

Resource Summary Report

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

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: 20260905T132749+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 306 mentions in open access literature.

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

Akwelle RN, et al. (2026) In Silico Design and Computational Characterization of Novel Chimeric Multiepitope Antigens for Mpox Serosurveillance: An Immunoinformatics Approach. Health science reports, 9(6), e72702.

Tang H, et al. (2026) Designing a novel multiepitope vaccine candidate against Treponema pallidum via adhesins using reverse vaccinology. Scientific reports, 16(1).

Santos-Rodriguez G, et al. (2026) Isoform-specific m6A deposition and coordinated splicing shape mammalian transcriptome evolution. Nature communications, 17(1).

Osmanli Z, et al. (2026) Protein tandem repeats that produce frameshifts can generate new structural states and functions. The FEBS journal, 293(3), 842.

Song Y, et al. (2026) Unleashed condensation by recurrent mutations of an epigenetic regulator promotes cancer. bioRxiv : the preprint server for biology.

Souza MFS, et al. (2026) Development of serologic diagnostic test based on in silico predicted synthetic peptides for Brucella canis in dogs. PloS one, 21(2), e0342574.

Saha A, et al. (2026) Proteome-wide prediction of interactions between structured domains and peptide motifs reveals functionally coherent subnetworks. Proceedings of the National Academy of Sciences of the United States of America, 123(15), e2527957123.

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.

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^Δ allele. G3 (Bethesda, Md.), 15(12).

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.

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

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.

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

Herrera MG, et al. (2025) TBK1 Induces the Formation of Optineurin Filaments That Condensate with Polyubiquitin and LC3 for Cargo Sequestration. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), e09927.

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

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

Sharma M, et al. (2025) Intrinsic disorder in CYP1B1 and its implications in primary congenital glaucoma pathogenesis. *Journal of proteins and proteomics*.

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