

Resource Summary Report

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CZ CELLxGENE Discover

RRID:SCR_024894

Type: Tool

Proper Citation

CZ CELLxGENE Discover (RRID:SCR_024894)

Resource Information

URL: <https://cellxgene.cziscience.com/>

Proper Citation: CZ CELLxGENE Discover (RRID:SCR_024894)

Description: Portal used to find and download any of data sets published on CELLxGENE. Allows to download and visually explore data to understand functionality of human tissues at cellular level. Optimized for finding, exploring, and reusing single cell data. Collections Page lists collections hosted on CELLxGENE Discover and metadata that define tissue, assay, disease, organism, and cell count for each collection. Once you find published dataset of interest on CELLxGENE Discover, you can click on the explore button below the dataset description to explore the cells of that dataset using the CELLxGENE Explorer.

Synonyms: Chan Zuckerberg CELL by GENE Discover

Resource Type: catalog, data or information resource, database, portal

Keywords: BICAN, visually explore data, functionality of human tissues at cellular level, tissue, assay, disease, organism, cell count, collection

Availability: Free, Freely available

Resource Name: CZ CELLxGENE Discover

Resource ID: SCR_024894

Record Creation Time: 20240118T050241+0000

Record Last Update: 20260905T133444+0000

Ratings and Alerts

No rating or validation information has been found for CZ CELLxGENE Discover.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 139 mentions in open access literature.

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

Yuan L, et al. (2026) Human assembloids recapitulate periportal liver tissue in vitro. Nature, 650(8101), 438.

He J, et al. (2026) A Microbiota- and IL-15-Dependent Innate-Like B Cell Progenitor Expressing E4BP4. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(8), e12444.

Zhao Z, et al. (2026) Multi-omics analysis unveils tumor heterogeneity and immunotherapy predictive model in breast cancer for precision medicine and early detection. Neoplasia (New York, N.Y.), 71, 101260.

Zhang H, et al. (2026) OmniCellTOSG: The First Cell Text-Omic Signaling Graphs Dataset for Graph Language Foundation Modeling. Research square.

Zhang X, et al. (2026) Single-Cell Transcriptome-Wide Mendelian Randomization and Colocalization Uncover Potential Immunocytes-Related Therapeutic Targets for Obesity. Journal of cellular and molecular medicine, 30(9), e71185.

Kunst M, et al. (2026) SCALPEL: A pipeline for processing large-scale spatial transcriptomics data. bioRxiv : the preprint server for biology.

Nguyen K, et al. (2026) Cell type annotation using large language models (LLMs) and CytoAnalyst. Bioinformatics advances, 6(1), vbag001.

Xu Z, et al. (2026) Single-cell multimodal profiling of pan-cancer cell lines uncovers gene regulatory principles underlying intrinsic cell states and environmental features. bioRxiv : the preprint server for biology.

Jiménez-Sánchez A, et al. (2026) Transcriptomic Plasticity Is a Hallmark of Metastatic Pancreatic Cancer. Cancer research, 86(7), 1769.

TanTai W, et al. (2026) SIRT5-RAC2 Axis Drives Monocyte-to-Macrophage Differentiation to Promote Inflammatory Injury in Premature Ovarian Insufficiency. Advanced science (Weinheim, Baden-Wurttemberg, Germany), e18417.

Quaynor SK, et al. (2026) Consensus-based Detection of Aetiologic Copy Number Variants For Syndromic Orofacial Clefts Utilising Whole Exome Sequencing of Case Parent Trios. Research square.

Li S, et al. (2026) Spatial transcriptomics uncovers lipid metabolic dysregulation driving immune-stroma crosstalk in Sjögren's Disease. *EBioMedicine*, 123, 106074.

Waldow A, et al. (2026) Nanoscopic analysis of tight junction organization in in vitro blood-brain barrier models. *Fluids and barriers of the CNS*, 23(1).

Kim JP, et al. (2026) Genetic architecture of plasma pTau217 and related biomarkers in Alzheimer's disease via genome-wide association studies. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 22(3), e71275.

Yu Z, et al. (2026) scMapNet: Marker-based cell type annotation of scRNA-seq data via vision transfer learning with tabular-to-image transformations. *Journal of advanced research*, 85, 633.

Park H, et al. (2026) MetaCCI: meta cell-cell interaction inference and its application to CCIs characteristics of MDS. *Bioinformatics (Oxford, England)*, 42(5).

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).

Fang M, et al. (2026) Multimodal integration of neuroimaging, transcriptomics and single-cell analysis reveals molecular correlates linking osteoporosis to brain abnormalities. *Frontiers in immunology*, 17, 1817475.

Chang CH, et al. (2026) In situ proteomics unveils specialized domains for extrasynaptic signaling on neuronal cilia. *Science advances*, 12(23), eaed5548.

Zhang X, et al. (2026) CSPG4+ extracellular vesicles carry fibronectin and interleukin-11 and reflect radiographic severity in knee osteoarthritis. *Osteoarthritis and cartilage open*, 8(2), 100769.