Resource Summary Report

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

Defining Citation: PMID:21816040

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

Funding:

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

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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 47 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Lopes-Paciencia S, et al. (2024) A senescence restriction point acting on chromatin integrates oncogenic signals. Cell reports, 43(4), 114044.

Liu H, et al. (2024) Integrative molecular and spatial analysis reveals evolutionary dynamics and tumor-immune interplay of in situ and invasive acral melanoma. Cancer cell, 42(6), 1067.

Camilleri-Robles C, et al. (2024) Long non-coding RNAs involved in Drosophila development and regeneration. NAR genomics and bioinformatics, 6(3), lqae091.

Du C, et al. (2024) Mitochondrial serine catabolism safeguards maintenance of the hematopoietic stem cell pool in homeostasis and injury. Cell stem cell, 31(10), 1484.

Sun Y, et al. (2024) Integrated multi-omics profiling to dissect the spatiotemporal evolution of metastatic hepatocellular carcinoma. Cancer cell, 42(1), 135.

Patton MH, et al. (2024) Synaptic plasticity in human thalamocortical assembloids. Cell reports, 43(8), 114503.

Shi D, et al. (2024) Pseudouridine synthase 1 regulates erythropoiesis via transfer RNAs

pseudouridylation and cytoplasmic translation. iScience, 27(3), 109265.

McDaniel JM, et al. (2024) p53R172H and p53R245W Hotspot Mutations Drive Distinct Transcriptomes in Mouse Mammary Tumors Through a Convergent Transcriptional Mediator. Cancer research communications, 4(8), 1991.

Haas R, et al. (2024) The Proteogenomics of Prostate Cancer Radioresistance. Cancer research communications, 4(9), 2463.

Gellert J, et al. (2024) Tumoral Interferon Beta Induces an Immune-Stimulatory Phenotype in Tumor-Associated Macrophages in Melanoma Brain Metastases. Cancer research communications, 4(8), 2189.

Murray GC, et al. (2024) Testing SIPA1L2 as a modifier of CMT1A using mouse models. Journal of neuropathology and experimental neurology.

Moskovljevic M, et al. (2024) Cognate antigen engagement induces HIV-1 expression in latently infected CD4+ T cells from people on long-term antiretroviral therapy. Immunity, 57(12), 2928.

Yue T, et al. (2024) Sex-biased regulatory changes in the placenta of native highlanders contribute to adaptive fetal development. eLife, 12.

Tang R, et al. (2024) Tandemly expanded OR17b in Himalaya ghost moth facilitates larval food allocation via olfactory reception of plant-derived tricosane. International journal of biological macromolecules, 268(Pt 1), 131503.

Koganemaru S, et al. (2024) The tumor immune microenvironment and therapeutic efficacy of trastuzumab deruxtecan in gastric cancer. Cancer research communications.

Bai M, et al. (2024) The telomere-to-telomere (T2T) genome of Peucedanum praeruptorum Dunn provides insights into the genome evolution and coumarin biosynthesis. GigaScience, 13.

Philip VM, et al. (2023) Gene expression genetics of the striatum of Diversity Outbred mice. Scientific data, 10(1), 522.

Farsi Z, et al. (2023) Brain-region-specific changes in neurons and glia and dysregulation of dopamine signaling in Grin2a mutant mice. Neuron, 111(21), 3378.

Takahashi G, et al. (2023) Control of stem cell behavior by CLE-JINGASA signaling in the shoot apical meristem in Marchantia polymorpha. Current biology : CB, 33(23), 5121.

Jorstad NL, et al. (2023) Comparative transcriptomics reveals human-specific cortical features. Science (New York, N.Y.), 382(6667), eade9516.