

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

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: 20260903T235020+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 1935 mentions in open access literature.

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

Liu H, et al. (2026) Phase separation of OPTN initiates mitophagy to orchestrate craniofacial bone mineralization. *Autophagy*, 22(5), 1021.

Zhu F, et al. (2026) Computational Validation of Multi-Epitope mRNA Vaccine Targeting *Streptococcus anginosus* Surface Protein (TMPC) as an Effective Alternative Treatment to Reduce Gastric Cancer. *MicrobiologyOpen*, 15(1), e70230.

Stong Tangan YA, et al. (2026) In-silico design of a multi-epitope vaccine candidate against *Strongyloides stercoralis*. *BMC infectious diseases*, 26(1).

Naveed M, et al. (2026) Computational design of a multiepitope vaccine targeting VP1 and VP2 capsid proteins of simian virus 40 (SV40) for enhanced immune activation. *Open medicine (Warsaw, Poland)*, 21(1), 20251284.

Wu Y, et al. (2026) E. coli-expressed chicken IL-17A enhances respiratory innate immunity by inducing proinflammatory cytokines and interferons. *Poultry science*, 105(7), 106873.

Hart JE, et al. (2026) Detecting the body's reproductive hormonal brake against tissue overgrowth: Micrin/SgII-70. *PloS one*, 21(3), e0340980.

Farhani I, et al. (2026) Design and immunogenicity of a recombinant *Saccharomyces boulardii* secreting the P2-VP8 subunit rotavirus vaccine. *Scientific reports*, 16(1), 6932.

Rezaei R, et al. (2026) Immunoinformatics-driven design of a conserved RNA-dependent RNA polymerase-based multi-epitope vaccine against avian infectious bronchitis virus. *Veterinary world*, 19(1), 448.

Yang Q, et al. (2026) Targeted mutagenesis of the ICP4 transactivation domain generates a protective DIVA vaccine against duck plague. *Poultry science*, 105(7), 106960.

Ben Mariem O, et al. (2026) Identification of neuronatin as a SERCA2b regulin-like protein and assessment of its aggregation propensity via coarse grained simulations. *PloS one*, 21(4), e0346335.

Bayat Z, et al. (2026) A bioinformatics pipeline for the design of a SART3-targeted cancer vaccine with enhanced immunogenicity. *Genomics & informatics*, 24(1).

Zhamalbekova A, et al. (2026) Effect of HIV-1 subtype-specific Tat protein polymorphisms on Tat-TAR interaction. *PloS one*, 21(4), e0346629.

Saber MA, et al. (2026) Pan-genome and reverse vaccinology for a multi-epitope vaccine against circulating post-2022 Monkeypox virus strains. *PloS one*, 21(6), e0351881.

Wang Y, et al. (2026) Identification of Conserved Cross-Reactive B-Cell Epitopes in CPV1 and CPV2 L1 Proteins with Vaccine Potential. *Vaccines*, 14(6).

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).

Abbas S, et al. (2026) Analyzing fourteen deleterious nsSNPs of CFTR as promising genetic markers for cancer prognosis. *Scientific reports*, 16(1).

Gollapalli P, et al. (2026) Designing and immuno-informatics evaluation of a multi-epitope vaccine targeting lipoprotein A-4'-phosphatase (LpxF) for *Helicobacter pylori* infection control. *Frontiers in bioinformatics*, 6, 1779654.

Creagh JW, et al. (2026) A Comprehensive Structural and Functional Analysis of *Saccharomyces* Killer Toxins. *Toxins*, 18(5).

Chen PP, et al. (2026) Cell Cycle-Specific Regulation of Centrosome Clustering Dynamics in Cancer Cells by the Multifunctional Kinesin HSET. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(26), e74651.

Waleed Iqbal M, et al. (2026) Delving Into the Depths of AGTR2: In Silico Identification of Deleterious Nonsynonymous SNPs Associated With Cardiovascular Diseases. *Human mutation*, 2026, 9394808.