

# Resource Summary Report

Generated by T1D on Sep 19, 2026

## QuasiSeq

RRID:SCR\_001715

Type: Tool

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### Proper Citation

QuasiSeq (RRID:SCR\_001715)

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### 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:** 20260919T194945+0000

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### Ratings and Alerts

No rating or validation information has been found for QuasiSeq.

No alerts have been found for QuasiSeq.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 20 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#).

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.

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

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.

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.

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

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.