

Resource Summary Report

Generated by [NIF](#) on Sep 22, 2026

How many cells

RRID:SCR_018184

Type: Tool

Proper Citation

How many cells (RRID:SCR_018184)

Resource Information

URL: <https://satijalab.org/howmanycells>

Proper Citation: How many cells (RRID:SCR_018184)

Description: Web tool for calculating number of cells that must be sampled in order to see at least n cells of each type for single cell genomics experiments.

Synonyms: Satija Lab: How Many Cells

Resource Type: analysis service resource, data access protocol, production service resource, service resource, software resource, web service

Keywords: Calculating cell number, single cell genomic, genomic experiment, cell type number, New York Genome Center, Satija Lab

Availability: Free, Freely available

Resource Name: How many cells

Resource ID: SCR_018184

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260919T195348+0000

Ratings and Alerts

No rating or validation information has been found for How many cells.

No alerts have been found for How many cells.

Data and Source Information

Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Canizo JR, et al. (2025) The guinea pig serves as an alternative model to study human preimplantation development. *Nature cell biology*, 27(4), 696.

Nadukkandy AS, et al. (2025) Clinical application of single-cell RNA sequencing in disease and therapy. *Clinical and translational medicine*, 15(11), e70512.

Grones C, et al. (2024) Best practices for the execution, analysis, and data storage of plant single-cell/nucleus transcriptomics. *The Plant cell*, 36(4), 812.

Li T, et al. (2024) Differential Contributions of Fibroblast Subpopulations to Intercellular Communication in Eosinophilic Esophagitis. *Biology*, 13(7).

Baker EAG, et al. (2023) In silico tissue generation and power analysis for spatial omics. *Nature methods*, 20(3), 424.

Li T, et al. (2023) Comparative transcriptomics reveals highly conserved regional programs between porcine and human colonic enteric nervous system. *Communications biology*, 6(1), 98.

Van de Sande B, et al. (2023) Applications of single-cell RNA sequencing in drug discovery and development. *Nature reviews. Drug discovery*, 22(6), 496.

Yoshihara M, et al. (2023) The Continued Absence of Functional Germline Stem Cells in Adult Ovaries. *Stem cells (Dayton, Ohio)*, 41(2), 105.

Jeon H, et al. (2023) Statistical Power Analysis for Designing Bulk, Single-Cell, and Spatial Transcriptomics Experiments: Review, Tutorial, and Perspectives. *Biomolecules*, 13(2).

Shekhar K, et al. (2022) Diversification of multipotential postmitotic mouse retinal ganglion cell precursors into discrete types. *eLife*, 11.

Liang S, et al. (2022) Sensei: how many samples to tell a change in cell type abundance? *BMC bioinformatics*, 23(1), 2.

Lim RG, et al. (2022) Huntington disease oligodendrocyte maturation deficits revealed by single-nucleus RNAseq are rescued by thiamine-biotin supplementation. *Nature communications*, 13(1), 7791.

Long H, et al. (2022) Mouse genomic and cellular annotations. *Mammalian genome : official journal of the International Mammalian Genome Society*, 33(1), 19.

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

Kozareva V, et al. (2021) A transcriptomic atlas of mouse cerebellar cortex comprehensively defines cell types. *Nature*, 598(7879), 214.

Surumbayeva A, et al. (2021) Preparation of mouse pancreatic tumor for single-cell RNA sequencing and analysis of the data. *STAR protocols*, 2(4), 100989.

Ding J, et al. (2021) Computational tools for analyzing single-cell data in pluripotent cell differentiation studies. *Cell reports methods*, 1(6), 100087.

Deng Y, et al. (2021) Expression characteristics of interferon-stimulated genes and possible regulatory mechanisms in lupus patients using transcriptomics analyses. *EBioMedicine*, 70, 103477.

Chen H, et al. (2021) Effects of Sample Size on Plant Single-Cell RNA Profiling. *Current issues in molecular biology*, 43(3), 1685.

Bernal C, et al. (2020) Functional Pro-metastatic Heterogeneity Revealed by Spiked-scRNAseq Is Shaped by Cancer Cell Interactions and Restricted by VSIG1. *Cell reports*, 33(6), 108372.