Resource Summary Report

Generated by dkNET on Apr 16, 2025

SAVES

RRID:SCR_018219
Type: Tool

Proper Citation

SAVES (RRID:SCR_018219)

Resource Information

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

Proper Citation: SAVES (RRID:SCR_018219)

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

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

Funding:

Availability: Free, Freely available

Resource Name: SAVES

Resource ID: SCR_018219

Record Creation Time: 20220129T080339+0000

Record Last Update: 20250416T063836+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

Source: SciCrunch Registry

Usage and Citation Metrics

We found 151 mentions in open access literature.

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

Ma L, et al. (2025) The Chlamydia pneumoniae inclusion membrane protein Cpn0308 interacts with host protein ACBD3. Journal of bacteriology, 207(1), e0027524.

Rahman MM, et al. (2025) Designing of an mRNA vaccine against high-risk human papillomavirus targeting the E6 and E7 oncoproteins exploiting immunoinformatics and dynamic simulation. PloS one, 20(1), e0313559.

Siddiki AZ, et al. (2025) Development of a multi-epitope chimeric vaccine in silico against Babesia bovis, Theileria annulata, and Anaplasma marginale using computational biology tools and reverse vaccinology approach. PloS one, 20(1), e0312262.

Rani V, et al. (2024) Genome-wide identification of nuclear factor -Y (NF-Y) transcription factor family in finger millet reveals structural and functional diversity. Heliyon, 10(18), e36370.

Lu L, et al. (2024) Avian pathogenic Escherichia coli T6SS effector protein Hcp2a causes mitochondrial dysfunction through interaction with LETM1 protein in DF-1 cells. Poultry science, 103(4), 103514.

Khichi S, et al. (2024) A Multi-epitope Subunit Vaccine Identification and Development Against Scrub Typhus (Orientia tsutsugamushi) Using Immunoinformatics Approaches. Cureus, 16(5), e61009.

Shah M, et al. (2024) Development of a subunit vaccine against the cholangiocarcinoma causing Opisthorchis viverrini: a computational approach. Frontiers in immunology, 15, 1281544.

Khanam A, et al. (2024) An immunoinformatics approach for a potential NY-ESO-1 and WT1 based multi-epitope vaccine designing against triple-negative breast cancer. Heliyon, 10(17), e36935.

Shetty S, et al. (2024) Immunoinformatics design of a multi-epitope vaccine for Chlamydia

trachomatis major outer membrane proteins. Scientific reports, 14(1), 29919.

Sarvmeili J, et al. (2024) Immunoinformatics design of a structural proteins driven multi-epitope candidate vaccine against different SARS-CoV-2 variants based on fynomer. Scientific reports, 14(1), 10297.

Shafique I, et al. (2024) Computational evaluation of efflux pump homologues and lignans as potent inhibitors against multidrug-resistant Salmonella typhi. PloS one, 19(6), e0303285.

Li X, et al. (2024) Discovery, characterization and mechanism of a Microbacterium esterase for key d-biotin chiral intermediate synthesis. Bioresources and bioprocessing, 11(1), 59.

Gouda MNR, et al. (2024) Variations in the expression of odorant binding and chemosensory proteins in the developmental stages of whitefly Bemisia tabaci Asia II-1. Scientific reports, 14(1), 15046.

Sulieman AME, et al. (2024) Comprehensive In Vitro Evaluation of Antibacterial, Antioxidant, and Computational Insights into Blepharis ciliaris (L.) B. L. Burtt from Hail Mountains, Saudi Arabia. Plants (Basel, Switzerland), 13(24).

Fu BW, et al. (2024) Engineering of Bacillus thuringiensis Cry2Ab toxin for improved insecticidal activity. AMB Express, 14(1), 15.

Arthur MN, et al. (2024) Design of Inhibitors That Target the Menin-Mixed-Lineage Leukemia Interaction. Computation (Basel, Switzerland), 12(1).

Li M, et al. (2024) Identification of TonB-dependent siderophore receptor inhibitors against Flavobacterium columnare using a structure-based high-throughput virtual screening method. Frontiers in microbiology, 15, 1392178.

Mahdeen AA, et al. (2024) Designing novel multiepitope mRNA vaccine targeting Hendra virus (HeV): An integrative approach utilizing immunoinformatics, reverse vaccinology, and molecular dynamics simulation. PloS one, 19(10), e0312239.

Ma X, et al. (2024) Genome-Wide Identification and Characterization of the Medium-Chain Dehydrogenase/Reductase Superfamily of Trichosporon asahii and Its Involvement in the Regulation of Fluconazole Resistance. Journal of fungi (Basel, Switzerland), 10(2).

Shabir A, et al. (2024) Exploring HMMR as a therapeutic frontier in breast cancer treatment, its interaction with various cell cycle genes, and targeting its overexpression through specific inhibitors. Frontiers in pharmacology, 15, 1361424.