

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

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: 20260912T195857+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 16 mentions in open access literature.

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

Palmer CR, et al. (2026) Single-cell multiomic human brain atlas reveals regulatory drivers of cortical regionality. Nature communications, 17(1).

Abraham E, et al. (2026) YAP1 and QSER1 are key modulators of embryonic signaling pathways in the mammalian epiblast. EMBO reports, 27(9), 2369.

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.

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.

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.