

Resource Summary Report

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QuasiSeq

RRID:SCR_001715

Type: Tool

Proper Citation

QuasiSeq (RRID:SCR_001715)

Resource Information

URL: <https://cran.r-project.org/src/contrib/Archive/QuasiSeq/>

Proper Citation: QuasiSeq (RRID:SCR_001715)

Description: Software package to apply the QL, QLShrink and QLSpline methods to quasi-Poisson or quasi-negative binomial models for identifying differentially expressed genes in RNA-seq data.

Abbreviations: QuasiSeq

Resource Type: software resource

Defining Citation: [PMID:23104842](#)

Keywords: differential expression, gene, rna-seq, next generation sequencing, gene expression, mrna

Availability: Free, Available for download, Freely available

Resource Name: QuasiSeq

Resource ID: SCR_001715

Alternate IDs: OMICS_01963

Old URLs: <http://cran.r-project.org/web/packages/QuasiSeq/index.html>

License: GNU General Public License, v2, v3

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260801T190148+0000

Ratings and Alerts

No rating or validation information has been found for QuasiSeq.

No alerts have been found for QuasiSeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Hatfield BM, et al. (2023) Light cues induce protective anticipation of environmental water loss in terrestrial bacteria. *Proceedings of the National Academy of Sciences of the United States of America*, 120(38), e2309632120.

Barth VC, et al. (2019) Toxin-mediated ribosome stalling reprograms the Mycobacterium tuberculosis proteome. *Nature communications*, 10(1), 3035.

Kappeler BIG, et al. (2019) MiRNAs differentially expressed in skeletal muscle of animals with divergent estimated breeding values for beef tenderness. *BMC molecular biology*, 20(1), 1.

Assefa AT, et al. (2018) Differential gene expression analysis tools exhibit substandard performance for long non-coding RNA-sequencing data. *Genome biology*, 19(1), 96.

Vestal B, et al. (2018) miRNA-regulated transcription associated with mouse strains predisposed to hypnotic effects of ethanol. *Brain and behavior*, 8(6), e00989.

Gonçalves TM, et al. (2018) Gene Co-expression Analysis Indicates Potential Pathways and Regulators of Beef Tenderness in Nellore Cattle. *Frontiers in genetics*, 9, 441.

Poillet-Perez L, et al. (2018) Autophagy maintains tumour growth through circulating arginine. *Nature*, 563(7732), 569.

Guo H, et al. (2018) FERONIA Receptor Kinase Contributes to Plant Immunity by Suppressing Jasmonic Acid Signaling in *Arabidopsis thaliana*. *Current biology : CB*, 28(20), 3316.

Johnson TA, et al. (2017) The In-Feed Antibiotic Carbadox Induces Phage Gene Transcription in the Swine Gut Microbiome. *mBio*, 8(4).

Lin HY, et al. (2017) Substantial contribution of genetic variation in the expression of transcription factors to phenotypic variation revealed by eRD-GWAS. *Genome biology*, 18(1), 192.

Ye H, et al. (2017) RD26 mediates crosstalk between drought and brassinosteroid signalling pathways. *Nature communications*, 8, 14573.

Liu H, et al. (2016) Post-weaning blood transcriptomic differences between Yorkshire pigs divergently selected for residual feed intake. *BMC genomics*, 17, 73.

Kambakam S, et al. (2016) PTOX Mediates Novel Pathways of Electron Transport in Etioplasts of Arabidopsis. *Molecular plant*, 9(9), 1240.

Lanubile A, et al. (2015) Transcriptome profiling of soybean (*Glycine max*) roots challenged with pathogenic and non-pathogenic isolates of *Fusarium oxysporum*. *BMC genomics*, 16, 1089.

Nguyen Y, et al. (2015) Detecting Differentially Expressed Genes with RNA-seq Data Using Backward Selection to Account for the Effects of Relevant Covariates. *Journal of agricultural, biological, and environmental statistics*, 20(4), 577.

Wilkins KE, et al. (2015) TAL effectors and activation of predicted host targets distinguish Asian from African strains of the rice pathogen *Xanthomonas oryzae* pv. *oryzicola* while strict conservation suggests universal importance of five TAL effectors. *Frontiers in plant science*, 6, 536.

Wang X, et al. (2014) Histone lysine methyltransferase SDG8 is involved in brassinosteroid-regulated gene expression in *Arabidopsis thaliana*. *Molecular plant*, 7(8), 1303.

Zhang Y, et al. (2014) The Aux/IAA gene *rum1* involved in seminal and lateral root formation controls vascular patterning in maize (*Zea mays* L.) primary roots. *Journal of experimental botany*, 65(17), 4919.

Tang HM, et al. (2014) The maize brown midrib2 (*bm2*) gene encodes a methylenetetrahydrofolate reductase that contributes to lignin accumulation. *The Plant journal : for cell and molecular biology*, 77(3), 380.

Coble DJ, et al. (2014) RNA-seq analysis of broiler liver transcriptome reveals novel responses to high ambient temperature. *BMC genomics*, 15(1), 1084.