

Resource Summary Report

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Jpred

RRID:SCR_016504

Type: Tool

Proper Citation

Jpred (RRID:SCR_016504)

Resource Information

URL: <http://www.compbio.dundee.ac.uk/jpred/>

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Description: Software tool for protein secondary structure prediction from the amino acid sequence by the JNet algorithm. Makes also predictions on Solvent Accessibility and Coiled-coil regions.

Synonyms: Jprotein secondary structure PREDiction

Resource Type: sequence analysis software, software application, data processing software, data analysis software, data analytics software, software resource

Defining Citation: [DOI:10.1093/nar/gkn238](https://doi.org/10.1093/nar/gkn238)

Keywords: protein, secondary, structure, prediction, amino, acid, sequence, accurate, JNet algorithm, solvent, accessibility, coiled, coil, region

Funding: Biotechnology and Biological Sciences Research Council ;
Wellcome Trust 355804783;
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Availability: Free, Available for download, Freely available, Tutorial available

Resource Name: Jpred

Resource ID: SCR_016504

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260804T043627+0000

Ratings and Alerts

No rating or validation information has been found for Jpred.

No alerts have been found for Jpred.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 126 mentions in open access literature.

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

Qiao X, et al. (2025) Characterization of Flexusin A, a Novel Circular Bacteriocin Produced by Marine Bacterium *Bacillus flexus* R29-2. *Marine drugs*, 23(3).

Mótyán JA, et al. (2025) Characterization of the E26H Mutant *Schistosoma japonicum* Glutathione S-Transferase. *Proteins*, 93(5), 1054.

Rakesh S, et al. (2025) Unveiling the structural and functional implications of uncharacterized NSPs and variations in the molecular toolkit across arteriviruses. *NAR genomics and bioinformatics*, 7(2), lqaf035.

Nath R, et al. (2025) Lineage-Specific Class-A GPCR Dynamics Reflect Diverse Chemosensory Adaptations in Lophotrochozoa. *Molecular biology and evolution*, 42(3).

Diallo S, et al. (2025) Identification of the trail-following pheromone receptor in termites. *eLife*, 13.

Sivakumar P, et al. (2025) Sporophyte-directed gametogenesis in *Arabidopsis*. *Nature plants*, 11(3), 398.

Yu Y, et al. (2024) Nuclear pore protein POM121 regulates subcellular localization and transcriptional activity of PPAR γ . *Cell death & disease*, 15(1), 7.

Hacker C, et al. (2024) Biogenesis, inheritance, and 3D ultrastructure of the microsporidian mitosome. *Life science alliance*, 7(1).

Garcia-Montojo M, et al. (2024) TDP-43 proteinopathy in ALS is triggered by loss of ASRGL1 and associated with HML-2 expression. *Nature communications*, 15(1), 4163.

Rakesh S, et al. (2024) Reappraisal of the DNA phosphorothioate modification machinery: uncovering neglected functional modalities and identification of new counter-invader defense systems. *Nucleic acids research*, 52(3), 1005.

Dewa KI, et al. (2024) Neuronal DSCAM regulates the peri-synaptic localization of GLAST in Bergmann glia for functional synapse formation. *Nature communications*, 15(1), 458.

Enge S, et al. (2023) A supergene in seaweed flies modulates male traits and female perception. *Proceedings. Biological sciences*, 290(2008), 20231494.

Harmer CJ, et al. (2023) Insertion sequences related to ISAjo2 target pdif and dif sites and belong to a new IS family, the IS1202 family. *Microbial genomics*, 9(3).

Gu B, et al. (2023) A single region of the *Phytophthora infestans* avirulence effector Avr3b functions in both cell death induction and plant immunity suppression. *Molecular plant pathology*, 24(4), 317.

Gu X, et al. (2023) Macrophage Migration Inhibitory Factor in *Psoroptes ovis*: Molecular Characterization and Potential Role in Eosinophil Accumulation of Skin in Rabbit and Its Implication in the Host-Parasite Interaction. *International journal of molecular sciences*, 24(6).

Kibby EM, et al. (2023) Bacterial NLR-related proteins protect against phage. *Cell*, 186(11), 2410.

Burroughs AM, et al. (2023) New biochemistry in the Rhodanese-phosphatase superfamily: emerging roles in diverse metabolic processes, nucleic acid modifications, and biological conflicts. *NAR genomics and bioinformatics*, 5(1), lqad029.

Stromberg KA, et al. (2023) Evolutionary diversification reveals distinct somatic versus germline cytoskeletal functions of the Arp2 branched actin nucleator protein. *Current biology : CB*, 33(24), 5326.

Reppert N, et al. (2022) A conserved sequence in the small intracellular loop of tetraspanins forms an M-shaped inter-helix turn. *Scientific reports*, 12(1), 4494.

Xu Y, et al. (2022) Genome-wide identification and expression analysis of the Hsp gene superfamily in Asian long-horned beetle (*Anoplophora glabripennis*). *International journal of biological macromolecules*, 200, 583.