

Resource Summary Report

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CellChat

RRID:SCR_021946

Type: Tool

Proper Citation

CellChat (RRID:SCR_021946)

Resource Information

URL: <https://github.com/sqjin/CellChat>

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Description: Software R toolkit for inference, visualization and analysis of cell-cell communication from single cell data. Quantitatively infers and analyzes intercellular communication networks from single-cell RNA-sequencing data. Predicts major signaling inputs and outputs for cells and how those cells and signals coordinate for functions using network analysis and pattern recognition approaches. Classifies signaling pathways and delineates conserved and context specific pathways across different datasets.

Resource Type: software resource, software toolkit

Defining Citation: [PMID:33597522](#)

Keywords: inference, visualization, analysis, cell-cell communication, single cell data, intercellular communication networks, single-cell RNA-sequencing data

Funding: Howard Hughes Medical Institute ;
LEO Foundation ;
NIGMS R01 GM123731;
NIH P30 AR07504;
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Simons Foundation ;
UC Irvine

Availability: Free, Available for download, Freely available

Resource Name: CellChat

Resource ID: SCR_021946

Alternate URLs: <http://www.cellchat.org/>

License: GNU General Public License v3.0

Record Creation Time: 20220421T050137+0000

Record Last Update: 20260912T200259+0000

Ratings and Alerts

No rating or validation information has been found for CellChat.

No alerts have been found for CellChat.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 753 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Zhang G, et al. (2026) Ubiquitylation-oxaliplatin-related prognosis signature reveals the landscapes of immune responses, cell communication, and therapeutic sensitivity for colorectal cancer. *Anti-cancer drugs*, 37(1), 67.

Johnson LA, et al. (2026) Clonal expansion of cytotoxic CD8⁺ T cells in lecanemab-associated ARIA. *Nature communications*, 17(1).

Yang J, et al. (2026) Hypoxia-Induced Osteopontin-Positive Glioma-Associated Macrophages Facilitate Glioma Mesenchymal Transition via NF- κ B Pathway Activation. *Cancer communications (London, England)*, 46, 0007.

Sun H, et al. (2026) Identification and characterization of MARCO-expressing tumor-associated macrophages in pancreatic ductal adenocarcinoma with pan-cancer relevance. *NPJ precision oncology*, 10(1).

Bi C, et al. (2026) cRGD-Functionalized macrophage extracellular vesicles loaded with GSK2033 enhance T cell antitumor immunity in GBM by disrupting the LXR/ABCA1-Mediated Myelin lipid transfer axis. *Journal of nanobiotechnology*, 24(1).

Wu LW, et al. (2026) Inactivation of AXL in Cardiac Fibroblasts Alleviates Right Ventricular Remodeling in Pulmonary Hypertension. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(9), e08995.

Kroehling L, et al. (2026) A highly resolved integrated single-cell atlas of HPV-negative head and neck cancer. *Communications medicine*, 6(1).

Yogo A, et al. (2026) Spatial Transcriptomics Reveals Location-Specific Tumor Cell Subtypes and Signaling within Multifocal Small Intestinal Neuroendocrine Tumors. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(10), 2098.

Ge M, et al. (2026) Senescent fibroblasts drive CD8+ T cell dysfunction in colorectal cancer via CD36-mediated lipid transfer and peroxidation. *Journal of translational medicine*, 24(1).

Zhang J, et al. (2026) Single-cell spatiotemporal transcriptomic and chromatin accessibility profiling in developing postnatal human and macaque prefrontal cortex. *Nature neuroscience*, 29(3), 746.

Zhou Q, et al. (2026) CD19+Ki67+B cells regulated by NAMPT as key modulators in triple-negative breast cancer with brain metastasis. *Breast cancer research : BCR*, 28(1).

Albuquerque RA, et al. (2026) Kinetics of local C3 production orchestrates neutrophil recruitment in lung injury. *bioRxiv : the preprint server for biology*.

Geng Z, et al. (2026) Prediction of tumor-infiltrating lymphocytes through habitat radiomics and exploration of response mechanisms in neoadjuvant immunochemotherapy-treated lung cancer. *Cancer immunology, immunotherapy : CII*, 75(2), 42.

Zhang H, et al. (2026) Single-cell transcriptomic analysis and machine learning identify ATAD3A as a key gene that stabilizes mitochondrial-endoplasmic reticulum membranes, promoting bladder cancer progression. *Journal of translational medicine*, 24(1).

Zhang M, et al. (2026) Combined single-cell transcriptome and immune repertoire analysis reveals hepatic and renal immune injury by heat stroke. *JCI insight*, 11(6).

Cao Z, et al. (2026) Single-cell transcriptomics reveals ADRB1 as a key immune checkpoint regulating T cell exhaustion in lung cancer and its prognostic value in lung cancer. *Discover oncology*, 17(1).

Li X, et al. (2026) Single-cell atlas of gastric cancer reveals malignant epithelial evolution and regulatory reprogramming of the tumor microenvironment. *PloS one*, 21(4), e0347679.

Hosseini ST, et al. (2026) Deciphering immune and cellular reprogramming during the progression from inflammatory bowel disease to colorectal cancer using multi-omics single-cell and spatial transcriptomics. *Journal of translational medicine*, 24(1).

Zhao B, et al. (2026) A pyroptosis-related molecular signature stratifies prognosis and highlights GSDMB-mediated malignancy in intrahepatic cholangiocarcinoma. *Biology direct*, 21(1).

Wang J, et al. (2026) Single-cell and machine learning-integrated bulk RNA-seq analysis reveals TKT as an oxidative stress-associated diagnostic biomarker in acute myocardial infarction. *Human genomics*, 20(1).