

Resource Summary Report

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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, software application, software resource, sequence analysis software, data processing software

Defining Citation: [PMID:28346451](#)

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

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Belgian Network DYSCO ;
FRS-FNRS ;
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Sanger Institute ;
University of Edinburgh ;
Bloodwise 13003;
MRC ;
Kay Kendall Leukaemia Fund ;
Cambridge NIHR Biomedical Research Center ;
Cambridge Experimental Cancer Medicine Centre ;
Leukemia and Lymphoma Society of America 07037

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: 20260801T190532+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 20 mentions in open access literature.

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

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. *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.

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

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.

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

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

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

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

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.

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

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.

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

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

Han S, et al. (2019) Defining the Identity and Dynamics of Adult Gastric Isthmus Stem Cells. *Cell stem cell*, 25(3), 342.

Gong W, et al. (2018) DrImpute: imputing dropout events in single cell RNA sequencing data. *BMC bioinformatics*, 19(1), 220.

Lopez-Baez JC, et al. (2018) Wilms Tumor 1b defines a wound-specific sheath cell subpopulation associated with notochord repair. *eLife*, 7.