

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

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>

License: LGPL

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260801T190754+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 43994 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Stern YE, et al. (2026) Targeting CDK12/13 Drives Mitotic Arrest to Overcome Resistance to KRASG12C Inhibitors. Cancer research, 86(2), 485.

Devapatla P, et al. (2026) Multi-Target Effects of Novel Synthetic Indanedione-Based Spirotransdicalinol Compound 4I in Autosomal Dominant Polycystic Kidney Disease. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 40(1), e71409.

Yang W, et al. (2026) Multi-omics reveals co-regulation of hepatic bile acid metabolism in laying hens by host genetics and the cecal Anaerostipes. Poultry science, 105(3), 106388.

Yan C, et al. (2026) RAS/MEK/PI3K pathway inhibition augments response to CD40 agonism by targeting CD11b+ Bregs thereby overcoming melanoma PD1-resistance. Nature communications, 17(1), 162.

Dunn LN, et al. (2026) Altered hepatic metabolism in Down syndrome. Cell reports, 45(1), 116835.

Herbrich S, et al. (2026) TET2-mutant clonal hematopoiesis enhances macrophage antigen presentation and improves immune checkpoint therapy in solid tumors. Cancer cell, 44(1), 187.

D'Alessio A, et al. (2026) Neurometabolic adaptations to intestinal inflammation in a mouse model of colitis. American journal of physiology. Gastrointestinal and liver physiology, 330(2), G98.

Nitsch S, et al. (2026) H4K16 acylations destabilize chromatin architecture and facilitate transcriptional response during metabolic perturbations. Molecular cell, 86(1), 24.

Cappadona C, et al. (2026) Multi-omics identifies oxidative stress, prothrombotic pathways, and lactoperoxidase variants as key factors in COVID-19 severity. EBioMedicine, 123, 106111.

Williams EC, et al. (2026) Expression of endogenous retroviral elements is associated with extracellular matrix remodeling in prostate cancer. *Mobile DNA*, 17(1), 1.

Allen AM, et al. (2026) Differential neuronal survival defines a novel axis of sexual dimorphism in the *Drosophila* brain. *Cell genomics*, 101125.

Lu G, et al. (2026) In vivo detection of immune responses via cytokine activity labeling. *Cell*.

Huang X, et al. (2026) Integrin/CD44-targeted liposomes remodel the pulmonary microenvironment to alleviate acute exacerbation of pulmonary fibrosis. *Journal of controlled release : official journal of the Controlled Release Society*, 389, 114427.

Yesupatham SK, et al. (2026) Transcriptome profiling suggests molecular sexual dimorphism in lumbosacral dorsal root ganglia and sex-specific mechanisms underlying visceral pain. *Physiological genomics*, 58(1), 12.

Kärkkäinen M, et al. (2026) Integrative omics approaches to uncover liquid-based cancer-predicting biomarkers in Lynch syndrome. *International journal of cancer*, 158(1), 243.

Sperschneider J, et al. (2026) The fungal pathogen *Rhizoctonia solani* AG-8 has 2 nuclear haplotypes that differ in abundance. *G3 (Bethesda, Md.)*, 16(1).

Chen K, et al. (2026) Liquid?liquid phase separation of PHLDB2 promotes oral squamous cell carcinoma metastasis through regulating epithelial mesenchymal transition and PIK3CA expression. *Molecular medicine reports*, 33(1).

Li X, et al. (2026) Site-Specific Mitochondrial RNA N1-Methyladenosine Demethylation via an Engineered MTS-PUF-ALKBH3 Fusion Protein. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(1), e10482.

Barnes-Vélez JA, et al. (2026) Peroxisomal integrity in demyelination-associated microglia enables cellular debris clearance and myelin renewal in mice. *The Journal of clinical investigation*, 136(1).

Zhu Z, et al. (2026) EP300/YAP1-SERPINE1 Signaling Regulates Ductular Reaction and Liver Fibrosis in Biliary Atresia. *Cellular and molecular gastroenterology and hepatology*, 20(1), 101640.