

Resource Summary Report

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SnapTools

RRID:SCR_018097

Type: Tool

Proper Citation

SnapTools (RRID:SCR_018097)

Resource Information

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

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

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

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: 20260801T042813+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 14 mentions in open access literature.

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

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.

Abraham E, et al. (2025) A retinoic acid:YAP1 signaling axis controls atrial lineage commitment. *Cell reports*, 44(5), 115687.

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.

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*.

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

Abraham E, et al. (2024) A Retinoic Acid:YAP1 signaling axis controls atrial lineage commitment. *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.

Li YE, et al. (2021) An atlas of gene regulatory elements in adult mouse cerebrum. *Nature*, 598(7879), 129.

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

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

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