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

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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: software application, software resource, data processing software

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

Funding:

Availability: Free, Available to download, Freely available

Resource Name: scATAC Pipeline

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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

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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 <u>NIF</u>.

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.

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