

Resource Summary Report

Generated by [dkNET](#) on Sep 11, 2026

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, software resource, web service

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: 20260905T132947+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 474 mentions in open access literature.

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

Paulo DGS, et al. (2026) Peptides Derived From Reactive Center Loops Inhibit Digestive Trypsin-Like Enzymes in Lepidopteran Pests. Archives of insect biochemistry and physiology, 121(1), e70123.

Li S, et al. (2026) In silico design of the multi-epitope vaccine for lung adenocarcinoma based on hub gene-derived neoantigens. BMC cancer, 26(1).

Nguyen TC, et al. (2026) Subtle Genetic Shifts of African Swine Fever Virus Among Vietnamese Domestic Swine Following Live-Attenuated Vaccine Commercialization. Transboundary and emerging diseases, 2026, 8776906.

Mallawarachchi S, et al. (2026) Evaluation of molecular interactions of vaping juice components with ACE2 receptor. Scientific reports, 16(1).

Seifi N, et al. (2026) Design and in silico evaluation of an mRNA vaccine against HTLV-1 using AI-driven reverse vaccinology approaches. PloS one, 21(5), e0340201.

Ribeiro JA, et al. (2026) Molecular Characterization of Tomato Brown Rugose Fruit Virus in Portugal and Its Global Phylogenetic Context. Plants (Basel, Switzerland), 15(8).

Hoda A, et al. (2026) Computational analysis of non-synonymous SNPs in the sheep MC4R gene. Journal, genetic engineering & biotechnology, 24(2), 100709.

Ali S, et al. (2026) Immunoinformatics-guided design of a universal chimeric multi-epitope subunit vaccine against Marburg virus disease and Ravn virus co-infection. Scientific reports, 16(1), 6984.

Emadi SH, et al. (2026) Design and computational evaluation of a prophylactic and therapeutic multi-epitope vaccine candidate against cervical cancer. Virology journal, 23(1), 45.

De Leon DO, et al. (2026) Immunoinformatics and molecular docking reveal potential multi-epitope vaccine against Pseudomonas aeruginosa. Clinical and experimental vaccine research, 15(1), 71.

Srivastava R, et al. (2026) Immunoinformatic insights for design and clinical prospects of pan-RAS cancer vaccine. Frontiers in medicine, 13, 1727976.

Shuvo MN, et al. (2026) Computational and immunoinformatics approaches for designing phytocompound-based drugs and a multi-epitope vaccine targeting FemA, a cell wall protein of Staphylococcus aureus. PloS one, 21(4), e0346271.

Liscano Y, et al. (2026) Spider Venom Peptides as Potential Allosteric Inhibitors of Undecaprenyl Diphosphatase (UppP) from *Acinetobacter baumannii*: In Silico Identification and Structural Analysis. *Toxins*, 18(5).

Zepeda-Cervantes J, et al. (2026) Identification of Conserved B and T Cell Epitopes in Glycoprotein S of Mexican Porcine Epidemic Diarrhea Virus (PEDV) Strains via Immunoinformatics Analysis, Molecular Docking, and Immunofluorescence. *Viruses*, 18(4).

Naveed M, et al. (2026) Designing a multi-epitope vaccine against yellow fever virus using immunoinformatics approaches. *Open medicine (Warsaw, Poland)*, 21(1), 20261453.

Ishabiyi FO, et al. (2026) Establishing FDA-approved oncology drugs as GPR176 inhibitor through homology modelling, molecular docking, MMGBSA, DFT, and molecular dynamics simulation. *Scientific reports*, 16(1), 1859.

Rivera MV, et al. (2026) Expression, Solubilization, and Refolding Recovery of a Novel I???Asparaginase-Arginase 1 Chimera from *E. coli* Inclusion Bodies. *ACS omega*, 11(10), 16333.

Attique L, et al. (2026) Multiepitope-Based Peptide Vaccine Against A35R Glycoprotein and E8L Membrane Protein of Monkeypox Virus Using an Immunoinformatics Approach. *Biology*, 15(7).

Tao X, et al. (2026) Preparation of a multiepitope vaccine candidate for camel bocavirus and evaluation of its immunogenicity in a mouse model. *Frontiers in immunology*, 17, 1786028.

Araneda J, et al. (2026) In silico design of a multiantigenic and multiepitope chimeric protein as a vaccine candidate against *Renibacterium salmoninarum*. *Frontiers in cellular and infection microbiology*, 16, 1814020.