

Resource Summary Report

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ArchR

RRID:SCR_020982

Type: Tool

Proper Citation

ArchR (RRID:SCR_020982)

Resource Information

URL: <https://www.archrproject.com/>

Proper Citation: ArchR (RRID:SCR_020982)

Description: Software R package for processing and analyzing single-cell ATAC-seq data. Used for integrative single cell chromatin accessibility analysis. Provides intuitive, user focused interface for complex single cell analysis, including doublet removal, single cell clustering and cell type identification, unified peak set generation, cellular trajectory identification, DNA element-to-gene linkage, transcription factor footprinting, mRNA expression level prediction from chromatin accessibility and multi-omic integration with single-cell RNA sequencing.

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

Defining Citation: [PMID:33633365](#)

Keywords: single-cell ATAC-seq data analysis, single-cell ATAC-seq data processing, single cell chromatin accessibility analysis, doublet removal, single cell clustering, cell type identification, unified peak set generation, cellular trajectory identification, transcription factor footprinting

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NIA K99 AG059918;
American Society of Hematology Scholar Award ;
International Collaborative Award ;
Defense Advanced Research Project Agency ;
Ray and Dagmar Dolby Family Fund ;

Stanford Cancer Institute-Goldman Sachs Foundation Cancer Research Award

Availability: Free, Available for download, Freely available

Resource Name: ArchR

Resource ID: SCR_020982

Alternate URLs: <https://github.com/GreenleafLab/ArchR>, <https://www.archrproject.com/>,
https://github.com/GreenleafLab/ArchR_2020

License: MIT License

Record Creation Time: 20220129T080353+0000

Record Last Update: 20260729T044504+0000

Ratings and Alerts

No rating or validation information has been found for ArchR.

No alerts have been found for ArchR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 358 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Leichter SM, et al. (2026) Polycomb misregulation in enterocytes drives tissue decline in the aging Drosophila intestine. Genome research, 36(1), 102.

Mout L, et al. (2025) Genetic and Epigenetic Reprogramming of Transposable Elements Drives ecDNA-Mediated Metastatic Prostate Cancer. bioRxiv : the preprint server for biology.

Xiao Y, et al. (2025) Tracking single-cell evolution using clock-like chromatin accessibility loci. Nature biotechnology, 43(5), 784.

Gur ER, et al. (2025) scATAC-seq generates more accurate and complete regulatory maps than bulk ATAC-seq. Scientific reports, 15(1), 3665.

Li J, et al. (2025) Organoid modeling reveals the tumorigenic potential of the alveolar progenitor cell state. The EMBO journal, 44(6), 1804.

Jin W, et al. (2025) Semi-automated IT-scATAC-seq profiles cell-specific chromatin accessibility in differentiation and peripheral blood populations. Nature communications,

16(1), 2635.

Nirgude S, et al. (2025) Single-nucleus multiomic analysis of Beckwith-Wiedemann syndrome liver reveals PPARA signaling enrichment and metabolic dysfunction. *Communications biology*, 8(1), 495.

Hamed AA, et al. (2025) Gliomagenesis mimics an injury response orchestrated by neural crest-like cells. *Nature*, 638(8050), 499.

Gerstner N, et al. (2025) Contrasting genetic predisposition and diagnosis in psychiatric disorders: A multi-omic single-nucleus analysis of the human OFC. *Science advances*, 11(10), eadq2290.

Okonechnikov K, et al. (2025) Oncogene aberrations drive medulloblastoma progression, not initiation. *Nature*, 642(8069), 1062.

Hammond NL, et al. (2025) Spatial gene regulatory networks driving cell state transitions during human liver disease. *EMBO molecular medicine*, 17(6), 1452.

Lin Z, et al. (2025) Androgen receptor promotes arachidonic acid metabolism and angiogenic microenvironment in AFP-negative hepatocellular carcinoma. *Nature communications*, 16(1), 6451.

Ma P, et al. (2025) Single-cell chromatin accessibility landscape profiling reveals the diversity of epigenetic regulation in the rat nervous system. *Scientific data*, 12(1), 140.

Hu R, et al. (2025) A Compound Screen Based on Isogenic hESC-Derived ? Cell Reveals an Inhibitor Targeting ZnT8-Mediated Zinc Transportation to Protect Pancreatic ? Cell from Stress-Induced Cell Death. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(20), e2413161.

Sur I, et al. (2025) Shared requirement for MYC upstream super-enhancer region in tissue regeneration and cancer. *Life science alliance*, 8(6).

Lobato-Moreno S, et al. (2025) Single-cell ultra-high-throughput multiplexed chromatin and RNA profiling reveals gene regulatory dynamics. *Nature methods*, 22(6), 1213.

Lu Z, et al. (2025) BIT: Bayesian Identification of Transcriptional regulators from epigenomics-based query region sets. *Nature communications*, 16(1), 4966.

Liu F, et al. (2025) BRD4 Signaling Maintains the Differentiated State of ? Cells. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(33), e05659.

Pereira MF, et al. (2025) YY1 mutations disrupt corticogenesis through a cell type specific rewiring of cell-autonomous and non-cell-autonomous transcriptional programs. *Molecular psychiatry*, 30(8), 3413.

Wang K, et al. (2025) Single-Cell Multi-omics Assessment of Spinal Cord Injury Blocking via Cerium-doped Upconversion Antioxidant Nanoenzymes. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(8), e2412526.