Resource Summary Report

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Subread

RRID:SCR_009803
Type: Tool

Proper Citation

Subread (RRID:SCR_009803)

Resource Information

URL: http://subread.sourceforge.net/

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Description: Software package for high-performance read alignment, quantification and mutation discovery.General purpose read aligner which can be used to map both genomic DNA-seq reads and RNA-seq reads. Subread aligner as fast, accurate and scalable read mapping by seed-and-vote.These programs were also implemented in Bioconductor R package Rsubread.

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

Defining Citation: PMID:23558742

Keywords: read alignment, DNA-seq reads mapping, RNA-seq reads mapping, mutation discovery, , bio.tools

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

Availability: Free, Freely available

Resource Name: Subread

Resource ID: SCR_009803

Alternate IDs: OMICS_01255, biotools:subread

Alternate URLs: https://bio.tools/subread, https://sources.debian.org/src/subread/

Record Creation Time: 20220129T080255+0000

Record Last Update: 20250411T055403+0000

Ratings and Alerts

No rating or validation information has been found for Subread.

No alerts have been found for Subread.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1497 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Lim B, et al. (2025) Cell deconvolution-based integrated time-series network of whole blood transcriptome reveals systemic antiviral activities and cell-specific immunological changes against PRRSV infection. Veterinary research, 56(1), 19.

Zluhan-Martínez E, et al. (2025) The MADS-box gene XAANTAL1 participates in Arabidopsis thaliana primary root growth and columella stem cell patterns in response to ROS, via direct regulation of PEROXIDASE 28 and RETINOBLASTOMA-RELATED genes. Journal of experimental botany, 76(2), 411.

Hathcock SF, et al. (2025) Transcriptomic analysis of coxsackievirus B3 infection in induced pluripotent stem cell-derived brain-like endothelial cells. Journal of virology, 99(1), e0182424.

Nayar S, et al. (2025) Molecular and spatial analysis of tertiary lymphoid structures in Sjogren's syndrome. Nature communications, 16(1), 5.

Clark AT, et al. (2025) A mutation in LXR? uncovers a role for cholesterol sensing in limiting metabolic dysfunction-associated steatohepatitis. Nature communications, 16(1), 1102.

Peralta M, et al. (2025) Endothelial calcium firing mediates the extravasation of metastatic tumor cells. iScience, 28(2), 111690.

Würth R, et al. (2025) Circulating tumor cell plasticity determines breast cancer therapy resistance via neuregulin 1-HER3 signaling. Nature cancer, 6(1), 67.

Mao F, et al. (2025) Unravelling the prognostic and operative role of intratumoural microbiota in non-small cell lung cancer: Insights from 16S rRNA and RNA sequencing. Clinical and translational medicine, 15(1), e70156.

Okonechnikov K, et al. (2025) Biglycan-driven risk stratification in ZFTA-RELA fusion supratentorial ependymomas through transcriptome profiling. Acta neuropathologica communications, 13(1), 4.

Nath SR, et al. (2025) Unraveling calcium dysregulation and autoimmunity in immune mediated rippling muscle disease. Acta neuropathologica communications, 13(1), 11.

Vigeland MD, et al. (2025) Gene Expression Correlates with Disability and Pain Intensity in Patients with Chronic Low Back Pain and Modic Changes in a Sex-Specific Manner. International journal of molecular sciences, 26(2).

Zheng C, et al. (2025) Integrative Omics Analysis Reveals Mechanisms of Anthocyanin Biosynthesis in Djulis Spikes. Plants (Basel, Switzerland), 14(2).

Soria E, et al. (2025) Segregation Between an Ornamental and a Disease Driver Gene Provides Insights Into Pigment Cell Regulation. Pigment cell & melanoma research, 38(1), e13196.

Huang X, et al. (2025) Predicting Alzheimer's disease subtypes and understanding their molecular characteristics in living patients with transcriptomic trajectory profiling. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(1), e14241.

Zakerzade R, et al. (2025) Diversification and recurrent adaptation of the synaptonemal complex in Drosophila. PLoS genetics, 21(1), e1011549.

Da Silva AJ, et al. (2025) Nuclear talin-1 provides a bridge between cell adhesion and gene expression. iScience, 28(2), 111745.

Zhang F, et al. (2025) Impact of Lysine to Methionine Ratios on Antioxidant Capacity and Immune Function in the Rumen of Tibetan Sheep: An RNA-Seq Analysis. Veterinary medicine and science, 11(1), e70173.

Zhang J, et al. (2025) Histone methyltransferases MLL2 and SETD1A/B play distinct roles in H3K4me3 deposition during the transition from totipotency to pluripotency. The EMBO journal, 44(2), 437.

Tenger-Trolander A, et al. (2025) Genomic Resources for the Scuttle Fly Megaselia abdita: A Model Organism for Comparative Developmental Studies in Flies. bioRxiv : the preprint server for biology.

Paulo DF, et al. (2025) Functional genomics implicates ebony in the black pupae phenotype of tephritid fruit flies. Communications biology, 8(1), 60.