

Resource Summary Report

Generated by [dkNET](#) on Jul 30, 2026

PSIPRED

RRID:SCR_010246

Type: Tool

Proper Citation

PSIPRED (RRID:SCR_010246)

Resource Information

URL: <http://bioinf.cs.ucl.ac.uk/psipred/>

Proper Citation: PSIPRED (RRID:SCR_010246)

Description: Web tool as secondary structure prediction method, incorporating two feed forward neural networks which perform analysis on output obtained from PSI-BLAST. Web server offering analyses of protein sequences.

Synonyms: PSIPRED Protein Sequence Analysis Workbench, PSIPRED 4.0

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

Defining Citation: [DOI:10.1093/nar/gkz297](https://doi.org/10.1093/nar/gkz297)

Keywords: Predict Secondary Structure, protein analysis, secondary structure prediction, protein sequence, sequence analysis, protein, analysis

Funding: Biotechnology and Biological Science Research Council ;
University College London

Availability: Free, Freely available

Resource Name: PSIPRED

Resource ID: SCR_010246

Alternate IDs: SCR_018546, nlx_156884

Alternate URLs: <https://sources.debian.org/src/psipred/>

Record Creation Time: 20220129T080257+0000

Record Last Update: 20260729T044244+0000

Ratings and Alerts

No rating or validation information has been found for PSIPRED.

No alerts have been found for PSIPRED.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1688 mentions in open access literature.

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

Minesso S, et al. (2026) Generation, characterization, and application of caprine herpesvirus 1 secreted glycoprotein D. Microbiology spectrum, 14(1), e0237325.

Raj M, et al. (2025) Cultural dynamics and endogeneity in psychological drivers of adoption of community-based water purification technology in rural India. iScience, 28(12), 113857.

Nobari MB, et al. (2025) The Lpp-OmpA-BtaE fusion protein causes a protective immune response against Brucella melitensis in mice. Scientific reports, 15(1), 27210.

Nahian M, et al. (2025) Immunoinformatic strategy for developing multi-epitope subunit vaccine against Helicobacter pylori. PloS one, 20(2), e0318750.

Taheri MN, et al. (2025) Clotide U1, a Novel Antimicrobial Peptide Isolated From Urtica Dioica Leaves. Bioinformatics and biology insights, 19, 11779322251315291.

Naveed M, et al. (2025) Insight into molecular and mutational scrutiny of epilepsy associated gene Gabrg2 leading to novel computer-aided drug designing. Scientific reports, 15(1), 6770.

Zubair A, et al. (2025) Targeting HIV-1 conserved regions: An immunoinformatic pathway to vaccine innovation for the Asia. PloS one, 20(3), e0317382.

Reglinski M, et al. (2025) A widely-occurring family of pore-forming effectors broadens the impact of the Serratia Type VI secretion system. The EMBO journal, 44(23), 6892.

Jia Y, et al. (2025) Design and Evaluation of a Broadly Multivalent Adhesins-Based Multi-Epitope Fusion Antigen Vaccine Against Enterotoxigenic Escherichia coli Infection. Vaccines, 13(10).

Salama MM, et al. (2025) Bioinformatics approach for discovery of potential lead compound of NSP6 of SARS-CoV-2 using structure based virtual screening and molecular dynamics simulations. Scientific reports, 15(1), 37347.

Gandvi D, et al. (2025) In silico design of a multi-epitope pan vaccine targeting *Schistosoma* species. *Genomics & informatics*, 23(1), 21.

Sahoo S, et al. (2025) An integrated structural and immunoinformatic approach to design a multi-epitope based vaccine against the foot-and-mouth disease virus. *Scientific reports*, 15(1), 35911.

Guío J, et al. (2025) NsrM (AlI0345) and NsrX (Alr1976), two FurC (PerR)-targeted transcriptional regulators, modulate nitrogen metabolism and heterocyst differentiation genes in the cyanobacterium *Anabaena* sp. strain PCC 7120. *Microbiology spectrum*, 13(11), e0231125.

Youssef EG, et al. (2025) In Silico Design of a Multiepitope Vaccine Against Intestinal Pathogenic *Escherichia coli* Based on the 2011 German O104:H4 Outbreak Strain Using Reverse Vaccinology and an Immunoinformatic Approach. *Diseases (Basel, Switzerland)*, 13(8).

Li H, et al. (2025) Sld3CBD-Cdc45 structural insights into Cdc45 recruitment for CMG complex formation during DNA replication. *eLife*, 13.

Heidarinia H, et al. (2025) Design a multi-epitope vaccine candidate against *Acinetobacter baumannii* using advanced computational methods. *AMB Express*, 15(1), 103.

Naveed M, et al. (2025) Rational computational design and development of an immunogenic multiepitope vaccine incorporating transmembrane proteins of *Fusobacterium necrophorum*. *Scientific reports*, 15(1), 15587.

Kandathil SM, et al. (2025) Foldclass and Merizo-search: scalable structural similarity search for single- and multi-domain proteins using geometric learning. *Bioinformatics (Oxford, England)*, 41(5).

Tariq TB, et al. (2025) Molecular modelling and gene expression analysis to probe the GT-? trihelix transcription factors in *Solanum tuberosum* under drought stress. *Scientific reports*, 15(1), 12471.

Suneesh NS, et al. (2025) Reverse vaccinology-based design of multivalent multiepitope mRNA vaccines targeting key viral proteins of Herpes Simplex Virus type-2. *Frontiers in immunology*, 16, 1586271.