

Resource Summary Report

Generated by [kravitz2](#) on Sep 17, 2026

scater

RRID:SCR_015954

Type: Tool

Proper Citation

scater (RRID:SCR_015954)

Resource Information

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

Proper Citation: scater (RRID:SCR_015954)

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

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

Funding: Cancer Research UK A17197;
European Molecular Biology Laboratory ;
National Health and Medical Research Council of Australia APP1112681;
Oxford Single Cell Biology Consortium ;
United Kingdom Medical Research Council

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

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260912T195832+0000

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 187 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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

Huerga Encabo H, et al. (2026) Human TET2-Mutant Clonal Hematopoiesis Expansion Is Driven by Distinct Inflammatory Signaling Responses in Stem Cells Versus Myeloid Progeny. Blood cancer discovery, 7(2), 287.

Huang Y, et al. (2026) Integration of Single-cell and Bulk Transcriptome Analyses Unravels a Macrophage-based Gene Signature for Prognostication and Treatment in Triple-negative Breast Cancer. International journal of medical sciences, 23(1), 253.

Luo XX, et al. (2026) Molecular Determinants of Macrophage Polarization in Glioblastoma and Implications for Tumor Progression. Cells, 15(6).

Mace JW, et al. (2026) Autoimmune neuroinflammation leads to neuronal death via MIF nuclease-mediated parthanatos. Nature neuroscience, 29(4), 796.

Van Lil K, et al. (2026) Protocol to annotate dendritic cell maturation types in vivo making use of lipid nanoparticle-based approaches. STAR protocols, 7(1), 104395.

Näsiaho J, et al. (2026) Spatial single-cell analysis reveals tumor microenvironment signatures predictive of oral cavity cancer outcome. Cell reports. Medicine, 7(2), 102615.

Ahuja K, et al. (2026) Human Myelin Spheres for in Vitro Oligodendrocyte Maturation, Myelination and Neurological Disease Modeling. Stem cell reviews and reports, 22(3), 1420.

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

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*.

Apostolov E, et al. (2026) Single-Cell and Spatial Transcriptomic Profiling Reveals Epithelial Functional States and Fibroblast Phenotypes in Hormone Therapy-Naïve Localized Prostate Cancer. *Cancer research*, 86(8), 1836.

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

Ernst KJ, et al. (2025) A simplified preparation method for single-nucleus RNA-sequencing using long-term frozen brain tumor tissues. *Scientific reports*, 15(1), 12849.

Azami T, et al. (2025) STAT3 signaling enhances tissue expansion during postimplantation mouse development. *Cell reports*, 44(4), 115506.

Zhang J, et al. (2025) Single-cell and bulk transcriptome analysis unveils a ligand-receptor-based signature for prognostication and reveals that TREM1 controls the malignant behaviors of hepatocellular carcinoma. *Acta biochimica et biophysica Sinica*, 57(11), 1847.

Herpelinck T, et al. (2025) A single-cell atlas of the murine limb skeleton integrating the developmental and adult stages. *Scientific reports*, 15(1), 22514.

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.

Shah K, et al. (2025) Spatio-molecular gene expression reflects dorsal anterior cingulate cortex structure and function in the human brain. *bioRxiv : the preprint server for biology*.

Ireland AS, et al. (2025) Basal cell of origin resolves neuroendocrine-tuft lineage plasticity in cancer. *Nature*, 647(8088), 257.

Van Nevel S, et al. (2025) Distinct Effects of Biological Treatments on Eosinophils and Neutrophils in Chronic Rhinosinusitis With Nasal Polyp Patients. *Clinical and translational allergy*, 15(12), e70117.