Resource Summary Report

Generated by <u>NIF</u> on Apr 29, 2025

AUCell

RRID:SCR_021327 Type: Tool

Proper Citation

AUCell (RRID:SCR_021327)

Resource Information

URL: https://bioconductor.org/packages/AUCell/

Proper Citation: AUCell (RRID:SCR_021327)

Description: Software R package to identify cells with active gene sets in single cell RNAseq data. Used for analysis of gene set activity in single cell RNA-seq data.Used to calculate whether critical subset of input gene set is enriched within expressed genes for each cell.

Synonyms: Area Under the Curve

Resource Type: data processing software, software toolkit, data analysis software, software resource, software application

Keywords: Identify cells with active gene sets, single cell RNA-seq data, gene set activity analysis

Funding:

Availability: Free, Available for download, Freely available

Resource Name: AUCell

Resource ID: SCR_021327

License: GPL v3

Record Creation Time: 20220129T080354+0000

Record Last Update: 20250429T060054+0000

Ratings and Alerts

No rating or validation information has been found for AUCell.

No alerts have been found for AUCell.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 20 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

Tasis A, et al. (2024) Single-Cell Analysis of Bone Marrow CD8+ T Cells in Myeloid Neoplasms Reveals Pathways Associated with Disease Progression and Response to Treatment with Azacitidine. Cancer research communications, 4(12), 3067.

Szabó D, et al. (2024) A single dose of cocaine rewires the 3D genome structure of midbrain dopamine neurons. bioRxiv : the preprint server for biology.

Lu Y, et al. (2024) ALDH1A3-acetaldehyde metabolism potentiates transcriptional heterogeneity in melanoma. Cell reports, 43(7), 114406.

Luo M, et al. (2024) Integrated single-cell and spatial transcriptomics reveal microenvironment disruptions by androgen in mouse ovary. iScience, 27(10), 111028.

Golec DP, et al. (2024) A PI3K?-Foxo1-FasL signaling amplification loop rewires CD4+ T helper cell signaling, differentiation and epigenetic remodeling. bioRxiv : the preprint server for biology.

Zhou C, et al. (2024) Single-Cell Atlas of Human Ovaries Reveals The Role Of The Pyroptotic Macrophage in Ovarian Aging. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(4), e2305175.

Jiang Z, et al. (2024) Revealing the crucial roles of suppressive immune microenvironment in cardiac myxoma progression. Signal transduction and targeted therapy, 9(1), 193.

Yuan D, et al. (2024) Co-expression of immune checkpoints in glioblastoma revealed by single-nucleus RNA sequencing and spatial transcriptomics. Computational and structural biotechnology journal, 23, 1534.

Wang H, et al. (2024) Preclinical study and phase II trial of adapting low-dose radiotherapy to immunotherapy in small cell lung cancer. Med (New York, N.Y.), 5(10), 1237.

Wang W, et al. (2024) Identification of hypoxic macrophages in glioblastoma with therapeutic potential for vasculature normalization. Cancer cell, 42(5), 815.

Xie XP, et al. (2024) Glioblastoma functional heterogeneity and enrichment of cancer stem cells with tumor recurrence. Neuron, 112(24), 4017.

Abdel-Hafiz HA, et al. (2023) Single-cell profiling of murine bladder cancer identifies sexspecific transcriptional signatures with prognostic relevance. iScience, 26(9), 107703.

Li W, et al. (2023) Single-cell RNA-seq of heart reveals intercellular communication drivers of myocardial fibrosis in diabetic cardiomyopathy. eLife, 12.

Ning B, et al. (2023) Convergence of YAP/TAZ, TEAD and TP63 activity is associated with bronchial premalignant severity and progression. Journal of experimental & clinical cancer research : CR, 42(1), 116.

Turan T, et al. (2023) iBRIDGE: A Data Integration Method to Identify Inflamed Tumors from Single-cell RNA-Seq Data and Differentiate Cell Type-Specific Markers of Immune-Cell Infiltration. Cancer immunology research, 11(6), 732.

Dai Y, et al. (2023) Integrative Single-Cell and Bulk Transcriptomes Analyses Identify Intrinsic HNSCC Subtypes with Distinct Prognoses and Therapeutic Vulnerabilities. Clinical cancer research : an official journal of the American Association for Cancer Research, 29(15), 2845.

Cannell IG, et al. (2023) FOXC2 promotes vasculogenic mimicry and resistance to antiangiogenic therapy. Cell reports, 42(8), 112791.

Xie XP, et al. (2022) Quiescent human glioblastoma cancer stem cells drive tumor initiation, expansion, and recurrence following chemotherapy. Developmental cell, 57(1), 32.

Bibby JA, et al. (2022) Systematic single-cell pathway analysis to characterize early T cell activation. Cell reports, 41(8), 111697.

Cebrian-Silla A, et al. (2021) Single-cell analysis of the ventricular-subventricular zone reveals signatures of dorsal and ventral adult neurogenesis. eLife, 10.