

Resource Summary Report

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MINT

RRID:SCR_001523

Type: Tool

Proper Citation

MINT (RRID:SCR_001523)

Resource Information

URL: <http://mint.bio.uniroma2.it/>

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Description: A database that focuses on experimentally verified protein-protein interactions mined from the scientific literature by expert curators. The curated data can be analyzed in the context of the high throughput data and viewed graphically with the MINT Viewer. This collection of molecular interaction databases can be used to search for, analyze and graphically display molecular interaction networks and pathways from a wide variety of species. MINT is comprised of separate database components. HomoMINT, is an inferred human protein interaction database. Domino, is database of domain peptide interactions. VirusMINT explores the interactions of viral proteins with human proteins. The MINT connect viewer allows you to enter a list of proteins (e.g. proteins in a pathway) to retrieve, display and download a network with all the interactions connecting them.

Abbreviations: MINT

Synonyms: MINT, the Molecular INTERaction database, Molecular Interactions Database, Molecular INTERaction database, MINT - the Molecular INTERaction database

Resource Type: data or information resource, database

Defining Citation: [PMID:22096227](#), [PMID:24234451](#), [PMID:19897547](#), [PMID:18592188](#), [PMID:18551417](#), [PMID:18428712](#), [PMID:17135203](#), [PMID:11911893](#)

Keywords: protein-protein interaction, protein, interaction, virus, peptide, organelle co-localization, pathway, molecular interaction, papillomavirus, epstein-barr virus, hepatitis b virus, hepatitis c virus, human adenovirus, human herpesvirus, human immunodeficiency virus, influenza a virus, vaccinia virus, simian virus 40, virus strains, virus protein, orthologous protein, network, proteomics, ortholog, FASEB list

Funding: European Union ;
ENFIN ;

Interaction Proteome Project ;
IMEx - The International Molecular Exchange Consortium ;
HUPO Proteomics Standards Initiative ;
AIRC Associazione Italiana per la Ricerca sul Cancro

Resource Name: MINT

Resource ID: SCR_001523

Alternate IDs: nlx_152821, r3d100010414

Alternate URLs: <https://doi.org/10.17616/R38S3B>

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Record Creation Time: 20220129T080208+0000

Record Last Update: 20260905T133114+0000

Ratings and Alerts

No rating or validation information has been found for MINT.

No alerts have been found for MINT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1141 mentions in open access literature.

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

Ho Han J, et al. (2026) Plasma extracellular vesicle sampling from glioblastoma demonstrates a small RNA signature indicative of disease and identifies lncRNA RPPH1 as a biomarker. Neuro-oncology advances, 8(1), vda273.

Sarker P, et al. (2026) Feature reduction using swarm optimization and random forest classifiers for early diabetes risk prediction. Scientific reports, 16(1).

Shivani , et al. (2026) Hydrogen sulfide modulates gene networks in hypoxia/reoxygenation-stressed trophoblasts: insights from transcriptome profiling. Frontiers in bioinformatics, 6, 1785302.

Rychlik KA, et al. (2026) Prenatal arsenic exposure and gene expression in fetal liver, heart, lung, and placenta. Toxicology, 522, 154420.

Myers IK, et al. (2026) Vagus Nerve Stimulation Paired With Tones Alters the Auditory Cortex Proteome in a Rat Model of Rett Syndrome. Developmental neurobiology, 86(3),

e70032.

Schmitt O, et al. (2026) Proteomic Characterization of Spinal Cord Myelin in the Mouse. *ASN neuro*, 18(1), 2595945.

Kotlyar M, et al. (2026) IID 2025: Physical protein interaction data with detection types, co-purified protein sets, molecular docking, and immune cell networks. *Nucleic acids research*, 54(D1), D593.

Wu L, et al. (2026) Lycorine inhibits the proliferation of acute myeloid leukemia cells by upregulating the expression of THBS1. *Annals of hematology*, 105(1), 24.

Gersting SW, et al. (2026) Peroxisomal interactome mapping enables network-based modelling of function and disease. *Life science alliance*, 9(9).

Pandit D, et al. (2026) Multi-omics analysis positions DNA2 at the interface of genome integrity programs and tumor behavior in pan-cancer. *Functional & integrative genomics*, 26(1).

Custodio N, et al. (2026) Cognitive impairment on the Alzheimer's Disease Centers' Uniform Data Set Version 3 Neuropsychological Test Battery in a Peruvian population with progressive supranuclear palsy. *Arquivos de neuro-psiquiatria*, 84(5), 1.

Ullanat V, et al. (2026) Learning the language of protein-protein interactions. *Nature communications*, 17(1), 1199.

Zhao Y, et al. (2026) Integrative Analysis of Triphala's Therapeutic Mechanisms in Periodontitis: Network Pharmacology-guided Investigation with Experimental Validation in Cellular and Animal Models. *Oral health & preventive dentistry*, 24, 375.

Alam A, et al. (2026) Targeting protein protein interactions and their modulators to enable new therapeutic strategies for human diseases. *NPJ systems biology and applications*, 12(1).

Karthick V, et al. (2026) Quantum-augmented graph differential geometry enhances accuracy in protein-protein interaction prediction. *Scientific reports*, 16(1).

Srinivasarao M, et al. (2026) Effects of EGR and Fe₃O₄ nanoadditives on performance of a variable compression ratio diesel engine fueled with tamarind biodiesel. *Scientific reports*, 16(1).

Noh SG, et al. (2026) Calorie Restriction Modulates Gene Expression of IL19 and IL24 during Renal Aging. *Annals of geriatric medicine and research*, 30(1), 28.

Reed TJ, et al. (2026) Exploring How Workflow Variations in Denaturation-Based Assays Impact Global Protein-Protein Interaction Predictions. *Molecular & cellular proteomics : MCP*, 25(2), 101479.

Vinogradov-Talyah E, et al. (2026) Human clearance systems have a layered architecture across tissues and cell types that supports varied proteome compositions. *Autophagy*, 22(1), 145.

Lambourne L, et al. (2026) Experimental assessment of AI-based interactome mapping. Nature communications, 17(1).