

Resource Summary Report

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Metacell

RRID:SCR_017013

Type: Tool

Proper Citation

Metacell (RRID:SCR_017013)

Resource Information

URL: <https://omictools.com/metacell-tool>

Proper Citation: Metacell (RRID:SCR_017013)

Description: Software package for single cell RNA-seq data analysis using k-NN graph partitions. Used to analyze group of scRNA profiles that are highly similar and provides features for deriving them. Can be used with large datasets., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: MetaCell

Resource Type: software application, software resource, data analysis software, data processing software

Defining Citation: [DOI:10.1101/437665](https://doi.org/10.1101/437665)

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Metacell

Resource ID: SCR_017013

Alternate IDs: OMICS_32475

Alternate URLs: <https://bitbucket.org/tanaylab/metacell/src/default/>

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260811T043547+0000

Ratings and Alerts

No rating or validation information has been found for Metacell.

No alerts have been found for Metacell.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 31 mentions in open access literature.

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

Gurevich-Shapiro A, et al. (2025) Distinct Cellular and Molecular Patterns in Pretreatment Peripheral Blood Are Associated with CAR T-cell Outcomes in Diffuse Large B-cell Lymphoma. Cancer research, 85(24), 5066.

Liu W, et al. (2024) An immune cell map of human lung adenocarcinoma development reveals an anti-tumoral role of the Tfh-dependent tertiary lymphoid structure. Cell reports. Medicine, 5(3), 101448.

Chen K, et al. (2024) Cellular Trojan Horse initiates bimetallic Fe-Cu MOF-mediated synergistic cuproptosis and ferroptosis against malignancies. Science advances, 10(15), eadk3201.

Larouche JD, et al. (2024) Transposable elements regulate thymus development and function. eLife, 12.

Lee CYC, et al. (2024) Tumour-retained activated CCR7+ dendritic cells are heterogeneous and regulate local anti-tumour cytolytic activity. Nature communications, 15(1), 682.

Huang L, et al. (2024) Tuft cells act as regenerative stem cells in the human intestine. Nature, 634(8035), 929.

Gillespie ER, et al. (2024) Single-cell RNA sequencing reveals peripheral blood leukocyte responses to spinal cord injury in mice with humanised immune systems. Journal of neuroinflammation, 21(1), 63.

Hu R, et al. (2024) Expanding GABAergic Neuronal Diversity in iPSC-Derived Disease Models. bioRxiv : the preprint server for biology.

Ding L, et al. (2023) scMINER: a mutual information-based framework for identifying hidden drivers from single-cell omics data. bioRxiv : the preprint server for biology.

van der Leun AM, et al. (2023) Dual Immune Checkpoint Blockade Induces Analogous Alterations in the Dysfunctional CD8+ T-cell and Activated Treg Compartment. Cancer discovery, 13(10), 2212.

Persad S, et al. (2023) SEACells infers transcriptional and epigenomic cellular states from single-cell genomics data. Nature biotechnology, 41(12), 1746.

Tung CC, et al. (2023) Single-cell transcriptomics unveils xylem cell development and evolution. *Genome biology*, 24(1), 3.

Chung JY, et al. (2023) Smad3 is essential for polarization of tumor-associated neutrophils in non-small cell lung carcinoma. *Nature communications*, 14(1), 1794.

Goldman O, et al. (2023) Early Infiltration of Innate Immune Cells to the Liver Depletes HNF4 α and Promotes Extrahepatic Carcinogenesis. *Cancer discovery*, 13(7), 1616.

Gil N, et al. (2023) Complex regulation of Eomes levels mediated through distinct functional features of the Meteor long non-coding RNA locus. *Cell reports*, 42(6), 112569.

Liu Y, et al. (2022) A specialized bone marrow microenvironment for fetal haematopoiesis. *Nature communications*, 13(1), 1327.

Gur C, et al. (2022) LGR5 expressing skin fibroblasts define a major cellular hub perturbed in scleroderma. *Cell*, 185(8), 1373.

Fu W, et al. (2022) Cellular features of localized microenvironments in human meniscal degeneration: a single-cell transcriptomic study. *eLife*, 11.

Miguel-Escalada I, et al. (2022) Pancreas agenesis mutations disrupt a lead enhancer controlling a developmental enhancer cluster. *Developmental cell*, 57(16), 1922.

Bresser K, et al. (2022) Replicative history marks transcriptional and functional disparity in the CD8 $^{+}$ T cell memory pool. *Nature immunology*, 23(5), 791.