

Resource Summary Report

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AUCell

RRID:SCR_021327

Type: Tool

Proper Citation

AUCell (RRID:SCR_021327)

Resource Information

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

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Description: Software R package to identify cells with active gene sets in single cell RNA-seq 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

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: 20260731T043055+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 40 mentions in open access literature.

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

Yao S, et al. (2025) SmartImpute is a targeted imputation framework for single-cell transcriptome data. Cell reports methods, 5(8), 101122.

Li Y, et al. (2025) Single-Cell Transcriptomic Landscape Deciphers Intratumoral Heterogeneity and Subtypes of Acral and Mucosal Melanomas. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(12), 2495.

Hu Y, et al. (2025) Accurate Transcription Factor Activity Inference to Decipher Cell Identity from Single-Cell Transcriptomic Data with MetaTF. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(23), e10745.

Williams AF, et al. (2025) DNA fragmentation factor B suppresses interferon to enable cancer persister cell regrowth. Nature cell biology, 27(12), 2143.

Hu W, et al. (2025) Single-cell RNA sequencing dissects the immunosuppressive signatures in Helicobacter pylori-infected human gastric ecosystem. Nature communications, 16(1), 3903.

Gong Z, et al. (2025) A single-cell transcriptome analysis reveals astrocyte heterogeneity and identifies CHI3L1 as a diagnostic biomarker in Parkinson's disease. Heliyon, 11(3), e42051.

Jiang X, et al. (2025) Depletion of Effector Regulatory T Cells Associates with Major Response to Induction Dual Immune Checkpoint Blockade. Cancer discovery, 15(8), 1569.

Yu B, et al. (2025) Neonatal-Inspired Reprogramming of Microglial Pan-Programmed Cell Death Enhances Regeneration in Adult Spinal Cord Injury. Research (Washington, D.C.), 8, 0759.

Chen J, et al. (2025) CD146+ CAFs mediate immunosuppression in gastric cancer via COL4A1: potential therapeutic targets. Journal for immunotherapy of cancer, 13(12).

Hatkevich T, et al. (2025) Gonadal sex and temperature independently influence germ cell differentiation and meiotic progression in Trachemys scripta. Proceedings of the National Academy of Sciences of the United States of America, 122(1), e2413191121.

Ju FE, et al. (2025) Integrative analysis of bulk and single-cell gene expression profiles to identify bone marrow mesenchymal cell heterogeneity and prognostic significance in multiple myeloma. Journal of translational medicine, 23(1), 659.

Costa-da-Silva AC, et al. (2025) Exhausted-like effector CD8 T cells mediate immune-stromal interactions at mucosal Chronic Graft-versus-Host Disease onset. *bioRxiv* : the preprint server for biology.

Allen AM, et al. (2025) A high-resolution atlas of the brain predicts lineage and birth order underlying neuronal identity. *Cell genomics*, 101103.

Gao Y, et al. (2025) Trilaciclib triggers a neutrophil-related immune response and sensitizes non-small cell lung cancer to anti-PD-1 therapy. *Cell reports. Medicine*, 6(11), 102434.

Xue HC, et al. (2025) A unified cell atlas of vascular plants reveals cell-type foundational genes and accelerates gene discovery. *Cell*.

Jayasinghe RG, et al. (2025) Single-cell transcriptomic profiling reveals diversity in human iNKT cells across hematologic tissues. *Cell reports*, 44(5), 115587.

Ligorio F, et al. (2025) Early downmodulation of tumor glycolysis predicts response to fasting-mimicking diet in triple-negative breast cancer patients. *Cell metabolism*, 37(2), 330.

Sharifi MN, et al. (2025) High-purity CTC RNA sequencing identifies prostate cancer lineage phenotypes prognostic for clinical outcomes. *Cancer discovery*, 15(5), 969.

Castresana-Aguirre M, et al. (2025) Computational decoding of cell-cycle phase effects on cancer hallmarks across breast cancer subtypes. *Breast cancer research : BCR*.

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.