

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

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: 20260805T044406+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 134 mentions in open access literature.

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

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

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.

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

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).

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

Almeida Machado Costa C, et al. (2025) Single-cell transcriptomics reveals stepwise transformation of epithelial cells into Non-Professional Phagocytes. PLoS genetics, 21(12), e1011953.

Guo Q, et al. (2025) Epithelial characteristics of ovarian clear cell carcinoma at single-cell resolution. Communications biology, 8(1), 1156.

Zhai M, et al. (2025) TEAD1-Mediated Trans-Differentiation of Vascular Smooth Muscle Cells into Fibroblast-Like Cells Contributes to the Stabilization and Repair of Disrupted Atherosclerotic Plaques. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(5), e2407408.

Neo SY, et al. (2025) Atypical memory B cells acquire Breg phenotypes in hepatocellular carcinoma. JCI insight, 10(7).

Ji P, et al. (2025) Single-cell delineation of the microbiota-gut-brain axis: Probiotic intervention in Chd8 haploinsufficient mice. Cell genomics, 5(2), 100768.

Bui HV, et al. (2025) White and brown adipose tissue share a convergent fibro-adipogenic progenitor population. *EMBO reports*, 26(22), 5612.

He F, et al. (2025) Integrative analysis of Ewing's sarcoma reveals that the MIF-CD74 axis is a target for immunotherapy. *Cell communication and signaling : CCS*, 23(1), 23.

Lv W, et al. (2025) SLC38A1 and STX11 are mitochondria-related biomarkers associated with immune infiltration in osteoarthritis. *Frontiers in genetics*, 16, 1585775.

Zhao B, et al. (2025) Integrative single-cell transcriptomics of sheep ovarian development reveals dynamic transcriptional programs relevant to reproductive traits. *iScience*, 28(5), 112422.

Yang Y, et al. (2025) Cross-modal contrastive learning decodes developmental regulatory features through chromatin potential analysis. *GigaScience*, 14.

Keller F, et al. (2025) Differentiation-associated ISG expression of NK cells in chronic viral infection. *iScience*, 28(9), 113216.

Castresana-Aguirre M, et al. (2025) Computational decoding of cell-cycle phase effects on cancer hallmarks across breast cancer subtypes. *Breast cancer research : BCR*.

Li X, et al. (2025) The Dynamically Evolving Cell States and Ecosystem from Benign Nevi to Melanoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(12), 2478.

Jones J, et al. (2025) Gut commensal microbiota drive tailored macrophage responses. *Cell reports*, 44(8), 116157.