

# Resource Summary Report

Generated by [dkNET](#) on Sep 19, 2026

## DeconRNASeq

RRID:SCR\_006713

Type: Tool

### Proper Citation

DeconRNASeq (RRID:SCR\_006713)

### Resource Information

**URL:** <http://www.bioconductor.org/packages/2.12/bioc/html/DeconRNASeq.html>

**Proper Citation:** DeconRNASeq (RRID:SCR\_006713)

**Description:** An R package for deconvolution of heterogeneous tissues based on mRNA-Seq data. It modeled expression levels from heterogeneous cell populations in mRNA-Seq as the weighted average of expression from different constituting cell types and predicted cell type proportions of single expression profiles.

**Abbreviations:** DeconRNASeq

**Resource Type:** software resource

**Resource Name:** DeconRNASeq

**Resource ID:** SCR\_006713

**Alternate IDs:** OMICS\_01230

**Record Creation Time:** 20220129T080237+0000

**Record Last Update:** 20260919T195116+0000

### Ratings and Alerts

No rating or validation information has been found for DeconRNASeq.

No alerts have been found for DeconRNASeq.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 44 mentions in open access literature.

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

Dumanis G, et al. (2026) Medulloblastoma immune microenvironment resembles early brain development and reveals novel basophil- B cell- associated signatures. *Neuro-oncology advances*, 8(1), vdag134.

Lin W, et al. (2026) transFusion: a novel comprehensive platform for integration analysis of single-cell and spatial transcriptomics. *Bioinformatics (Oxford, England)*, 42(2).

Hamilton MS, et al. (2026) Protocol for a biomarker discovery study to identify correlates of risk for future tuberculosis disease progression in South African children (INTREPID). *BMJ open*, 16(2), e099348.

Pant S, et al. (2026) Erdafitinib in Patients with FGFR-Altered Advanced or Metastatic Cholangiocarcinoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(6), 1136.

Zhao L, et al. (2026) Transcriptomic analysis reveals the impact of concurrent, resistance, and endurance training on skeletal muscle. *PloS one*, 21(2), e0340309.

Cao D, et al. (2025) Time-series single-cell transcriptomic profiling of luteal-phase endometrium uncovers dynamic characteristics and its dysregulation in recurrent implantation failures. *Nature communications*, 16(1), 137.

S??mon M, et al. (2025) Comparative transcriptomics in serial organs uncovers early and pan-organ developmental changes associated with organ-specific morphological adaptation. *Nature communications*, 16(1), 768.

Yu H, et al. (2025) Identification of the body fluid donors from mixture stains using bulk transcriptomes data. *Briefings in bioinformatics*, 26(6).

Amblard E, et al. (2025) A robust workflow to benchmark deconvolution of multi-omic data. *Genome biology*, 26(1), 429.

Zhang W, et al. (2025) Deconer: An Evaluation Toolkit for Reference-based Deconvolution Methods Using Gene Expression Data. *Genomics, proteomics & bioinformatics*, 23(1).

Wang L, et al. (2024) Single-cell transcriptomic-informed deconvolution of bulk data identifies immune checkpoint blockade resistance in urothelial cancer. *iScience*, 27(6), 109928.

Larsen JH, et al. (2024) Benchmarking transcriptome deconvolution methods for estimating tissue- and cell-type-specific extracellular vesicle abundances. *Journal of extracellular vesicles*, 13(9), e12511.

Hurtado M, et al. (2024) Transcriptomics profiling of the non-small cell lung cancer microenvironment across disease stages reveals dual immune cell-type behaviors. *Frontiers in immunology*, 15, 1394965.

Wang C, et al. (2024) Deconvolution from bulk gene expression by leveraging sample-wise and gene-wise similarities and single-cell RNA-Seq data. BMC genomics, 25(1), 875.

Armero AS, et al. (2024) Co-analysis of methylation platforms for signatures of biological aging in the domestic dog reveals previously unexplored confounding factors. Aging, 16(13), 10724.

Ahn C, et al. (2024) An optimized pipeline for high-throughput bulk RNA-Seq deconvolution illustrates the impact of obesity and weight loss on cell composition of human adipose tissue. bioRxiv : the preprint server for biology.

Lu Q, et al. (2024) Inferring tumor purity using multi-omics data based on a uniform machine learning framework MoTP. Briefings in bioinformatics, 26(1).

Revkov E, et al. (2023) PUREE: accurate pan-cancer tumor purity estimation from gene expression data. Communications biology, 6(1), 394.

Barone DG, et al. (2022) Prevention of the foreign body response to implantable medical devices by inflammasome inhibition. Proceedings of the National Academy of Sciences of the United States of America, 119(12), e2115857119.

Schmidt AF, et al. (2022) Fetal maturation revealed by amniotic fluid cell-free transcriptome in rhesus macaques. JCI insight, 7(18).