

Resource Summary Report

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Single Cell Portal

RRID:SCR_014816

Type: Tool

Proper Citation

Single Cell Portal (RRID:SCR_014816)

Resource Information

URL: https://singlecell.broadinstitute.org/single_cell

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Description: Portal specializes in visualizing and disseminating single cell data. Allows you to use natural language and faceted search to discover other scientists' research and share your own findings. Each study includes information on cell types, singular or multiple gene expression, and spatial transcriptomics. Interactive visualizations allow to explore cell clusters and search for related genes.

Abbreviations: SCP

Synonyms: Single-Cell RNA-Seq Portal for Brain Research

Resource Type: data or information resource, portal

Keywords: Single cell data visualization, disseminating single cell data, single cell data, brain, RNA, rna seq, multiple gene expression, spatial transcriptomics, open science

Availability: Free, Available for download, Freely available

Resource Name: Single Cell Portal

Resource ID: SCR_014816

Alternate URLs: https://portals.broadinstitute.org/single_cell?utf8=?&search_terms=e+coli&order=&commit=

Record Creation Time: 20220129T080322+0000

Record Last Update: 20260905T133049+0000

Ratings and Alerts

No rating or validation information has been found for Single Cell Portal.

No alerts have been found for Single Cell Portal.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 366 mentions in open access literature.

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

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.

Franciosa G, et al. (2026) The proteomics and phosphoproteomics landscape of melanoma under T cell attack. *Cell reports. Medicine*, 7(6), 102829.

Betti M, et al. (2026) Biopsy RNA-seq captures TROP-2-linked migration and clonal resistance to forecast aggressiveness in metastatic melanoma. *Journal of experimental & clinical cancer research : CR*, 45(1).

Rider A, et al. (2026) Transcriptomic profiling and machine learning uncover gene signatures of psoriasis endotypes and disease severity. *Communications medicine*, 6(1), 65.

Yan C, et al. (2026) RAS/MEK/PI3K pathway inhibition augments response to CD40 agonism by targeting CD11b+ Bregs thereby overcoming melanoma PD1-resistance. *Nature communications*, 17(1), 162.

Fujikura K, et al. (2026) Genome-wide analysis of somatic noncoding mutation patterns and mitochondrial heteroplasmic shift in type B1 and B2 thymomas. *The Journal of pathology*, 268(2), 135.

Lee H, et al. (2026) Platelets induce VISTA expression and modulate the ovarian tumor microenvironment. *Platelets*, 37(1), 2644366.

Martinez-Daunis A, et al. (2026) Alternative Pathways of Acetylcholine Release in the Colon: Role of High-Affinity Choline Transporters. *Neurogastroenterology and motility*, 38(3), e70280.

Yang T, et al. (2026) Identification of MTURN as a trained immunity-related biomarker for heart failure via integrative transcriptomic machine learning analysis and experimental validation. *Frontiers in immunology*, 17, 1739660.

Xuan J, et al. (2026) Cardiomyocyte-derived TGFB3 attenuates cardiac fibrosis and preserves cardiac function in heart failure. *Scientific reports*, 16(1).

Tommasini D, et al. (2026) The Extreme Diversity Of Retinal Amacrine Cells Has Deep Evolutionary Roots. *bioRxiv : the preprint server for biology*.

Gou X, et al. (2026) Identification of a Two-Gene Biomarker Correlated with Sensitivity to Combined PARP7 Inhibition and AHR Activation in Cancer Cells. *Cancer research communications*, 6(1), 5.

Manoukian P, et al. (2026) Estrogen Production in Pancreatic Cancer Shapes a Tumor-Suppressive Stromal Microenvironment. *Cancer research*, 86(3), 571.

Li Y, et al. (2026) Ion channel gene signature for diagnosis and antifibrotic therapy in liver fibrosis. *Journal of translational medicine*, 24(1).

Zhang S, et al. (2026) Identification and Validation of Key Purine Metabolism-Related Genes in Ulcerative Colitis Using Bioinformatics and Machine Learning. *Journal of inflammation research*, 19, 557806.

Yue Y, et al. (2026) Genetic and functional characterization of AMH Signaling in Zebrafish - Evidence for Roles of Amh-Bmpr2a-Bmpr1bb Pathway in Controlling Gonadal Homeostasis. *PLoS genetics*, 22(3), e1011958.

Fan Z, et al. (2026) Establishing an atherosclerosis diagnostic model based on WGCNA and machine learning algorithms with key genes in cholesterol metabolism and ferroptosis, and revealing the regulatory role of HMOX1 in cellular ferroptosis. *Frontiers in cardiovascular medicine*, 13, 1715946.

Saldanha OL, et al. (2026) SwarmMAP: swarm learning for decentralized cell type annotation in single cell sequencing data. *NPJ systems biology and applications*, 12(1).

He Y, et al. (2026) Macrophage NEDD4L restrains liver fibrosis by preventing scar-associated macrophage expansion via ubiquitination of phospho-SMAD3. *International journal of biological sciences*, 22(7), 3304.

Yin X, et al. (2026) Identification of Cell Subpopulation-Specific Driver Genes Reveals Ideal Candidates for Renal Cell Carcinoma Immunotherapy. *International journal of molecular sciences*, 27(8).