

Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 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: software application, web application, data analysis software, sequence analysis software, software resource, data processing software

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: 20260729T044333+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 [nidm-terms](#) .

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^ΔN allele. *bioRxiv : the preprint server for biology*.

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.

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

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

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.

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

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).

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

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.

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.