimization of Sorafenib derivatives targeting VEGFR2 for angiogenesis-related pathologies: a structure-based in-silico study. *Scientific reports*, 16(1).

Nandish V, et al. (2026) Comparative pangenomics of *Pasteurella multocida* uncovers adhesins specific to capsular serogroup B strains associated with bovine host tropism. *BMC microbiology*, 26(1).

Doostmohammadi A, et al. (2026) Phylogeny-guided multi-epitope vaccine design targeting conserved and divergent regions of *Brucella* OMP2, OMP25, and OMP31: an immunoinformatics study. *BMC immunology*, 27(1).

Baniasadi Nejad N, et al. (2026) Computational design of a multi-epitope vaccine against *Helicobacter pylori* targeting CagA, FltD, urease, and OipA with cholera toxin B subunit (CTB) adjuvant. *BMC microbiology*, 26(1).

Muflikhati Z, et al. (2026) Integrative structural and physicochemical characterization of chalcone synthase enzymes from medicinal plants using AlphaFold, molecular docking, and molecular dynamics. *Scientific reports*, 16(1).

Sripath K, et al. (2026) Proteome-Based Antigen Screening and Multi-Epitope Design Against *Cutibacterium acnes*: An In Silico Study. *Biology*, 15(12).

Li J, et al. (2026) Molecular Characterization and Mechanistic Insights of a Thermostable Neoagarobiose Hydrolase Aga2457 from *Alteromonas* sp. *Marine drugs*, 24(4).

Xu J, et al. (2026) *Schistosoma japonicum* histone acetyltransferase 1 (SjHAT1): A novel anti-schistosomal drug target. *PLoS pathogens*, 22(6), e1014334.

Choudhary H, et al. (2026) In silico assessment of 4 methoxypelargonidin and luteolinidin from *Parthenium hysterophorus* as acetylcholinesterase inhibitors of *Phlebotomus Papatasi*. *Scientific reports*, 16(1), 3598.

Naveed M, et al. (2026) In silico design and immunoinformatics assessment of a multiepitope vaccine targeting borealpox virus. *Scientific reports*, 16(1), 3885.

Javaid S, et al. (2026) Identification of natural FGFR3 inhibitor for glioma using integrated computational and microRNA regulatory analysis. *Scientific reports*, 16(1).

Siddiquee NH, et al. (2026) Design of a global population-covering multi-epitope mRNA vaccine against Lassa virus using immunoinformatics. *Scientific reports*, 16(1).

Berrahou S, et al. (2026) HAp@Cell bio-films engineered from local resources involving molecular mechanisms of dye adsorption and antibacterial activity. *Scientific reports*, 16(1).

Yuan W, et al. (2026) Structural Prioritization of FatB Thioesterase Candidates Potentially Related to Lauric Acid-Rich Seed Oil in *Litsea cubeba*. *Biomolecules*, 16(6).

Almaghrabi M, et al. (2026) AI-Driven Discovery of Prototype CLEC4M Inhibitors Targeting Marburg Virus Entry via Integrated Machine Learning and Molecular Modeling. *International journal of molecular sciences*, 27(12).

Nguyen TD, et al. (2026) Genetic polymorphism and natural selection of apical membrane antigen-1 in *Plasmodium malariae* isolated from Vietnam. *BMC infectious diseases*, 26(1).

Dabiri M, et al. (2026) Computational optimization of DEK1 calpain domain solubility through integrated structural modelling and data-driven targeted mutagenesis. *Scientific reports*, 16(1).

Mechri S, et al. (2026) Hybrid Whole-Genome Sequencing of *Penicillium crustosum* CTM10622 Uncovers a Highly Thermostable Alkaline Serine Lipase with Biotechnological Relevance. *International journal of molecular sciences*, 27(12).