

Resource Summary Report

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SnapATAC

RRID:SCR_020981

Type: Tool

Proper Citation

SnapATAC (RRID:SCR_020981)

Resource Information

URL: <https://github.com/r3fang/SnapATAC>

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Description: Software package for analyzing scATAC-seq datasets.Used to dissect cellular heterogeneity in unbiased manner and map trajectories of cellular states. Can process data from up to million cells. Incorporates existing tools into comprehensive package for analyzing single cell ATAC-seq dataset.

Synonyms: Single Nucleus Analysis Pipeline for ATAC-seq

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

Defining Citation: [PMID:33637727](#)

Keywords: scATAC-seq datasets analysis, dissects cellular heterogeneity, cellular states, map trajectories

Funding: NCI K99 CA252020;
NIMH U19 MH114831;
UCSD School of Medicine

Availability: Free, Available for download, Freely available

Resource Name: SnapATAC

Resource ID: SCR_020981

Alternate URLs: <https://github.com/r3fang/SnapATAC>

License: GNU General Public License v3.0

Record Creation Time: 20220129T080353+0000

Ratings and Alerts

No rating or validation information has been found for SnapATAC.

No alerts have been found for SnapATAC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Hao G, et al. (2025) Topological identification and interpretation for single-cell epigenetic regulation elucidation in multi-tasks using scAGDE. *Nature communications*, 16(1), 1691.

Li X, et al. (2025) Multi-omics delineate growth factor network underlying exercise effects in an Alzheimer's mouse model. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 21(3), e70024.

Zhang W, et al. (2025) Molecular architecture of mesoderm cells across early to middle stage of human embryo development at single-cell resolution. *BMC molecular and cell biology*, 27(1), 3.

Ak Ç, et al. (2024) Multiplex imaging of localized prostate tumors reveals altered spatial organization of AR-positive cells in the microenvironment. *iScience*, 27(9), 110668.

Yuan J, et al. (2024) Single-nucleus multi-omics analyses reveal cellular and molecular innovations in the anterior cingulate cortex during primate evolution. *Cell genomics*, 4(12), 100703.

Li X, et al. (2024) Multi-omics delineate growth factor network underlying exercise effects in an Alzheimer's mouse model. *bioRxiv : the preprint server for biology*.

Kim JH, et al. (2023) Integrative analysis of single-cell RNA-seq and ATAC-seq reveals heterogeneity of induced pluripotent stem cell-derived hepatic organoids. *iScience*, 26(9), 107675.

Safi F, et al. (2022) Concurrent stem- and lineage-affiliated chromatin programs precede hematopoietic lineage restriction. *Cell reports*, 39(6), 110798.

Wang L, et al. (2022) A single-cell atlas of glioblastoma evolution under therapy reveals cell-intrinsic and cell-extrinsic therapeutic targets. *Nature cancer*, 3(12), 1534.

Michelson DA, et al. (2022) Thymic epithelial cells co-opt lineage-defining transcription factors to eliminate autoreactive T cells. *Cell*, 185(14), 2542.

Ranzoni AM, et al. (2021) Integrative Single-Cell RNA-Seq and ATAC-Seq Analysis of Human Developmental Hematopoiesis. *Cell stem cell*, 28(3), 472.

Schwartz GW, et al. (2021) TooManyPeaks identifies drug-resistant-specific regulatory elements from single-cell leukemic epigenomes. *Cell reports*, 36(8), 109575.

Gally F, et al. (2021) The MUC5B-associated variant rs35705950 resides within an enhancer subject to lineage- and disease-dependent epigenetic remodeling. *JCI insight*, 6(2).

Miao Z, et al. (2021) Single cell regulatory landscape of the mouse kidney highlights cellular differentiation programs and disease targets. *Nature communications*, 12(1), 2277.

Wimmers F, et al. (2021) The single-cell epigenomic and transcriptional landscape of immunity to influenza vaccination. *Cell*, 184(15), 3915.

Ziffra RS, et al. (2021) Single-cell epigenomics reveals mechanisms of human cortical development. *Nature*, 598(7879), 205.

Li Z, et al. (2021) Chromatin-accessibility estimation from single-cell ATAC-seq data with scOpen. *Nature communications*, 12(1), 6386.

Fang R, et al. (2021) Comprehensive analysis of single cell ATAC-seq data with SnapATAC. *Nature communications*, 12(1), 1337.

Rondini EA, et al. (2021) Single cell functional genomics reveals plasticity of subcutaneous white adipose tissue (WAT) during early postnatal development. *Molecular metabolism*, 53, 101307.

Bakken TE, et al. (2021) Comparative cellular analysis of motor cortex in human, marmoset and mouse. *Nature*, 598(7879), 111.