

Resource Summary Report

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ATACseqQC

RRID:SCR_023103

Type: Tool

Proper Citation

ATACseqQC (RRID:SCR_023103)

Resource Information

URL: <https://bioconductor.org/packages/ATACseqQC/>

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Description: Software R package for post alignment quality assessment of ATAC-seq data. Package also contains functions to preprocess aligned ATAC-seq data for subsequent peak calling.

Synonyms: Assays for Transposase-Accessible Chromatin using sequencing Quality Control

Resource Type: software resource, software toolkit

Defining Citation: [PMID:29490630](#)

Keywords: Assays for Transposase-Accessible Chromatin, sequencing, quality control, assaying chromatin accessibility, post alignment quality assessment, ATAC-seq data, preprocess aligned ATAC-seq data, subsequent peak calling,

Funding: Department of Molecular ;
Cell and Cancer Biology at UMass Medical School

Availability: Free, Available for download, Freely available

Resource Name: ATACseqQC

Resource ID: SCR_023103

License: GNU GPL v2

Record Creation Time: 20230105T050209+0000

Record Last Update: 20260905T133313+0000

Ratings and Alerts

No rating or validation information has been found for ATACseqQC.

No alerts have been found for ATACseqQC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 60 mentions in open access literature.

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

Chen X, et al. (2026) Stiff matrix-induced KRTAP2-3 expression suppresses ciliogenesis via actin tension-driven chromatin remodeling. *Cell death & disease*, 17(1).

Zhang Y, et al. (2026) Integration of ATAC-seq and RNA-seq reveals temperature-responsive regulatory regions in *Plasmodium falciparum* asexual stages. *Parasites & vectors*, 19(1).

Schulz K, et al. (2026) ERG is a regulator of dynamic and reversible endothelial plasticity. *Genome medicine*, 18(1).

Murphy DM, et al. (2026) IFN- γ -induced trained immunity enhances killing of priority pathogens in healthy and genetically vulnerable individuals. *JCI insight*, 11(6).

Cathell ML, et al. (2026) SoxB1-mediated chromatin remodeling promotes sensory neuron differentiation in planarians. *Genetics*, 232(3).

F Sousa J, et al. (2026) Comparative multi-omic analysis reveals conserved and derived mechanisms of fin and limb regeneration. *Nature communications*, 17(1).

Huang K, et al. (2026) Epigenetic analysis of sheep mycoplasma pneumonia and the effect of FOXF1 on *Mycoplasma ovipneumoniae* infection. *Virulence*, 17(1), 2665898.

Okamoto AS, et al. (2026) Modular genetic architecture underlies human hand and foot evolution. *Proceedings of the National Academy of Sciences of the United States of America*, 123(20), e2603297123.

Cathell ML, et al. (2025) SoxB1-Mediated Chromatin Remodeling Promotes Sensory Neuron Differentiation in Planarians. *bioRxiv : the preprint server for biology*.

Karagyozyova T, et al. (2025) HIRA defines early replication initiation zones independently of their genome compartment. *Nature communications*, 16(1), 9715.

Sharp JA, et al. (2025) Role of the SAF-A/HNRNPU ATPase and RGG domains in X chromosome inactivation, nuclear dynamics, transcription, splicing, and cell proliferation. *bioRxiv : the preprint server for biology*.

Zhang W, et al. (2025) NRF2-mediated persistent adaptation of oesophageal adenocarcinoma cells to HER2 inhibition. *Oncogene*, 44(33), 2929.

Frenette B, et al. (2025) HOXA5-driven transcriptional program in lung development. *Developmental biology*, 527, 191.

Kwon G, et al. (2025) Epigenomic landscapes define differential Janus kinases inhibitor sensitivity in IFN- γ -primed human macrophages. *iScience*, 28(5), 112502.

Barragán-Rosillo AC, et al. (2025) The role of DNA content in shaping chromatin architecture and gene expression. *The Plant journal : for cell and molecular biology*, 121(6), e70116.

Xu X, et al. (2025) 3D genome landscape of primary and metastatic colorectal carcinoma reveals the regulatory mechanism of tumorigenic and metastatic gene expression. *Communications biology*, 8(1), 365.

Matthews ER, et al. (2025) Anthracyclines induce global changes in cardiomyocyte chromatin accessibility that overlap with cardiovascular disease loci. *bioRxiv : the preprint server for biology*.

Sarbaugh DK, et al. (2025) The Chromatin Remodeler Protein CHD4 Cooperates With NKX2.2 to Regulate Pancreatic Beta Cell Integrity. *bioRxiv : the preprint server for biology*.

Van de Velde S, et al. (2025) Med14 phosphorylation shapes genomic response to GLP-1 Agonist. *bioRxiv : the preprint server for biology*.

Matthews ER, et al. (2025) Anthracyclines induce global changes in cardiomyocyte chromatin accessibility that overlap with cardiovascular disease loci. *PLoS genetics*, 21(10), e1011900.