

Resource Summary Report

Generated by [ASWG](#) on Aug 23, 2026

SC3

RRID:SCR_015953

Type: Tool

Proper Citation

SC3 (RRID:SCR_015953)

Resource Information

URL: <http://bioconductor.org/packages/release/bioc/html/SC3.html>

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Description: Software tool for the unsupervised clustering of cells from single cell RNA-Seq experiments. SC3 is capable of identifying subclones from the transcriptomes of neoplastic cells collected from patients.

Synonyms: SC3 package, Single-Cell Consensus Clustering

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

Defining Citation: [PMID:28346451](#)

Keywords: scRNA-seq, interactive, cluster, clustering, cell, single, rna, rnaseq, bio.tools

Funding: ARC (Action de Recherche Concerte) ;
Belgian Network DYSCO ;
Belgian State Science Policy Office ;
Bloodwise 13003;
Cambridge Experimental Cancer Medicine Centre ;
Cambridge NIHR Biomedical Research Center ;
EPSRC EP/N014529/1;
FRS-FNRS ;
Kay Kendall Leukaemia Fund ;
Leukemia and Lymphoma Society of America 07037;
MRC ;
Sanger Institute ;
University of Edinburgh ;
Wallonia-Brussels Federation ;
Wellcome Trust 104710/Z/14/Z

Availability: Free, Available for download

Resource Name: SC3

Resource ID: SCR_015953

Alternate IDs: biotools:sc3

Alternate URLs: <https://bio.tools/sc3>

License: GPL3

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260821T194031+0000

Ratings and Alerts

No rating or validation information has been found for SC3.

No alerts have been found for SC3.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

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

Van Der Byl W, et al. (2024) The CD8+ T cell tolerance checkpoint triggers a distinct differentiation state defined by protein translation defects. Immunity, 57(6), 1324.

Ding L, et al. (2023) scMINER: a mutual information-based framework for identifying hidden drivers from single-cell omics data. Research square.

Ding L, et al. (2023) scMINER: a mutual information-based framework for identifying hidden drivers from single-cell omics data. bioRxiv : the preprint server for biology.

He J, et al. (2022) Practical bioinformatics pipelines for single-cell RNA-seq data analysis. Biophysics reports, 8(3), 158.

Lowe MG, et al. (2022) EED is required for mouse primordial germ cell differentiation in the embryonic gonad. Developmental cell, 57(12), 1482.

Tian T, et al. (2021) Model-based deep embedding for constrained clustering analysis of single cell RNA-seq data. *Nature communications*, 12(1), 1873.

Kim J, et al. (2021) Single-cell RNA sequencing for the identification of early-stage lung cancer biomarkers from circulating blood. *NPJ genomic medicine*, 6(1), 87.

FitzPatrick MEB, et al. (2021) Human intestinal tissue-resident memory T cells comprise transcriptionally and functionally distinct subsets. *Cell reports*, 34(3), 108661.

Astro V, et al. (2021) Pseudoautosomal Region 1 Overdosage Affects the Global Transcriptome in iPSCs From Patients With Klinefelter Syndrome and High-Grade X Chromosome Aneuploidies. *Frontiers in cell and developmental biology*, 9, 801597.

Camps J, et al. (2020) Interstitial Cell Remodeling Promotes Aberrant Adipogenesis in Dystrophic Muscles. *Cell reports*, 31(5), 107597.

Dias A, et al. (2020) A *Tgfb β 1*/*Snai1*-dependent developmental module at the core of vertebrate axial elongation. *eLife*, 9.

Zand M, et al. (2020) Network-Based Single-Cell RNA-Seq Data Imputation Enhances Cell Type Identification. *Genes*, 11(4).

Sheng X, et al. (2020) Cycling Stem Cells Are Radioresistant and Regenerate the Intestine. *Cell reports*, 32(4), 107952.

Dibaeinia P, et al. (2020) SERGIO: A Single-Cell Expression Simulator Guided by Gene Regulatory Networks. *Cell systems*, 11(3), 252.

Youk J, et al. (2020) Three-Dimensional Human Alveolar Stem Cell Culture Models Reveal Infection Response to SARS-CoV-2. *Cell stem cell*, 27(6), 905.

Teo YV, et al. (2019) Notch Signaling Mediates Secondary Senescence. *Cell reports*, 27(4), 997.

Planas-Paz L, et al. (2019) YAP, but Not RSPO-LGR4/5, Signaling in Biliary Epithelial Cells Promotes a Ductular Reaction in Response to Liver Injury. *Cell stem cell*, 25(1), 39.

Märtn A, et al. (2019) A Spatiomolecular Map of the Striatum. *Cell reports*, 29(13), 4320.

van Galen P, et al. (2019) Single-Cell RNA-Seq Reveals AML Hierarchies Relevant to Disease Progression and Immunity. *Cell*, 176(6), 1265.