

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 2026

[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](#)

Resource Name: baySeq

Resource ID: SCR_012795

Alternate IDs: OMICS_01299

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260912T195753+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 121 mentions in open access literature.

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

Gonzalo L, et al. (2025) The nuclear pore complex acts as a hub for pri-miRNA transcription and processing in plants. *Nucleic acids research*, 53(17).

Tanaka T, et al. (2025) Early Enhancement in Contrast-Enhanced Computed Tomography Is an Index of DUSP9, SLPI, ALDH1L2, and SLC1A1 Expression in Canine Hepatocellular Carcinoma: A Preliminary Study. *Veterinary sciences*, 12(2).

Kamii M, et al. (2025) PARP inhibitors elicit a cellular senescence mediated inflammatory response in homologous recombination proficient cancer cells. *Scientific reports*, 15(1), 15458.

Kappala D, et al. (2025) Resiquimod induces a mixed Th1 and Th2 response via STAT1 and STAT3 signalling in chickens. *Biochemistry and biophysics reports*, 41, 101941.

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.

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.

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.

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).

Krejřová 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.

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.

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

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.

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).

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.

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

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.