

Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

IUPRED

RRID:SCR_014632

Type: Tool

Proper Citation

IUPRED (RRID:SCR_014632)

Resource Information

URL: <http://iupred.enzim.hu/>

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Description: A web server which recognizes tertiary structures from an amino acid sequence based on estimated pairwise energy content. Users can input SWISS-PROT/TrEMBL identifier or accession number, or paste the amino acid sequence.

Synonyms: Prediction of Intrinsically Unstructured Proteins, Prediction of Intrinsically Unstructured Proteins (IUPRED)

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

Defining Citation: [PMID:15955779](#)

Keywords: web application, sequence analysis, web server, territory structure, amino acid sequence, swiss prot, trembl

Availability: Available to academic users, Available for download, Commercial users must enquire

Resource Name: IUPRED

Resource ID: SCR_014632

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260804T043549+0000

Ratings and Alerts

No rating or validation information has been found for IUPRED.

No alerts have been found for IUPRED.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 295 mentions in open access literature.

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

Gul L, et al. (2025) Protocol for predicting host-microbe interactions and their downstream effect on host cells using MicrobioLink. STAR protocols, 6(1), 103570.

Parreiras de Jesus AC, et al. (2025) Identifying promising peptide targets for leprosy serological tests: From prediction to ELISA. Journal, genetic engineering & biotechnology, 23(1), 100475.

Shumaker KA, et al. (2025) A screen for synthetic genetic interactions with the *Saccharomyces cerevisiae* hrq1^Δ allele. bioRxiv : the preprint server for biology.

Kane EI, et al. (2025) Characterization of meiotic axis proteins in the model brown alga *Ectocarpus*. EMBO reports, 26(23), 5673.

Shumaker KA, et al. (2025) A screen for synthetic genetic interactions with the *Saccharomyces cerevisiae* hrq1^Δ allele. G3 (Bethesda, Md.), 15(12).

Choteau SA, et al. (2025) mimicINT: A workflow for microbe-host protein interaction inference. F1000Research, 14, 128.

Dong T, et al. (2025) Stress granule clearance mediated by V-ATPase-interacting protein NCOA7 mitigates ovarian aging. Nature aging, 5(8), 1548.

Hu G, et al. (2025) Neutralizing antibody levels as a key factor in determining the immunogenic efficacy of the novel PEDV alpha coronavirus vaccine. The veterinary quarterly, 45(1), 1.

Rajeevan A, et al. (2025) Aurora A regulates the material property of spindle poles to orchestrate nuclear organization at mitotic exit. The EMBO journal.

Park SO, et al. (2025) Cross-species rescue reveals sequence requirements for a rapidly evolving intrinsically disordered region. PLoS biology, 23(9), e3003396.

Geist JL, et al. (2024) Generation of a high confidence set of domain-domain interface types to guide protein complex structure predictions by AlphaFold. Bioinformatics (Oxford, England), 40(8).

Zatorski N, et al. (2024) Structural analysis of genomic and proteomic signatures reveal dynamic expression of intrinsically disordered regions in breast cancer. iScience, 27(9), 110640.

Gosztyla ML, et al. (2024) Integrated multi-omics analysis of zinc-finger proteins uncovers roles in RNA regulation. *Molecular cell*, 84(19), 3826.

Singer A, et al. (2024) Elaboration of the Homer1 Recognition Landscape Reveals Incomplete Divergence of Paralogous EVH1 Domains. *bioRxiv : the preprint server for biology*.

Erdős G, et al. (2024) AIUPred: combining energy estimation with deep learning for the enhanced prediction of protein disorder. *Nucleic acids research*, 52(W1), W176.

Weibel CA, et al. (2024) The protein domains of vertebrate species in which selection is more effective have greater intrinsic structural disorder. *eLife*, 12.

Esparza D, et al. (2024) Pancreatic β -cells package double C2-like domain beta protein into extracellular vesicles via tandem C2 domains. *Frontiers in endocrinology*, 15, 1451279.

Cao J, et al. (2024) Predicting cysteine reactivity changes upon phosphorylation using XGBoost. *FEBS open bio*, 14(1), 51.

Hannon CE, et al. (2024) Intrinsic protein disorder is insufficient to drive subnuclear clustering in embryonic transcription factors. *eLife*, 12.

Sun H, et al. (2024) Nuclear and cytoplasmic specific RNA binding proteome enrichment and its changes upon ferroptosis induction. *Nature communications*, 15(1), 852.