Resource Summary Report

Generated by dkNET on Apr 26, 2025

Goseq

RRID:SCR_017052
Type: Tool

Proper Citation

Goseq (RRID:SCR_017052)

Resource Information

URL: https://bioconductor.org/packages/release/bioc/html/goseq.html

Proper Citation: Goseq (RRID:SCR_017052)

Description: Software application for performing Gene Ontology analysis on RNAseq data and other length biased data. Used to reduce complexity and highlight biological processes in genome wide expression studies.

Resource Type: data analysis software, software application, software resource, data processing software

Defining Citation: PMID:20132535

Keywords: Gene, Ontology, analysis, RNAseq, data, sequencing, genome, expression, bio.tools

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Goseq

Resource ID: SCR_017052

Alternate IDs: biotools:goseq

Alternate URLs: https://bio.tools/goseq

License: LGPL

Record Creation Time: 20220129T080333+0000

Record Last Update: 20250426T060616+0000

Ratings and Alerts

No rating or validation information has been found for Goseq.

No alerts have been found for Goseq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 330 mentions in open access literature.

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

Wang Z, et al. (2025) OsFKBP12 transduces the sucrose signal from OsNIN8 to the OsTOR pathway in a loosely binding manner for cell division. iScience, 28(1), 111555.

Yan Y, et al. (2024) Metabolome integrated with transcriptome reveals the mechanism of three different color formations in Taxus mairei arils. Frontiers in plant science, 15, 1330075.

Zhang Y, et al. (2024) CWF19L1 promotes T-cell cytotoxicity through the regulation of alternative splicing. The Journal of biological chemistry, 300(12), 107982.

Ngubo M, et al. (2024) Progeria-based vascular model identifies networks associated with cardiovascular aging and disease. Aging cell, 23(7), e14150.

Dai M, et al. (2024) Analysis of lettuce transcriptome reveals the mechanism of different light/dark cycle in promoting the growth and quality. Frontiers in plant science, 15, 1394434.

Wang C, et al. (2024) Integrative transcriptomic and metabolomic analysis to elucidate the effect of gossypol on Enterobacter sp. GD5. PloS one, 19(8), e0306597.

Mustafa EH, et al. (2024) Selective inhibition of CDK9 in triple negative breast cancer. Oncogene, 43(3), 202.

Song L, et al. (2024) SHMT2 Mediates Small-Molecule-Induced Alleviation of Alzheimer Pathology Via the 5'UTR-dependent ADAM10 Translation Initiation. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(11), e2305260.

Gibu K, et al. (2024) Polyamine impact on physiology of early stages of reef-building corals-

insights from rearing experiments and RNA-Seq analysis. Scientific reports, 14(1), 23465.

Li H, et al. (2024) Transcriptomic and metabolomic analysis of poplar response to feeding by Hyphantria cunea. BMC plant biology, 24(1), 920.

García-Beltrán JM, et al. (2024) The susceptibility of shi drum juveniles to betanodavirus increases with rearing densities in a process mediated by neuroactive ligand-receptor interaction. Frontiers in immunology, 15, 1304603.

Zhen X, et al. (2024) Leaf Senescence Regulation Mechanism Based on Comparative Transcriptome Analysis in Foxtail Millet. International journal of molecular sciences, 25(7).

Bakhsh T, et al. (2024) Molecular detection of exosomal miRNAs of blood serum for prognosis of colorectal cancer. Scientific reports, 14(1), 8902.

Nowell RW, et al. (2024) Bdelloid rotifers deploy horizontally acquired biosynthetic genes against a fungal pathogen. Nature communications, 15(1), 5787.

Yang B, et al. (2024) Integrated analysis of BSA-seq and RNA-seq identified the candidate genes for seed weight in Brassica juncea. Frontiers in plant science, 15, 1458294.

Tang Y, et al. (2024) Enhancing diabetic foot ulcer healing: Impact of the regulation of the FUS and ILF2 RNA?binding proteins through negative pressure wound therapy. International journal of molecular medicine, 54(5).

Huang H, et al. (2024) Jag1/2 maintain esophageal homeostasis and suppress foregut tumorigenesis by restricting the basal progenitor cell pool. Nature communications, 15(1), 4124.

Huang Y, et al. (2024) Enhanced resistance to heat and fungal infection in transgenic Trichoderma via over-expressing the HSP70 gene. AMB Express, 14(1), 34.

Reynolds ES, et al. (2024) Comparative Pathogenesis of Two Lineages of Powassan Virus Reveals Distinct Clinical Outcome, Neuropathology, and Inflammation. Viruses, 16(6).

Jiang Y, et al. (2024) Effect of folA gene in human breast milk-derived Limosilactobacillus reuteri on its folate biosynthesis. Frontiers in microbiology, 15, 1402654.