

Resource Summary Report

Generated by [RRID](#) on Sep 10, 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: 20260905T132444+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 35 mentions in open access literature.

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

Zhou X, et al. (2026) AI-derived constrained conditional model for screening marker genes through integrated high-throughput transcriptome big data. BMC medical research methodology, 26(1).

Olivas-Bernal CA, et al. (2026) Transcriptomic Meta-Analysis as a Framework for Robust Cross-Study Biological Inference. International journal of molecular sciences, 27(11).

Ge M, et al. (2026) Comprehensive profiling of circRNAs reveals stimulus-specific networks and core regulators of cellular senescence. PloS one, 21(2), e0343300.

Hajibarat Z, et al. (2026) Integrative Analysis of Abiotic Stress-Responsive Genes in Soybean Using Differential Gene Expression and Validation With Machine Learning. Plant-environment interactions (Hoboken, N.J.), 7(3), e70174.

Jajoo A, et al. (2025) Leveraging genomic and transcriptomic data of diverse ancestry to uncover mechanisms of psychiatric risk in the adult and developing brain. Nature communications, 17(1), 1179.

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.

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

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.

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.

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

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).