Resource Summary Report

Generated by NIF on Apr 17, 2025

SnapTools

RRID:SCR_018097
Type: Tool

Proper Citation

SnapTools (RRID:SCR_018097)

Resource Information

URL: https://github.com/r3fang/SnapTools

Proper Citation: SnapTools (RRID:SCR_018097)

Description: Software tool as module for working with snap files in Python. Snap files are designed for storing single nucleus ATAC-seq datasets.

Abbreviations: SnapTools

Synonyms: Single Nucleus Accessibility Profile Tools, Single nucleus accessibility profile Tools

Resource Type: alignment software, image analysis software, software application, data processing software, software resource

Keywords: Sequence, snap file, single nucleus, ATACseq dataset, data

Funding:

Availability: Free, Available for download, Freely available

Resource Name: SnapTools

Resource ID: SCR_018097

License: Apache License 2.0

Record Creation Time: 20220129T080338+0000

Record Last Update: 20250417T065626+0000

Ratings and Alerts

No rating or validation information has been found for SnapTools.

No alerts have been found for SnapTools.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Ye F, et al. (2024) Fast and flexible profiling of chromatin accessibility and total RNA expression in single nuclei using Microwell-seq3. Cell discovery, 10(1), 33.

Abraham E, et al. (2024) A Retinoic Acid:YAP1 signaling axis controls atrial lineage commitment. bioRxiv : the preprint server for biology.

Wang X, et al. (2024) Benchmarking Algorithms for Gene Set Scoring of Single-cell ATAC-seq Data. Genomics, proteomics & bioinformatics, 22(2).

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.

Okafor AE, et al. (2023) Single-cell chromatin accessibility profiling reveals a self-renewing muscle satellite cell state. The Journal of cell biology, 222(8).

Lu Z, et al. (2023) Tracking cell-type-specific temporal dynamics in human and mouse brains. Cell, 186(20), 4345.

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

Yao Z, et al. (2021) A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. Nature, 598(7879), 103.

Navidi Z, et al. (2021) simATAC: a single-cell ATAC-seq simulation framework. Genome biology, 22(1), 74.

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

Li YE, et al. (2021) An atlas of gene regulatory elements in adult mouse cerebrum. Nature,

598(7879), 129.

Malkani S, et al. (2020) Circulating miRNA Spaceflight Signature Reveals Targets for Countermeasure Development. Cell reports, 33(10), 108448.