

Resource Summary Report

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PoissonSeq

RRID:SCR_001784

Type: Tool

Proper Citation

PoissonSeq (RRID:SCR_001784)

Resource Information

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

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

Availability: Free, Available for download, Freely available

Resource Name: PoissonSeq

Resource ID: SCR_001784

Alternate IDs: OMICS_01950

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

License: GNU General Public License, v2, v3

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260725T190510+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 33 mentions in open access literature.

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

Rishi JK, et al. (2025) Ovarian SUMO-2/3 targets and their differential response to genotoxic stress induced by 7,12-dimethylbenz(a) anthracene exposure in lean and obese female mice†. *Biology of reproduction*, 113(4), 962.

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.

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

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.

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.

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.

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.

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.