

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: 20260729T044151+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 204 mentions in open access literature.

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

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.

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

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.

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

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.

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.

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.

Zhang F, et al. (2025) Evaluation of predictions of disordered binding regions in the CAID2 experiment. *Computational and structural biotechnology journal*, 27, 78.

Bonnet DMVJ, et al. (2025) Structural characterization of plum pox virus by cryo-electron microscopy. *Archives of virology*, 171(1), 11.

Thomas SD, et al. (2025) Impact of intrinsically disordered regions and functional disorder hotspots in the human kinome. *Briefings in bioinformatics*, 26(6).

Yang H, et al. (2025) A multimodal framework for comprehensive driver variant prediction in cancer. *Communications medicine*, 5(1), 499.

Fossat MJ, et al. (2025) MEDOC: A Fast, Scalable, and Mathematically Exact Algorithm for the Site-Specific Prediction of the Protonation Degree in Large Disordered Proteins. *Journal of chemical information and modeling*, 65(2), 873.

Pintado-Grima C, et al. (2025) Comprehensive protein datasets and benchmarking for liquid-liquid phase separation studies. *Genome biology*, 26(1), 198.

Shukla S, et al. (2025) Intrinsic Disorder and Phase Separation Coordinate Exocytosis, Motility, and Chromatin Remodeling in the Human Acrosomal Proteome. *Proteomes*, 13(2).

Gonay V, et al. (2025) Developing machine-learning-based amyloidogenicity predictors with Cross-Beta DB. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 21(2), e14510.

Zhang H, et al. (2025) Heterochromatome wide analyses reveal MBD2 as a phase separation scaffold for heterochromatin compartmentalization and composition. *Nucleic acids research*, 53(22).

Fich?? E, et al. (2025) MFIB 2.0: a major update of the database of protein complexes formed by mutual folding of the constituting protein chains. *Nucleic acids research*, 53(D1), D487.

Vagiona AC, et al. (2025) Unraveling cooperative and competitive interactions within protein triplets in the human interactome. *Scientific reports*, 15(1), 32548.

Kipp OL, et al. (2025) Missense mutations in intrinsically disordered protein regions link pathogenicity and phase separation. *The Journal of biological chemistry*, 301(11), 110773.