

Resource Summary Report

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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: data or information resource, database, 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: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MatrixDB

Resource ID: SCR_001727

Alternate IDs: biotools:matrixdb, r3d100010672, nif-0000-10226

Alternate URLs: <https://bio.tools/matrixdb>, <https://doi.org/10.17616/R3M03H>

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

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260821T193633+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 95 mentions in open access literature.

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

Iacobucci I, et al. (2026) Proteomic and degradomic signatures of extracellular matrix remodeling in calcific aortic valve stenosis. Molecular medicine (Cambridge, Mass.), 32(1).

He F, et al. (2026) Acellular nerve perineurium repairs peripheral nerve injuries in a rat model via ECM-mediated barrier and optimization of the regenerative microenvironment. Regenerative biomaterials, 13, rbag047.

Lohia S, et al. (2026) Integrative Analysis on the Urinary Proteome of Diabetic Kidney Disease, with an Emphasis on Extracellular Matrix Proteins. *International journal of molecular sciences*, 27(5).

Rizvi SA, et al. (2026) Scaling Large Language Models for Next-Generation Single-Cell Analysis. *bioRxiv : the preprint server for biology*.

Kotlyar M, et al. (2026) IID 2025: Physical protein interaction data with detection types, co-purified protein sets, molecular docking, and immune cell networks. *Nucleic acids research*, 54(D1), D593.

Maurencova D, et al. (2026) Cellular senescence escape and antiviral response discriminate glioblastoma from lower-grade gliomas. *Neuro-oncology advances*, 8(1), vdag122.

Farahi N, et al. (2025) Phase-separating fusion proteins drive cancer by upsetting transcription regulation. *Genome biology*, 26(1), 330.

Bhutada S, et al. (2025) Degradomics defines proteolysis information flow from human knee osteoarthritis cartilage to matched synovial fluid and the contributions of secreted proteases ADAMTS5, MMP13 and CMA1 to articular cartilage breakdown. *Osteoarthritis and cartilage*, 33(1), 116.

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. (2025) MatriCom, a single-cell RNA-sequencing data mining tool to infer cell-extracellular matrix interactions. *Journal of cell science*, 138(13).

Ling Z, et al. (2025) Chemoselective Characterization of New Extracellular Matrix Deposition in Bioengineered Tumor Tissues. *Advanced materials (Deerfield Beach, Fla.)*, 37(47), e05445.

Richard JB, et al. (2025) Synovial matrix turnover controls immune cell spatial patterning in inflammation resolution. *Molecular systems biology*, 21(11), 1638.

Okoye GD, et al. (2025) Single-cell map of innate-like lymphocyte response to *Francisella tularensis* infection reveals interleukin-17-dependent protection by MAIT cells. *iScience*, 28(3), 111810.

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

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*.

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.

Novoseleetskaya ES, et al. (2023) Extracellular matrix-induced signaling pathways in mesenchymal stem/stromal cells. *Cell communication and signaling : CCS*, 21(1), 244.