

Resource Summary Report

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scATAC Pipeline

RRID:SCR_018919

Type: Tool

Proper Citation

scATAC Pipeline (RRID:SCR_018919)

Resource Information

URL:

https://broadinstitute.github.io/warp/docs/Pipelines/Single_Cell_ATAC_Seq_Pipeline/README

Proper Citation: scATAC Pipeline (RRID:SCR_018919)

Description: Pipeline developed in collaboration with Bing Ren lab and supports processing of BICCN single-cell/nucleus ATAC-seq datasets. Pipeline uses python module SnapTools to align and process paired reads in form of FASTQ files. Produces hdf5-structured Snap file that includes cell-by-bin count matrix. Final outputs also include GA4GH compliant aligned BAM and QC metrics.

Synonyms: single cell ATAC, scATAC

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

Keywords: Data, data processing, single nuclei, ATAC-seq datasets, paired reads processing, FASTQ file

Availability: Free, Available to download, Freely available

Resource Name: scATAC Pipeline

Resource ID: SCR_018919

Alternate URLs:

<https://github.com/broadinstitute/warp/tree/master/pipelines/skylab/scATAC>,
<https://app.terra.bio/#workspaces/brain-initiative-bcdc/scATAC>

Old URLs: <https://github.com/HumanCellAtlas/skylab/tree/master/pipelines/snap-atac>

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260821T194152+0000

Ratings and Alerts

No rating or validation information has been found for scATAC Pipeline.

No alerts have been found for scATAC Pipeline.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Hawrylycz M, et al. (2023) A guide to the BRAIN Initiative Cell Census Network data ecosystem. PLoS biology, 21(6), e3002133.

Ament SA, et al. (2023) The Neuroscience Multi-Omic Archive: a BRAIN Initiative resource for single-cell transcriptomic and epigenomic data from the mammalian brain. Nucleic acids research, 51(D1), D1075.