

Resource Summary Report

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MobiDB

RRID:SCR_014542

Type: Tool

Proper Citation

MobiDB (RRID:SCR_014542)

Resource Information

URL: <http://mobidb.bio.unipd.it>

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Description: A database of protein disorder and mobility annotations. The database features three levels of annotation: manually curated data (which are extracted from the DisProt database), indirect data, and predicted data. Additional annotations are included from external sources, including UniProt, Pfam, PDB, and STRING.

Resource Type: database, data or information resource

Keywords: database, protein disorder, mobility, annotation, intrinsic protein disorder, bio.tools, FASEB list

Availability: Available to the research community

Resource Name: MobiDB

Resource ID: SCR_014542

Alternate IDs: biotools:mobidb

Alternate URLs: <https://bio.tools/mobidb>

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260803T040634+0000

Ratings and Alerts

No rating or validation information has been found for MobiDB.

No alerts have been found for MobiDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 130 mentions in open access literature.

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

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

Ramirez-Aguirre E, et al. (2025) Structural disorder and distinctive motifs in the C-terminal region of the MADS-domain transcription factors are conserved across diverse taxa. *PLoS one*, 20(8), e0330098.

Mellgren AEC, et al. (2025) On subcellular distribution of the zinc finger 469 protein (ZNF469) and observed discrepancy in the localization of endogenous and overexpressed ZNF469. *FEBS open bio*, 15(7), 1054.

Pesce G, et al. (2025) Dissecting Henipavirus W proteins conformational and fibrillation properties: contribution of their N- and C-terminal constituent domains. *The FEBS journal*, 292(3), 556.

Williams CJ, et al. (2025) Categorizing prediction modes within low-pLDDT regions of AlphaFold2 structures: near-predictive, pseudostructure and barbed wire. *Acta crystallographica. Section D, Structural biology*, 81(Pt 10), 558.

Gondelaud F, et al. (2025) Unraveling the molecular grammar and the structural transitions underlying the fibrillation of a viral fibrillogenic domain. *Protein science : a publication of the Protein Society*, 34(3), e70068.

Breunig K, et al. (2025) SERBP1 interacts with PARP1 and is present in PARylation-dependent protein complexes regulating splicing, cell division, and ribosome biogenesis. *eLife*, 13.

Aspromonte MC, et al. (2025) Genetic variants and phenotypic data curated for the CAGI6 intellectual disability panel challenge. *Human genetics*, 144(2-3), 309.

Veinstein M, et al. (2025) The "DDVF" motif used by viral and bacterial proteins to hijack RSK kinases mimics a short linear motif (SLiM) found in proteins related to the RAS-ERK MAP kinase pathway. *PLoS pathogens*, 21(3), e1013016.

Sangster AG, et al. (2025) Zero-shot segmentation using embeddings from a protein language model identifies functional regions in the human proteome. *PLoS computational biology*, 21(11), e1012929.

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

Schumbera E, et al. (2025) Computational investigation of the sequence context of arginine/glycine-rich motifs in the human proteome. *BMC genomics*, 26(1), 883.

Kuno S, et al. (2025) Multivalent afadin interaction promotes IDR-mediated condensate formation and junctional separation of epithelial cells. *Cell reports*, 44(3), 115335.

Garcia-Hernandez S, et al. (2025) Concerted transport and phosphorylation of diacylglycerol at ER-PM contact sites regulate phospholipid dynamics during stress. *Proceedings of the National Academy of Sciences of the United States of America*, 122(23), e2421334122.

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

Gavalda-Garcia J, et al. (2024) Data-driven probabilistic definition of the low energy conformational states of protein residues. *NAR genomics and bioinformatics*, 6(3), lqae082.

Yu X, et al. (2024) Time-course swRNA-seq uncovers a hierarchical gene regulatory network in controlling the response-repair-remodeling after wounding. *Communications biology*, 7(1), 694.

Petrin AL, et al. (2024) Whole genome sequencing of a family with autosomal dominant features within the oculoauriculovertebral spectrum. *medRxiv : the preprint server for health sciences*.

Harrison PM, et al. (2024) Intrinsically Disordered Compositional Bias in Proteins: Sequence Traits, Region Clustering, and Generation of Hypothetical Functional Associations. *Bioinformatics and biology insights*, 18, 11779322241287485.

Xing YH, et al. (2024) DisP-seq reveals the genome-wide functional organization of DNA-associated disordered proteins. *Nature biotechnology*, 42(1), 52.