

Resource Summary Report

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DEXSeq

RRID:SCR_012823

Type: Tool

Proper Citation

DEXSeq (RRID:SCR_012823)

Resource Information

URL: <http://bioconductor.org/packages/release/bioc/html/DEXSeq.html>

Proper Citation: DEXSeq (RRID:SCR_012823)

Description: Software package focused on finding differential exon usage using RNA-seq exon counts between samples with different experimental designs. It provides functions that allows the user to make the necessary statistical tests based on a model that uses the negative binomial distribution to estimate the variance between biological replicates and generalized linear models for testing. The package also provides functions for the visualization and exploration of the results.

Abbreviations: DEXSeq

Resource Type: software resource

Keywords: bio.tools

Resource Name: DEXSeq

Resource ID: SCR_012823

Alternate IDs: OMICS_01329, biotools:dexseq

Alternate URLs: <https://bio.tools/dexseq>

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260808T190016+0000

Ratings and Alerts

No rating or validation information has been found for DEXSeq.

No alerts have been found for DEXSeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 540 mentions in open access literature.

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

Hu Z, et al. (2026) CRISPR/Cas9 screening with destabilized bicistronic fluorescent protein reporter revealed PABPN1 as a hub of regulators for alternative polyadenylation. *Nucleic acids research*, 54(5).

Nunes de Almeida F, et al. (2026) A forward genetic screen identifies Sirtuin1 as a driver of neuroendocrine prostate cancer. *The Journal of experimental medicine*, 223(7).

Polizel GHG, et al. (2026) Maternal nutrition alters mRNA isoform expression, usage, and splicing dynamics in skeletal muscle of beef cattle offspring. *Frontiers in genetics*, 17, 1734234.

Zhao LN, et al. (2026) Alternative splicing regulates FGGY-derived neoantigen presentation and promotes immune evasion in metabolic-associated hepatocellular carcinoma. *iScience*, 29(6), 115999.

Margetts AV, et al. (2026) Morphine and methamphetamine trigger divergent post-transcriptional neuroimmune landscapes in the dorsal striatum. *bioRxiv : the preprint server for biology*.

Yu H, et al. (2026) Transcriptome Profiling of Powdery Mildew-Stressed 'Yeniang No. 2' Grapevine Reveals Differential Expression, Alternative Splicing, and the Identification of 1232 Annotated Novel Genes. *Metabolites*, 16(3).

Mao Y, et al. (2026) TAR syndrome causal gene RBM8A is critical for embryonic bone development and proper Hedgehog signaling. *Research square*.

Hao S, et al. (2026) Genomic basis underlying alternative transcripts-mediated drought tolerance in maize. *Genome biology*, 27(1), 47.

Zhang J, et al. (2026) Alternative Polyadenylation Drives Runaway Pro-Inflammatory Macrophages in Periodontitis by Enabling Escape From miRNA Repression. *Cell proliferation*, 59(6), e70156.

Fardellas A, et al. (2026) ADAR1 Controls Macrophage Scavenging and Lipid-Buffering Programs in Metabolic Tissues. *European journal of immunology*, 56(4), e70189.

Abou Karam P, et al. (2026) Nuclear import of malaria RNA rewires splicing in host immune cells. *Cell reports*, 45(2), 116953.

Vendramin R, et al. (2026) Nonsense-mediated mRNA decay inhibition reshapes the cancer immunopeptidome. *Immunity*, 59(5), 1398.

Baltazar-Soares M, et al. (2026) Transcriptomics Reveal Molecular Signatures of a Resolved Sexual Conflict and Potential Association With Colour Polymorphism in Tawny Owls. *Molecular ecology*, 35(7), e70338.

Kopczyńska M, et al. (2026) SETD2 methyltransferase activity promotes correct transcription initiation and termination. *EMBO reports*, 27(9), 2218.

Ruan T, et al. (2026) A novel dual histone mark reader ZCWPW2 regulates meiotic recombination through lactylation and transcriptional regulation in humans and mice. *Nucleic acids research*, 54(3).

Huang Y, et al. (2026) Long-read sequencing and proteomics reveal blood transcriptome and protein expression profiles in multiple primary lung cancers. *BMC cancer*, 26(1).

Stevens MB, et al. (2026) The human branchpoint-interacting stem-loop sequence and structure regulates U2 snRNA expression, branchpoint recognition, and the transcriptome. *Nucleic acids research*, 54(6).

Behrouz Sharif S, et al. (2026) WSTF deficiency reprograms regulatory networks by linking locus-specific chromatin remodeling to altered isoform expression and misdirected signaling. *Nucleic acids research*, 54(11).

Khavesh N, et al. (2026) Integrative multi-omics analysis of growth plate regulation underlying body size in miniature pigs. *Communications biology*, 9(1).

Maeda M, et al. (2026) CRISPR screen of human pancreatic cancer xenografts identifies a KLF5 proliferation vulnerability through epigenetic modifiers NCAPD2 and MTHFD1. *Molecular cancer*, 25(1).