

Resource Summary Report

Generated by [NIF](#) on Sep 1, 2026

Multiome Pipeline

RRID:SCR_024217

Type: Tool

Proper Citation

Multiome Pipeline (RRID:SCR_024217)

Resource Information

URL: https://broadinstitute.github.io/warp/docs/Pipelines/Multiome_Pipeline/README

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Description: Software open-source, cloud-optimized pipeline developed in collaboration with members of the BRAIN Initiative (BICCN and BICAN Sequencing Working Group) and SCORCH. It supports the processing of 10x 3' single-cell and single-nucleus gene expression (GEX) and chromatin accessibility (ATAC) data generated with the 10x Genomics Multiome assay.

Synonyms: , Multiome GEX and scATAC Pipeline, Multiome Pipeline

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

Keywords: data processing, 10x Genomics Multiome assay data, single cell data, single nucleus gene expression data, single cell chromatin accessibility data,

Availability: Free, Available for download, Freely available

Resource Name: Multiome Pipeline

Resource ID: SCR_024217

Old URLs: <https://github.com/broadinstitute/warp/tree/master/pipelines/skylab/multiome>

Record Creation Time: 20230829T050218+0000

Record Last Update: 20260829T182827+0000

Ratings and Alerts

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

No alerts have been found for Multiome Pipeline.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

, et al. (2026) A Community Standard Multispecies Cell Atlas of the Basal Ganglia. bioRxiv : the preprint server for biology.