

Resource Summary Report

Generated by [dkNET](#) on Aug 6, 2026

Bustools

RRID:SCR_018210

Type: Tool

Proper Citation

Bustools (RRID:SCR_018210)

Resource Information

URL: <https://github.com/BUStools/bustools/>

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Description: Software tool for manipulating BUS files for single cell RNA-Seq datasets. Used to error correct barcodes, collapse UMIs, produce gene count or transcript compatibility count matrices, and is useful for many other tasks.

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

Defining Citation: [DOI:10.1101/673285](https://doi.org/10.1101/673285)

Keywords: Single cell RNAseq workflow, single cell RNAseq dataset, error correct barcode, collapse UMI, produce gene count, produce transcript compatibility count matrix

Availability: Free, Available for download, Freely available

Resource Name: Bustools

Resource ID: SCR_018210

Alternate IDs: OMICS_33004

Alternate URLs: <https://sources.debian.org/src/bustools/>

License: BSD 2-Clause "Simplified" License

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260806T054659+0000

Ratings and Alerts

No rating or validation information has been found for Bustools.

No alerts have been found for Bustools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Cruz J, et al. (2025) Single-cell transcriptomics of X-ray irradiated *Drosophila* wing discs reveals heterogeneity related to cell-cycle status and cell location. *bioRxiv : the preprint server for biology*.

Marchand V, et al. (2025) Monocytes generated by interleukin-6-treated human hematopoietic stem and progenitor cells secrete calprotectin that inhibits erythropoiesis. *iScience*, 28(1), 111522.

Sullivan DK, et al. (2024) kallisto, bustools, and kb-python for quantifying bulk, single-cell, and single-nucleus RNA-seq. *bioRxiv : the preprint server for biology*.

Booeshaghi AS, et al. (2024) Quantifying orthogonal barcodes for sequence census assays. *Bioinformatics advances*, 4(1), vbad181.

Deschamps P, et al. (2024) CXCL8 secreted by immature granulocytes inhibits WT hematopoiesis in chronic myelomonocytic leukemia. *The Journal of clinical investigation*, 134(22).

Ramirez MD, et al. (2024) Cellular-resolution gene expression mapping reveals organization in the head ganglia of the gastropod, *Berghia stephanieae*. *The Journal of comparative neurology*, 532(6), e25628.

Cui G, et al. (2023) Molecular insights into the Darwin paradox of coral reefs from the sea anemone *Aiptasia*. *Science advances*, 9(11), eadf7108.

Einarsson PH, et al. (2023) BUSZ: compressed BUS files. *Bioinformatics (Oxford, England)*, 39(5).

Hsu CW, et al. (2022) Protocol for fast scRNA-seq raw data processing using scKB and non-arbitrary quality control with COPILOT. *STAR protocols*, 3(4), 101729.

Pronier E, et al. (2022) Macrophage migration inhibitory factor is overproduced through EGR1 in TET2^{low} resting monocytes. *Communications biology*, 5(1), 110.

Melhem H, et al. (2022) Epithelial GPR35 protects from *Citrobacter rodentium* infection by preserving goblet cells and mucosal barrier integrity. *Mucosal immunology*, 15(3), 443.

Rohm TV, et al. (2022) Targeting colonic macrophages improves glycemic control in high-fat diet-induced obesity. *Communications biology*, 5(1), 370.

Ren X, et al. (2021) COVID-19 immune features revealed by a large-scale single-cell transcriptome atlas. *Cell*, 184(7), 1895.

Friedrich M, et al. (2021) IL-1-driven stromal-neutrophil interactions define a subset of patients with inflammatory bowel disease that does not respond to therapies. *Nature medicine*, 27(11), 1970.

Booeshaghi AS, et al. (2021) Isoform cell-type specificity in the mouse primary motor cortex. *Nature*, 598(7879), 195.

Pasquini G, et al. (2020) Using Transcriptomic Analysis to Assess Double-Strand Break Repair Activity: Towards Precise in vivo Genome Editing. *International journal of molecular sciences*, 21(4).

Bernstein NJ, et al. (2020) Solo: Doublet Identification in Single-Cell RNA-Seq via Semi-Supervised Deep Learning. *Cell systems*, 11(1), 95.

Du Y, et al. (2020) Evaluation of STAR and Kallisto on Single Cell RNA-Seq Data Alignment. *G3 (Bethesda, Md.)*, 10(5), 1775.