Resource Summary Report

Generated by kravitz2 on Jul 31, 2026

EDASeq

RRID:SCR_006751
Type: Tool

Proper Citation

EDASeq (RRID:SCR_006751)

Resource Information

URL: http://watson.nci.nih.gov/bioc_mirror/packages/2.11/bioc/html/EDASeq.html

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Description: Software for numerical and graphical summaries of RNA-Seq read data. Within-lane normalization procedures to adjust for GC-content effect (or other gene-level effects) on read counts: loess robust local regression, global-scaling, and full-quantile normalization (Risso et al., 2011). Between-lane normalization procedures to adjust for distributional differences between lanes (e.g., sequencing depth): global-scaling and full-quantile normalization (Bullard et al., 2010)., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: EDASeq

Synonyms: EDASeq: Exploratory Data Analysis and Normalization for RNA-Seq data

Resource Type: software resource

Keywords: data analysis, normalization, rna-seq

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: EDASeq

Resource ID: SCR_006751

Alternate IDs: OMICS_01231

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260725T190627+0000

Ratings and Alerts

No rating or validation information has been found for EDASeq.

No alerts have been found for EDASeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 254 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Hulbert A, et al. (2025) CEACAM7 Expression and DNA Methylation: Prognostic Biomarkers for Lung Adenocarcinoma in African Americans. Journal of thoracic oncology : official publication of the International Association for the Study of Lung Cancer.

Sulaiman F, et al. (2025) Characterizing Circulating microRNA Signatures of Type 2 Diabetes Subtypes. International journal of molecular sciences, 26(2).

Zhang C, et al. (2025) HBO1 determines epithelial-mesenchymal transition and promotes immunotherapy resistance in ovarian cancer cells. Cellular oncology (Dordrecht, Netherlands), 48(4), 943.

Huang J, et al. (2025) Model-to-crop conserved NUE Regulons enhance machine learning predictions of nitrogen use efficiency. The Plant cell, 37(5).

Guan Y, et al. (2025) Abundant Parent-of-origin Effect eQTL: The Framingham Heart Study. bioRxiv : the preprint server for biology.

Bodmer NK, et al. (2025) Latent transforming growth factor binding protein-2 (LTBP2), an IPF biomarker of clinical decline, promotes TGF-beta signaling and lung fibrosis in mice. bioRxiv : the preprint server for biology.

Hanna AD, et al. (2025) Mechanisms underlying dilated cardiomyopathy associated with FKBP12 deficiency. The Journal of general physiology, 157(1).

Castelvecchi G, et al. (2025) Regulation of the Yolk Microtubule and Actin Cytoskeleton by Dachsous Cadherins during Zebrafish Epiboly. bioRxiv : the preprint server for biology.

Dheedene W, et al. (2025) Loss of endothelial ZEB2 in mice attenuates steatosis early during metabolic dysfunction-associated steatotic liver disease. Scientific reports, 15(1), 23434.

Zhao K, et al. (2025) METTL13 is essential for the survival of acute myeloid leukemia cells by regulating MYC. Cell death discovery, 11(1), 240.

Wang F, et al. (2025) ELK4 induced upregulation of HOMER3 promotes the proliferation and metastasis in glioma via Wnt/?-catenin/EMT signaling pathway. Biology direct, 20(1),

48.

Petrohilos C, et al. (2025) No Evidence for Distinct Transcriptomic Subgroups of Devil Facial Tumor Disease (DFTD). Evolutionary applications, 18(4), e70091.

van Oost S, et al. (2025) Divergent therapeutic and prognostic impacts of immunogenic features in undifferentiated pleomorphic sarcoma and myxofibrosarcoma. Cancer immunology, immunotherapy : CII, 74(8), 258.

Khodaparast L, et al. (2025) Co-translational protein aggregation and ribosome stalling as a broad-spectrum antibacterial mechanism. Nature communications, 16(1), 1561.

Zheng D, et al. (2025) CD4+ anti-TGF-? CAR T cells and CD8+ conventional CAR T cells exhibit synergistic antitumor effects. Cell reports. Medicine, 6(3), 102020.

Lawrence SS, et al. (2025) Interferon-?/Janus Kinase 1/STAT1 Signaling Represses Forkhead Box A1 and Drives a Basal Transcriptional State in Muscle-Invasive Bladder Cancer. The American journal of pathology, 195(5), 1013.

González JT, et al. (2025) Age-invariant genes: multi-tissue identification and characterization of murine reference genes. Aging, 17(1), 170.

Kelley LH, et al. (2024) Poly(U) polymerase activity in Caenorhabditis elegans regulates abundance and tailing of sRNA and mRNA. Genetics, 228(2).

Fouziya S, et al. (2024) Genome wide nucleosome landscape shapes 3D chromatin organization. Science advances, 10(23), eadn2955.

Zhu Y, et al. (2024) Disruption of MAM integrity in mutant FUS oligodendroglial progenitors from hiPSCs. Acta neuropathologica, 147(1), 6.