Resource Summary Report

Generated by NIF on Sep 2, 2026

scran

RRID:SCR_016944
Type: Tool

Proper Citation

scran (RRID:SCR_016944)

Resource Information

URL: https://bioconductor.org/packages/release/bioc/html/scran.html

Proper Citation: scran (RRID:SCR_016944)

Description: Software package for low-level analyses of single-cell RNA-seq data. Used for quality control, data exploration and normalization, cell cycle phase assignment, identification of highly variable and correlated genes, clustering into subpopulations and marker gene detection.

Abbreviations: SCRAN

Synonyms: Single-Cell Rna-seq data ANalysis, SCRAN

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

Defining Citation: PMID:27909575

Keywords: low, level, analysis, scRNA-seq, data, normalization, cell, cycle, phase, gene, variable, correlation, cluster, subpopulation, marker, bio.tools

Funding: Cancer Research UK ;
EMBL ;
National Health and Medical Research Council of Australia

Availability: Free, Available for download, Freely available

Resource Name: scran

Resource ID: SCR_016944

Alternate IDs: biotools:scran

Alternate URLs: https://bio.tools/scran

License: GPL 3

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260829T182553+0000

Ratings and Alerts

No rating or validation information has been found for scran.

No alerts have been found for scran.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 100 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Salvidge W, et al. (2026) Lineage priming and cell type proportioning depends on the interplay between stochastic and deterministic factors. eLife, 14.

Laubreton D, et al. (2026) Transient tumor exposure induces persistent functional defects in memory CD8+ T cells. iScience, 29(5), 115556.

Branco MA, et al. (2026) Modeling embryonic heart vascular plexus development and sympathetic innervation on a human heart organoid. iScience, 29(3), 115071.

Sierra-Rodero B, et al. (2026) Decoding B-cell Signatures of Complete Pathologic Response to Perioperative Chemoimmunotherapy in Non-Small Cell Lung Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(8), 1499.

Bardet PMR, et al. (2026) Multiomics immune profiling of a patient-relevant orthotopic lung cancer model using SEPARATE-Seq. Nature communications, 17(1).

Fang R, et al. (2026) PD-L1 on Tumor-Derived Extracellular Vesicles Induces CD8+ T Cell Terminal Exhaustion and Mediates Anti-PD-1 Resistance in Head and Neck Squamous Cell Carcinoma. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(4), e16348.

Kim H, et al. (2026) Myelin antigen capture in the CNS by B cells expressing EBV latent membrane protein 1 leads to demyelinating lesion formation. Cell.

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.

Richman CM, et al. (2025) Carbonic Anhydrase Inhibition Sensitizes Group 3 Medulloblastoma to Radiotherapy. Cancer research, 85(19), 3737.

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

Yata T, et al. (2025) Contribution of germline and somatic mutations to risk of neuromyelitis optica spectrum disorder. Cell genomics, 5(3), 100776.

Kuett L, et al. (2025) Distant Metastases of Breast Cancer Resemble Primary Tumors in Cancer Cell Composition but Differ in Immune Cell Phenotypes. Cancer research, 85(1), 15.

Priego N, et al. (2025) TIMP1 Mediates Astrocyte-Dependent Local Immunosuppression in Brain Metastasis Acting on Infiltrating CD8+ T Cells. Cancer discovery, 15(1), 179.

Ali M, et al. (2025) Multi-cohort cerebrospinal fluid proteomics identifies robust molecular signatures across the Alzheimer disease continuum. Neuron, 113(9), 1363.

Zhao H, et al. (2025) Single-Cell Analysis of Posttranslational Modifications Identifies Immunosuppressive Macrophage Subtypes in the HBV-Positive Hepatocellular Carcinoma Microenvironment. Cancer immunology research, 13(8), 1303.

Chandramohan D, et al. (2025) Dual role of Oct4 and Sox2 in controlling the developmental capacity and timing of tissue morphogenesis in the embryonic lineage. Developmental cell.

Oh MS, et al. (2025) Characteristics of a CCL21 Gene-Modified Dendritic Cell Vaccine Utilized for a Clinical Trial in Non-Small Cell Lung Cancer. Molecular cancer therapeutics, 24(2), 286.

Iyer DP, et al. (2024) mTOR activity paces human blastocyst stage developmental progression. Cell, 187(23), 6566.

Khetan N, et al. (2024) Single-cell RNA sequencing algorithms underestimate changes in transcriptional noise compared to single-molecule RNA imaging. Cell reports methods, 4(12), 100933.

Jakobsen NA, et al. (2024) Selective advantage of mutant stem cells in human clonal hematopoiesis is associated with attenuated response to inflammation and aging. Cell stem cell, 31(8), 1127.