

Resource Summary Report

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Signac

RRID:SCR_021158

Type: Tool

Proper Citation

Signac (RRID:SCR_021158)

Resource Information

URL: <https://satijalab.org/signac/index.html>

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Description: Software framework for analysis of single cell chromatin data. Used for analysis, interpretation, and exploration of single cell chromatin datasets including datasets that co-assay DNA accessibility with gene expression, protein abundance, and mitochondrial genotype. Analysis of single-cell chromatin data including peak calling, quantification, quality control, dimension reduction, clustering, integration with single-cell gene expression datasets, DNA motif analysis, and interactive visualization.

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

Defining Citation: [DOI:10.1101/2020.11.09.373613](https://doi.org/10.1101/2020.11.09.373613)

Keywords: Single cell chromatin data, single cell multimodal analysis, peak calling, quantification, quality control, dimension reduction, clustering, integration with single-cell gene expression datasets, DNA motif analysis, interactive visualization

Availability: Free, Available for download, Freely available

Resource Name: Signac

Resource ID: SCR_021158

Alternate URLs: <https://CRAN.R-project.org/package=Signac>

License: MIT + file LICENSE

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260821T194203+0000

Ratings and Alerts

No rating or validation information has been found for Signac.

No alerts have been found for Signac.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 90 mentions in open access literature.

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

Roberts RR, et al. (2026) Gene regulatory programs underlying diversification of facial ligaments and tendons in zebrafish. *Development (Cambridge, England)*, 153(2).

Wang K, et al. (2026) Ontogeny Dictates Oncogenic Potential, Lineage Hierarchy, and Therapy Response in Pediatric Leukemia. *Cancer discovery*, 16(3), 541.

Nguyen TDT, et al. (2026) Pan-Cancer Single-Cell RNA Sequencing Analysis Refines Multi-Origin Monocyte and Macrophage Lineages. *Cancer immunology research*, 14(2), 350.

Fan H, et al. (2026) Single-cell transcriptomic and chromatin accessibility atlas of peripheral blood mononuclear cells reveals immune cell heterogeneity and breed-specific characteristics in Duroc and Meishan pigs. *BMC genomics*, 27(1).

Pastinen T, et al. (2026) Evolving epigenomics of immune cells at single-nucleus resolution in children en route to type 1 diabetes. *Nature communications*, 17(1).

Sussman JH, et al. (2026) A longitudinal single-cell and spatial multiomic atlas of pediatric high-grade glioma. *Cell reports. Medicine*, 7(5), 102766.

López-Fuentes E, et al. (2026) Epigenetic and Transcriptional Programs Define Osteosarcoma Subtypes and Establish Targetable Vulnerabilities. *Cancer discovery*, 16(2), 296.

Adams NM, et al. (2026) Chromatin-mediated anticipatory control of type I interferon production in plasmacytoid dendritic cells. *Immunity*, 59(2), 270.

Al Souz J, et al. (2026) Organ injury in systemic autoimmunity is mediated by stem-like CD8+ T cells arising from tissue-draining lymph nodes. *Immunity*, 59(6), 1667.

Hilgart E, et al. (2026) DNA Methylation Stochasticity Is Linked to Transcriptional Variability and Convergent Epigenetic Disruption across Genetic Subtypes of Acute Myeloid Leukemia. *Cancer research*, 86(13), 3325.

Foidart P, et al. (2026) Whole-genome doubling drives immune evasion by silencing antigen presentation. *Cancer cell*, 44(7), 1418.

Soltys V, et al. (2026) Flexible and high-throughput simultaneous profiling of gene expression and chromatin accessibility in single cells. *eLife*, 15.

Katko A, et al. (2026) Gene regulatory network determinants of rapid recall in human memory CD4⁺ T cells. *Cell reports*, 45(4), 117103.

Cao C, et al. (2025) Blocking CXCR4⁺ CD4⁺ T cells reprograms Treg-mediated immunosuppression via modulating the Rho-GTPase/NF- κ B signaling axis. *Genome medicine*, 17(1), 85.

Hu Z, et al. (2025) CellWalker2: Multi-omic discovery using hierarchical cell type relationships. *Cell genomics*, 5(7), 100886.

Chen Z, et al. (2025) reDA: differential abundance testing on scATAC-seq data using random walk with restart. *Bioinformatics (Oxford, England)*, 41(10).

Ortiz A, et al. (2025) Cell-type-specific roles of FOXP1 in the excitatory neuronal lineage during early neocortical murine development. *Cell reports*, 44(3), 115384.

Pucella JN, et al. (2025) Tonic type I interferon signaling optimizes the antiviral function of plasmacytoid dendritic cells. *Nature immunology*, 26(11), 1946.

Kaur N, et al. (2025) Specification of claustroramygdalar and palaeocortical neurons and circuits. *Nature*, 638(8050), 469.

Pastinen T, et al. (2025) Evolving epigenomics of immune cells in type 1 diabetes at single nuclei resolution. *Research square*.