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

Proper Citation: Signac (RRID:SCR_021158)

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

Defining Citation: DOI: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

Funding:

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: 20250329T061422+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 56 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Littleton SH, et al. (2024) Variant-to-function analysis of the childhood obesity chr12q13 locus implicates rs7132908 as a causal variant within the 3' UTR of FAIM2. Cell genomics, 4(5), 100556.

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.

Jessa S, et al. (2024) FOXR2 targets LHX6+/DLX+ neural lineages to drive CNS neuroblastoma. Cancer research.

Hu Z, et al. (2024) CellWalker2: multi-omic discovery of hierarchical cell type relationships and their associations with genomic annotations. bioRxiv : the preprint server for biology.

Aggarwal A, et al. (2024) Distinct melanocyte subpopulations defined by stochastic expression of proliferation or maturation programs enable a rapid and sustainable pigmentation response. PLoS biology, 22(8), e3002776.

Henon C, et al. (2024) Single-cell multiomics profiling reveals heterogeneous transcriptional programs and microenvironment in DSRCTs. Cell reports. Medicine, 5(6), 101582.

Ortiz A, et al. (2024) Cell type specific roles of FOXP1 during early neocortical murine development. bioRxiv : the preprint server for biology.

Dorgau B, et al. (2024) Deciphering the spatiotemporal transcriptional and chromatin accessibility of human retinal organoid development at the single-cell level. iScience, 27(4), 109397.

Chen PB, et al. (2024) Complementation testing identifies genes mediating effects at quantitative trait loci underlying fear-related behavior. Cell genomics, 4(5), 100545.

Gordon WE, et al. (2024) Integrative single-cell characterization of a frugivorous and an insectivorous bat kidney and pancreas. Nature communications, 15(1), 12.

Li Y, et al. (2024) Single-Cell Transcriptome Atlas and Regulatory Dynamics in Developing Cotton Anthers. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(3), e2304017.

Feng AC, et al. (2024) The transcription factor NF-?B orchestrates nucleosome remodeling during the primary response to Toll-like receptor 4 signaling. Immunity, 57(3), 462.

Singh PNP, et al. (2024) Transcription factor dynamics, oscillation, and functions in human enteroendocrine cell differentiation. Cell stem cell, 31(7), 1038.

Cai S, et al. (2023) Integrative single-cell RNA-seq and ATAC-seq analysis of myogenic differentiation in pig. BMC biology, 21(1), 19.

Bagheri M, et al. (2023) Pharmacological Induction of mesenchymal-epithelial transition chemosensitizes breast cancer cells and prevents metastatic progression. bioRxiv : the preprint server for biology.

Littleton SH, et al. (2023) Variant-to-function analysis of the childhood obesity chr12q13 locus implicates rs7132908 as a causal variant within the 3' UTR of FAIM2. bioRxiv : the preprint server for biology.

Krienen FM, et al. (2023) A marmoset brain cell census reveals regional specialization of cellular identities. Science advances, 9(41), eadk3986.

Noack F, et al. (2023) Joint epigenome profiling reveals cell-type-specific gene regulatory programmes in human cortical organoids. Nature cell biology, 25(12), 1873.

Fan H, et al. (2023) Single-cell chromatin accessibility profiling of acute myeloid leukemia reveals heterogeneous lineage composition upon therapy-resistance. Communications biology, 6(1), 765.