

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

SCENIC+

RRID:SCR_026702

Type: Tool

Proper Citation

SCENIC+ (RRID:SCR_026702)

Resource Information

URL: <https://github.com/aertslab/scenicplus>

Proper Citation: SCENIC+ (RRID:SCR_026702)

Description: Software Python package to build gene regulatory networks using combined or separate single-cell gene expression and single-cell chromatin accessibility (scATAC-seq) data. Used for inferring and analyzing enhancer-driven gene regulatory networks using single-cell multiomic data.

Resource Type: software toolkit, source code, software resource

Defining Citation: [PMID:37443338](#)

Keywords: build gene regulatory networks, inferring and analyzing enhancer-driven gene regulatory networks, single-cell multiomic data,

Funding: Foundation Against Cancer ;
ERC Consolidator Grant ;
ERC Proof of Concept

Availability: Free, Available for download, Freely available

Resource Name: SCENIC+

Resource ID: SCR_026702

License URLs: <https://github.com/aertslab/scenicplus?tab=License-1-ov-file#readme>

Record Creation Time: 20250404T060341+0000

Record Last Update: 20260815T042921+0000

Ratings and Alerts

No rating or validation information has been found for SCENIC+.

No alerts have been found for SCENIC+.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 25 mentions in open access literature.

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

Nirgude S, et al. (2026) Beckwith-Wiedemann syndrome multiomic analysis of hepatoblastoma uncovers unique tumour heterogeneity and cellular landscapes, including transition cells leading to tumour formation. BJC reports, 4(1).

Palmer CR, et al. (2026) Single-cell multiomic human brain atlas reveals regulatory drivers of cortical regionality. Nature communications, 17(1).

Kim D, et al. (2026) Discovery of key regulators in classical monocyte phenotypes linked to COVID-19 severity using single-cell multi-omics sequencing. iScience, 29(3), 114849.

Kim Y, et al. (2026) Single-nucleus multi-omics delineates distinct epigenetic programs associated with tumor progression in lung adenocarcinoma. Clinical epigenetics, 18(1).

Kempynck N, et al. (2026) CREsted: modeling genomic and synthetic cell-type-specific enhancers across tissues and species. Nature methods, 23(5), 946.

Zhang M, et al. (2026) A pipeline for single-cell chromatin accessibility data analysis. Blood science (Baltimore, Md.), 8(1), e00259.

Sarropoulos I, et al. (2026) The evolution of gene regulation in mammalian cerebellum development. Science (New York, N.Y.), 391(6784), eadw9154.

Stevens HP, et al. (2026) Architectural fragility of gene regulatory networks underlies hematopoietic stem cell aging. bioRxiv : the preprint server for biology.

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

Kim SK, et al. (2026) Human-specific features of the cerebellum and ZP2-regulated synapse development. Cell, 189(6), 1802.

Liu D, et al. (2025) A stem cell knockout village reveals lineage rewiring and a non-canonical islet cell fate in monogenic diabetes. bioRxiv : the preprint server for biology.

Yoo J, et al. (2025) Establishing a continuum of cell types in the visual cortex. bioRxiv : the preprint server for biology.

Smela MP, et al. (2025) Initiation of meiosis from human iPSCs under defined conditions through identification of regulatory factors. *Science advances*, 11(33), eadu0384.

Moore H, et al. (2025) Stimulation modulates cell assemblies linked with gene networks in the human temporal cortex ex vivo. *bioRxiv* : the preprint server for biology.

Keshavarzian T, et al. (2025) Prostate cancer cells converge to an inflammatory-like state upon metastatic dissemination. *Nature communications*, 16(1), 11339.

Kim DW, et al. (2025) Decoding gene networks controlling hypothalamic and prethalamic neuron development. *Cell reports*, 44(6), 115858.

Leonard R, et al. (2025) Single-nuclei multiomics analysis identifies abnormal cardiomyocytes in a murine model of cardiac development. *Nature communications*, 16(1), 6947.

O'Leary TS, et al. (2025) Single-nuclei multiome ATAC and RNA sequencing reveals the molecular basis of thermal plasticity in *Drosophila melanogaster* embryos. *bioRxiv* : the preprint server for biology.

Kim DW, et al. (2025) Decoding Gene Networks Controlling Hypothalamic and Prethalamic Neuron Development. *bioRxiv* : the preprint server for biology.

Krauter D, et al. (2025) Spatial organization, chromatin accessibility and gene-regulatory programs defining mouse sensory neurons. *Communications biology*, 8(1), 908.