

Resource Summary Report

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sctransform

RRID:SCR_022146

Type: Tool

Proper Citation

sctransform (RRID:SCR_022146)

Resource Information

URL: <https://github.com/satijalab/sctransform>

Proper Citation: sctransform (RRID:SCR_022146)

Description: Software R package for normalization and variance stabilization of single-cell RNA-seq data using regularized negative binomial regression.

Resource Type: software toolkit, software resource

Defining Citation: [DOI:10.1186/s13059-019-1874-1](https://doi.org/10.1186/s13059-019-1874-1)

Keywords: normalization and variance stabilization, single-cell RNA-seq data, regularized negative binomial regression

Funding:

Availability: Free, Available for download, Freely available

Resource Name: sctransform

Resource ID: SCR_022146

License: GNU GPL v3.0

Record Creation Time: 20220421T050138+0000

Record Last Update: 20250508T070006+0000

Ratings and Alerts

No rating or validation information has been found for sctransform.

No alerts have been found for sctransform.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 37 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Soni J, et al. (2025) Protocol for investigating intracellular microbial diversity using single-cell RNA-seq in immune cells of SARS-CoV-2-positive and recovered patients. STAR protocols, 6(1), 103546.

Chen F, et al. (2025) miR-142 deficit in T cells during blast crisis promotes chronic myeloid leukemia immune escape. Nature communications, 16(1), 1253.

Chen PB, et al. (2024) Complementation testing identifies genes mediating effects at quantitative trait loci underlying fear-related behavior. Cell genomics, 4(5), 100545.

Segui-Perez C, et al. (2024) MUC13 negatively regulates tight junction proteins and intestinal epithelial barrier integrity via protein kinase C. Journal of cell science, 137(5).

Jung S, et al. (2024) Detecting expressed genes in cell populations at the single-cell level with scGeneXpress. Briefings in bioinformatics, 25(6).

Ghasemi DR, et al. (2024) Compartments in medulloblastoma with extensive nodularity are connected through differentiation along the granular precursor lineage. Nature communications, 15(1), 269.

Chang JJ, et al. (2024) Uncovering strain- and age-dependent innate immune responses to SARS-CoV-2 infection in air-liquid-interface cultured nasal epithelia. iScience, 27(6), 110009.

Lanman NA, et al. (2024) Infiltrating lipid-rich macrophage subpopulations identified as a regulator of increasing prostate size in human benign prostatic hyperplasia. bioRxiv : the preprint server for biology.

Brand J, et al. (2024) Fallopian tube single cell analysis reveals myeloid cell alterations in high-grade serous ovarian cancer. iScience, 27(3), 108990.

Qu S, et al. (2024) The effects of methylphenidate and atomoxetine on Drosophila brain at single-cell resolution and potential drug repurposing for ADHD treatment. *Molecular psychiatry*, 29(1), 165.

Xu L, et al. (2024) A comprehensive single-cell breast tumor atlas defines epithelial and immune heterogeneity and interactions predicting anti-PD-1 therapy response. *Cell reports. Medicine*, 5(5), 101511.

Littleton SH, et al. (2024) Variant-to-function analysis of the childhood obesity chr12q13 locus implicates rs7132908 as a causal variant within the 3' UTR of FAIM2. *Cell genomics*, 4(5), 100556.

Zhang F, et al. (2024) Tumor-specific activation of folate receptor beta enables reprogramming of immune cells in the tumor microenvironment. *Frontiers in immunology*, 15, 1354735.

Li B, et al. (2024) Tissue characterization at an enhanced resolution across spatial omics platforms with deep generative model. *Nature communications*, 15(1), 6541.

Drouillard D, et al. (2024) CXCL12 chemokine dimer signaling modulates acute myelogenous leukemia cell migration through altered receptor internalization. *bioRxiv : the preprint server for biology*.

Benthal JT, et al. (2024) Meta-atlas of Juvenile and Adult Enteric Neuron scRNA-seq for Dataset Comparisons and Consensus on Transcriptomic Definitions of Enteric Neuron Subtypes. *bioRxiv : the preprint server for biology*.

Braithwaite AT, et al. (2024) Multi-organ single-cell RNA sequencing in mice reveals early hyperglycemia responses that converge on fibroblast dysregulation. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 38(3), e23448.

Zhang L, et al. (2024) Regulation of muscle hypertrophy through granulin: Relayed communication among mesenchymal progenitors, macrophages, and satellite cells. *Cell reports*, 43(4), 114052.

Lawrence AR, et al. (2024) Microglia maintain structural integrity during fetal brain morphogenesis. *Cell*, 187(4), 962.

Jeong H, et al. (2023) Functional analysis of structural variants in single cells using Strand-seq. *Nature biotechnology*, 41(6), 832.