Resource Summary Report

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DESeq2

RRID:SCR_015687
Type: Tool

Proper Citation

DESeq2 (RRID:SCR_015687)

Resource Information

URL: https://bioconductor.org/packages/release/bioc/html/DESeq2.html

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Description: Software package for differential gene expression analysis based on the negative binomial distribution. Used for analyzing RNA-seq data for differential analysis of count data, using shrinkage estimation for dispersions and fold changes to improve stability and interpretability of estimates.

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

Keywords: differential, gene, expression, analysis, binominal, distribution, RNA-seq data, Bioconductor, bio.tools

Funding: International Max Planck Research School for Computational Biology and Scientific Computing ;
NCI T32 CA009337;
European Union’s 7th Framework Programme

Availability: Free, Available for download, Freely available

Resource Name: DESeq2

Resource ID: SCR_015687

Alternate IDs: biotools:deseq2

Alternate URLs: https://github.com/mikelove/DESeq2, https://bio.tools/deseq2

Record Creation Time: 20220129T080327+0000

Record Last Update: 20250517T060223+0000

Ratings and Alerts

No rating or validation information has been found for DESeq2.

No alerts have been found for DESeq2.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 34538 mentions in open access literature.

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

Bryan E, et al. (2025) Nucleosomal asymmetry shapes histone mark binding and promotes poising at bivalent domains. Molecular cell, 85(3), 471.

Ramponi V, et al. (2025) H4K20me3-Mediated Repression of Inflammatory Genes Is a Characteristic and Targetable Vulnerability of Persister Cancer Cells. Cancer research, 85(1), 32.

Guillou MC, et al. (2025) Phytocytokine genes newly discovered in Malus domestica and their regulation in response to Erwinia amylovora and acibenzolar-S-methyl. The plant genome, 18(1), e20540.

Gabiatti BP, et al. (2025) Trypanosoma cruzi eIF4E3- and eIF4E4-containing complexes bind different mRNAs and may sequester inactive mRNAs during nutritional stress. Nucleic acids research, 53(2).

Tejedor JR, et al. (2025) Integration of multi-omics layers empowers precision diagnosis through unveiling pathogenic mechanisms on maple syrup urine disease. Journal of inherited metabolic disease, 48(1), e12829.

Wu Q, et al. (2025) Defects in the H3t Gene Cause an Increase in Leydig Cells With Impaired Spermatogenesis in Mice. Genes to cells : devoted to molecular & cellular mechanisms, 30(1), e13182.

Xu X, et al. (2025) Endonuclease G promotes hepatic mitochondrial respiration by selectively

increasing mitochondrial tRNAThr production. Proceedings of the National Academy of Sciences of the United States of America, 122(1), e2411298122.

Chen YC, et al. (2025) PreLect: Prevalence leveraged consistent feature selection decodes microbial signatures across cohorts. NPJ biofilms and microbiomes, 11(1), 3.

Huang XX, et al. (2025) Effects of RAR? ligand binding domain mutations on breast fibroepithelial tumor function and signaling. NPJ breast cancer, 11(1), 1.

Qin Q, et al. (2025) Enhanced glycolysis-derived lactate promotes microglial activation in Parkinson's disease via histone lactylation. NPJ Parkinson's disease, 11(1), 3.

Würth R, et al. (2025) Circulating tumor cell plasticity determines breast cancer therapy resistance via neuregulin 1-HER3 signaling. Nature cancer, 6(1), 67.

Kirmizakis P, et al. (2025) Microbial fuel cells to monitor natural attenuation around groundwater plumes. Environmental science and pollution research international, 32(4), 2069.

Hu W, et al. (2025) CYP3A5 promotes glioblastoma stemness and chemoresistance through fine-tuning NAD+/NADH ratio. Journal of experimental & clinical cancer research : CR, 44(1), 3.

Xu C, et al. (2025) Predicting hepatocellular carcinoma outcomes and immune therapy response with ATP-dependent chromatin remodeling-related genes, highlighting MORF4L1 as a promising target. Cancer cell international, 25(1), 4.

Wang Y, et al. (2025) hAMSCs regulate EMT in the progression of experimental pulmonary fibrosis through delivering miR-181a-5p targeting TGFBR1. Stem cell research & therapy, 16(1), 2.

Orlovskis Z, et al. (2025) The phytoplasma SAP54 effector acts as a molecular matchmaker for leafhopper vectors by targeting plant MADS-box factor SVP. eLife, 13.

Raiter A, et al. (2025) Galectin-3 secreted by triple-negative breast cancer cells regulates T cell function. Neoplasia (New York, N.Y.), 60, 101117.

Dong J, et al. (2025) ZNF143 binds DNA and stimulates transcription initiation to activate and repress direct target genes. Nucleic acids research, 53(2).

Nishino K, et al. (2025) Functional dissection of metabolic trait-associated gene regulation in steady state and stimulated human skeletal muscle cells. bioRxiv : the preprint server for biology.

Bae S, et al. (2025) Lonafarnib Protects Against Muscle Atrophy Induced by Dexamethasone. Journal of cachexia, sarcopenia and muscle, 16(1), e13665.