

# Resource Summary Report

Generated by [NIF](#) on Aug 29, 2026

## MobiDB

RRID:SCR\_014542

Type: Tool

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### Proper Citation

MobiDB (RRID:SCR\_014542)

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### Resource Information

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

**Proper Citation:** MobiDB (RRID:SCR\_014542)

**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:** data or information resource, database

**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:** 20260829T183032+0000

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### 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 145 mentions in open access literature.

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

Kálmán ZE, et al. (2026) Structural Modeling and Dynamics of the Full-Length Homer1 Multimer. *Proteins*, 94(4), 947.

Cagliani R, et al. (2026) Positive Selection Targeted Primate Genes that Encode Transposable Element Repressors. *Genome biology and evolution*, 18(3).

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

Zhao Y, et al. (2026) IDR-driven LLPS of GAS2L3 scaffolds CHMP4B condensates to accelerate cytokinesis in hepatocellular carcinoma cells. *Journal of advanced research*, 85, 455.

Soman SP, et al. (2026) IsoProDB: an integrated map of human protein isoforms for accelerated research. *Database : the journal of biological databases and curation*, 2026.

Yalaev BI, et al. (2026) Genetic Determinants of Microvascular Complications of Type 1 Diabetes Mellitus: New Data from a Replication Study. *Biomedicines*, 14(6).

Zhang Y, et al. (2026) The transcription factor TaWRKY58 coordinates growth and drought sensitivity in wheat by repressing TaLRR and TaBCS1. *PLoS genetics*, 22(4), e1012124.

Barter IK, et al. (2026) ClpC1-targeting peptide natural products differentially dysregulate the proteome of *Mycobacterium tuberculosis*. *Nature communications*, 17(1), 1725.

Li Y, et al. (2026) BOLL-Containing Aggregates Mediate the Translational Regulation During Human Oogenesis. *Cell proliferation*, 59(4), e70181.

Ramírez-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.

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

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.

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.

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

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.

Omkar S, et al. (2025) Mechanosensor-mediated Hsp70 phosphorylation orchestrates the landscape of the heat shock response. *Nature communications*, 17(1), 507.

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.

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.