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/

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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: analysis service resource, data analysis service, data or information resource, storage service resource, production service resource, database, service resource, data repository

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: Account required, Creative Commons Attribution-NoDerivs License, Trial accounts for commercial users are available, Terms of Use, The community can contribute to this resource

Resource Name: Database of Interacting Proteins (DIP)

Resource ID: SCR_003167

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

Alternate URLs: https://dip.doe-mbi.ucla.edu/dip/Main.cgi, https://bio.tools/dip

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250425T055319+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 149 mentions in open access literature.

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

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.

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.

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.

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

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.

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

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.

Yan VKC, et al. (2021) Drug Repurposing for the Treatment of COVID-19: A Knowledge Graph Approach. Advanced therapeutics, 4(7), 2100055.

Yoshioka H, et al. (2021) Overexpression of miR-1306-5p, miR-3195, and miR-3914 Inhibits Ameloblast Differentiation through Suppression of Genes Associated with Human Amelogenesis Imperfecta. International journal of molecular sciences, 22(4).

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.

Chen S, et al. (2021) Establishment of an anti-inflammation-based bioassay for the quality control of the 13-component TCM formula (Lianhua Qingwen). Pharmaceutical biology, 59(1), 537.

Potrony M, et al. (2021) DNA Repair and Immune Response Pathways Are Deregulated in Melanocyte-Keratinocyte Co-cultures Derived From the Healthy Skin of Familial Melanoma Patients. Frontiers in medicine, 8, 692341.