Resource Summary Report

Generated by NIF on Apr 25, 2025

rSeq

RRID:SCR_000562 Type: Tool

Proper Citation

rSeq (RRID:SCR_000562)

Resource Information

URL: http://www-personal.umich.edu/~jianghui/rseq/

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Description: A software toolkit for RNA sequence data analysis. It contains programs that cover several aspects of RNA-Seq data analysis such as read quality assessment, reference sequence generation, sequence mapping, and gene and isoform expressions estimations.

Synonyms: RNA-Seq Analyzer, rSeq: RNA-Seq Analyzer

Resource Type: software resource, source code, software toolkit

Keywords: rna, sequence, read quality assessment, reference sequence generation, sequence mapping, gene, isoform expressions estimations, bio.tools

Funding:

Availability: Non-commercial, Open Source

Resource Name: rSeq

Resource ID: SCR_000562

Alternate IDs: OMICS_01288, biotools:rseq

Alternate URLs: https://bio.tools/rseq

License: Anyone can use the source codes, documents or the excutable file of rSeq free of charge for non-commercial use. For commercial use, please contact the author.

Record Creation Time: 20220129T080202+0000

Record Last Update: 20250425T055132+0000

Ratings and Alerts

No rating or validation information has been found for rSeq.

No alerts have been found for rSeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

Scott LJ, et al. (2016) The genetic regulatory signature of type 2 diabetes in human skeletal muscle. Nature communications, 7, 11764.

Gibbons JG, et al. (2012) The evolutionary imprint of domestication on genome variation and function of the filamentous fungus Aspergillus oryzae. Current biology : CB, 22(15), 1403.

Salzman J, et al. (2011) Statistical Modeling of RNA-Seq Data. Statistical science : a review journal of the Institute of Mathematical Statistics, 26(1).

Jiang H, et al. (2009) Statistical inferences for isoform expression in RNA-Seq. Bioinformatics (Oxford, England), 25(8), 1026.