Resource Summary Report

Generated by dkNET on Apr 25, 2025

Rsubread

RRID:SCR_016945
Type: Tool

Proper Citation

Rsubread (RRID:SCR_016945)

Resource Information

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

Proper Citation: Rsubread (RRID:SCR_016945)

Description: Software R package for sequence alignment and counting for R. Used for analyses of second and third generation sequencing data, for read mapping, read counting, SNP calling, short and long read alignment, quantification and mutation discovery. Includes assessment of sequence reads, read alignment, read summarization, exon-exon junction detection, fusion detection, detection of short and long indels, absolute expression calling and SNP calling. Can be used with reads generated from any of the major sequencing platforms including Illumina GA/HiSeq/MiSeq, Roche GS-FLX, ABI SOLiD and LifeTech Ion PGM/Proton sequencers.

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

Defining Citation: PMID:23558742

Keywords: sequence, alignment, counting, multi, seed, strategy, mapping, read, reference, genome, analysis, data, SNP, calling, mutation, discovery, bio.tools

Funding: Australian National Health and Medical Research Council ;
Victorian State Government Operational Infrastructure Support ;
Australian Government

Availability: Free, Available for download, Freely available

Resource Name: Rsubread

Resource ID: SCR_016945

Alternate IDs: biotools:rsubread

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

License: GPL 3

Record Creation Time: 20220129T080332+0000

Record Last Update: 20250425T060207+0000

Ratings and Alerts

No rating or validation information has been found for Rsubread.

No alerts have been found for Rsubread.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 169 mentions in open access literature.

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

Ginley-Hidinger M, et al. (2024) Cis-regulatory control of transcriptional timing and noise in response to estrogen. Cell genomics, 4(5), 100542.

Senn KA, et al. (2024) Control of 3' splice site selection by the yeast splicing factor Fyv6. eLife, 13.

Wang Z, et al. (2024) Loss-of-Function but Not Gain-of-Function Properties of Mutant TP53 Are Critical for the Proliferation, Survival, and Metastasis of a Broad Range of Cancer Cells. Cancer discovery, 14(2), 362.

Benjaskulluecha S, et al. (2024) O6-methylguanine DNA methyltransferase regulates ?-glucan-induced trained immunity of macrophages via farnesoid X receptor and AMPK. iScience, 27(1), 108733.

Nicolas-Martinez EC, et al. (2024) RNA variant assessment using transactivation and transdifferentiation. American journal of human genetics, 111(8), 1673.

Kettunen K, et al. (2024) Profiling steroid hormone landscape of bladder cancer reveals

depletion of intratumoural androgens to castration levels: a cross-sectional study. EBioMedicine, 108, 105359.

Lehle JD, et al. (2024) An in vitro approach reveals molecular mechanisms underlying endocrine disruptor-induced epimutagenesis. eLife, 13.

Senatorov IS, et al. (2024) Castrate-resistant prostate cancer response to taxane is determined by an HNF1-dependent apoptosis resistance circuit. Cell reports. Medicine, 5(12), 101868.

Jokelainen O, et al. (2024) Differential expression analysis identifies a prognostically significant extracellular matrix-enriched gene signature in hyaluronan-positive clear cell renal cell carcinoma. Scientific reports, 14(1), 10626.

Leonard J, et al. (2024) Whole blood coagulation in an ex vivo thrombus is sufficient to induce clot neutrophils to adopt a myeloid-derived suppressor cell signature and shed soluble Lox-1. Journal of thrombosis and haemostasis : JTH, 22(4), 1031.

Moore J, et al. (2024) Lack of TGF? signaling competency predicts conversion of immune poor cancer to immune rich and response to checkpoint blockade. bioRxiv : the preprint server for biology.

Xu H, et al. (2024) PP2A complex disruptor SET prompts widespread hypertranscription of growth-essential genes in the pancreatic cancer cells. Science advances, 10(4), eadk6633.

Lind-Holm Mogensen F, et al. (2024) PARK7/DJ-1 deficiency impairs microglial activation in response to LPS-induced inflammation. Journal of neuroinflammation, 21(1), 174.

Lanshakov DA, et al. (2024) Brainstem transcriptomic changes in male Wistar rats after acute stress, comparing the use of duplex specific nuclease (DSN). Scientific reports, 14(1), 21856.

Tsuchiya J, et al. (2024) Time course transcriptomic profiling suggests Crp/Fnr transcriptional regulation of nosZ gene in a N2O-reducing thermophile. iScience, 27(11), 111074.

De Bellis C, et al. (2024) Genomic, epigenomic and transcriptomic inter- and intra-tumor heterogeneity in desmoid tumors. Clinical cancer research : an official journal of the American Association for Cancer Research.

Martins SG, et al. (2024) Laminin-?2 chain deficiency in skeletal muscle causes dysregulation of multiple cellular mechanisms. Life science alliance, 7(12).

Shen X, et al. (2024) Transcriptome profiling reveals SLC5A5 regulates chicken ovarian follicle granulosa cell proliferation, apoptosis, and steroid hormone synthesis. Poultry science, 103(1), 103241.

Muhammad T, et al. (2024) Non-cell-autonomous regulation of germline proteostasis by insulin/IGF-1 signaling-induced dietary peptide uptake via PEPT-1. The EMBO journal,

43(21), 4892.

Chen Q, et al. (2024) Transcriptome analysis identifies the NR4A subfamily involved in the alleviating effect of folic acid on mastitis induced by high concentration of Staphylococcus aureus lipoteichoic acid. BMC genomics, 25(1), 1051.