

Resource Summary Report

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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, software resource, web service, analysis service 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: 20260801T042817+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 104 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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.

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.

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.

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.

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.

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.

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.

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).

Zheng X, et al. (2021) Identification of Potential Inhibitors of MurD Enzyme of *Staphylococcus aureus* from a Marine Natural Product Library. *Molecules (Basel, Switzerland)*, 26(21).

Yılmaz Çolak Ç, et al. (2021) Computational Design of a Multi-epitope Vaccine Against *Clostridium chauvoei*: An Immunoinformatics Approach. *International journal of peptide research and therapeutics*, 27(4), 2639.

Madlala T, et al. (2021) Designing multiepitope-based vaccine against *Eimeria* from immune mapped protein 1 (IMP-1) antigen using immunoinformatic approach. *Scientific reports*, 11(1), 18295.

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

Shankar C, et al. (2021) Aerobactin Seems To Be a Promising Marker Compared With Unstable RmpA2 for the Identification of Hypervirulent Carbapenem-Resistant *Klebsiella pneumoniae*: In Silico and In Vitro Evidence. *Frontiers in cellular and infection microbiology*, 11, 709681.

Fadaka AO, et al. (2021) Immunoinformatics design of a novel epitope-based vaccine candidate against dengue virus. *Scientific reports*, 11(1), 19707.

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.

Tang Q, et al. (2021) Alpha-Synuclein defects autophagy by impairing SNAP29-mediated autophagosome-lysosome fusion. *Cell death & disease*, 12(10), 854.