Resource Summary Report

Generated by NIF on Apr 9, 2025

MatrixDB

RRID:SCR_001727
Type: Tool

Proper Citation

MatrixDB (RRID:SCR_001727)

Resource Information

URL: http://matrixdb.univ-lyon1.fr/

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Description: Freely available database focused on interactions established by extracellular proteins and polysaccharides, taking into account the multimeric nature of the extracellular proteins (e.g. collagens, laminins and thrombospondins are multimers). MatrixDB is an active member of the International Molecular Exchange (IMEx) consortium and has adopted the PSI-MI standards for annotating and exchanging interaction data. It includes interaction data extracted from the literature by manual curation, and offers access to relevant data involving extracellular proteins provided by the IMEx partner databases through the PSICQUIC webservice, as well as data from the Human Protein Reference Database. The database reports mammalian protein-protein and protein-carbohydrate interactions involving extracellular molecules. Interactions with lipids and cations are also reported. MatrixDB is focused on mammalian interactions, but aims to integrate interaction datasets of model organisms when available. MatrixDB provides direct links to databases recapitulating mutations in genes encoding extracellular proteins, to UniGene and to the Human Protein Atlas that shows expression and localization of proteins in a large variety of normal human tissues and cells. MatrixDB allows researchers to perform customized queries and to build tissue- and disease-specific interaction networks that can be visualized and analyzed with Cytoscape or Medusa. Statistics (2013): 2283 extracellular matrix interactions including 2095 protein-protein and 169 protein-glycosaminoglycan interactions.

Abbreviations: MatrixDB

Synonyms: MatrixDB: Extracellular Matrix Interactions Database, Extracellular Matrix Interactions Database

Resource Type: database, data or information resource, production service resource, service resource

Defining Citation: PMID:20852260, PMID:19147664

Keywords: extracellular, protein fragment, biomolecule, cation, cleavage, collagen, glycosaminoglycan, human, interaction, laminin, lipid, mammalian, matricryptin, matrikin, matrix, molecule, monomer, mulimerization, multimer, polysaccharide, protein, protein-carbohydrate interaction, protein-protein interaction, recognition, thrombospondin, interactome, extracellular protein, protein-polysaccharide interaction, extracellular interaction, molecular interaction, model organism, inorganic, small molecule-protein, small molecule, extracellular matrix protein, protein-glycosaminoglycan interaction, bio.tools, FASEB list

Funding: European Union contract FP7-HEALTH-2007-223411

Availability: Free, Public, Acknowledgement requested

Resource Name: MatrixDB

Resource ID: SCR_001727

Alternate IDs: biotools:matrixdb, nif-0000-10226

Alternate URLs: https://bio.tools/matrixdb

Old URLs: http://matrixdb.ibcp.fr/

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250409T060143+0000

Ratings and Alerts

No rating or validation information has been found for MatrixDB.

No alerts have been found for MatrixDB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 79 mentions in open access literature.

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

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.

Wright SN, et al. (2025) State of the interactomes: an evaluation of molecular networks for generating biological insights. Molecular systems biology, 21(1), 1.

Lamba R, et al. (2024) MatriCom: a scRNA-Seq data mining tool to infer ECM-ECM and cell-ECM communication systems. bioRxiv : the preprint server for biology.

Enríquez-Rodríguez CJ, et al. (2024) Proteomic Blood Profiles Obtained by Totally Blind Biological Clustering in Stable and Exacerbated COPD Patients. Cells, 13(10).

Martinez K, et al. (2024) Functional implications of glycans and their curation: insights from the workshop held at the 16th Annual International Biocuration Conference in Padua, Italy. Database : the journal of biological databases and curation, 2024.

Li N, et al. (2024) Glycosaminoglycans: Participants in Microvascular Coagulation of Sepsis. Thrombosis and haemostasis, 124(7), 599.

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.

Kyriakopoulou K, et al. (2023) Trends in extracellular matrix biology. Molecular biology reports, 50(1), 853.

Chaussé AM, et al. (2023) Epithelial cell invasion by salmonella typhimurium induces modulation of genes controlled by aryl hydrocarbon receptor signaling and involved in extracellular matrix biogenesis. Virulence, 14(1), 2158663.

Naba A, et al. (2023) Ten Years of Extracellular Matrix Proteomics: Accomplishments, Challenges, and Future Perspectives. Molecular & cellular proteomics : MCP, 22(4), 100528.

Petrov PB, et al. (2023) Matrisome AnalyzeR: A suite of tools to annotate and quantify ECM molecules in big datasets across organisms. bioRxiv : the preprint server for biology.

Petrov PB, et al. (2023) Matrisome AnalyzeR - a suite of tools to annotate and quantify ECM molecules in big datasets across organisms. Journal of cell science, 136(17).

Li X, et al. (2022) dbBIP: a comprehensive bipolar disorder database for genetic research. Database : the journal of biological databases and curation, 2022.

Kotlyar M, et al. (2022) IID 2021: towards context-specific protein interaction analyses by increased coverage, enhanced annotation and enrichment analysis. Nucleic acids research, 50(D1), D640.

Zingg D, et al. (2022) Truncated FGFR2 is a clinically actionable oncogene in multiple cancers. Nature, 608(7923), 609.

Kondoh K, et al. (2022) Identification of Key Genes and Pathways Associated with Preeclampsia by a WGCNA and an Evolutionary Approach. Genes, 13(11).

Trbojevi?-Akma?i? I, et al. (2022) High-Throughput Glycomic Methods. Chemical reviews, 122(20), 15865.

Kontio J, et al. (2022) Analysis of extracellular matrix network dynamics in cancer using the MatriNet database. Matrix biology : journal of the International Society for Matrix Biology, 110, 141.

Grillo PK, et al. (2021) Prognostic impact of the glypican family of heparan sulfate proteoglycans on the survival of breast cancer patients. Journal of cancer research and clinical oncology, 147(7), 1937.

Messina F, et al. (2021) Looking for pathways related to COVID-19: confirmation of pathogenic mechanisms by SARS-CoV-2-host interactome. Cell death & disease, 12(8), 788.