Resource Summary Report

Generated by dkNET on May 21, 2025

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

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

Funding:

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: 20250521T061812+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 33 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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

Akindehin S, et al. (2024) Loss of GIPR in LEPR cells impairs glucose control by GIP and GIP:GLP-1 co-agonism without affecting body weight and food intake in mice. Molecular metabolism, 83, 101915.

Qian X, et al. (2024) Spatial Single-cell Analysis Decodes Cortical Layer and Area Specification. bioRxiv : the preprint server for biology.

Piki E, et al. (2024) Molecular and functional profiling of primary normal ovarian cells defines insights into cancer development and drug responses. Molecular therapy. Oncology, 32(4), 200903.

Goumenaki P, et al. (2024) The innate immune regulator MyD88 dampens fibrosis during zebrafish heart regeneration. Nature cardiovascular research, 3(9), 1158.

Hall S, et al. (2024) Cellular and molecular characterization of peripheral glia in the lung and other organs. PloS one, 19(12), e0310303.

N M P, et al. (2024) A multi-region single nucleus transcriptomic atlas of Parkinson's disease. Scientific data, 11(1), 1274.

Brooks ER, et al. (2024) A single-cell atlas of spatial and temporal gene expression in the mouse cranial neural plate. bioRxiv : the preprint server for biology.

Xu Y, et al. (2024) PDGFRA is a conserved HAND2 effector during early cardiac development. Nature cardiovascular research, 3(12), 1531.

Cao C, et al. (2024) CXCR4 orchestrates the TOX-programmed exhausted phenotype of CD8+ T cells via JAK2/STAT3 pathway. Cell genomics, 4(10), 100659.

Mangiola S, et al. (2024) A multi-organ map of the human immune system across age, sex and ethnicity. bioRxiv : the preprint server for biology.

Fischer F, et al. (2024) scTab: Scaling cross-tissue single-cell annotation models. Nature communications, 15(1), 6611.

Hutchison WJ, et al. (2024) The tidyomics ecosystem: Enhancing omic data analyses. bioRxiv : the preprint server for biology.

Kwak JW, et al. (2024) CXCR1/2 antagonism inhibits neutrophil function and not recruitment in cancer. Oncoimmunology, 13(1), 2384674.

Yang X, et al. (2024) GeneCompass: deciphering universal gene regulatory mechanisms with a knowledge-informed cross-species foundation model. Cell research, 34(12), 830.

Bush SJ, et al. (2024) Adult Human, but Not Rodent, Spermatogonial Stem Cells Retain States with a Foetal-like Signature. Cells, 13(9).

Luo Y, et al. (2024) Systems biology-based analysis exploring shared biomarkers and pathogenesis of myocardial infarction combined with osteoarthritis. Frontiers in immunology, 15, 1398990.

Hai L, et al. (2024) A clinically applicable connectivity signature for glioblastoma includes the tumor network driver CHI3L1. Nature communications, 15(1), 968.

Ergen C, et al. (2024) Consensus prediction of cell type labels in single-cell data with popV. Nature genetics, 56(12), 2731.

Corcoran TE, et al. (2024) CFTR expression decreases with age in several airway cell types. Scientific reports, 14(1), 28832.