Resource Summary Report

Generated by NIF on May 20, 2025

ProSA-web

RRID:SCR_018540
Type: Tool

Proper Citation

ProSA-web (RRID:SCR_018540)

Resource Information

URL: https://prosa.services.came.sbg.ac.at/prosa.php

Proper Citation: ProSA-web (RRID:SCR_018540)

Description: Web service is extension of classic ProSA program used for refinement and validation of experimental protein structures and in structure prediction and modeling.

Synonyms: Protein Structure Analysis web

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

Defining Citation: PMID:17517781

Keywords: Protein structure, protein, protein structure refinement, protein structure validation, protein structure prediction, protein structure modeling, bio.tools

Funding: FWF Austria ;
University of Salzburg ;
Austria.

Availability: Free, Freely available

Resource Name: ProSA-web

Resource ID: SCR_018540

Alternate IDs: biotools:prosa-web

Alternate URLs: https://bio.tools/prosa-web

Record Creation Time: 20220129T080340+0000

Record Last Update: 20250519T204038+0000

Ratings and Alerts

No rating or validation information has been found for ProSA-web.

No alerts have been found for ProSA-web.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 102 mentions in open access literature.

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

Banico EC, et al. (2024) Advancing one health vaccination: In silico design and evaluation of a multi-epitope subunit vaccine against Nipah virus for cross-species immunization using immunoinformatics and molecular modeling. PloS one, 19(9), e0310703.

Zhou P, et al. (2024) Innovative epitopes in Staphylococcal Protein-A an immuno-informatics approach to combat MDR-MRSA infections. Frontiers in cellular and infection microbiology, 14, 1503944.

Albaqami FF, et al. (2024) From proteome to candidate vaccines: target discovery and molecular dynamics-guided multi-epitope vaccine engineering against kissing bug. Frontiers in immunology, 15, 1413893.

Ru Y, et al. (2023) Identification of Potential Novel B-Cell Epitopes of Capsid Protein VP2 in Senecavirus A. Microbiology spectrum, 11(4), e0447222.

Sarkar B, et al. (2022) Immunoinformatics-guided designing and in silico analysis of epitope-based polyvalent vaccines against multiple strains of human coronavirus (HCoV). Expert review of vaccines, 21(12), 1851.

Jyotisha , et al. (2022) Multi-epitope vaccine against SARS-CoV-2 applying immunoinformatics and molecular dynamics simulation approaches. Journal of biomolecular structure & dynamics, 40(7), 2917.

Kalachova T, et al. (2022) DIACYLGLYCEROL KINASE 5 participates in flagellin-induced

signaling in Arabidopsis. Plant physiology, 190(3), 1978.

Ayyagari VS, et al. (2022) Design of a multi-epitope-based vaccine targeting M-protein of SARS-CoV2: an immunoinformatics approach. Journal of biomolecular structure & dynamics, 40(7), 2963.

Samad A, et al. (2022) Designing a multi-epitope vaccine against SARS-CoV-2: an immunoinformatics approach. Journal of biomolecular structure & dynamics, 40(1), 14.

Behbahani M, et al. (2021) In silico design of a multi-epitope peptide construct as a potential vaccine candidate for Influenza A based on neuraminidase protein. In silico pharmacology, 9(1), 36.

Behera SK, et al. (2021) Immunoinformatic Study of Recombinant LigA/BCon1-5 Antigen and Evaluation of Its Diagnostic Potential in Primary and Secondary Binding Tests for Serodiagnosis of Porcine Leptospirosis. Pathogens (Basel, Switzerland), 10(9).

Chatterjee R, et al. (2021) Development of a Conserved Chimeric Vaccine for Induction of Strong Immune Response against Staphylococcus aureus Using Immunoinformatics Approaches. Vaccines, 9(9).

Rahman S, et al. (2021) Integrated Multi-omics, Virtual Screening and Molecular Docking Analysis of Methicillin-Resistant Staphylococcus aureus USA300 for the Identification of Potential Therapeutic Targets: An In-Silico Approach. International journal of peptide research and therapeutics, 27(4), 2735.

Rostaminia S, et al. (2021) Computational Design and Analysis of a Multi-epitope Against Influenza A virus. International journal of peptide research and therapeutics, 27(4), 2625.

Nath P, et al. (2021) Structure and dynamics analysis of multi-domain putative ?-1,4-glucosidase of family 3 glycoside hydrolase (PsGH3) from Pseudopedobacter saltans. Journal of molecular modeling, 27(4), 106.

Aljahdali MO, et al. (2021) Compounds Identified from Marine Mangrove Plant (Avicennia alba) as Potential Antiviral Drug Candidates Against WDSV, an In-Silico Approach. Marine drugs, 19(5).

Rossi S, et al. (2021) Transamidation Down-Regulates Intestinal Immunity of Recombinant ?-Gliadin in HLA-DQ8 Transgenic Mice. International journal of molecular sciences, 22(13).

Sanami S, et al. (2021) Design of a multi-epitope vaccine against cervical cancer using immunoinformatics approaches. Scientific reports, 11(1), 12397.

Shey RA, et al. (2021) Computational Design and Preliminary Serological Analysis of a Novel Multi-Epitope Vaccine Candidate against Onchocerciasis and Related Filarial Diseases. Pathogens (Basel, Switzerland), 10(2).

Kumar M, et al. (2021) Addressing the potential role of curcumin in the prevention of COVID-19 by targeting the Nsp9 replicase protein through molecular docking. Archives of microbiology, 203(4), 1691.