Resource Summary Report

Generated by NIF on Apr 28, 2025

baySeq

RRID:SCR_012795
Type: Tool

Proper Citation

baySeq (RRID:SCR_012795)

Resource Information

URL: http://www.bioconductor.org/packages/release/bioc/html/baySeq.html

Proper Citation: baySeq (RRID:SCR_012795)

Description: Software package that identifies differential expression in high-throughput "count" data, such as that derived from next-generation sequencing machines.

Abbreviations: baySeq

Resource Type: software resource

Defining Citation: PMID:20698981

Funding:

Resource Name: baySeq

Resource ID: SCR_012795

Alternate IDs: OMICS_01299

Record Creation Time: 20220129T080312+0000

Record Last Update: 20250420T014619+0000

Ratings and Alerts

No rating or validation information has been found for baySeq.

No alerts have been found for baySeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 117 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Ohashi Y, et al. (2024) Heterogeneous gene expression during early arteriovenous fistula remodeling suggests that downregulation of metabolism predicts adaptive venous remodeling. Scientific reports, 14(1), 13287.

Sato Y, et al. (2024) Autonomous differentiation of transgenic cells requiring no external hormone application: the endogenous gene expression and phytohormone behaviors. Frontiers in plant science, 15, 1308417.

Xue J, et al. (2024) Comparative study on differential expression analysis methods for single-cell RNA sequencing data with small biological replicates: Based on single-cell transcriptional data of PBMCs from COVID-19 severe patients. PloS one, 19(3), e0299358.

Zhebrun A, et al. (2024) Two H3K23 histone methyltransferases, SET-32 and SET-21, function synergistically to promote nuclear RNAi-mediated transgenerational epigenetic inheritance in Caenorhabditis elegans. bioRxiv : the preprint server for biology.

Kumar AJ, et al. (2023) Pneumosepsis survival in the setting of obesity leads to persistent steatohepatitis and metabolic dysfunction. Hepatology communications, 7(9).

Krej?ová G, et al. (2023) Macrophage-derived insulin antagonist ImpL2 induces lipoprotein mobilization upon bacterial infection. The EMBO journal, 42(23), e114086.

Buffa JA, et al. (2022) The microbial gbu gene cluster links cardiovascular disease risk associated with red meat consumption to microbiota L-carnitine catabolism. Nature microbiology, 7(1), 73.

Suzuki S, et al. (2022) Xenopus laevis il11ra.L is an experimentally proven interleukin-11 receptor component that is required for tadpole tail regeneration. Scientific reports, 12(1), 1903.

Zytnicki M, et al. (2021) Finding differentially expressed sRNA-Seq regions with srnadiff. PloS one, 16(8), e0256196.

Tente E, et al. (2021) Reprogramming of the wheat transcriptome in response to infection with Claviceps purpurea, the causal agent of ergot. BMC plant biology, 21(1), 316.

Spanka DT, et al. (2021) Impact of PNPase on the transcriptome of Rhodobacter sphaeroides and its cooperation with RNase III and RNase E. BMC genomics, 22(1), 106.

Sfikakis PP, et al. (2021) Blood Transcriptomes of Anti-SARS-CoV-2 Antibody-Positive Healthy Individuals Who Experienced Asymptomatic Versus Clinical Infection. Frontiers in immunology, 12, 746203.

Wallen ZD, et al. (2021) Comparison study of differential abundance testing methods using two large Parkinson disease gut microbiome datasets derived from 16S amplicon sequencing. BMC bioinformatics, 22(1), 265.

Orsi RH, et al. (2021) Alternative ? Factors Regulate Overlapping as Well as Distinct Stress Response and Metabolic Functions in Listeria monocytogenes under Stationary Phase Stress Condition. Pathogens (Basel, Switzerland), 10(4).

Wong PS, et al. (2021) Improvement of Free Fatty Acid Secretory Productivity in Aspergillus oryzae by Comprehensive Analysis on Time-Series Gene Expression. Frontiers in microbiology, 12, 605095.

Cambiagno DA, et al. (2021) HASTY modulates miRNA biogenesis by linking pri-miRNA transcription and processing. Molecular plant, 14(3), 426.

Benda M, et al. (2021) Quasi-essentiality of RNase Y in Bacillus subtilis is caused by its critical role in the control of mRNA homeostasis. Nucleic acids research, 49(12), 7088.

Lai PF, et al. (2021) Labour classified by cervical dilatation & fetal membrane rupture demonstrates differential impact on RNA-seq data for human myometrium tissues. PloS one, 16(11), e0260119.

Boher P, et al. (2021) Silencing of StRIK in potato suggests a role in periderm related to RNA processing and stress. BMC plant biology, 21(1), 409.

Detcharoen M, et al. (2021) Differential gene expression in Drosophila melanogaster and D. nigrosparsa infected with the same Wolbachia strain. Scientific reports, 11(1), 11336.