Resource Summary Report

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scater

RRID:SCR_015954
Type: Tool

Proper Citation

scater (RRID:SCR_015954)

Resource Information

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

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Description: Software toolkit for doing various analyses of single-cell RNA-seq gene expression data, with a focus on quality control. This package facilitates pre-processing, quality control, normalization and visualization of scRNA-seq data.

Synonyms: scater (single-cell analysis toolkit for gene expression data in R)

Resource Type: software application, software toolkit, data visualization software, data analysis software, data processing software, sequence analysis software, software resource

Keywords: scRNA-seq, rna, rnaseq, single, cell, analysis, gene, expression, quality, control, preprocessing, normalization, visualization, r, bio.tools

Funding: National Health and Medical Research Council of Australia APP1112681;
European Molecular Biology Laboratory ;
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United Kingdom Medical Research Council ;
Oxford Single Cell Biology Consortium

Availability: Free, Available for download

Resource Name: scater

Resource ID: SCR_015954

Alternate IDs: biotools:scater

Alternate URLs: https://bioconductor.org/packages/scater/, https://bio.tools/scater

License: GPL

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Ratings and Alerts

No rating or validation information has been found for scater.

No alerts have been found for scater.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 157 mentions in open access literature.

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

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.

Gallaccio G, et al. (2024) Protocol to characterize immune cell subpopulations in cerebrospinal fluid of patients with neuroinflammatory diseases using mass cytometry. STAR protocols, 5(2), 103038.

Billiet L, et al. (2024) ThymoSpheres culture: A model to study human polyclonal unconventional T cells. European journal of immunology, 54(12), e2451265.

Valdeolivas A, et al. (2024) Profiling the heterogeneity of colorectal cancer consensus molecular subtypes using spatial transcriptomics. NPJ precision oncology, 8(1), 10.

Bai H, et al. (2024) Progressive senescence programs induce intrinsic vulnerability to aging-related female breast cancer. Nature communications, 15(1), 5154.

Bonder MJ, et al. (2024) scEpiAge: an age predictor highlighting single-cell ageing heterogeneity in mouse blood. Nature communications, 15(1), 7567.

Zheng D, et al. (2024) snRNA-seq analysis in multinucleated myogenic FSHD cells identifies heterogeneous FSHD transcriptome signatures associated with embryonic-like program activation and oxidative stress-induced apoptosis. Human molecular genetics, 33(3), 284.

Hai L, et al. (2024) A clinically applicable connectivity signature for glioblastoma includes the tumor network driver CHI3L1. Nature communications, 15(1), 968.

Vu Manh TP, et al. (2024) SARS-CoV2 infection in whole lung primarily targets macrophages that display subset-specific responses. Cellular and molecular life sciences : CMLS, 81(1), 351.

Gonzalez Galofre ZN, et al. (2024) Runx1+ vascular smooth muscle cells are essential for hematopoietic stem and progenitor cell development in vivo. Nature communications, 15(1), 1653.

Gillespie ER, et al. (2024) Single-cell RNA sequencing reveals peripheral blood leukocyte responses to spinal cord injury in mice with humanised immune systems. Journal of neuroinflammation, 21(1), 63.

Wong MMK, et al. (2024) The neocortical infrastructure for language involves region-specific patterns of laminar gene expression. Proceedings of the National Academy of Sciences of the United States of America, 121(34), e2401687121.

Ye X, et al. (2024) Transcriptional signature of durable effector T cells elicited by a replication defective HCMV vaccine. NPJ vaccines, 9(1), 70.

Duijvelaar E, et al. (2024) Longitudinal plasma proteomics reveals biomarkers of alveolar-capillary barrier disruption in critically ill COVID-19 patients. Nature communications, 15(1), 744.

Hanhart D, et al. (2024) ScLinear predicts protein abundance at single-cell resolution. Communications biology, 7(1), 267.

Popp JM, et al. (2024) Cell type and dynamic state govern genetic regulation of gene expression in heterogeneous differentiating cultures. Cell genomics, 4(12), 100701.

Kiourtis C, et al. (2024) Hepatocellular senescence induces multi-organ senescence and dysfunction via TGF?. Nature cell biology, 26(12), 2075.

Zhou R, et al. (2024) Involvement of S100A6/S100A11 in T-Cell Immune Regulatory in HCC Revealed by Single Cell RNA-seq. Technology in cancer research & treatment, 23, 15330338241252610.

Lando D, et al. (2024) Enhancer-promoter interactions are reconfigured through the formation of long-range multiway hubs as mouse ES cells exit pluripotency. Molecular cell.

Kwon DI, et al. (2024) Fc-fused IL-7 provides broad antiviral effects against respiratory virus infections through IL-17A-producing pulmonary innate-like T cells. Cell reports. Medicine, 5(1), 101362.