

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/>

Proper Citation: Subread (RRID:SCR_009803)

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, data processing software, software application

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: 20260803T040536+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 1854 mentions in open access literature.

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

Zhang Q, et al. (2026) Integrated analysis of DNA methylation and transcriptome profiles in broiler heart and lung tissues reveals epigenetic regulatory mechanisms underlying ascites syndrome. Poultry science, 105(1), 106034.

Chen J, et al. (2026) Genomic and transcriptomic analysis of yield enhancement mechanism of lipopeptide iturin W by tryptone supplementation. Microbiology spectrum, 14(1), e0324725.

Al-Ahmadi W, et al. (2026) Spaceflight alters molecular networks linked to diverse human diseases in a single cellular model. Science advances, 12(1), eadw7832.

Chiang Y, et al. (2026) High-CD14-expressing urothelial cancer cells foster a neutrophil-rich tumor microenvironment that increases the risk of radiation-promoted distant metastasis. Journal of biomedical science, 33(1), 2.

Shi M, et al. (2026) Genomic architecture and evolution of heterostyly: new insights from Cordia subcordata (Boraginaceae). Molecular biology and evolution, 43(1).

Xie H, et al. (2026) Ubc9-Mediated SUMOylation of RPL3, an Unappreciated Mechanism against Hepatocyte Senescence by Repressing the DHX9-p16 Axis. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(1), e10240.

Muppirala AN, et al. (2026) Tachykinin signaling defines distinct populations of glia in the enteric nervous system. Neuron.

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

Wang J, et al. (2025) DNA methyltransferase 1 modulates mitochondrial function through bridging m5C RNA methylation. Molecular cell, 85(10), 1999.

Doro Pereira L, et al. (2025) PARP Inhibitors Differentially Regulate Immune Responses in Distinct Genetic Backgrounds of High-Grade Serous Tubo-Ovarian Carcinoma. Cancer research communications, 5(2), 339.

Gu J, et al. (2025) Suppressing SENP1 inhibits esophageal squamous carcinoma cell growth via SIRT6 SUMOylation. *Cellular oncology (Dordrecht, Netherlands)*, 48(1), 67.

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.

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

Lubrano P, et al. (2025) Metabolic mutations reduce antibiotic susceptibility of *E. coli* by pathway-specific bottlenecks. *Molecular systems biology*, 21(3), 274.

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.

Gregory AL, et al. (2025) Impacts of perR on oxygen sensitivity, gene expression, and murine infection in *Clostridioides difficile* 630^{erm}. *Journal of bacteriology*, 207(2), e0046824.

Abdulai-Saiku S, et al. (2025) The maternal X chromosome affects cognition and brain ageing in female mice. *Nature*, 638(8049), 152.

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.

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

Terashima Y, et al. (2025) Discovery of Novel RASGRF2 Fusions as a Therapeutic Target in Lung Adenocarcinoma of Never or Light Smokers. *Cancer science*.