

# Resource Summary Report

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

## umis

RRID:SCR\_024381

Type: Tool

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### Proper Citation

umis (RRID:SCR\_024381)

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### Resource Information

**URL:** <https://github.com/vals/umis>

**Proper Citation:** umis (RRID:SCR\_024381)

**Description:** Software tools for estimating expression in RNA-Seq data which performs sequencing of end tags of transcript, and incorporate molecular tags to correct for amplification bias.

**Resource Type:** software resource, software toolkit

**Defining Citation:** [PMID:28263961](#)

**Keywords:** estimating expression in RNA-Seq data, sequencing of end tags of transcript, incorporate molecular tags, correct for amplification bias,

**Availability:** Free, Available for download, Freely available,

**Resource Name:** umis

**Resource ID:** SCR\_024381

**Alternate IDs:** OMICS\_12783

**Alternate URLs:** <https://sources.debian.org/src/umis/>

**Record Creation Time:** 20230830T050217+0000

**Record Last Update:** 20260801T190902+0000

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### Ratings and Alerts

No rating or validation information has been found for umis.

No alerts have been found for umis.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Menezes NA, et al. (2025) Cell-context response to germ layer differentiation signals is predetermined by the epigenome in regionalized epiblast populations. Nature communications, 16(1), 5000.

Takahama M, et al. (2024) A pairwise cytokine code explains the organism-wide response to sepsis. Nature immunology, 25(2), 226.