

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

Defining Citation: [DOI:10.1101/153940](https://doi.org/10.1101/153940)

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

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: 20260801T190528+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 118 mentions in open access literature.

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

Peralta Ramos JM, et al. (2025) Targeting CD38 immunometabolic checkpoint improves metabolic fitness and cognition in a mouse model of Alzheimer's disease. *Nature communications*, 16(1), 3736.

Cerrizuela S, et al. (2025) Protocol update to: High-throughput scNMT protocol for multiomics profiling of single cells from mouse brain and pancreatic organoids. *STAR protocols*, 6(3), 103980.

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.

Luzak V, et al. (2025) SLAM-seq reveals independent contributions of RNA processing and stability to gene expression in African trypanosomes. *Nucleic acids research*, 53(3).

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.

Liu H, et al. (2025) Aging alters the effect of adiponectin receptor signaling on bone marrow-derived mesenchymal stem cells. *Aging cell*, 24(2), e14390.

Hartmanis L, et al. (2025) Deciphering direct transcriptional effects of epigenetic compounds through large-scale new RNA profiling. *Nature communications*, 16(1), 6629.

Niehhs A, et al. (2025) Transient tissue residency and lymphatic egress define human CD56bright NK cell homeostasis. *Nature immunology*, 26(11), 2004.

Zhao A, et al. (2025) Maternal diabetes programs sexually dimorphic early-onset cardiovascular dysfunction in metabolically healthy offspring. *Cell reports. Medicine*, 6(11), 102454.

O'Keeffe P, et al. (2025) TIRE-seq simplifies transcriptomics via integrated RNA capture and library preparation. *Scientific reports*, 15(1), 15385.

Nattress CB, et al. (2025) Phenoscaping Reveals Multimodal ?? T-cell Cytotoxicity as a Strategy to Overcome Cancer Cell-Mediated Immunomodulation. *Cancer research*, 85(22), 4415.

Yan Y, et al. (2025) Single-cell dissection of chronic lung allograft dysfunction reveals convergent and distinct fibrotic mechanisms. *JCI insight*, 10(20).

Papanicolaou N, et al. (2025) Multi-layered dosage compensation of the avian Z chromosome by increased transcriptional burst frequency and elevated translational rates. *Nature communications*, 16(1), 9088.

Vlassakev I, et al. (2025) The liver clock modulates circadian rhythms in white adipose tissue. *Molecular metabolism*, 101, 102249.

Sponheimer M, et al. (2025) TNF-? and IFN-? differentially regulate AML cell susceptibility to CD70-antibody-mediated cytotoxicity. *Journal for immunotherapy of cancer*, 13(12).

Coskun H, et al. (2025) 3D spatial organization of heterogeneous nkx2.5+ progenitors in the zebrafish heart field pre-patterns cardiovascular development. *Nature communications*, 16(1), 11624.

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.

He W, et al. (2025) X-Linked Gene Dosage and SOX2 Act as Key Roadblocks for Human Germ Cell Specification in Klinefelter Syndrome. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(15), e2410533.

Cougoux 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.

Antoniolli M, et al. (2025) ARID1A mutations protect follicular lymphoma from FAS-dependent immune surveillance by reducing RUNX3/ETS1-driven FAS-expression. *Cell death and differentiation*, 32(5), 899.