

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

RSEM

RRID:SCR_000262

Type: Tool

Proper Citation

RSEM (RRID:SCR_000262)

Resource Information

URL: <http://deweylab.biostat.wisc.edu/rsem/>

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Description: Software package for quantifying gene and isoform abundances from single end or paired end RNA Seq data. Accurate transcript quantification from RNA Seq data with or without reference genome. Used for accurate quantification of gene and isoform expression from RNA-Seq data.

Synonyms: RSEM, RNA-Seq by Expectation-Maximization, RSEM-v1.3.0

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

Defining Citation: [PMID:21816040](#)

Keywords: quantifying, gene, isoform, abundance, single, end, paired, RNA seq, data, transcript, reference, genome, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: RSEM

Resource ID: SCR_000262

Alternate IDs: OMICS_01966, OMICS_01287, biotools:rsem, SCR_013027

Alternate URLs: <https://github.com/deweylab/RSEM>,
<https://github.com/deweylab/RSEM/releases>, <https://bio.tools/rsem>,
<https://sources.debian.org/src/rsem/>

License: GNU GPL

License URLs: <http://www.gnu.org/copyleft/gpl.html>

Record Creation Time: 20220129T080200+0000

Record Last Update: 20260805T044005+0000

Ratings and Alerts

No rating or validation information has been found for RSEM.

No alerts have been found for RSEM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 94 mentions in open access literature.

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

Nitsch S, et al. (2026) H4K16 acylations destabilize chromatin architecture and facilitate transcriptional response during metabolic perturbations. *Molecular cell*, 86(1), 24.

Stern YE, et al. (2026) Targeting CDK12/13 Drives Mitotic Arrest to Overcome Resistance to KRASG12C Inhibitors. *Cancer research*, 86(2), 485.

Lee H, et al. (2025) Hi-GDT: A Hi-C-based 3D gene domain analysis tool for analyzing local chromatin contacts in plants. *GigaScience*, 14.

Arthur TD, et al. (2025) Multiomic QTL mapping reveals phenotypic complexity of GWAS loci and prioritizes putative causal variants. *Cell genomics*, 5(3), 100775.

Lee SM, et al. (2025) Phase II Open-Label Trial of Brentuximab Vedotin with Pembrolizumab in PD-1-Pretreated Metastatic Non-Small Cell Lung Cancer and Metastatic Cutaneous Melanoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(5), 848.

Ma Y, et al. (2025) Updated efficacy and predictive biomarkers of QL1706, a bifunctional PD-1/CTLA-4 dual blocker in advanced solid tumors-A phase 1/1b study. *Cell reports. Medicine*, 6(10), 102396.

Yim KM, et al. (2025) Cell-type-specific dysregulation of gene expression due to Chd8 haploinsufficiency during mouse cortical development. *Cell genomics*, 100986.

Xiao T, et al. (2025) RAD23B acquires a copper metalloadaptor function in amphibian-to-reptile evolution to increase metabolism and regulate genomic integrity. *Molecular cell*, 85(18), 3443.

Suda K, et al. (2025) Low OLFM1 and BMP6 Expression Predicts Recurrence in Early-Stage Nonsquamous NSCLC with Pure Solid Tumor Appearance. *Cancer research*

communications, 5(12), 2186.

Tayari MM, et al. (2025) Balancing Activation and Repression: CoREST-p300 Antagonism Controls Retinoic Acid-Driven Differentiation in AML. *bioRxiv : the preprint server for biology*.

Lopez-Pajares V, et al. (2025) Glucose modulates IRF6 transcription factor dimerization to enable epidermal differentiation. *Cell stem cell*, 32(5), 795.

Nayak PK, et al. (2025) Transcriptome profiling of tendon fibroblasts at the onset of embryonic muscle contraction reveals novel force-responsive genes. *eLife*, 14.

Ishikawa H, et al. (2025) Effects of aging on diurnal transcriptome change in the mouse corpus callosum. *iScience*, 28(1), 111556.

Neill NJ, et al. (2025) Integrative Proteogenomics and Forward Genetics Reveal a Novel Mitotic Vulnerability in Triple-Negative Breast Cancer. *Cancer discovery*, 15(11), 2326.

Wang M, et al. (2025) Vascular Normalization Augments the Antitumor Efficacy of Combined HDAC Inhibitor with Immunotherapy in Solid Tumors. *Cancer discovery*, 15(9), 1883.

Xu X, et al. (2025) Genomic Analyses Reveal the Evolving Characteristics of Intestinal Metaplasia and Gastric Cancer. *Cancer research*, 85(16), 3123.

Tayari MM, et al. (2025) Co-targeting menin and LSD1 dismantles oncogenic programs and restores differentiation in MLL-rearranged AML. *bioRxiv : the preprint server for biology*.

Hamanaka G, et al. (2025) Protocol for sex-specific isolation of microglia, oligodendrocyte precursor cells, and astrocytes from neonatal rats using shake-off technique. *STAR protocols*, 6(3), 103902.

Fouque A, et al. (2025) Constructing chimeric mouse islets to study alpha- and delta-cell influence on beta-cell feature. *Molecular metabolism*, 101, 102245.

Tingvall-Gustafsson J, et al. (2025) Chromatin interaction-based annotation of regulatory elements reveals dynamic promoter-enhancer interactions in lymphocyte development. *iScience*, 28(7), 112855.