

Resource Summary Report

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Drop-seq tools

RRID:SCR_018142

Type: Tool

Proper Citation

Drop-seq tools (RRID:SCR_018142)

Resource Information

URL: <https://github.com/broadinstitute/Drop-seq>

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Description: Software Java tools for analyzing Drop-seq data. Used to analyze gene expression from thousands of individual cells simultaneously. Analyzes mRNA transcripts while remembering origin cell transcript.

Synonyms: Droplet sequencing tools, Droplet sequencing data analysis software tools

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

Defining Citation: [PMID:26000488](#)

Keywords: Simultaneous analysis, Drop-seq data, gene expression, thousands individual cells

Funding: Stanley Center for Psychiatric Research ;
MGH Psychiatry Residency Research Program ;
Stanley-MGH Fellowship in Psychiatric Neuroscience ;
Stewart Trust Fellows Award ;
Simons Foundation ;
NHGRI P50 HG006193;
Klarman Cell Observatory ;
NIMH U01 MH105960;
NIMH R25 MH094612;
NICHD F32 HD075541;
NSF ECS 0335765;
NSF DMR 1310266;
NSF DMR 1420570

Resource Name: Drop-seq tools

Resource ID: SCR_018142

Alternate URLs: <https://sources.debian.org/src/drop-seq-tools/>

License: MIT License

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260801T190757+0000

Ratings and Alerts

No rating or validation information has been found for Drop-seq tools.

No alerts have been found for Drop-seq tools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 94 mentions in open access literature.

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

Mbano IM, et al. (2026) Single-cell and spatial profiling highlights TB-induced myofibroblasts as drivers of lung pathology. The Journal of experimental medicine, 223(3).

Chintala S, et al. (2025) Reduction of NFX1-123 and HPV 16 E6 and E7 Decreased Telomerase and CENP-F in Cervical Cancer Cell Lines. Cancers, 17(12).

Zhao C, et al. (2025) A comprehensive human embryo reference tool using single-cell RNA-sequencing data. Nature methods, 22(1), 193.

Emili E, et al. (2025) Allometry of cell types in planarians by single-cell transcriptomics. Science advances, 11(19), eadm7042.

Wallén E, et al. (2025) Effects of alcohol on the transcriptome, methylome and metabolome of in vitro gastrulating human embryonic cells. Disease models & mechanisms, 18(6).

Gupta S, et al. (2025) Systems genomics of salinity stress response in rice. eLife, 13.

Sarnataro R, et al. (2025) Mitochondrial origins of the pressure to sleep. Nature, 645(8081), 722.

Theobald SJ, et al. (2025) Deep immune profiling delineates hallmarks of disease heterogeneity in extrapulmonary tuberculosis. Nature communications, 16(1), 9662.

Pérez-Posada A, et al. (2025) Multimodal single cell analyses reveal gene networks of planarian stem cell differentiation. *Nature communications*, 16(1), 10683.

Shen Y, et al. (2025) m6A deficiency impairs hypothalamic neurogenesis of feeding-related neurons in mice and human organoids and leads to adult obesity in mice. *Cell stem cell*, 32(5), 727.

Krause R, et al. (2024) B cell heterogeneity in human tuberculosis highlights compartment-specific phenotype and functional roles. *Communications biology*, 7(1), 584.

Yin K, et al. (2024) Dyna-vivo-seq unveils cellular RNA dynamics during acute kidney injury via in vivo metabolic RNA labeling-based scRNA-seq. *Nature communications*, 15(1), 9866.

Ziegler CGK, et al. (2024) An enhanced IL17 and muted type I interferon nasal epithelial cell state characterizes severe COVID-19 with fungal coinfection. *Microbiology spectrum*, 12(6), e0351623.

Paquette SE, et al. (2024) Loss of developmentally derived Irf8+ macrophages promotes hyperinnervation and arrhythmia in the adult zebrafish heart. *bioRxiv : the preprint server for biology*.

Schott M, et al. (2024) Protocol for high-resolution 3D spatial transcriptomics using Open-ST. *STAR protocols*, 6(1), 103521.

Ling E, et al. (2024) Concerted neuron-astrocyte gene expression declines in aging and schizophrenia. *bioRxiv : the preprint server for biology*.

Gupta S, et al. (2024) Systems genomics of salinity stress response in rice. *bioRxiv : the preprint server for biology*.

Auvinen P, et al. (2024) Genome-wide DNA methylation and gene expression in human placentas derived from assisted reproductive technology. *Communications medicine*, 4(1), 267.

Maxwell S, et al. (2024) Set7 Methyltransferase and Phenotypic Switch in Diabetic Glomerular Endothelial Cells. *Journal of the American Society of Nephrology : JASN*, 35(6), 733.

Wegmann R, et al. (2024) Molecular and functional landscape of malignant serous effusions for precision oncology. *Nature communications*, 15(1), 8544.