

Resource Summary Report

Generated by PRECISE-TBI on Sep 7, 2026

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

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: 20260905T132838+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 109 mentions in open access literature.

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

Tombari W, et al. (2025) A novel mRNA-based multi-epitope vaccine for rabies virus computationally designed via reverse vaccinology and immunoinformatics. Scientific reports, 15(1), 30355.

Singh K, et al. (2025) Comprehensive Evolutionary and Structural Analysis of the H5N1 Clade 2.4.3.4b Influenza A Virus Based on the Sequences and Data Mining of the Hemagglutinin, Nucleoprotein and Neuraminidase Genes Across Multiple Hosts. Pathogens (Basel, Switzerland), 14(9).

Sattari Sarvari S, et al. (2025) Protective Immunity of a Novel Multi-Epitope Vaccine Encoding OMP31, TF, BLS, SOD, BP26, and L9 Against Brucella spp. Infection. Iranian biomedical journal, 29(1 & 2), 36.

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.

Rabienia M, et al. (2024) Designing of a new multi-epitope vaccine against Leishmania major using Leish-F1 epitopes: An In-silico study. PloS one, 19(1), e0295495.

Zhou P, et al. (2024) Innovative epitopes in Staphylococcal Protein-A an immunoinformatics 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.

Wu S, et al. (2024) Revealing the Hypoglycemic Effect of Red Yeast Rice: Perspectives from the Inhibition of α -Glucosidase and the Anti-Glycation Capability by Ankaflavin and Monascin. Foods (Basel, Switzerland), 13(10).

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

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.

Movahedpour A, et al. (2022) Designing a Multi-Epitope Antigen for Serodiagnosis of *Strongyloides stercoralis* Based on L3Nie.01 and IgG Immunoreactive Epitopes. *Avicenna journal of medical biotechnology*, 14(2), 114.

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.

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.

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.

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).

Rossi S, et al. (2021) Transamidation Down-Regulates Intestinal Immunity of Recombinant γ -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.

Hasanshahi Z, et al. (2021) First report on molecular docking analysis and drug resistance substitutions to approved HCV NS5A and NS5B inhibitors amongst Iranian patients. *BMC gastroenterology*, 21(1), 443.