

Resource Summary Report

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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 analysis software, data processing 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: 20260905T132817+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 145 mentions in open access literature.

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

Simmons SK, et al. (2026) Experimental and computational methods for allelic imbalance analysis from single-nucleus RNA-seq data. *Genome biology*, 27(1).

Klink N, et al. (2026) Targeted degradation of USP7 in solid cancer cells reveals distinct effects of deubiquitinase degraders and inhibitors. *Nature communications*, 17(1).

Veysi A, et al. (2026) Psilocybin elicits a conserved glucocorticoid-responsive gene signature across five 5-HT2A receptor-rich brain regions in rat. *Acta neuropsychiatrica*, 38, e37.

Eriksson J, et al. (2026) Single-Cell Lineage Tracing Uncovers Resistance Signatures and Sensitizing Strategies to FLT3 Inhibitors in Acute Myeloid Leukemia. *Cancer research*, 86(7), 1724.

Maple R, et al. (2026) Co-transcriptional splicing changes combine with reduced productive transcription initiation for cold-induced repression of FLC. *Nucleic acids research*, 54(1).

Thienger P, et al. (2026) A Double-Negative Prostate Cancer Subtype Is Vulnerable to SWI/SNF-Targeting Degradar Molecules. *Cancer research*, 86(7), 1570.

Zhang Z, et al. (2026) Simultaneous epigenomic profiling and regulatory activity measurement using e2MPRA. *Nature communications*, 17(1), 1724.

Tisch M, et al. (2026) Aberrant calcium signaling and neuronal activity in the L271H CACNA1D (Cav1.3) iPSC model of neurodevelopmental disease. *Molecular psychiatry*.

Salvidge W, et al. (2026) Lineage priming and cell type proportioning depends on the interplay between stochastic and deterministic factors. *eLife*, 14.

Soltys V, et al. (2026) Flexible and high-throughput simultaneous profiling of gene expression and chromatin accessibility in single cells. *eLife*, 15.

Ye Y, et al. (2026) DCPS modulates TDP-43-linked neurodegeneration through P-body-mediated RNA decay. *Neuron*, 114(11), 1970.

Mao X, et al. (2026) Cytoplasmic mRNA decay by the antiviral nuclease RNase L promotes transcriptional repression. *Cell reports*, 45(3), 117028.

Yao B, et al. (2026) Divergent tumor immunity determined by bacteria-cancer cell engagement. *Cell*, 189(6), 1748.

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).

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

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

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).

Jung H, et al. (2025) Sensitizing tumor response to topoisomerase I antibody drug conjugate by selective CDK7 inhibition. *bioRxiv : the preprint server for biology*.

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*.

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.