

Resource Summary Report

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PSIPRED

RRID:SCR_010246

Type: Tool

Proper Citation

PSIPRED (RRID:SCR_010246)

Resource Information

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

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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: data access protocol, service resource, production service resource, software 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: 20260801T042705+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 [PRECISE-TBI](#) .

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.

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

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.

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

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.

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).

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

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

Gil-Gomez A, et al. (2025) Proteome remodeling in the zoospore-to-vegetative cell transition of the stramenopile *Aurantiochytrium limacinum* reveals candidate ectoplasmic network proteins. *PloS one*, 20(7), e0326651.

Gharazi H, et al. (2025) Brucellosis novel multi-epitope vaccine design based on in silico analysis focusing on *Brucella abortus*. *BMC immunology*, 26(1), 46.

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.

Ullah S, et al. (2025) In Silico Designed Multi-Epitope Vaccine Based on the Conserved Fragments in Viral Proteins for Broad-Spectrum Protection Against Porcine Reproductive and Respiratory Syndrome Virus. *Veterinary sciences*, 12(6).

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

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.

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).

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.

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.