

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

umis

RRID:SCR_024381

Type: Tool

Proper Citation

umis (RRID:SCR_024381)

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: 20260725T191112+0000

Ratings and Alerts

No rating or validation information has been found for umis.

No alerts have been found for umis.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

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.