

Resource Summary Report

Generated by [T1D](#) on Aug 2, 2026

[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: 20260801T190208+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 [T1D](#).

Öztemur Islakoğlu 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.

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

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.

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.

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.

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.

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.

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).

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.

Mota APZ, et al. (2021) Defining the combined stress response in wild *Arachis*. *Scientific reports*, 11(1), 11097.