

Resource Summary Report

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CellPhoneDB

RRID:SCR_017054

Type: Tool

Proper Citation

CellPhoneDB (RRID:SCR_017054)

Resource Information

URL: <https://www.cellphonedb.org/>

Proper Citation: CellPhoneDB (RRID:SCR_017054)

Description: Collection of publicly available data of curated receptors, ligands and their interactions. Integrates existing datasets that pertain to cellular communication and new manually reviewed information. Used to search for particular ligand or receptor or to interrogate single cell transcriptomics data.

Resource Type: database, data or information resource

Defining Citation: [PMID:30429548](#)

Keywords: collection, publicly, available, data, curated, receptor, ligand, interaction, heterometric, complex, dataset, cellular, transcriptomic, FASEB list

Funding:

Availability: Free, Available for download, Freely available

Resource Name: CellPhoneDB

Resource ID: SCR_017054

Alternate URLs: <https://github.com/Teichlab/cellphonedb>

License: MIT

Record Creation Time: 20220129T080333+0000

Record Last Update: 20250412T060050+0000

Ratings and Alerts

No rating or validation information has been found for CellPhoneDB.

No alerts have been found for CellPhoneDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 288 mentions in open access literature.

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

Mei J, et al. (2025) Altered Atlas of Exercise-Responsive MicroRNAs Revealing miR-29a-3p Attacks Armored and Cold Tumors and Boosts Anti-B7-H3 Therapy. *Research* (Washington, D.C.), 8, 0590.

Zhang XP, et al. (2025) The heterogeneity of cellular metabolism in the tumour microenvironment of hepatocellular carcinoma with portal vein tumour thrombus. *Cell proliferation*, 58(1), e13738.

Kandror EK, et al. (2025) Enhancer Dynamics and Spatial Organization Drive Anatomically Restricted Cellular States in the Human Spinal Cord. *bioRxiv : the preprint server for biology*.

Weigert M, et al. (2025) A cell atlas of the human fallopian tube throughout the menstrual cycle and menopause. *Nature communications*, 16(1), 372.

Chen Z, et al. (2025) Single-Nucleus RNA Sequencing Reveals Cellular Transcriptome Features at Different Growth Stages in Porcine Skeletal Muscle. *Cells*, 14(1).

Wang Q, et al. (2025) The profiles of immunosuppressive microenvironment in the Lauren intestinal-type gastric adenocarcinoma. *Cancer immunology, immunotherapy : CII*, 74(3), 82.

De Vriendt S, et al. (2025) Single-cell transcriptome atlas of male mouse pituitary across postnatal life highlighting its stem cell landscape. *iScience*, 28(2), 111708.

Wang X, et al. (2025) Elucidating cardiomyocyte heterogeneity and maturation dynamics through integrated single-cell and spatial transcriptomics. *iScience*, 28(1), 111596.

Hu X, et al. (2024) Single-cell transcriptomic profiling reveals immune cell heterogeneity in acute myeloid leukaemia peripheral blood mononuclear cells after chemotherapy. *Cellular*

oncology (Dordrecht), 47(1), 97.

Zhan W, et al. (2024) Sputum Transcriptomics Reveals FCN1+ Macrophage Activation in Mild Eosinophilic Asthma Compared to Non-Asthmatic Eosinophilic Bronchitis. *Allergy, asthma & immunology research*, 16(1), 55.

Wang Y, et al. (2024) Extracellular cancer-associated fibroblasts: A novel subgroup in the cervical cancer microenvironment that exhibits tumor-promoting roles and prognosis biomarker functions. *Oncology letters*, 27(4), 167.

Carabaña C, et al. (2024) Spatially distinct epithelial and mesenchymal cell subsets along progressive lineage restriction in the branching embryonic mammary gland. *The EMBO journal*, 43(12), 2308.

Wang L, et al. (2024) Integrative cross-species analysis reveals conserved and unique signatures in fatty skeletal muscles. *Scientific data*, 11(1), 290.

Wang D, et al. (2024) Single-cell transcriptome analysis deciphers the CD74-mediated immune evasion and tumour growth in lung squamous cell carcinoma with chronic obstructive pulmonary disease. *Clinical and translational medicine*, 14(8), e1786.

Cui J, et al. (2024) Identification of Therapy-Induced Clonal Evolution and Resistance Pathways in Minimal Residual Clones in Multiple Myeloma through Single-Cell Sequencing. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(17), 3919.

Yang W, et al. (2024) Analyses of single-cell and bulk RNA sequencing combined with machine learning reveal the expression patterns of disrupted mitophagy in schizophrenia. *Frontiers in psychiatry*, 15, 1429437.

Su W, et al. (2024) Tumor microenvironment remodeling after neoadjuvant chemoradiotherapy in local advanced rectal cancer revealed by single-cell RNA sequencing. *Journal of translational medicine*, 22(1), 1037.

Niu Y, et al. (2024) Decoding neuronal genes in stroke-induced pain: insights from single-nucleus sequencing in mice. *BMC neurology*, 24(1), 459.

Zerrouk N, et al. (2024) Building a modular and multi-cellular virtual twin of the synovial joint in Rheumatoid Arthritis. *NPJ digital medicine*, 7(1), 379.

Liang Y, et al. (2024) Bariatric surgery induces pancreatic cell transdifferentiation as indicated by single-cell transcriptomics in Zucker diabetic rats. *Journal of diabetes*, 16(8), e13521.