

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 analysis software, data processing software, software application, software resource, software toolkit

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: 20260912T200022+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 56 mentions in open access literature.

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

Zhang L, et al. (2026) Retinoic Acid Reprograms Mast Cells Toward a Proinflammatory State to Enhance Antitumor Immunity. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(6), e09340.

Ratnawati H, et al. (2026) The ubiquitin-proteasome system is an important driver of EBV-associated nasopharyngeal carcinoma progression: a meta-analysis of transcriptomic data. *Scientific reports*, 16(1).

Yang J, et al. (2026) A Malignant Subpopulation of H2AFZ+ Cells Interacts with Myeloid Cells to Promote an Anti-inflammatory Microenvironment and Drive Hepatic Metastasis, Revealing an Immunotherapeutic Strategy for Pancreatic Ductal Adenocarcinoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(12), 2479.

Wang F, et al. (2026) SpaHE-Infil: A spatial heterogeneity framework for decoding TME infiltration from H&E-stained slides. *iScience*, 29(4), 115155.

Altendorf L, et al. (2026) Molecular changes during AT/RT progression associated with epithelial-mesenchymal transition and extracellular matrix changes. *Acta neuropathologica*, 152(1).

Wang Z, et al. (2026) Spatial multi-omics unveils the monoclonal origin, neuroendocrine plasticity, and microenvironment niches in combined small-cell lung cancer. *Cell reports. Medicine*, 7(4), 102741.

Zhang L, et al. (2026) Bcl11a orchestrates multilineage integrity in aging hematopoiesis by regulating multipotent progenitor fate decisions. *Cell reports*, 45(7), 117716.

Wang J, et al. (2026) The phosphatase DUSP2 constrains lymphoid remodeling and immunotherapy response in lung squamous carcinoma. *Molecular therapy : the journal of the American Society of Gene Therapy*, 34(7), 4279.

Xu X, et al. (2026) A Multistep Immune-Competent Genetically Engineered Mouse Model Reveals Phenotypic Plasticity in Uveal Melanoma. *Cancer research*, 86(15), 3666.

Zink A, et al. (2026) Pluripotent stem-cell-based screening uncovers sildenafil as a mitochondrial disease therapy. *Cell*, 189(6), 1656.

Gong Y, et al. (2026) Human retinal organoids functionally bridge a transected optic nerve in a rat model. *Cell stem cell*, 33(7), 1161.

Apostolov E, et al. (2026) Single-Cell and Spatial Transcriptomic Profiling Reveals Epithelial Functional States and Fibroblast Phenotypes in Hormone Therapy-Na⁺ve Localized Prostate Cancer. *Cancer research*, 86(8), 1836.

Clubb JD, et al. (2026) Armored Chimeric Antigen Receptor T-cell Therapy Targets Antigen-Heterogeneous Glioma. *Cancer research*, 86(15), 3781.

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.

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

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

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.

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