Resource Summary Report

Generated by dkNET on Apr 24, 2025

edgeR

RRID:SCR_012802

Type: Tool

Proper Citation

edgeR (RRID:SCR_012802)

Resource Information

URL: http://bioconductor.org/packages/edgeR/

Proper Citation: edgeR (RRID:SCR_012802)

Description: Bioconductor software package for Empirical analysis of Digital Gene Expression data in R. Used for differential expression analysis of RNA-seq and digital gene expression data with biological replication.

Abbreviations: edgeR

Synonyms: edgeR, empirical analysis of digital gene expression data in R, Empirical analysis of Digital Gene Expression data in R

Resource Type: data analysis software, data processing software, software resource, software application

Defining Citation: PMID:19910308, DOI:10.1093/bioinformatics/btp616

Keywords: empirical, analysis, digital, gene, expression, data, R, RNA-seq data, bio.tools

Funding: NHMRC 406657;

Independent Research Institutes Infrastructure Support Scheme 361646;

Victorian State Government OIS grant;

Melbourne International Research Scholarship;

Harris and IBS Honours scholarships

Availability: Free, Available for download, Freely available

Resource Name: edgeR

Resource ID: SCR_012802

Alternate IDs: OMICS_01308, biotools:edger

Alternate URLs: https://bio.tools/edger, https://sources.debian.org/src/r-bioc-edger/

License: GPL

Record Creation Time: 20220129T080312+0000

Record Last Update: 20250423T060700+0000

Ratings and Alerts

No rating or validation information has been found for edgeR.

No alerts have been found for edgeR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 18878 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Wang K, et al. (2025) Exploring the Role of Ccn3 in Type III Cell of Mice Taste Buds. Journal of neurochemistry, 169(1), e16291.

Meng J, et al. (2025) Porcine granulosa cell transcriptomic analyses reveal the differential regulation of IncRNAs and mRNAs in response to all-trans retinoic acid in vitro. Animal bioscience, 38(2), 267.

Zhang MJ, et al. (2025) Oncolytic herpes simplex virus propagates tertiary lymphoid structure formation via CXCL10/CXCR3 to boost antitumor immunity. Cell proliferation, 58(1), e13740.

Hellen DJ, et al. (2025) A Microphysiological Model of Progressive Human Hepatic Insulin Resistance. bioRxiv: the preprint server for biology.

Krasik SV, et al. (2025) Systematic evaluation of intratumoral and peripheral BCR repertoires in three cancers. eLife, 13.

Albano F, et al. (2025) Selective expression and significance of ACKR2 in lung aerocytes.

Journal for immunotherapy of cancer, 13(1).

Candela ME, et al. (2025) Cryopreserved human alternatively activated macrophages promote resolution of acetaminophen-induced liver injury in mouse. NPJ Regenerative medicine, 10(1), 5.

Cook PC, et al. (2025) Mgl2+ cDC2s coordinate fungal allergic airway type 2, but not type 17, inflammation in mice. Nature communications, 16(1), 928.

Martins V, et al. (2025) Subregional pedoclimatic conditions with contrasted UV-radiation shape host-microbiome and metabolome phenotypes in the grape berry. Food chemistry: X, 25, 102139.

Tombácz D, et al. (2025) Temporal transcriptional profiling of host cells infected by a veterinary alphaherpesvirus using nanopore sequencing. Scientific reports, 15(1), 3247.

Yeh H, et al. (2025) Development and characterization of in vitro inducible immortalization of a murine microglia cell line for high throughput studies. Scientific reports, 15(1), 3207.

Kiesworo K, et al. (2025) Nicotinamide mononucleotide restores impaired metabolism, endothelial cell proliferation and angiogenesis in old sedentary male mice. iScience, 28(1), 111656.

Leshem R, et al. (2025) Combined PARP14 inhibition and PD-1 blockade promotes cytotoxic T cell quiescence and modulates macrophage polarization in relapsed melanoma. Journal for immunotherapy of cancer, 13(1).

Li D, et al. (2025) Seed microbiomes promote Astragalus mongholicus seed germination through pathogen suppression and cellulose degradation. Microbiome, 13(1), 23.

Zhang H, et al. (2025) Omics-Based Interaction Analysis Reveals Interplay of Chemical Pollutant (Ozone) and Photoradiation (UVSSR) Stressors in Skin Damage. Biology, 14(1).

Hong JY, et al. (2025) Differential Gene Expression Analysis in a Lumbar Spinal Stenosis Rat Model via RNA Sequencing: Identification of Key Molecular Pathways and Therapeutic Insights. Biomedicines, 13(1).

Benkhalifa M, et al. (2025) Quantification of Free Circulating DNA and Differential Methylation Profiling of Selected Genes as Novel Non-Invasive Biomarkers for Endometriosis Diagnosis. Biomolecules, 15(1).

Shi L, et al. (2025) CRISPRepi: a multi-omic atlas for CRISPR-based epigenome editing. Nucleic acids research, 53(D1), D901.

Faliti CE, et al. (2025) Disease-associated B cells and immune endotypes shape adaptive immune responses to SARS-CoV-2 mRNA vaccination in human SLE. Nature immunology, 26(1), 131.

Bergamasco MI, et al. (2025) KAT6B is required for histone 3 lysine 9 acetylation and SOX gene expression in the developing brain. Life science alliance, 8(2).