

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: data analysis software, data processing software, software application, software resource, 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

Funding: American Society of Hematology Scholar Award ;
Defense Advanced Research Project Agency ;
International Collaborative Award ;
NCI R35 CA209919;
NCI U2C CA233311;
NHGRI RM1 HG007735;
NHGRI UM1 HG009436;
NHGRI UM1 HG009442;
NIAID U19 AI057266;
NIA K99 AG059918;
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

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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 424 mentions in open access literature.

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

Wang BS, et al. (2026) Single-cell multiomic approaches define a gradual, spatially regulated epigenetic and transcriptional transition from embryonic to adult neural stem cells. Stem cell reports, 21(7), 102967.

Li R, et al. (2026) Single-nucleus multiple-organ chromatin accessibility landscape in the adult rat. GigaScience, 15.

Ren Y, et al. (2026) Cell type-specific gene regulatory atlas prioritizes drug targets and repurposable medicines in Alzheimer's disease. Genome research, 36(3), 645.

Lee H, et al. (2026) Multimodal antigenic escape to GPRC5D-targeted T cell engagers in multiple myeloma. Nature medicine, 32(3), 964.

Mu Z, et al. (2026) Impact of disease-associated chromatin accessibility QTLs across immune cell types and contexts. Cell genomics, 6(1), 101061.

Weir K, et al. (2026) Heterochronic transcription factor expression drives cone-dominant retina development in 13-lined ground squirrels. eLife, 14.

Furukawa T, et al. (2026) Patient-derived orthotopic xenograft models recapitulate the peritoneal dissemination of pancreatic cancer and delineate its transcriptional and regulatory programs. *Journal of experimental & clinical cancer research* : CR, 45(1).

Lorenzi V, et al. (2026) Spatiotemporal cellular map of the developing human reproductive tract. *Nature*, 650(8101), 428.

Meng J, et al. (2026) Single-cell spatial map of cis-regulatory elements for disease-related genes in the macaque cortex. *Nature communications*, 17(1).

Zhao Y, et al. (2026) Integrated Single-Cell Multi-Omics Analysis Reveals That a CD8+ TPex-Monocyte Interaction Axis Coordinates Immune Infiltration in Alzheimer's Disease. *International journal of molecular sciences*, 27(4).

Menon S, et al. (2026) Massive-scale single-nucleus multi-omics identifies novel rare noncoding drivers of Parkinson's disease. *bioRxiv* : the preprint server for biology.

Sun W, et al. (2026) CoCUT&Tag maps linked chromatin states at single-molecule, single-cell resolution. *bioRxiv* : the preprint server for biology.

Wang J, et al. (2026) BART-spatial unravels biologically significant transcriptional regulators from spatial omics data. *bioRxiv* : the preprint server for biology.

Liu V, et al. (2026) Clonal lineage tracing of innate immune cells in human cancer. *Cancer cell*, 44(7), 1509.

Li A, et al. (2026) Ganoderma lucidum spore powder enhances IFN- γ -mediated antiviral capacity of COVID-19 vaccine boosters revealed by single-cell multi-omics sequencing. *Journal of advanced research*, 85, 737.

Cooper E, et al. (2026) Childhood brain tumors instruct cranial hematopoiesis and immunotolerance. *Nature genetics*, 58(2), 317.

Cowley CJ, et al. (2026) Distinctive DNA sequence features define epigenetic longevity of inflammatory memory. *Science (New York, N.Y.)*, 391(6792), eadz6830.

Chen Z, et al. (2026) Single-cell chromatin accessibility landscape of cardiac non-myocytes identifies tissue repair program during heart regeneration. *NPJ Regenerative medicine*, 11(1).

Rathgeber AC, et al. (2026) Single-cell epigenetic and transcriptomic states across the continuum of monoclonal B cell lymphocytosis to chronic lymphocytic leukemia. *Genome biology*, 27(1).

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.