

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 9, 2026

Souporcell

RRID:SCR_027462

Type: Tool

Proper Citation

Souporcell (RRID:SCR_027462)

Resource Information

URL: <https://github.com/wheaton5/souporcell>

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Description: Software tool to cluster cells using the genetic variants detected within the scRNAseq reads. Robust clustering of single-cell RNA-seq data by genotype without reference genotypes. Used for clustering scRNAseq by genotypes.

Resource Type: software resource, software application, source code

Defining Citation: [PMID:32366989](#)

Keywords: Clustering scRNAseq by genotypes, cluster cells, genetic variants, scRNAseq reads,

Funding: Wellcome Trust ;
UK Medical Research Council ;
British Heart Foundation

Availability: Free, Available for download, Freely available

Resource Name: Souporcell

Resource ID: SCR_027462

License: MIT license

Record Creation Time: 20250926T061848+0000

Record Last Update: 20260808T190813+0000

Ratings and Alerts

No rating or validation information has been found for Souporcell.

No alerts have been found for Souporcell.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Lee J, et al. (2026) Robust effector memory features of human T-bethi B cells induced by repeated mRNA vaccination. iScience, 29(2), 114804.

Randolph HE, et al. (2026) Widespread gene-environment interactions shape the immune response to SARS-CoV-2 infection in hospitalized COVID-19 patients. Nature communications, 17(1).

Ferrena A, et al. (2026) Single-Cell RNA Analysis of Murine Osteosarcoma Uncovers Skp2 Function in Metastasis, Genomic Instability, and Immune Activation and Reveals Additional Target Pathways. Cancer research communications, 6(4), 923.

Weerakoon M, et al. (2026) Souporcell3: robust demultiplexing for high-donor single-cell RNA-seq datasets. Bioinformatics (Oxford, England), 42(3).

Stevens HP, et al. (2026) Architectural fragility of gene regulatory networks underlies hematopoietic stem cell aging. bioRxiv : the preprint server for biology.

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

Katko A, et al. (2026) Gene regulatory network determinants of rapid recall in human memory CD4+ T cells. Cell reports, 45(4), 117103.

Youlten SE, et al. (2025) In vivo differentiation of embryonic cells devoid of key reprogramming factors. Cell reports, 44(11), 116498.