

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-delimited 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, consortium, data or information resource, data repository, database, organization portal, portal, service resource, storage service

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

Availability: Free, Freely available, Available for download

Resource Name: IMEx - The International Molecular Exchange Consortium

Resource ID: SCR_002805

Alternate IDs: nif-0000-00447, OMICS_01545, r3d100010669, biotools:imex

Alternate URLs: <http://imex.sourceforge.net/>, <https://bio.tools/imex>, <https://doi.org/10.17616/R3090W>

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Record Creation Time: 20220129T080215+0000

Record Last Update: 20260903T234548+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 161 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

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

Liu H, et al. (2026) The genomes of 5 mantises provide insights into sex chromosome evolution and Mantodea phylogeny clarification. GigaScience, 15.

Piel iii RB, et al. (2026) Progesterone receptor membrane component 1 (PGRMC1) regulates Heme trafficking through mitochondria-ER junctions. Journal of inorganic

biochemistry, 275, 113093.

Young V, et al. (2026) Effector-host interactome map links type III secretion systems in healthy gut microbiomes to immune modulation. *Nature microbiology*, 11(2), 442.

Piroozmand S, et al. (2026) Suboptimal Responses to Anti-VEGF in Retinal Neurovascular Diseases: Linking Aging and Alternative Angioinflammatory Pathways. *Investigative ophthalmology & visual science*, 67(5), 4.

Azadeh F, et al. (2026) Development of a global screening system for detecting protein-protein interactions by luminescence complementation in fission yeast. *Scientific reports*, 16(1), 5034.

Konstantinou A, et al. (2025) Elucidation of short linear motif-based interactions of the MIT and rhodanese domains of the ubiquitin-specific protease 8. *Biology direct*, 20(1), 59.

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.

Orchard SE, et al. (2025) What Have Data Standards Ever Done for Us? *Molecular & cellular proteomics : MCP*, 24(6), 100933.

Girault V, et al. (2025) Multi-proteomic profiling of the varicella-zoster virus-host interface reveals host susceptibilities to severe infection. *Nature microbiology*, 10(8), 2048.

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).

Frommelt F, et al. (2025) The solute carrier superfamily interactome. *Molecular systems biology*, 21(6), 632.

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

Meriranta L, et al. (2024) Disruption of KLHL6 Fuels Oncogenic Antigen Receptor Signaling in B-Cell Lymphoma. *Blood cancer discovery*, 5(5), 331.

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.

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.

Wang S, et al. (2024) Gene interactions analysis of brain spatial transcriptome for Alzheimer's disease. *Genes & diseases*, 11(6), 101337.

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