

Resource Summary Report

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metaRNASeq

RRID:SCR_002174

Type: Tool

Proper Citation

metaRNASeq (RRID:SCR_002174)

Resource Information

URL: <http://cran.r-project.org/web/packages/metaRNASeq/>

Proper Citation: metaRNASeq (RRID:SCR_002174)

Description: Software package for meta-analysis of RNA-seq data. This package implements two p-value combination techniques (inverse normal and Fisher methods). It also provides a vignette explaining how to combine data from multiple RNA-seq experiments.

Synonyms: metaRNASeq: Meta-analysis of RNA-seq data

Resource Type: software resource

Defining Citation: [PMID:24678608](#)

Keywords: standalone software, unix/linux, mac os x, windows, r

Availability: Free, Available for download, Freely available

Resource Name: metaRNASeq

Resource ID: SCR_002174

Alternate IDs: OMICS_03527

License: GNU General Public License, v2, v3

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260725T190521+0000

Ratings and Alerts

No rating or validation information has been found for metaRNASeq.

No alerts have been found for metaRNASeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 30 mentions in open access literature.

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

Öztemur Islako?lu Y, et al. (2025) Fusion transcripts landscape in hepatocellular carcinoma and potential impact on the expression of fusion partners. RNA biology, 22(1), 1.

Karami S, et al. (2025) Molecular investigation of how drought stress affects chlorophyll metabolism and photosynthesis in leaves of C3 and C4 plant species: A transcriptome meta-analysis. Heliyon, 11(3), e42368.

Farhan M, et al. (2025) Identification of Leaf Rust-Related Gene Signature in Wheat (Triticum Aestivum L.) Using High-Throughput Sequencing, Network Analysis, and Machine Learning Algorithms. Rice (New York, N.Y.), 18(1), 82.

Lin YT, et al. (2025) Temporal analysis of doxorubicin-induced cardiac toxicity and hypertrophy. NPJ systems biology and applications, 11(1), 67.

Panahi B, et al. (2024) Global transcriptome analysis identifies critical functional modules associated with multiple abiotic stress responses in microalgae Chromochloris zofingiensis. PloS one, 19(8), e0307248.

Kissel LT, et al. (2024) Sex-Differential Gene Expression in Developing Human Cortex and Its Intersection With Autism Risk Pathways. Biological psychiatry global open science, 4(4), 100321.

Beric A, et al. (2024) Circulating blood circular RNA in Parkinson's Disease; a systematic study. medRxiv : the preprint server for health sciences.

Nagarajan G, et al. (2024) Distinct expression profile reveals glia involvement in the trigeminal system attributing to post-traumatic headache. The journal of headache and pain, 25(1), 203.

López-Martínez A, et al. (2024) lncRNA-mRNA Co-Expression and Regulation Analysis in Lung Fibroblasts from Idiopathic Pulmonary Fibrosis. Non-coding RNA, 10(2).

Tabatabaeipour SN, et al. (2024) Comprehensive transcriptomic meta-analysis unveils new responsive genes to methyl jasmonate and ethylene in Catharanthus roseus. Heliyon, 10(5), e27132.

Schall PZ, et al. (2024) Predictive modeling of oocyte maternal mRNA features for five mammalian species reveals potential shared and species-restricted regulators during maturation. *Physiological genomics*, 56(1), 9.

Pandey D, et al. (2023) Improved meta-analysis pipeline ameliorates distinctive gene regulators of diabetic vasculopathy in human endothelial cell (hECs) RNA-Seq data. *PloS one*, 18(11), e0293939.

Asadi A, et al. (2023) Meta-analysis of transcriptome reveals key genes relating to oil quality in olive. *BMC genomics*, 24(1), 566.

Salina EG, et al. (2022) A New Benzothiazolthiazolidine Derivative, 11726172, Is Active In Vitro, In Vivo, and against Nonreplicating Cells of Mycobacterium tuberculosis. *mSphere*, 7(6), e0036922.

Di Fraia D, et al. (2022) Conserved exchange of paralog proteins during neuronal differentiation. *Life science alliance*, 5(6).

Amar M, et al. (2021) Autism-linked Cullin3 germline haploinsufficiency impacts cytoskeletal dynamics and cortical neurogenesis through RhoA signaling. *Molecular psychiatry*, 26(7), 3586.

Ghahramani N, et al. (2021) Integrative Systems Biology Analysis Elucidates Mastitis Disease Underlying Functional Modules in Dairy Cattle. *Frontiers in genetics*, 12, 712306.

Rahman MR, et al. (2021) Discovering common pathogenetic processes between COVID-19 and diabetes mellitus by differential gene expression pattern analysis. *Briefings in bioinformatics*, 22(6).

Zhao H, et al. (2021) Integrated multi-omics approach identified molecular mechanism and pathogenetic processes of COVID-19 that affect patient with Parkinson's disorder. *Saudi journal of biological sciences*, 28(12), 6939.

Malik A, et al. (2021) Role of Transportome in the Gills of Chinese Mitten Crabs in Response to Salinity Change: A Meta-Analysis of RNA-Seq Datasets. *Biology*, 10(1).