Resource Summary Report

Generated by <u>NIF</u> on Apr 25, 2025

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: database, data or information resource

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

Funding:

Resource Name: DisProt - Database of Protein Disorder

Resource ID: SCR_007097

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

Alternate URLs: https://bio.tools/disprot

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

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250425T055555+0000

Ratings and Alerts

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

No alerts have been found for DisProt - Database of Protein Disorder.

Data and Source Information

Source: <u>SciCrunch Registry</u>

Usage and Citation Metrics

We found 186 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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

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

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.

Fichó 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.

Zhang J, et al. (2024) HybridDBRpred: improved sequence-based prediction of DNA-binding amino acids using annotations from structured complexes and disordered proteins. Nucleic acids research, 52(2), e10.

Jahn LR, et al. (2024) Protein embeddings predict binding residues in disordered regions. Scientific reports, 14(1), 13566.

Janson G, et al. (2024) Transferable deep generative modeling of intrinsically disordered protein conformations. PLoS computational biology, 20(5), e1012144.

Desai H, et al. (2024) Chemoproteogenomic stratification of the missense variant cysteinome. Nature communications, 15(1), 9284.

Antonietti M, et al. (2024) Effects of Aging on Intrinsic Protein Disorder in Human Lenses and Zonules. Cell biochemistry and biophysics, 82(4), 3667.

Vincoff S, et al. (2024) FusOn-pLM: A Fusion Oncoprotein-Specific Language Model via

Focused Probabilistic Masking. bioRxiv : the preprint server for biology.

Chow CFW, et al. (2024) SHARK enables sensitive detection of evolutionary homologs and functional analogs in unalignable and disordered sequences. Proceedings of the National Academy of Sciences of the United States of America, 121(42), e2401622121.

Tomasini C, et al. (2024) Decoding the biogenesis of HIV-induced CPSF6 puncta and their fusion with the nuclear speckle. bioRxiv : the preprint server for biology.

Erd?s G, et al. (2024) AIUPred: combining energy estimation with deep learning for the enhanced prediction of protein disorder. Nucleic acids research, 52(W1), W176.

Hoenger Ramazanova RD, et al. (2024) PhoXplex: Combining Phospho-enrichable Cross-Linking with Isobaric Labeling for Quantitative Proteome-Wide Mapping of Protein Interfaces. Journal of proteome research, 23(11), 5209.

Janson G, et al. (2024) Transferable deep generative modeling of intrinsically disordered protein conformations. bioRxiv : the preprint server for biology.

Pandi B, et al. (2024) Tissue Usage Preference and Intrinsically Disordered Region Remodeling of Alternative Splicing Derived Proteoforms in the Heart. Journal of proteome research, 23(8), 3161.

An Y, et al. (2024) Active learning of the thermodynamics-dynamics trade-off in protein condensates. Science advances, 10(1), eadj2448.

Zhang H, et al. (2024) There will always be variants of uncertain significance. Analysis of VUSs. NAR genomics and bioinformatics, 6(4), Iqae154.

Hou C, et al. (2024) SeqDance: A Protein Language Model for Representing Protein Dynamic Properties. bioRxiv : the preprint server for biology.

Zhang F, et al. (2023) HybridRNAbind: prediction of RNA interacting residues across structure-annotated and disorder-annotated proteins. Nucleic acids research, 51(5), e25.