Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 13, 2025

ProSA web

RRID:SCR_021879
Type: Tool

Proper Citation

ProSA web (RRID:SCR_021879)

Resource Information

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

Proper Citation: ProSA web (RRID:SCR_021879)

Description: Interactive web service for recognition of errors in three dimensional structures of proteins.

Synonyms: ProSA-web

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

Defining Citation: PMID:17517781

Keywords: structure errors recognition, proteins three dimensional structures, protein structure errors

Funding: FWF Austria ;
University of Salzburg Austria

Availability: Free, Freely available

Resource Name: ProSA web

Resource ID: SCR_021879

Record Creation Time: 20220421T050137+0000

Record Last Update: 20250412T060414+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 200 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Naveed M, et al. (2025) Exploration of alcohol dehydrogenase EutG from Bacillus tropicus as an eco-friendly approach for the degradation of polycyclic aromatic compounds. Scientific reports, 15(1), 3466.

Aganja RP, et al. (2025) Expression and delivery of HA1-M2e antigen using an innovative attenuated Salmonella-mediated delivery system confers promising protection against H9N2 avian influenza challenge. Poultry science, 104(1), 104602.

Nahian M, et al. (2025) Development of a broad-spectrum epitope-based vaccine against Streptococcus pneumoniae. PloS one, 20(1), e0317216.

Abuzahra M, et al. (2025) A novel p.127Val>Ile single nucleotide polymorphism in the MTNR1A gene and its relation to litter size in Thin-tailed Indonesian ewes. Animal bioscience, 38(2), 209.

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.

Gül A, et al. (2024) Immunogenicity and protection efficacy of a COVID-19 DNA vaccine encoding spike protein with D614G mutation and optimization of large-scale DNA vaccine production. Scientific reports, 14(1), 13865.

Bai Y, et al. (2024) Causative role of a novel intronic indel variant in FBN1 and maternal germinal mosaicism in Marfan syndrome. Orphanet journal of rare diseases, 19(1), 209.

Zhu X, et al. (2024) Design of multi-epitope vaccine against porcine rotavirus using computational biology and molecular dynamics simulation approaches. Virology journal, 21(1), 160.

Barazesh M, et al. (2024) Bioinformatics analysis to design a multi-epitope mRNA vaccine against S. agalactiae exploiting pathogenic proteins. Scientific reports, 14(1), 28294.

Shi H, et al. (2024) Development of innovative multi-epitope mRNA vaccine against central nervous system tuberculosis using in silico approaches. PloS one, 19(9), e0307877.

Saadh MJ, et al. (2024) Design of a novel multi-epitope vaccine candidate against Yersinia pestis using advanced immunoinformatics approaches: An in silico study. Biochemistry and biophysics reports, 40, 101871.

Hashempour A, et al. (2024) Design of multivalent-epitope vaccine models directed toward the world's population against HIV-Gag polyprotein: Reverse vaccinology and immunoinformatics. PloS one, 19(9), e0306559.

Momajadi L, et al. (2024) Designing a multi-epitope influenza vaccine: an immunoinformatics approach. Scientific reports, 14(1), 25382.

Singh G, et al. (2024) Structural characterization of DNA-binding domain of essential mammalian protein TTF 1. Bioscience reports, 44(8).

Nebangwa DN, et al. (2024) Predictive immunoinformatics reveal promising safety and anti-onchocerciasis protective immune response profiles to vaccine candidates (Ov-RAL-2 and Ov-103) in anticipation of phase I clinical trials. PloS one, 19(10), e0312315.

Lei X, et al. (2024) A Universal Multi-Epitope Vaccine Design Against Porcine Reproductive and Respiratory Syndrome Virus via Bioinformatics and Immunoinformatics Approaches. Veterinary sciences, 11(12).

Y?lmaz Çolak Ç, et al. (2024) In silico analysis of virulence factors of Streptococcus uberis for a chimeric vaccine design. In silico pharmacology, 12(1), 7.

Shi J, et al. (2024) In silico designed novel multi-epitope mRNA vaccines against Brucella by targeting extracellular protein BtuB and LptD. Scientific reports, 14(1), 7278.

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.

Li M, et al. (2024) Designing a conjugate vaccine targeting Klebsiella pneumoniae ST258 and ST11. Heliyon, 10(5), e27417.