Resource Summary Report

Generated by dkNET on Apr 30, 2025

Bustools

RRID:SCR_018210
Type: Tool

Proper Citation

Bustools (RRID:SCR_018210)

Resource Information

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

Proper Citation: Bustools (RRID:SCR_018210)

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

Defining Citation: DOI:10.1101/673285

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

Funding:

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: 20250429T055947+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 17 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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).

Pronier E, et al. (2022) Macrophage migration inhibitory factor is overproduced through EGR1 in TET2low resting monocytes. Communications biology, 5(1), 110.

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.

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

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.

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.

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

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).

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