

Resource Summary Report

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ENCODE ATAC-seq pipeline

RRID:SCR_023100

Type: Tool

Proper Citation

ENCODE ATAC-seq pipeline (RRID:SCR_023100)

Resource Information

URL: <https://github.com/ENCODE-DCC/atac-seq-pipeline>

Proper Citation: ENCODE ATAC-seq pipeline (RRID:SCR_023100)

Description: Software pipeline to process ATAC-Seq data. Used for automated end-to-end quality control and processing of ATAC-seq and DNase-seq data.

Resource Type: software toolkit, software resource

Keywords: automated end-to-end quality control and processing, ATAC-seq, DNase-seq data,

Availability: Free, Available for download, Freely available

Resource Name: ENCODE ATAC-seq pipeline

Resource ID: SCR_023100

License: MIT license

Record Creation Time: 20230104T050211+0000

Record Last Update: 20260810T040813+0000

Ratings and Alerts

No rating or validation information has been found for ENCODE ATAC-seq pipeline.

No alerts have been found for ENCODE ATAC-seq pipeline.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 155 mentions in open access literature.

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

Zhou C, et al. (2026) Decoding the cell intrinsic and extrinsic roles of PRC2 in early embryogenesis. *bioRxiv : the preprint server for biology*.

Keshishian H, et al. (2026) Integrative Multi-omics Analysis of the Human Skeletal Muscle Response to Endurance or Resistance Exercise: Findings from the Molecular Transducers of Physical Activity Consortium (MoTrPAC). *bioRxiv : the preprint server for biology*.

Camp SY, et al. (2026) Single-cell epigenetic profiling reveals a tumor-intrinsic interferon response program in ccRCC tied to poor prognosis and BAP1 loss. *Science advances*, 12(8), eadv5457.

Yang Q, et al. (2026) NFYA regulates two sequential genome-wide transcriptional activation events during oocyte to embryo transition. *bioRxiv : the preprint server for biology*.

Wang SK, et al. (2026) Single-cell multiome and enhancer connectome of human retinal pigment epithelium and choroid nominate causal variants in macular degeneration. *Cell reports*, 45(1), 116814.

Smith GR, et al. (2026) Multi-omic identification of key transcriptional regulatory programs during endurance exercise training in rats. *Nature communications*, 17(1).

Li B, et al. (2026) Reprogramming of neuronal genome function and phenotype by astrocytes. *bioRxiv : the preprint server for biology*.

Hossain M, et al. (2026) ChromAcS: an automated and flexible GUI for end-to-end reproducible ATAC-seq analysis across multiple species. *BMC bioinformatics*, 27(1).

Vr A, et al. (2026) Multi-omics Differential Inference for Functional Interpretation (MoDIFI): A Statistical Framework to Prioritize Cell Lines for Neurodevelopmental Variants. *bioRxiv : the preprint server for biology*.

Zhang Z, et al. (2026) Exercise modulation of the alternative splicing landscape in human tissues. *bioRxiv : the preprint server for biology*.

Tingvall-Gustafsson J, et al. (2026) B-lineage commitment is dependent on a reversible epigenetic switch. *Genes & development*, 40(3-4), 233.

Kong X, et al. (2026) OTX2 inhibits human pluripotent stem cell reprogramming toward 8-cell-like and morula-like states. *Nature communications*, 17(1), 1685.

Gjoni K, et al. (2026) Machine learning-predicted chromatin organization landscape across pediatric tumors. *Scientific reports*, 16(1).

Bonilauri B, et al. (2026) The long non-coding RNA landscape of endurance exercise training. *Molecular metabolism*, 108, 102358.

, et al. (2026) Multi-Omic, Multi-Tissue Responses to Acute Exercise in Sedentary Adults: Findings from the Molecular Transducers of Physical Activity Consortium. bioRxiv : the preprint server for biology.

Gunnell A, et al. (2025) NSD2-epigenomic reprogramming and maintenance of plasma cell phenotype in t(4;14) myeloma. *Oncotarget*, 16, 220.

Zhang J, et al. (2025) Dynamic properties of enhancer and promoter during DNA damage in hepatocellular carcinoma. *iScience*, 28(6), 112565.

Wang SK, et al. (2025) Single-cell multiome and enhancer connectome of human retinal pigment epithelium and choroid nominate pathogenic variants in age-related macular degeneration. bioRxiv : the preprint server for biology.

Tingvall-Gustafsson J, et al. (2025) Chromatin interaction-based annotation of regulatory elements reveals dynamic promoter-enhancer interactions in lymphocyte development. *iScience*, 28(7), 112855.

Sun S, et al. (2025) Single-cell multiomics analysis reveals CTCF as a key regulator of lung morphogenesis and progenitor maintenance. *Nature communications*, 16(1), 10729.