RSEM
RRID:SCR_013027
Type: Tool

Proper Citation

RSEM (RRID:SCR_013027)

Resource Information

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

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 quantifying transcript abundances from RNA Seq data.

Resource Name: RSEM

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

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

Resource ID: SCR_013027

Parent Organization: University of Wisconsin-Madison; Wisconsin; USA

Funding Agency: Dr. James Thomson MacArthur Professorship, Morgridge Institute for Research support for Computation and Informatics in Biology and Medicine, NHGRI

References: PMID:21816040

Availability: Free, Available for download, Freely available

Website Status: Last checked up
Alternate IDs: OMICS_01287

Alternate URLs: https://github.com/deweylab/RSEM/releases

Abbreviations: RSEM

Mentions Count: 1717

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 1717 mentions in open access literature.

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


Li Q, et al. (2020) SMRT sequencing of a full-length transcriptome reveals transcript variants involved in C18 unsaturated fatty acid biosynthesis and metabolism pathways at chilling temperature in Pennisetum giganteum. BMC genomics, 21(1), 52.

Tong D, et al. (2020) Contact-dependent delivery of IL-2 by dendritic cells to CD4 T cells in the contraction phase promotes their long-term survival. Protein & cell, 11(2), 108-123.
