Resource Summary Report

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zUMIs

RRID:SCR_016139
Type: Tool

Proper Citation

zUMIs (RRID:SCR_016139)

Resource Information

URL: https://github.com/sdparekh/zUMIs

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Description: Software pipeline to process RNA-seq data with UMIs. The input to this pipeline is paired-end fastq files, where one read contains the cDNA sequence and the other read contains UMI and Cell Barcode information.

Synonyms: zumi

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

Defining Citation: DOI:10.1101/153940

Keywords: single-cell, RNA-seq, UMI, Genomics, shell, r, perl, rna, cdna, cell, sequencing, bio.tools

Funding:

Availability: Open source, Free, Available for download

Resource Name: zUMIs

Resource ID: SCR_016139

Alternate IDs: biotools:zumis

Alternate URLs: https://bio.tools/zumis

License: GPLv3.0

Record Creation Time: 20220129T080329+0000

Record Last Update: 20250407T220313+0000

Ratings and Alerts

No rating or validation information has been found for zUMIs.

No alerts have been found for zUMIs.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 96 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Cardon A, et al. (2025) Single cell profiling of circulating autoreactive CD4 T cells from patients with autoimmune liver diseases suggests tissue imprinting. Nature communications, 16(1), 1161.

Yang J, et al. (2025) MARTRE family proteins negatively regulate CCR4-NOT activity to protect poly(A) tail length and promote translation of maternal mRNA. Nature communications, 16(1), 248.

Zeng J, et al. (2025) CancerSCEM 2.0: an updated data resource of single-cell expression map across various human cancers. Nucleic acids research, 53(D1), D1278.

Cougnoux A, et al. (2025) Diffusion Smart-seq3 of breast cancer spheroids to explore spatial tumor biology and test evolutionary principles of tumor heterogeneity. Scientific reports, 15(1), 3811.

Xie Z, et al. (2024) Vacuolar H+-ATPase determines daughter cell fates through asymmetric segregation of the nucleosome remodeling and deacetylase complex. eLife, 12.

Tang Z, et al. (2024) MitoSort: Robust Demultiplexing of Pooled Single-cell Genomic Data Using Endogenous Mitochondrial Variants. Genomics, proteomics & bioinformatics, 22(5).

Ko BS, et al. (2024) Baf-mediated transcriptional regulation of teashirt is essential for the development of neural progenitor cell lineages. Experimental & molecular medicine, 56(2), 422.

Wu SS, et al. (2024) Red2Flpe-SCON: a versatile, multicolor strategy for generating mosaic conditional knockout mice. Nature communications, 15(1), 4963.

Noble JC, et al. (2024) Introducing synthetic thermostable RNase inhibitors to single-cell RNA-seq. Nature communications, 15(1), 8373.

Radmand A, et al. (2024) Cationic cholesterol-dependent LNP delivery to lung stem cells, the liver, and heart. Proceedings of the National Academy of Sciences of the United States of America, 121(11), e2307801120.

Pekayvaz K, et al. (2024) Multiomic analyses uncover immunological signatures in acute and chronic coronary syndromes. Nature medicine, 30(6), 1696.

Carrelha J, et al. (2024) Alternative platelet differentiation pathways initiated by nonhierarchically related hematopoietic stem cells. Nature immunology, 25(6), 1007.

Chen ZK, et al. (2024) Septo-dentate gyrus cholinergic circuits modulate function and morphogenesis of adult neural stem cells through granule cell intermediaries. Proceedings of the National Academy of Sciences of the United States of America, 121(40), e2405117121.

Chang SH, et al. (2024) Therapeutic single-cell landscape: methotrexate exacerbates interstitial lung disease by compromising the stemness of alveolar epithelial cells under systemic inflammation. EBioMedicine, 108, 105339.

Lu YA, et al. (2024) Sex-specific proximal tubular cell differentiation pathways identified by single-nucleus RNA sequencing. Scientific reports, 14(1), 24041.

Lu H, et al. (2024) Dissecting the Impact of Maternal Androgen Exposure on Developmental Programming through Targeting the Androgen Receptor. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(36), e2309429.

Techameena P, et al. (2024) The single-cell transcriptomic atlas iPain identifies senescence of nociceptors as a therapeutical target for chronic pain treatment. Nature communications, 15(1), 8585.

Kliesmete Z, et al. (2024) Evidence for compensatory evolution within pleiotropic regulatory elements. Genome research, 34(10), 1528.

Kremer LPM, et al. (2024) DNA methylation controls stemness of astrocytes in health and ischaemia. Nature, 634(8033), 415.

Borrelli C, et al. (2024) In vivo interaction screening reveals liver-derived constraints to metastasis. Nature, 632(8024), 411.