

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

zUMIs

RRID:SCR_016139

Type: Tool

Proper Citation

zUMIs (RRID:SCR_016139)

Resource Information

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

Proper Citation: zUMIs (RRID:SCR_016139)

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, software application, data analysis software, 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: 20260731T042959+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 [kravitz2](#) .

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.

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.

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).

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.

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.

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.

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.

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.

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

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.

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).

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.

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.

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.