

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

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

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: 20260728T043616+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 75 mentions in open access literature.

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

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.

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).

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

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.

Kaur N, et al. (2025) Specification of claustrum-amygdala and paleocortical neurons and circuits. *Nature*, 638(8050), 469.

Garnica J, et al. (2025) BLIMP-1-dependent differentiation of T follicular helper cells into Foxp3+ T regulatory type 1 cells. *Frontiers in immunology*, 16, 1519780.

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

Han Y, et al. (2025) A Human Immuno-Lung Organoid Model to Study Macrophage-Mediated Lung Cell Senescence Upon SARS-CoV-2 Infection. *Advanced science (Weinheim, Baden-Wuerttemberg, Germany)*, 12(36), e03932.

Wang K, et al. (2025) Ontogeny Dictates Oncogenic Potential, Lineage Hierarchy, and Therapy Response in Pediatric Leukemia. *bioRxiv : the preprint server for biology*.

Du C, et al. (2025) Multiomic analyses on the contribution of transposable elements to the cis-regulatory landscape of different types of immune cells. *BMC genomics*, 26(1), 1077.

Reid MM, et al. (2025) Human brain vascular multi-omics elucidates disease-risk associations. *Neuron*.

Bhattacharya S, et al. (2025) Intestinal secretory differentiation reflects niche-driven phenotypic and epigenetic plasticity of a common signal-responsive terminal cell. *Cell stem cell*, 32(6), 952.

Ver Heul AM, et al. (2025) RAG suppresses group 2 innate lymphoid cells. *eLife*, 13.

Stomper J, et al. (2025) Sex differences in DNMT3A-mutant clonal hematopoiesis and the effects of estrogen. *Cell reports*, 44(4), 115494.

Köhne M, et al. (2025) *Satb1* directs the differentiation of TH17 cells through suppression of IL-2 expression. *Cell reports*, 44(7), 115866.

Wu Y, et al. (2025) Neurodevelopmental hijacking of oligodendrocyte lineage programs drives glioblastoma infiltration. *Developmental cell*.

Gao Y, et al. (2025) Multimodal analyses reveal genes driving electrophysiological maturation of neurons in the primate prefrontal cortex. *Neuron*, 113(15), 2490.

Cao C, et al. (2024) CXCR4 orchestrates the TOX-programmed exhausted phenotype of CD8⁺ T cells via JAK2/STAT3 pathway. *Cell genomics*, 4(10), 100659.

Yuan J, et al. (2024) Single-nucleus multi-omics analyses reveal cellular and molecular innovations in the anterior cingulate cortex during primate evolution. *Cell genomics*, 4(12), 100703.