

Resource Summary Report

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easyRNASeq

RRID:SCR_012020

Type: Tool

Proper Citation

easyRNASeq (RRID:SCR_012020)

Resource Information

URL: <http://www.bioconductor.org/packages/2.11/bioc/html/easyRNASeq.html>

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Description: Software that calculates the coverage of high-throughput short-reads against a genome of reference and summarizes it per feature of interest (e.g. exon, gene, transcript). The data can be normalized as "RPKM" or by the "DESeq" or "edgeR" package.

Abbreviations: easyRNASeq

Synonyms: easyRNASeq - Count summarization and normalization for RNA-Seq data

Resource Type: software resource

Defining Citation: [PMID:22847932](#)

Keywords: rna-seq, gene expression, genetics, preprocessing, bio.tools

Availability: Artistic License, v2

Resource Name: easyRNASeq

Resource ID: SCR_012020

Alternate IDs: OMICS_01938, biotools:easyrnaseq

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

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260725T190726+0000

Ratings and Alerts

No rating or validation information has been found for easyRNASeq.

No alerts have been found for easyRNASeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 29 mentions in open access literature.

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

Saenz C, et al. (2025) Muscle transcriptome profiles in elite male ultra-endurance athletes acclimated to a high-carbohydrate versus low-carbohydrate diet. *Scientific reports*, 15(1), 8419.

Mora P, et al. (2024) Sex-biased gene content is associated with sex chromosome turnover in Danaini butterflies. *Molecular ecology*, 33(24), e17256.

Pal J, et al. (2021) Systematic analysis of migration factors by MigExpress identifies essential cell migration control genes in non-small cell lung cancer. *Molecular oncology*, 15(7), 1797.

Zhang M, et al. (2021) Identification of Differentially Expressed Genes and Lipid Metabolism Signaling Pathways between Muscle and Fat Tissues in Broiler Chickens. *The journal of poultry science*, 58(2), 131.

Newell NR, et al. (2020) The Drosophila Post-mating Response: Gene Expression and Behavioral Changes Reveal Perdurance and Variation in Cross-Tissue Interactions. *G3 (Bethesda, Md.)*, 10(3), 967.

Liu W, et al. (2020) Identification of lncRNA-associated differential subnetworks in oesophageal squamous cell carcinoma by differential co-expression analysis. *Journal of cellular and molecular medicine*, 24(8), 4804.

Mola S, et al. (2020) A transcriptome-based approach to identify functional modules within and across primary human immune cells. *PloS one*, 15(5), e0233543.

Bray ER, et al. (2019) Thrombospondin-1 Mediates Axon Regeneration in Retinal Ganglion Cells. *Neuron*, 103(4), 642.

Cocce KJ, et al. (2019) The Lineage Determining Factor GRHL2 Collaborates with FOXA1 to Establish a Targetable Pathway in Endocrine Therapy-Resistant Breast Cancer. *Cell reports*, 29(4), 889.

Hans CP, et al. (2019) Transcriptomics Analysis Reveals New Insights into the Roles of Notch1 Signaling on Macrophage Polarization. *Scientific reports*, 9(1), 7999.

Bundy JL, et al. (2019) Sex-biased hippocampal pathology in the 5XFAD mouse model of Alzheimer's disease: A multi-omic analysis. *The Journal of comparative neurology*, 527(2), 462.

Nordquist E, et al. (2018) Postnatal and Adult Aortic Heart Valves Have Distinctive Transcriptional Profiles Associated With Valve Tissue Growth and Maintenance Respectively. *Frontiers in cardiovascular medicine*, 5, 30.

Bundy JL, et al. (2017) Sex differences in the molecular signature of the developing mouse hippocampus. *BMC genomics*, 18(1), 237.

Piras IS, et al. (2017) Whole transcriptome profiling of the human hippocampus suggests an involvement of the KIBRA rs17070145 polymorphism in differential activation of the MAPK signaling pathway. *Hippocampus*, 27(7), 784.

Chen J, et al. (2017) A systems-level approach reveals new gene regulatory modules in the developing ear. *Development (Cambridge, England)*, 144(8), 1531.

Li CQ, et al. (2017) Integrative analyses of transcriptome sequencing identify novel functional lncRNAs in esophageal squamous cell carcinoma. *Oncogenesis*, 6(2), e297.

DiCarlo LM, et al. (2017) The stability of the transcriptome during the estrous cycle in four regions of the mouse brain. *The Journal of comparative neurology*, 525(15), 3360.

Jones BC, et al. (2016) A somatic piRNA pathway in the *Drosophila* fat body ensures metabolic homeostasis and normal lifespan. *Nature communications*, 7, 13856.

D'Argenio V, et al. (2016) The complete 12 Mb genome and transcriptome of *Nonomuraea gerenzanensis* with new insights into its duplicated "magic" RNA polymerase. *Scientific reports*, 6(1), 18.

Xing K, et al. (2016) Identification of genes for controlling swine adipose deposition by integrating transcriptome, whole-genome resequencing, and quantitative trait loci data. *Scientific reports*, 6, 23219.