

Resource Summary Report

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Database of Interacting Proteins (DIP)

RRID:SCR_003167

Type: Tool

Proper Citation

Database of Interacting Proteins (DIP) (RRID:SCR_003167)

Resource Information

URL: <http://dip.doe-mbi.ucla.edu/>

Proper Citation: Database of Interacting Proteins (DIP) (RRID:SCR_003167)

Description: Database to catalog experimentally determined interactions between proteins combining information from a variety of sources to create a single, consistent set of protein-protein interactions that can be downloaded in a variety of formats. The data were curated, both, manually and also automatically using computational approaches that utilize the the knowledge about the protein-protein interaction networks extracted from the most reliable, core subset of the DIP data. Because the reliability of experimental evidence varies widely, methods of quality assessment have been developed and utilized to identify the most reliable subset of the interactions. This CORE set can be used as a reference when evaluating the reliability of high-throughput protein-protein interaction data sets, for development of prediction methods, as well as in the studies of the properties of protein interaction networks. Tools are available to analyze, visualize and integrate user's own experimental data with the information about protein-protein interactions available in the DIP database. The DIP database lists protein pairs that are known to interact with each other. By interact they mean that two amino acid chains were experimentally identified to bind to each other. The database lists such pairs to aid those studying a particular protein-protein interaction but also those investigating entire regulatory and signaling pathways as well as those studying the organization and complexity of the protein interaction network at the cellular level. Registration is required to gain access to most of the DIP features. Registration is free to the members of the academic community. Trial accounts for the commercial users are also available.

Abbreviations: DIP

Synonyms: , Database of Interacting Proteins, DIP, Database of Interacting Proteins (DIP)

Resource Type: data repository, production service resource, data analysis service, service resource, database, storage service resource, analysis service resource, data or

information resource

Defining Citation: [PMID:14681454](#)

Keywords: blast, cellular network, ligand-receptor complex, ligand, network, protein, protein interaction, protein ligand, protein-protein interaction, protein receptor, receptor, sequence, interaction, regulatory pathway, signaling pathway, protein binding, bio.tools, FASEB list

Funding: NIGMS

Availability: Free, Available for download, Freely available

Resource Name: Database of Interacting Proteins (DIP)

Resource ID: SCR_003167

Alternate IDs: OMICS_01905, nif-0000-00569, r3d100010882, biotools:dip

Alternate URLs: <https://dip.doe-mbi.ucla.edu/dip/Main.cgi>, <https://bio.tools/dip>, <https://doi.org/10.17616/R3431F>

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260804T043159+0000

Ratings and Alerts

No rating or validation information has been found for Database of Interacting Proteins (DIP).

No alerts have been found for Database of Interacting Proteins (DIP).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 153 mentions in open access literature.

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

Meng Y, et al. (2025) Protein structure prediction via deep learning: an in-depth review. *Frontiers in pharmacology*, 16, 1498662.

Al Ghafari M, et al. (2025) Key genes altered in glioblastoma based on bioinformatics (Review). *Oncology letters*, 29(5), 243.

Nogueira-Rodríguez A, et al. (2025) Towards a more accurate and reliable evaluation of machine learning protein-protein interaction prediction model performance in the presence

of unavoidable dataset biases. *Journal of integrative bioinformatics*, 22(2).

Zhou S, et al. (2025) Predicting protein-protein interactions in microbes associated with cardiovascular diseases using deep denoising autoencoders and evolutionary information. *Frontiers in pharmacology*, 16, 1565860.

Narula K, et al. (2024) Combining extracellular matrix proteome and phosphoproteome of chickpea and meta-analysis reveal novel proteoforms and evolutionary significance of clade-specific wall-associated events in plant. *Plant direct*, 8(3), e572.

Murdoch E, et al. (2024) Hypothesis: evidence that the PRS gene products of *Saccharomyces cerevisiae* support both PRPP synthesis and maintenance of cell wall integrity. *Current genetics*, 70(1), 6.

Han SY, et al. (2024) Identifying Candidate Polyphenols Beneficial for Oxidative Liver Injury through Multiscale Network Analysis. *Current issues in molecular biology*, 46(4), 3081.

Chen H, et al. (2024) Bioinformatic Resources for Exploring Human-virus Protein-protein Interactions Based on Binding Modes. *Genomics, proteomics & bioinformatics*, 22(5).

Kim K, et al. (2024) Differential gene expression and pathway analysis in growth hormone-secreting pituitary tumors according to granulation pattern. *Frontiers in oncology*, 14, 1423606.

Kim GB, et al. (2024) Identifying Herbal Candidates and Active Compounds for Psoriasis Through Multiscale Network Analysis. *Current issues in molecular biology*, 46(11), 11993.

Wang X, et al. (2023) Cross-Talk between N6-Methyladenosine and Their Related RNAs Defined a Signature and Confirmed m6A Regulators for Diagnosis of Endometriosis. *International journal of molecular sciences*, 24(2).

Luo L, et al. (2023) Identification of kukoamine A as an anti-osteoporosis drug target using network pharmacology and experiment verification. *Molecular medicine (Cambridge, Mass.)*, 29(1), 36.

Jiang Y, et al. (2022) Senkyunolide H protects PC12 cells from OGD/R-induced injury via cAMP-PI3K/AKT signaling pathway. *Journal of ethnopharmacology*, 282, 114659.

Sadeghi M, et al. (2022) lncRNA-miRNA-mRNA ceRNA Network Involved in Sheep Prolificacy: An Integrated Approach. *Genes*, 13(8).

Asim MN, et al. (2022) ADH-PPI: An attention-based deep hybrid model for protein-protein interaction prediction. *iScience*, 25(10), 105169.

Kang P, et al. (2021) A Network Pharmacology and Molecular Docking Strategy to Explore Potential Targets and Mechanisms Underlying the Effect of Curcumin on Osteonecrosis of the Femoral Head in Systemic Lupus Erythematosus. *BioMed research international*, 2021, 5538643.

Li Y, et al. (2021) Robust and accurate prediction of protein-protein interactions by exploiting evolutionary information. *Scientific reports*, 11(1), 16910.

Xu H, et al. (2021) A comprehensive review of integrative pharmacology-based investigation: A paradigm shift in traditional Chinese medicine. *Acta pharmaceutica Sinica. B*, 11(6), 1379.

Xu Y, et al. (2021) Identification of the Key Role of NF- κ B Signaling Pathway in the Treatment of Osteoarthritis With Bushen Zhuangjin Decoction, a Verification Based on Network Pharmacology Approach. *Frontiers in pharmacology*, 12, 637273.

Jin Z, et al. (2021) Protective effect of Qingre Huoxue decoction against myocardial infarction via PI3K/Akt autophagy pathway based on UPLC-MS, network pharmacology, and in vivo evidence. *Pharmaceutical biology*, 59(1), 1607.