

Resource Summary Report

Generated by [dkNET](#) on Aug 23, 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: 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: 20260821T194005+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 [dkNET](#) .

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

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.

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.

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).

Shumaker KA, et al. (2025) A screen for synthetic genetic interactions with the *Saccharomyces cerevisiae* hrq1^ΔN 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.

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.

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.

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

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*.