

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 1, 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: 20260801T190318+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 39 mentions in open access literature.

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

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.

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

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.

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.

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.

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.

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.

Rostovskaya M, et al. (2022) Amniogenesis occurs in two independent waves in primates. *Cell stem cell*, 29(5), 744.

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).

Sutton GJ, et al. (2022) Comprehensive evaluation of deconvolution methods for human brain gene expression. *Nature communications*, 13(1), 1358.

Tran TH, et al. (2022) Whole-transcriptome analysis in acute lymphoblastic leukemia: a report from the DFCI ALL Consortium Protocol 16-001. *Blood advances*, 6(4), 1329.

Betto RM, et al. (2021) Metabolic control of DNA methylation in naive pluripotent cells. *Nature genetics*, 53(2), 215.

Elosua-Bayes M, et al. (2021) SPOTlight: seeded NMF regression to deconvolute spatial transcriptomics spots with single-cell transcriptomes. *Nucleic acids research*, 49(9), e50.