

Resource Summary Report

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SCENIC

RRID:SCR_017247

Type: Tool

Proper Citation

SCENIC (RRID:SCR_017247)

Resource Information

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

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Description: Software R package as single cell regulatory network inference and clustering. Used for simultaneous gene regulatory network reconstruction and cell state identification from single cell RNA-seq data.

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

Defining Citation: [PMID:28991892](#)

Keywords: single, cell, regulatory, network, inference, clustering, simultaneous, gene, reconstruction, single, RNA-seq, data

Funding: ERC Consolidator Grant ;
Foundation Against Cancer ;
Special Research Fund (BOF) KU Leuven ;
The Research Foundation - Flanders

Availability: Free, Available for download, Freely available

Resource Name: SCENIC

Resource ID: SCR_017247

Alternate URLs: <https://aertslab.org/#scenic>

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260829T182847+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 161 mentions in open access literature.

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

Wang X, et al. (2026) An insulin receptor activity surge in follicle cells drives vitellogenesis by upregulating CrebA. EMBO reports, 27(3), 748.

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.

Han Z, et al. (2026) Single-Nucleus Transcriptome Reveals Cellular Heterogeneity and Transcriptional Response to Heat Stress in Skeletal Muscle. Journal of cachexia, sarcopenia and muscle, 17(1), e70217.

Zhang H, et al. (2026) Insights from pooled CRISPRi single-cell screens in K562 cells reveal gene functions, regulatory networks, and highlight opportunities and limitations. BMC genomics, 27(1).

Wang R, et al. (2026) IL-1 β /EPAS1-Associated Ferroptotic Stress Impairs Skeletal Stem/Progenitor Cell Function in Inflammation-Associated Fracture Nonunion. Current issues in molecular biology, 48(6).

Baurès M, et al. (2026) Targeting pre-existing club-like cells in prostate cancer potentiates androgen deprivation therapy. EMBO molecular medicine, 18(3), 943.

Lyu J, et al. (2026) A convenient single-cell assay for the newly synthesized transcriptome reveals FLI1 regulon downregulation during T cell activation. Cell reports methods, 6(1), 101252.

Leshem R, et al. (2026) A cell atlas of the developing human outflow tract of the heart and its adult aortic valve derivatives. eLife, 14.

Wang S, et al. (2026) A pan-cancer single-cell transcriptomic atlas of human bone metastases. Cell reports. Medicine, 7(2), 102583.

Huang Y, et al. (2026) cGAS-mediated IFN-I signaling contributes to disease progression in drug-refractory epilepsy. bioRxiv : the preprint server for biology.

Zhao ZH, et al. (2026) Multi-omics atlas of ovarian cellular and molecular responses to diabetes. *Molecular metabolism*, 103, 102307.

Wang P, et al. (2026) *Helicobacter pylori*-induced PPFIA4 orchestrates immune network-promoting gastritis and gastric bacterial colonization. *The Journal of clinical investigation*, 136(9).

Xu X, et al. (2026) A Multistep Immune-Competent Genetically Engineered Mouse Model Reveals Phenotypic Plasticity in Uveal Melanoma. *Cancer research*, 86(15), 3666.

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

Arya A, et al. (2025) Navigating single-cell RNA-sequencing: protocols, tools, databases, and applications. *Genomics & informatics*, 23(1), 13.

Ma T, et al. (2025) Pan-Cancer Analyses Refine the Single-Cell Portrait of Tumor-Infiltrating Dendritic Cells. *Cancer research*, 85(19), 3596.

James A, et al. (2025) Elevation of master autophagy regulator Tfeb in osteoblast lineage cells increases bone mass and strength. *JCI insight*, 10(17).

Lee D, et al. (2025) Multi-omics single-cell analysis reveals key regulators of HIV-1 persistence and aberrant host immune responses in early infection. *eLife*, 14.

Hua Y, et al. (2025) SeuratExtend: streamlining single-cell RNA-seq analysis through an integrated and intuitive framework. *GigaScience*, 14.

Xiao X, et al. (2025) Single-cell transcriptomic profiling reveals cell type heterogeneity between HFpEF and HFrEF. *Communications biology*, 8(1), 1436.