

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, software application, data analysis software, software resource

Defining Citation: [PMID:26000488](#)

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

Funding: Stanley Center for Psychiatric Research ;
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NHGRI P50 HG006193;
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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: 20260815T182715+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 112 mentions in open access literature.

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

Tsaktanis T, et al. (2026) Interferon- γ and FTY720 ameliorate progressive CNS inflammation via SOCS1-associated astrocyte signaling. Scientific reports, 16(1).

Li T, et al. (2026) Identification of a Small-Molecule Modulator of Astrocyte Reactivity for Optic Nerve Protection. Investigative ophthalmology & visual science, 67(5), 73.

Ishiguro S, et al. (2026) A multi-kingdom genetic barcoding system for precise clone isolation. Nature biotechnology, 44(4), 616.

Shirasawa K, et al. (2026) Chromosome-scale genome assembly of *Malcolmia littorea* using long-read sequencing and single-pollen genotyping technologies. DNA research : an international journal for rapid publication of reports on genes and genomes, 33(1).

Chu CC, et al. (2026) NanoPrePro: a fully equipped, fast, and memory-efficient preprocessor for nanopore transcriptomic sequencing. Briefings in bioinformatics, 27(1).

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).

Burger S, et al. (2026) Inter-individual variation of cellular and gene-expression properties of the human striatum. bioRxiv : the preprint server for biology.

Chen CY, et al. (2026) Transcriptome-guided development of a fibrosis-reversal compound reduces skin scarring and allows regeneration via mitochondrial uncoupling. Cell reports. Medicine, 7(5), 102821.

Li Y, et al. (2026) A spatial and projection-based transcriptomic atlas of paraventricular hypothalamic cell types. *Cell reports*, 45(2), 116904.

Li S, et al. (2025) Chemical reprogramming of fibroblasts into retinal pigment epithelium cells for vision restoration. *Nature communications*, 17(1), 409.

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

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).

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

Gemünd I, et al. (2025) Characterization of human CMV-specific CD8+ T cells using multi-layer single-cell omics. *Cell reports methods*, 5(7), 101085.

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).

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

Stendahl AM, et al. (2025) A partially automated method for DNA extraction from marmoset hair follicles to avoid blood chimerism. *Frontiers in genetics*, 16, 1608504.

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

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

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