

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;
Wellcome Trust WT092340;
Wellcome Trust WT083481;
Wellcome Trust 106370Z14

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](#).

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

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).

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?. 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.

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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.