

Resource Summary Report

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cellxgene

RRID:SCR_021059

Type: Tool

Proper Citation

cellxgene (RRID:SCR_021059)

Resource Information

URL: <https://chanzuckerberg.com/science/programs-resources/single-cell-biology/cellxgene/>

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Description: Software tool as interactive explorer for single cell transcriptomics datasets. Used to explore and visualize high dimensional single cell datasets in interactive way. Can visualize gene expression at level of entire dataset or particular subset of cells to help identify cell types, which can in turn help identify diseases. Enables plotting gene expression level against another gene to compare how these different genes are expressed across dataset. Open source cell visualization tool integrates with tools like SciPy and Jupyter.

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

Keywords: Single cell transcriptomics datasets explorer, gene expression visualization, identify cell types, identify diseases, plotting gene expression level

Availability: Free, Available for download, Freely available

Resource Name: cellxgene

Resource ID: SCR_021059

Alternate URLs: <https://github.com/chanzuckerberg/cellxgene>

License: MIT License

Record Creation Time: 20220129T080353+0000

Record Last Update: 20260731T043040+0000

Ratings and Alerts

No rating or validation information has been found for cellxgene.

No alerts have been found for cellxgene.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 61 mentions in open access literature.

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

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

Shao JS, et al. (2025) Pulmonary fibroblast-derived stem cell factor promotes neutrophilic asthma by augmenting IL-17A production from ILC3s. The Journal of clinical investigation, 135(16).

Huang L, et al. (2025) scValue: value-based subsampling of large-scale single-cell transcriptomic data for machine and deep learning tasks. Briefings in bioinformatics, 26(3).

Mao T, et al. (2025) CART-GPT: A T Cell-Informed AI Linguistic Framework for Interpreting Neurotoxicity and Therapeutic Outcomes in CAR-T Therapy. bioRxiv : the preprint server for biology.

Agboraw E, et al. (2025) paraCell: a novel software tool for the interactive analysis and visualization of standard and dual host-parasite single-cell RNA-seq data. Nucleic acids research, 53(4).

Shao J, et al. (2025) Orphan receptor GPR153 facilitates vascular damage responses by modulating cAMP levels, YAP/TAZ signaling, and NF- κ B activation. Nature communications, 16(1), 6232.

Keramati F, et al. (2025) Systemic inflammation impairs myelopoiesis and interferon type I responses in humans. Nature immunology, 26(5), 737.

Wang T, et al. (2025) GPRC5B preserves a mature γ cell state in obesity by controlling MafA expression. JCI insight, 10(20).

Brooks ER, et al. (2025) A single-cell atlas of spatial and temporal gene expression in the mouse cranial neural plate. eLife, 13.

Ito K, et al. (2025) Mouse-Geneformer: A deep learning model for mouse single-cell transcriptome and its cross-species utility. PLoS genetics, 21(3), e1011420.

Li C, et al. (2025) SUV39H1 maintains cancer stem cell chromatin state and properties in glioblastoma. JCI insight, 10(5).

Goclowski CL, et al. (2025) Galaxy as a gateway to bioinformatics: Multi-Interface Galaxy Hands-on Training Suite (MIGHTS) for scRNA-seq. *GigaScience*, 14.

Stachelek K, et al. (2025) Chevreul: an R bioconductor package for exploratory analysis of full-length single cell sequencing. *GigaByte* (Hong Kong, China), 2025, gigabyte158.

Li W, et al. (2025) Single-cell immune aging clocks reveal inter-individual heterogeneity during infection and vaccination. *Nature aging*, 5(4), 607.

Qian J, et al. (2025) Identification and characterization of cell niches in tissue from spatial omics data at single-cell resolution. *Nature communications*, 16(1), 1693.

Fullard JF, et al. (2025) Population-scale cross-disorder atlas of the human prefrontal cortex at single-cell resolution. *Scientific data*, 12(1), 954.

Constanty F, et al. (2025) Border-zone cardiomyocytes and macrophages regulate extracellular matrix remodeling to promote cardiomyocyte protrusion during cardiac regeneration. *Nature communications*, 16(1), 3823.

Mangiola S, et al. (2025) Circulating immune cells exhibit distinct traits linked to metastatic burden in breast cancer. *Breast cancer research : BCR*, 27(1), 73.

Wang Y, et al. (2025) Macrophages drive a fibrogenic gene program of periductal fibroblasts in pediatric primary sclerosing cholangitis. *bioRxiv : the preprint server for biology*.

Mañas A, et al. (2025) Targeted ferroptosis induction enhances chemotherapy efficacy in chemoresistant neuroblastoma. *NPJ precision oncology*, 9(1), 311.