

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, data visualization software, software application, software resource

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: 20260919T195448+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 82 mentions in open access literature.

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

Dang X, et al. (2026) Investigating the shared genetic architecture between selective immunoglobulin A deficiency and autoimmune diseases. *Human genetics*, 145(1).

Wang FQ, et al. (2026) DisCP-Atlas: a comprehensive resource mapping cellular processes to complex diseases. *Nucleic acids research*, 54(D1), D1376.

Dong M, et al. (2026) Stack: In-Context Learning of Single-Cell Biology. *bioRxiv* : the preprint server for biology.

Que D, et al. (2026) Identification of PANoptosis-related biomarkers in myocardial infarction via bioinformatics and single-cell analyses. *Medicine*, 105(4), e46750.

Van Loh BM, et al. (2026) The Transcription Factors Six3 and Six6 in Neuromedin-S Neurons Differentially Affect Circadian Rhythms. *Journal of neuroscience research*, 104(4), e70123.

Huffman A, et al. (2026) SEA CDM: Study-Experiment-Assay Common Data Model and Databases for Cross-Domain Data Integration and Analysis. *Scientific data*, 13(1), 238.

Feng X, et al. (2026) Ribonuclease 4 Functions in Nociceptor-Mediated Nerve Homeostasis. *Nature communications*, 17(1).

Deng Y, et al. (2026) Scalable cell-specific coexpression networks for granular regulatory pattern discovery with NeighbourNet. *Genome research*, 36(4), 785.

Sun R, et al. (2026) SexTumorDB: a comprehensive resource of sex-dependent tumor landscape at single-cell resolution. *Scientific data*, 13(1).

Zhang Y, et al. (2026) Co-occurrence of transcriptionally distinct persister cell states underpins neoadjuvant therapy resistance in triple-negative breast cancer. *Genome medicine*, 18(1).

Song Y, et al. (2026) GFetch2R: fetching single-cell/bulk RNA-seq data from public repositories to R and benchmarking the subsequent format conversion tools. *GigaScience*, 15.

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

Kim S, et al. (2026) Bazedoxifene reverses sexually dimorphic autistic-like abnormalities in biallelic MDGA1-mutant mice. *EMBO molecular medicine*, 18(4), 1358.

Malagoli G, et al. (2026) Geometry-aware graph attention networks to explain single-cell chromatin states and gene expression with SEAGALL. *Genome biology*, 27(1).

Bueckle A, et al. (2026) Cell Type Populations for 3D Anatomical Structures of the Human Reference Atlas. *Scientific data*, 13(1).

Yang Y, et al. (2026) HSD11B1 suppresses ferroptosis in endometrial stromal cells through the JUND/IL-10 axis to promote endometriosis progression. *Reproductive biology and endocrinology : RB&E*, 24(1).

Chechekhina E, et al. (2026) scParadise: tunable, highly accurate multi-level cell type annotation, unknown cell type identification, and modality imputation. *Nucleic acids research*, 54(11).

Yuan DJ, et al. (2026) Genotype-to-Phenotype Mapping of Somatic Clonal Mosaicism via Single-Cell Co-Capture of DNA Mutations and mRNA Transcripts. *Cancer discovery*, 16(4), 721.

Hutchings ED, et al. (2026) The cellular correlates and adolescent reorganisation of cortical myelination networks in the common marmoset. *Communications biology*.

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).