

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

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: 20260810T040518+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 [NIF](#) .

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

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

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.

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

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.

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

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.

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.

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

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.

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.

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.

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).

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.

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).

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).

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