

Resource Summary Report

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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, software toolkit, source code

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

Availability: Free, Available for download, Freely available,

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 executable 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: 20260821T193612+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 [NIF](#) .

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.