

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: database, data or information resource

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: 20260725T191119+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 1109 mentions in open access literature.

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

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.

Marino GB, et al. (2025) GeneSetCart: assembling, augmenting, combining, visualizing, and analyzing gene sets. GigaScience, 14.

Noh SG, et al. (2025) Co-regulation of Nr1d1 and Ppar?? in age-related changes of lipid metabolism and its modulation by calorie restriction. Aging, 17(7), 1810.

Hammers DB, et al. (2025) Differences in baseline cognitive performance between participants with early-onset and late-onset Alzheimer's disease: Comparison of LEADS and ADNI. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(1), e14218.

- Feng Y, et al. (2025) Microstructural mapping of neural pathways in Alzheimer's disease using macrostructure-informed normative tractometry. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 21(1), e14371.
- Zhu IY, et al. (2025) Structure and function of MDM2 and MDM4 in health and disease. *The Biochemical journal*, 482(4).
- Di Stefano G, et al. (2025) MicroRNA Expression in High-Grade B-Cell Lymphoma With 11q Aberration. *Genes, chromosomes & cancer*, 64(1), e70021.
- Brunt T, et al. (2025) Environmental DNA Reveals Habitat Variables Driving Platypus (*Ornithorhynchus anatinus*) Distribution Across an Urbanised Landscape. *Ecology and evolution*, 15(1), e70783.
- Rahman RL, et al. (2025) Neoadjuvant Chemotherapy for T3 Tumors in the Era of Precision Medicine-Biology Is Still King. *International journal of molecular sciences*, 26(2).
- Zaverdas H, et al. (2025) Unravelling the human taste receptor interactome: machine learning and molecular modelling insights into protein-protein interactions. *NPJ science of food*, 9(1), 113.
- Gianni GM, et al. (2025) Slab underthrusting is the primary control on flat-slab size. *Science advances*, 11(28), eadv8872.
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- Jiang L, et al. (2025) Graph neural network integrated with pretrained protein language model for predicting human-virus protein-protein interactions. *Briefings in bioinformatics*, 26(5).
- Jousse C, et al. (2025) Identification of a specific set of genes predicting obesity before phenotype appearance. *iScience*, 28(5), 112377.
- Azizova NA, et al. (2025) Comparative Assessment of the Critical Condition of Newborns with Congenital Anomalies on the Basis of Different Scales. *Turkish archives of pediatrics*, 60(2), 182.
- Junyent M, et al. (2025) Unravelling Convergent Signaling Mechanisms Underlying the Aging-Disease Nexus Using Computational Language Analysis. *Current issues in molecular biology*, 47(3).
- Kurz KS, et al. (2025) Age- and gender-specific molecular characteristics of diffuse large B-cell lymphoma: Results from clinical trials of the DSHNHL/GLA. *HemaSphere*, 9(3), e70093.
- Qian H, et al. (2025) Exploring the mechanism of *Inula japonica* Thunb. against non-small cell lung cancer using a computer-aided drug design approach. *Medicine*, 104(51), e46660.

Suchy-Dicey AM, et al. (2025) Cognitive reserve is associated with education, social determinants, and cognitive outcomes among older American Indians in the Strong Heart Study. *Communications psychology*, 3(1), 14.

Zhai Y, et al. (2025) Network pharmacology: a crucial approach in traditional Chinese medicine research. *Chinese medicine*, 20(1), 8.