

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, software resource, data analysis software, 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: 20260819T044427+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 50789 mentions in open access literature.

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

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.

Fresques T, et al. (2026) YAP1 Dysfunction Promotes Molecular Properties Linked to Breast Cancer Susceptibility. *Cancer prevention research (Philadelphia, Pa.)*, 19(4), 203.

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.

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.

Tollenaere A, et al. (2026) Mechanisms of gene regulation by SRCAP and H2A.Z. *Nature communications*, 17(1).

Yang Z, et al. (2026) Syndecan-1-targeted therapeutic antibody impairs macropinocytosis and elicits antitumor immunity in pancreatic cancer. *Cell reports. Medicine*, 7(2), 102613.

Ito T, et al. (2026) RLF/ZFP292 stabilize CoREST-linked LSD1 engagement at bivalent promoters to safeguard pluripotency. *Cell reports*, 45(4), 117293.

Sun JL, et al. (2026) Ferroptotic tumor cells reprogram tumor-associated macrophage antigen presentation to enhance the efficacy of immune checkpoint blockade. *Cell reports. Medicine*, 7(5), 102774.

Petrova V, et al. (2026) A human iPSC-derived sensory neuron platform for high-throughput discovery of neuroprotectants against chemotherapy-induced peripheral neuropathy. *Cell reports. Medicine*, 7(5), 102787.

Weerasopon K, et al. (2026) Loss of Ezh2 promotes M2-like macrophage polarization in hepatocellular carcinoma. *iScience*, 29(4), 115180.

van der Elst A, et al. (2026) Molecular and Immune Landscape of Recurrent and/or Distant Metastatic Squamous Cell Carcinoma of the Head and Neck: An EORTC/IMMUCAN Project. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(13), 2732.

Kelly B, et al. (2026) Sulfur partitioning from cysteine controls T cell proliferation and effector function. *Cell*, 189(12), 3669.

Sato K, et al. (2026) Aberrant Hippo-YAP/TEAD Signaling Drives Malignant Transcriptional Reprogramming in External Auditory Canal Squamous Cell Carcinoma. *Cancer research communications*, 6(2), 260.

Al-Azzam S, et al. (2026) Multi-omics profiling reveals microenvironmental remodeling as a key driver of house dust mite-induced lung cancer progression. *Neoplasia (New York, N.Y.)*, 73, 101275.

Prasad M, et al. (2026) Genomic Enrichment and Functional Impact of TP53 and CYLD Alterations in Recurrent and Metastatic HPV-Associated Head and Neck Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(9), 1809.

Tsymala I, et al. (2026) Innate lymphoid cells integrate sensing and plasticity to control fungal infections. *Cell reports*, 45(4), 117140.

Li H, et al. (2026) Tumor Extracellular Vesicles IncOSLMT Drives Lung Inflammatory Premetastatic Niche Formation in Osteosarcoma via m6A-Dependent hnRNPA2B1/COX-2 Axis. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(17), e19490.

Huang Y, et al. (2026) A positive feedback loop between FGR and p65 sustains satellite glial cell activation and chronic neuropathic pain. *Cell reports*, 45(2), 116899.

Yang J, et al. (2026) A Malignant Subpopulation of H2AFZ+ Cells Interacts with Myeloid Cells to Promote an Anti-inflammatory Microenvironment and Drive Hepatic Metastasis, Revealing an Immunotherapeutic Strategy for Pancreatic Ductal Adenocarcinoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(12), 2479.