# **Resource Summary Report**

Generated by NIF on Apr 26, 2025

# **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

Funding:

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: 20250420T014620+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 464 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

Kim MS, et al. (2025) A combination of upstream alleles involved in rice heading hastens natural long-day responses. Genes & genomics, 47(2), 245.

Lu X, et al. (2024) Transcriptional Determinism and Stochasticity Contribute to the Complexity of Autism Associated SHANK Family Genes. bioRxiv : the preprint server for biology.

Bhattacharyya N, et al. (2024) Deciphering novel TCF4-driven mechanisms underlying a common triplet repeat expansion-mediated disease. PLoS genetics, 20(5), e1011230.

Jones EF, et al. (2024) Long-read RNA sequencing identifies region- and sex-specific C57BL/6J mouse brain mRNA isoform expression and usage. bioRxiv : the preprint server for biology.

Mironov A, et al. (2024) Leveraging multi-omics data to infer regulators of mRNA 3' end processing in glioblastoma. Frontiers in molecular biosciences, 11, 1363933.

II?k ?A, et al. (2024) Autonomous transposons tune their sequences to ensure somatic suppression. Nature, 626(8001), 1116.

Long T, et al. (2024) Odorant receptor co-receptors affect expression of tuning receptors in Drosophila. Frontiers in cellular neuroscience, 18, 1390557.

Cho HM, et al. (2024) Transcriptome analysis of cynomolgus macaques throughout their lifespan reveals age-related immune patterns. npj aging, 10(1), 30.

Krueger A, et al. (2024) The essential kinase TgGSK regulates centrosome division and endodyogeny in Toxoplasma gondii. bioRxiv : the preprint server for biology.

Fowler CE, et al. (2024) The PRMT5-splicing axis is a critical oncogenic vulnerability that regulates detained intron splicing. bioRxiv : the preprint server for biology.

Zeng Y, et al. (2024) TDP-43 nuclear loss in FTD/ALS causes widespread alternative polyadenylation changes. bioRxiv : the preprint server for biology.

Lio CT, et al. (2024) Comprehensive benchmark of differential transcript usage analysis for static and dynamic conditions. bioRxiv : the preprint server for biology.

Yamanaka T, et al. (2024) The transcription factor NF-YA is crucial for neural progenitor maintenance during brain development. The Journal of biological chemistry, 300(2), 105629.

Li Y, et al. (2024) Comparative transcriptomics analysis on Senecavirus A-infected and non-infected cells. Frontiers in veterinary science, 11, 1431879.

Lu X, et al. (2024) Transcriptional determinism and stochasticity contribute to the complexity of autism-associated SHANK family genes. Cell reports, 43(7), 114376.

Shayler DWH, et al. (2024) Identification and characterization of early human photoreceptor states and cell-state-specific retinoblastoma-related features. bioRxiv : the preprint server for biology.

Nikonova E, et al. (2024) Bruno 1/CELF regulates splicing and cytoskeleton dynamics to ensure correct sarcomere assembly in Drosophila flight muscles. PLoS biology, 22(4), e3002575.

Weng Y, et al. (2024) Male-specific behavioral and transcriptomic changes in aging C. elegans neurons. iScience, 27(6), 109910.

Vieira de Sá R, et al. (2024) ATAXIN-2 intermediate-length polyglutamine expansions elicit ALS-associated metabolic and immune phenotypes. Nature communications, 15(1), 7484.

Guisasola-Serrano A, et al. (2024) Identifying transcriptomic profiles in ovine spleen after repetitive vaccination. Frontiers in immunology, 15, 1386590.