

Resource Summary Report

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DisProt - Database of Protein Disorder

RRID:SCR_007097

Type: Tool

Proper Citation

DisProt - Database of Protein Disorder (RRID:SCR_007097)

Resource Information

URL: <http://www.disprot.org/>

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Description: The Database of Protein Disorder (DisProt) is a curated database that provides information about proteins that lack fixed 3D structure in their putatively native states, either in their entirety or in part. Users can BLAST sequences, browse by protein name, or view by protein function and functional subclass.

Synonyms: DisProt

Resource Type: data or information resource, database

Keywords: protein, protein structure, bio.tools, FASEB list

Resource Name: DisProt - Database of Protein Disorder

Resource ID: SCR_007097

Alternate IDs: nif-0000-02754, r3d100010561, biotools:disprot

Alternate URLs: <https://bio.tools/disprot>, <https://doi.org/10.17616/R3NG75>

Old URLs: <http://divac.ist.temple.edu/disprot>

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260905T133138+0000

Ratings and Alerts

No rating or validation information has been found for DisProt - Database of Protein Disorder.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 223 mentions in open access literature.

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

Mehdiabadi M, et al. (2026) Critical Assessment of Protein Intrinsic Disorder Round 3 - Predicting Disorder in the Era of Protein Language Models. *Proteins*, 94(1), 414.

Zhang H, et al. (2026) Proteome-Wide Analysis of Human Deletions. *Proteins*, 94(3), 853.

Yoon JG, et al. (2026) A predictive framework for stop-loss variants with C-terminal extensions. *Nucleic acids research*, 54(2).

Song H, et al. (2026) Phylogenomic Insights into High Conservation and Lineage-Specific Expansion of the ABAPT Gene Family in Plants. *International journal of molecular sciences*, 27(8).

Liang J, et al. (2026) Hybrid deep learning with protein language models and dual-path architecture for predicting IDP functions. *Briefings in bioinformatics*, 27(2).

Kumar S, et al. (2026) Liquid liquid phase separation of the intrinsically disordered protein JPT2 compartmentalizes components of NAADP-evoked Ca²⁺ signaling. *bioRxiv : the preprint server for biology*.

Chatterjee A, et al. (2026) A benchmarking framework for comparative evaluation of low-complexity region detection tools in the human proteome. *Scientific reports*, 16(1).

Zhang H, et al. (2026) PON-Del predictor for sequence retaining protein deletions. *PLoS computational biology*, 22(2), e1014020.

Luo H, et al. (2026) ProteoformDB: an integrative database for functional roles of proteoforms. *Database : the journal of biological databases and curation*, 2026.

Fu R, et al. (2026) Prediction of plant phase-separating proteins using positive-unlabeled learning. *Genome biology*, 27(1).

Lee H, et al. (2026) Protein folding stability estimation with explicit consideration of unfolded states. *Nature communications*, 17(1).

Robles NDJ, et al. (2026) Missense Constraint in Intrinsically Disordered Proteins Enhances Missense Variant Interpretation in Neurodevelopmental Disorders. *Genes*, 17(2).

Kijima S, et al. (2025) RNA Binding Mechanism of the FUS Zinc Finger in Concert with Its Flanking Intrinsically Disordered Region. *Journal of chemical information and modeling*, 65(15), 8262.

Sulaiman X, et al. (2025) Enrichment of G-to-U Substitution in SARS-CoV-2 Functional Regions and Its Compensation via Concurrent Mutations. *Journal of medical virology*, 97(4), e70353.

Sil S, et al. (2025) Use of AI-methods over MD simulations in the sampling of conformational ensembles in IDPs. *Frontiers in molecular biosciences*, 12, 1542267.

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

Antonietti M, et al. (2025) An Analysis of Intrinsic Protein Disorder in Antimicrobial Peptides. *The protein journal*, 44(2), 175.

Majila K, et al. (2025) A deep learning method for predicting interactions for intrinsically disordered regions of proteins. *bioRxiv : the preprint server for biology*.

Gondelaud F, et al. (2025) A conserved motif in Henipavirus P/V/W proteins drives the fibrillation of the W protein from Hendra virus. *Protein science : a publication of the Protein Society*, 34(4), e70085.

Yu J, et al. (2025) Comprehensive assessment of AlphaFold's predictions of secondary structure and solvent accessibility at the amino acid-level in eukaryotic, bacterial and archaeal proteins. *Computational and structural biotechnology journal*, 27, 2443.