Resource Summary Report

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IMEx - The International Molecular Exchange Consortium

RRID:SCR_002805
Type: Tool

Proper Citation

IMEx - The International Molecular Exchange Consortium (RRID:SCR_002805)

Resource Information

URL: http://www.imexconsortium.org/

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Description: Interaction database from international collaboration between major public interaction data providers who share curation effort and develop set of curation rules when capturing data from both directly deposited interaction data or from publications in peer reviewed journals. Performs complete curation of all protein-protein interactions experimentally demonstrated within publication and makes them available in single search interface on common website. Provides data in standards compliant download formats. IMEx partners produce their own separate resources, which range from all encompassing molecular interaction databases, such as are maintained by IntAct, MINT and DIP, organism-centric resources such as BioGrid or MPIDB or biological domain centric, such as MatrixDB. They have committed to making records available, via PSICQUIC webservice, which have been curated to IMEx rules and are available to users as single, non-redundant set of curated publications which can be searched at the IMEx website. Data is made available in standards-compliant tab-deliminated and XML formats, enabling to visualize data using wide range of tools. Consortium is open to participation of additional partners and encourages deposition of data, prior to publication, and will supply unique accession numbers which may be referenced within final article. Submitters may send their data directly to any of member databases using variety of formats, but should conform to guidelines as to minimum information required to describe data.

Abbreviations: IMEx

Synonyms: The International Molecular Exchange Consortium, International Molecular

Exchange Consortium

Resource Type: community building portal, organization portal, portal, database, consortium, service resource, storage service resource, data repository, data or information resource

Defining Citation: PMID:22453911, PMID:17893861

Keywords: protein-protein interaction, nonredundant, protein interaction, interaction, proteomics, metadata standard, short course, molecular interaction, bio.tools, FASEB list

Funding: European Union

Resource Name: IMEx - The International Molecular Exchange Consortium

Resource ID: SCR_002805

Alternate IDs: nif-0000-00447, OMICS_01545, biotools:imex

Alternate URLs: http://imex.sourceforge.net/, https://bio.tools/imex

Record Creation Time: 20220129T080215+0000

Record Last Update: 20250508T064816+0000

Ratings and Alerts

No rating or validation information has been found for IMEx - The International Molecular Exchange Consortium.

No alerts have been found for IMEx - The International Molecular Exchange Consortium.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 140 mentions in open access literature.

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

Smith JR, et al. (2025) Standardized pipelines support and facilitate integration of diverse datasets at the Rat Genome Database. Database : the journal of biological databases and curation, 2025.

Samarasinghe KW, et al. (2025) MatrixDB 2024: an increased coverage of extracellular matrix interactions, a new Network Explorer and a new web interface. Nucleic acids research, 53(D1), D1677.

Panni S, et al. (2025) Integrated Analysis of microRNA Targets Reveals New Insights into Transcriptional-Post-Transcriptional Regulatory Cross-Talk. Biology, 14(1).

Kliche J, et al. (2024) Proteome-scale characterisation of motif-based interactome rewiring by disease mutations. Molecular systems biology, 20(9), 1025.

Persyn F, et al. (2024) A Nitrogen-specific Interactome Analysis Sheds Light on the Role of the SnRK1 and TOR Kinases in Plant Nitrogen Signaling. Molecular & cellular proteomics : MCP, 23(10), 100842.

Zhu A, et al. (2024) Single-cell analysis reveals T cell dysfunction driven by macrophages and differential expression of transposable elements in severe COVID-19 patients. Heliyon, 10(19), e38688.

Trepte P, et al. (2024) AI-guided pipeline for protein-protein interaction drug discovery identifies a SARS-CoV-2 inhibitor. Molecular systems biology, 20(4), 428.

Lee CY, et al. (2024) Systematic discovery of protein interaction interfaces using AlphaFold and experimental validation. Molecular systems biology, 20(2), 75.

Olivier JF, et al. (2024) CCDC88B interacts with RASAL3 and ARHGEF2 and regulates dendritic cell function in neuroinflammation and colitis. Communications biology, 7(1), 77.

Ferrarese R, et al. (2023) ZBTB18 inhibits SREBP-dependent lipid synthesis by halting CTBPs and LSD1 activity in glioblastoma. Life science alliance, 6(1).

Kliche J, et al. (2023) Large-scale phosphomimetic screening identifies phospho-modulated motif-based protein interactions. Molecular systems biology, e11164.

Kim DK, et al. (2023) A proteome-scale map of the SARS-CoV-2-human contactome. Nature biotechnology, 41(1), 140.

P?un O, et al. (2023) Pioneer factor ASCL1 cooperates with the mSWI/SNF complex at distal regulatory elements to regulate human neural differentiation. Genes & development, 37(5-6), 218.

Iglesias-Martinez LF, et al. (2023) Interactome dynamics of RAF1-BRAF kinase monomers and dimers. Scientific data, 10(1), 203.

Trepte P, et al. (2023) AI-guided pipeline for protein-protein interaction drug discovery

identifies a SARS-CoV-2 inhibitor. bioRxiv : the preprint server for biology.

Sherwood M, et al. (2023) Integrated re-analysis of transcriptomic and proteomic datasets reveals potential mechanisms for Zika viral-based oncolytic therapy in neuroblastoma. F1000Research, 12, 719.

Mihali? F, et al. (2023) Large-scale phage-based screening reveals extensive pan-viral mimicry of host short linear motifs. Nature communications, 14(1), 2409.

Bridges MC, et al. (2023) Actin-dependent recruitment of AGO2 to the zonula adherens. Molecular biology of the cell, 34(13), ar129.

Cheraghi-Shavi T, et al. (2023) TGM2, HMGA2, FXYD3, and LGALS4 genes as biomarkers in acquired oxaliplatin resistance of human colorectal cancer: A systems biology approach. PloS one, 18(8), e0289535.

Wang L, et al. (2023) GTPBP8 is required for mitoribosomal biogenesis and mitochondrial translation. Cellular and molecular life sciences : CMLS, 80(12), 361.