

Resource Summary Report

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Michigan Molecular Interactions

RRID:SCR_003521

Type: Tool

Proper Citation

Michigan Molecular Interactions (RRID:SCR_003521)

Resource Information

URL: <http://mimi.ncibi.org/MimiWeb/main-page.jsp>

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Description: MiMi Web gives you an easy to use interface to a rich NCIBI data repository for conducting your systems biology analyses. This repository includes the MiMI database, PubMed resources updated nightly, and text mined from biomedical research literature. The MiMI database comprehensively includes protein interaction information that has been integrated and merged from diverse protein interaction databases and other biological sources. With MiMI, you get one point of entry for querying, exploring, and analyzing all these data. MiMI provides access to the knowledge and data merged and integrated from numerous protein interactions databases and augments this information from many other biological sources. MiMI merges data from these sources with deep integration into its single database with one point of entry for querying, exploring, and analyzing all these data. MiMI allows you to query all data, whether corroborative or contradictory, and specify which sources to utilize. MiMI displays results of your queries in easy-to-browse interfaces and provides you with workspaces to explore and analyze the results. Among these workspaces is an interactive network of protein-protein interactions displayed in Cytoscape and accessed through MiMI via a MiMI Cytoscape plug-in. MiMI gives you access to more information than you can get from any one protein interaction source such as: * Vetted data on genes, attributes, interactions, literature citations, compounds, and annotated text extracts through natural language processing (NLP) * Linkouts to integrated NCIBI tools to: analyze overrepresented MeSH terms for genes of interest, read additional NLP-mined text passages, and explore interactive graphics of networks of interactions * Linkouts to PubMed and NCIBI's MiSearch interface to PubMed for better relevance rankings * Querying by keywords, genes, lists or interactions * Provenance tracking * Quick views of missing information across databases. Data Sources include: BIND, BioGRID, CCSB at Harvard, cPath, DIP, GO (Gene Ontology), HPRD, IntAct, InterPro, IPI, KEGG, Max Delbreuck Center, MiBLAST, NCBI Gene, Organelle DB, OrthoMCL DB, Pfam, ProtoNet, PubMed, PubMed NLP Mining, Reactome, MINT, and Finley Lab. The data integration service is supplied under the conditions of the original data sources and the specific terms of use for MiMI. Access to this website is

provided free of charge. The MiMI data is queryable through a web services api. The MiMI data is available in PSI-MITAB Format. These files represent a subset of the data available in MiMI. Only UniProt and RefSeq identifiers are included for each interactor, pathways and metabolomics data is not included, and provenance is not included for each interaction. If you need access to the full MiMI dataset please send an email to mimi-help (at) umich.edu.

Abbreviations: MiMI

Resource Type: analysis service resource, data access protocol, data analysis service, data or information resource, database, production service resource, service resource, software resource, web service

Defining Citation: [PMID:18978014](#), [PMID:17130145](#)

Keywords: gene, interaction, molecule, protein, protein interaction, protein-protein interaction

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Resource Name: Michigan Molecular Interactions

Resource ID: SCR_003521

Alternate IDs: nif-0000-00214

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260903T234627+0000

Ratings and Alerts

No rating or validation information has been found for Michigan Molecular Interactions.

No alerts have been found for Michigan Molecular Interactions.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Wang J, et al. (2015) Pathway and network approaches for identification of cancer signature markers from omics data. *Journal of Cancer*, 6(1), 54.

Dijksterhuis JP, et al. (2015) High levels of WNT-5A in human glioma correlate with increased presence of tumor-associated microglia/monocytes. *Experimental cell research*, 339(2), 280.

Lee SM, et al. (2014) Biological network inferences for a protection mechanism against familial Creutzfeldt-Jakob disease with E200K pathogenic mutation. *BMC medical genomics*, 7, 52.

Junker A, et al. (2012) Visual analysis of transcriptome data in the context of anatomical structures and biological networks. *Frontiers in plant science*, 3, 252.

Meyers KJ, et al. (2010) SNP-SNP interactions dominate the genetic architecture of candidate genes associated with left ventricular mass in African-Americans of the GENOA study. *BMC medical genetics*, 11, 160.