

Resource Summary Report

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UCSC Cell Browser

RRID:SCR_023293

Type: Tool

Proper Citation

UCSC Cell Browser (RRID:SCR_023293)

Resource Information

URL: <https://cells.ucsc.edu/>

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Description: Web based tool to visualize gene expression and metadata annotation distribution throughout single cell dataset or multiple datasets. Interactive viewer for single cell expression. You can click on and hover over cells to get meta information, search for genes to color on and click clusters to show cluster specific marker genes.

Resource Type: data access protocol, software resource, web service

Defining Citation: [PMID:34244710](#)

Keywords: visualize gene expression, metadata annotation distribution, single cell data viewer, cluster specific marker genes, single cell expression,

Funding: Brain and Behavior Research Foundation ;
California Institute for Regenerative Medicine ;
Chan Zuckerberg Initiative Foundation ;
NHGRI 1U41HG010972;
NHGRI 5R01HG010329;
NHGRI 5U41HG002371;
NIMH DP2MH122400;
NIMH RF1MH121268;
NIMH U01MH114825;
NINDS K99 NS111731;
Silicon Valley Community Foundation ;
Simons Foundation ;
University of California Office of the President Emergency COVID-19 Research Seed Funding

Availability: Free, Freely available

Resource Name: UCSC Cell Browser

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Alternate URLs: <https://cellbrowser.readthedocs.io/en/master/>,
<https://github.com/maximilianh/cellBrowser>

License: GNU GPL v3.0

Record Creation Time: 20230222T050208+0000

Record Last Update: 20260919T195533+0000

Ratings and Alerts

No rating or validation information has been found for UCSC Cell Browser.

No alerts have been found for UCSC Cell Browser.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 155 mentions in open access literature.

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

Wang Q, et al. (2026) JUND-driven stress-responsive astrocytes promote neuronal apoptosis via enhanced gap junction signaling in autism spectrum disorder. Molecular autism, 17(1).

Avila TU, et al. (2026) Repeat expansions in C9orf72 rewire the 3D chromatin landscape in ALS. bioRxiv : the preprint server for biology.

Li B, et al. (2026) Reprogramming of neuronal genome function and phenotype by astrocytes. bioRxiv : the preprint server for biology.

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).

Nguyen TDT, et al. (2026) Pan-Cancer Single-Cell RNA Sequencing Analysis Refines Multi-Origin Monocyte and Macrophage Lineages. Cancer immunology research, 14(2), 350.

Wang R, et al. (2026) PTGDS is a potential marker for lung adenocarcinoma identified in a pancancer analysis. Scientific reports, 16(1).

Huang Y, et al. (2026) scDenorm: a denormalization tool for integrating single-cell transcriptomics data. *GigaScience*, 15.

Virga F, et al. (2026) Transcriptome changes in circulating immune cells of critical COVID-19 patients predict a specific metabolic and epigenetic imprint. *Journal of translational medicine*, 24(1), 247.

Zhu N, et al. (2026) Bioinformatic validation of LCN2 as a common hub gene for ferroptosis, pyroptosis and necroptosis in ulcerative colitis. *BMC gastroenterology*, 26(1).

González-Hernández S, et al. (2026) Endothelial PROX1 induces blood-brain barrier disruption in the central nervous system. *JCI insight*, 11(1).

Gao W, et al. (2026) An integrative single-nucleus multiomic atlas of the human left ventricle identifies gene regulatory network dynamics across cardiac development, aging, and disease. *Genome biology*, 27(1).

Song Y, et al. (2026) GEfetch2R: fetching single-cell/bulk RNA-seq data from public repositories to R and benchmarking the subsequent format conversion tools. *GigaScience*, 15.

Li X, et al. (2026) RECOMBINE identifies recurrent composite markers of cell types and states. *Genome research*, 36(6), 1221.

Liu Y, et al. (2026) Inference of marker genes of subtle cell state changes via iLR: iterative logistic regression. *Bioinformatics (Oxford, England)*, 42(2).

Cancino-Maldonado K, et al. (2026) Deciphering the single-cell molecular landscape of ampullary cancer: A rare gastrointestinal malignancy. *iScience*, 29(6), 116015.

Keane L, et al. (2026) Microglia in diffuse midline glioma contribute to extracellular matrix remodelling and cancer cell invasion. *Cell death & disease*, 17(1).

Shim N, et al. (2026) Novel role of the lncRNA EPR as oncosuppressor in intestinal cancer. *bioRxiv : the preprint server for biology*.

Currie R, et al. (2026) CytoVerse: Single-Cell AI Foundation Models in the Browser. *bioRxiv : the preprint server for biology*.

Brandt A, et al. (2026) Toll-like receptor 2 drives liver senescence and fibrosis in aging through gut-derived microbial signaling. *Cellular & molecular biology letters*, 31(1).

Municio C, et al. (2026) Choroid plexus organoids mimic amyloid uptake at the blood-cerebrospinal fluid-barrier. *Frontiers in cellular neuroscience*, 20, 1769911.