

Resource Summary Report

Generated by [dkNET](#) on May 7, 2025

PoissonSeq

RRID:SCR_001784

Type: Tool

Proper Citation

PoissonSeq (RRID:SCR_001784)

Resource Information

URL: <http://cran.r-project.org/web/packages/PoissonSeq/index.html>

Proper Citation: PoissonSeq (RRID:SCR_001784)

Description: Software package that implements a method for normalization, testing, and false discovery rate estimation for RNA-sequencing data.

Abbreviations: PoissonSeq

Synonyms: PoissonSeq: Significance analysis of sequencing data based on a Poisson log linear model

Resource Type: software resource

Defining Citation: [PMID:22003245](#)

Keywords: normalization, testing, false discovery rate, rna-seq

Funding:

Availability: GNU General Public License, v2, v3

Resource Name: PoissonSeq

Resource ID: SCR_001784

Alternate IDs: OMICS_01950

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250420T014039+0000

Ratings and Alerts

No rating or validation information has been found for PoissonSeq.

No alerts have been found for PoissonSeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Watkins JM, et al. (2024) Phosphorylation Dynamics in a flg22-Induced, G Protein-Dependent Network Reveals the AtRGS1 Phosphatase. *Molecular & cellular proteomics : MCP*, 23(2), 100705.

Song G, et al. (2024) Quantitative proteomics reveals extensive lysine ubiquitination and transcription factor stability states in Arabidopsis. *The Plant cell*, 37(1).

Muhammad D, et al. (2024) Global impacts of peroxisome and pexophagy dysfunction revealed through multi-omics analyses of lon2 and atg2 mutants. *The Plant journal : for cell and molecular biology*, 120(6), 2563.

Yin L, et al. (2023) Transcription Factor Dynamics in Cross-Regulation of Plant Hormone Signaling Pathways. *bioRxiv : the preprint server for biology*.

Olatunji D, et al. (2023) The class VIII myosin ATM1 is required for root apical meristem function. *Development (Cambridge, England)*, 150(20).

Buratin A, et al. (2023) Systematic benchmarking of statistical methods to assess differential expression of circular RNAs. *Briefings in bioinformatics*, 24(1).

Wang P, et al. (2022) Integrated omics reveal novel functions and underlying mechanisms of the receptor kinase FERONIA in Arabidopsis thaliana. *The Plant cell*, 34(7), 2594.

Llinas RJ, et al. (2022) An Arabidopsis pre-RNA processing8a (prp8a) missense allele restores splicing of a subset of mis-spliced mRNAs. *Plant physiology*, 189(4), 2175.

Rang FJ, et al. (2022) Single-cell profiling of transcriptome and histone modifications with EpiDamID. *Molecular cell*, 82(10), 1956.

Wang P, et al. (2021) The F-box E3 ubiquitin ligase BAF1 mediates the degradation of the brassinosteroid-activated transcription factor BES1 through selective autophagy in

Arabidopsis. The Plant cell, 33(11), 3532.

Yin S, et al. (2021) SMIXnorm: Fast and Accurate RNA-Seq Data Normalization for Formalin-Fixed Paraffin-Embedded Samples. Frontiers in genetics, 12, 650795.

Clark NM, et al. (2021) Integrated omics networks reveal the temporal signaling events of brassinosteroid response in Arabidopsis. Nature communications, 12(1), 5858.

Dash L, et al. (2021) slim shady is a novel allele of PHYTOCHROME B present in the T-DNA line SALK_015201. Plant direct, 5(6), e00326.

Qin LX, et al. (2020) Statistical Assessment of Depth Normalization for Small RNA Sequencing. JCO clinical cancer informatics, 4, 567.

Baik B, et al. (2020) Benchmarking RNA-seq differential expression analysis methods using spike-in and simulation data. PloS one, 15(4), e0232271.

Yegorov S, et al. (2019) Schistosoma mansoni treatment reduces HIV entry into cervical CD4+ T cells and induces IFN-I pathways. Nature communications, 10(1), 2296.

Lee AS, et al. (2019) Rare mutations in the complement regulatory gene CSMD1 are associated with male and female infertility. Nature communications, 10(1), 4626.

Hersh CP, et al. (2019) High-Throughput Sequencing in Respiratory, Critical Care, and Sleep Medicine Research. An Official American Thoracic Society Workshop Report. Annals of the American Thoracic Society, 16(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.

Santamaria ME, et al. (2018) Dehydration Stress Contributes to the Enhancement of Plant Defense Response and Mite Performance on Barley. Frontiers in plant science, 9, 458.