Resource Summary Report

Generated by RRID on Apr 28, 2025

UMI-tools

RRID:SCR_017048
Type: Tool

Proper Citation

UMI-tools (RRID:SCR_017048)

Resource Information

URL: https://github.com/CGATOxford/UMI-tools

Proper Citation: UMI-tools (RRID:SCR_017048)

Description: Open source software package for handling Unique Molecular Identifiers in NGS data sets.

Synonyms: Unique Molecular Identifiers tools

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

Defining Citation: PMID:28100584

Keywords: unique, molecular, identifier, NGS, data, dataset, random, oligonucleotide, barcode, sequencing, copy, molecule, PCR, amplification, bio.tools

Funding: Medical Research Council

Availability: Free, Available for download, Freely available

Resource Name: UMI-tools

Resource ID: SCR_017048

Alternate IDs: biotools:umi-tools

Alternate URLs: https://bio.tools/umi-tools

License: MIT License

Record Creation Time: 20220129T080333+0000

Record Last Update: 20250428T054035+0000

Ratings and Alerts

No rating or validation information has been found for UMI-tools.

No alerts have been found for UMI-tools.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 105 mentions in open access literature.

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

Fajardo-Despaigne JE, et al. (2025) Characterization and effective expansion of CD4-CD8-TCR??+ T cells from individuals living with type 1 diabetes. Molecular therapy. Methods & clinical development, 33(1), 101400.

Al-Amoodi AS, et al. (2024) ?1,3-fucosylation treatment improves cord blood CD34 negative hematopoietic stem cell navigation. iScience, 27(2), 108882.

Villanueva E, et al. (2024) System-wide analysis of RNA and protein subcellular localization dynamics. Nature methods, 21(1), 60.

Glauninger H, et al. (2024) Transcriptome-wide mRNA condensation precedes stress granule formation and excludes stress-induced transcripts. bioRxiv : the preprint server for biology.

Tay T, et al. (2024) Degradation of IKZF1 prevents epigenetic progression of T cell exhaustion in an antigen-specific assay. Cell reports. Medicine, 5(11), 101804.

Verheyden NA, et al. (2024) A high-resolution map of functional miR-181 response elements in the thymus reveals the role of coding sequence targeting and an alternative seed match. Nucleic acids research, 52(14), 8515.

Gaballa A, et al. (2024) PAF1c links S-phase progression to immune evasion and MYC function in pancreatic carcinoma. Nature communications, 15(1), 1446.

Simmons SK, et al. (2024) Experimental and Computational Methods for Allelic Imbalance Analysis from Single-Nucleus RNA-seq Data. bioRxiv : the preprint server for biology.

Lehto P, et al. (2024) Postmortem analyses of myocardial microRNA expression in sepsis. Scientific reports, 14(1), 29476.

Del-Valle-Anton L, et al. (2024) Multiple parallel cell lineages in the developing mammalian cerebral cortex. Science advances, 10(13), eadn9998.

Giulietti M, et al. (2024) Effects of Eribulin on the RNA Content of Extracellular Vesicles Released by Metastatic Breast Cancer Cells. Cells, 13(6).

Cherubini A, et al. (2024) Exploring human pancreatic organoid modelling through single-cell RNA sequencing analysis. Communications biology, 7(1), 1527.

Alashkar Alhamwe B, et al. (2024) BAG6 restricts pancreatic cancer progression by suppressing the release of IL33-presenting extracellular vesicles and the activation of mast cells. Cellular & molecular immunology, 21(8), 918.

April-Monn SL, et al. (2024) Patient derived tumoroids of high grade neuroendocrine neoplasms for more personalized therapies. NPJ precision oncology, 8(1), 59.

Ikeda H, et al. (2024) Protocol for high-quality single-cell RNA-seq from tissue sections with DRaqL. STAR protocols, 5(2), 103050.

Roberts BS, et al. (2024) Probabilistic association of differentially expressed genes with cis-regulatory elements. Genome research, 34(4), 620.

Mangkalaphiban K, et al. (2024) Pleiotropic effects of PAB1 deletion: Extensive changes in the yeast proteome, transcriptome, and translatome. PLoS genetics, 20(9), e1011392.

Bi R, et al. (2024) Epigenetic characterization of adult rhesus monkey spermatogonial stem cells identifies key regulators of stem cell homeostasis. Nucleic acids research, 52(22), 13644.

Beiki H, et al. (2024) Detection of ac4C in human mRNA is preserved upon data reassessment. Molecular cell, 84(8), 1611.

Van Der Byl W, et al. (2024) The CD8+ T cell tolerance checkpoint triggers a distinct differentiation state defined by protein translation defects. Immunity, 57(6), 1324.