

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

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: 20260801T190600+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 126 mentions in open access literature.

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

Giridhar NJ, et al. (2025) Temporal transcriptomic profiling of human three-dimensional neuromuscular co-cultures. *Biology open*, 14(9).

Fonta N, et al. (2025) Oligodendrocyte-derived IL-33 regulates self-reactive CD8+ T cells in CNS autoimmunity. *The Journal of experimental medicine*, 222(7).

Li YS, et al. (2025) Cellular dynamics in cerebrospinal fluid unveils the key regulators of intracranial response to immune checkpoint inhibitors in NSCLC brain metastases. *Journal for immunotherapy of cancer*, 13(11).

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.

Lee JY, et al. (2025) Imp/IGF2BP and Syp/SYNCRIP temporal RNA interactomes uncover combinatorial networks of regulators of Drosophila brain development. *Science advances*, 11(6), eadr6682.

Omonijo FA, et al. (2025) Small nucleolar RNA dysregulation and potential roles in bovine subclinical mastitis. *Journal of animal science and biotechnology*, 16(1), 124.

Glauninger H, et al. (2025) Transcriptome-wide mRNP condensation precedes stress granule formation and excludes new mRNAs. *Molecular cell*, 85(23), 4393.

Pérez-Arques C, et al. (2025) RNAi epimutations conferring antifungal drug resistance are inheritable. *Nature communications*, 16(1), 7293.

Kolakada D, et al. (2025) Systematic analysis of nonsense variants uncovers peptide release rate as a novel modifier of nonsense-mediated mRNA decay. *Cell genomics*, 5(7), 100882.

Sakhawala RM, et al. (2025) A noncanonical Pol III-dependent, Microprocessor-independent biogenesis pathway generates a germline enriched miRNA family. *bioRxiv* : the preprint server for biology.

Zhou S, et al. (2025) Cancer-associated snaR-A noncoding RNA interacts with core splicing machinery and disrupts processing of mRNA subpopulations. *Nature communications*, 16(1), 10460.

Teimuri S, et al. (2025) *Drosophila* Topoisomerase 3 β binds to mRNAs in vivo, contributes to their localization and stability, and counteracts premature aging. *PLoS one*, 20(2), e0318142.

Chatsirisupachai K, et al. (2025) Mouse promoters are characterised by low occupancy and high turnover of RNA polymerase II. *Molecular systems biology*, 21(5), 447.

Huang J, et al. (2025) Model-to-crop conserved NUE Regulons enhance machine learning predictions of nitrogen use efficiency. *The Plant cell*, 37(5).

Satomura A, et al. (2025) Robustness of urinary extracellular vesicle-derived MiRNA profiles over multiple days and the impact of urine concentration. *Scientific reports*, 15(1), 34334.

Zhang Z, et al. (2025) Simultaneous epigenomic profiling and regulatory activity measurement using e2MPRA. *bioRxiv* : the preprint server for biology.

Zhong S, et al. (2025) Modular DNA barcoding of nanobodies enables multiplexed in situ protein imaging and high-throughput biomolecule detection. *eLife*, 14.

Bestehorn A, et al. (2025) Cytoplasmic mRNA decay controlling inflammatory gene expression is determined by pre-mRNA fate decision. *Molecular cell*, 85(4), 742.

Liu JF, et al. (2025) Decoding m6Am by simultaneous transcription-start mapping and methylation quantification. *eLife*, 13.

Taoka H, et al. (2025) Transcriptional dynamics uncover the role of BNIP3 in mitophagy during muscle remodeling in *Drosophila*. *eLife*, 14.