

Resource Summary Report

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rsamtools

RRID:SCR_024257

Type: Tool

Proper Citation

rsamtools (RRID:SCR_024257)

Resource Information

URL: <https://bioconductor.org/packages/Rsamtools/>

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Description: Software R package provides interface to the 'samtools', 'bcftools', and 'tabix' utilities for manipulating Sequence Alignment Map, FASTA, binary variant call and compressed indexed tab-delimited files.

Resource Type: software resource, software toolkit

Keywords: tabix interface, samtools interface, bcftools interface, Sequence Alignment Map manipulation, SAM manipulation, FASTA manipulation, binary variant call manipulation, compressed indexed tab delimited files manipulation,

Availability: Free, Available for download, Freely available,

Resource Name: rsamtools

Resource ID: SCR_024257

Alternate URLs: <https://sources.debian.org/src/r-bioc-rsamtools/>

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260801T042919+0000

Ratings and Alerts

No rating or validation information has been found for rsamtools.

No alerts have been found for rsamtools.

Data and Source Information

Usage and Citation Metrics

We found 58 mentions in open access literature.

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

Ahrend F, et al. (2025) Protocol for assembling, prioritizing, and characterizing piRNA clusters using the piRNA Cluster Builder. STAR protocols, 6(2), 103759.

Tsang J, et al. (2025) Identification of novel genetic mutations for the treatment prognostication of canine lymphoma. NPJ precision oncology, 9(1), 174.

Morgunova V, et al. (2025) RNA-binding protein Ars2 mediates transcriptional silencing of telomeric repeats and transposable elements in the Drosophila germline. Nucleic acids research, 53(10).

Song J, et al. (2025) DEMINERS enables clinical metagenomics and comparative transcriptomic analysis by increasing throughput and accuracy of nanopore direct RNA sequencing. Genome biology, 26(1), 76.

Gretzinger J, et al. (2025) Ancient DNA connects large-scale migration with the spread of Slavs. Nature, 646(8084), 384.

Jelcic I, et al. (2025) T-bet+ CXCR3+ B cells drive hyperreactive B-T cell interactions in multiple sclerosis. Cell reports. Medicine, 6(3), 102027.

Pérez MJ, et al. (2025) Rewriting nuclear epigenetic scripts in mitochondrial diseases as a strategy for heteroplasmy control. EMBO molecular medicine, 17(9), 2354.

Klein N, et al. (2025) Type I-Fv and engineered type IV-A1 CRISPR-Cas effectors facilitate genome reduction in Escherichia coli. Nucleic acids research, 53(22).

Hori C, et al. (2025) Characterizing heterogeneous cis-regulatory elements in gene regulatory programs associated with breast cancer. Genome medicine, 17(1), 145.

Mitina A, et al. (2024) Genome-wide enhancer-associated tandem repeats are expanded in cardiomyopathy. EBioMedicine, 101, 105027.

Zhang K, et al. (2024) VISTA promotes the metabolism and differentiation of myeloid-derived suppressor cells by STAT3 and polyamine-dependent mechanisms. Cell reports, 43(1), 113661.

Gretzinger J, et al. (2024) Evidence for dynastic succession among early Celtic elites in Central Europe. Nature human behaviour, 8(8), 1467.

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

Szeky B, et al. (2024) Efficient derivation of functional astrocytes from human induced pluripotent stem cells (hiPSCs). *PLoS one*, 19(12), e0313514.

Newaz K, et al. (2024) Prognostic importance of splicing-triggered aberrations of protein complex interfaces in cancer. *NAR genomics and bioinformatics*, 6(3), lqae133.

Lonare A, et al. (2024) 14-3-3 σ restricts YY1 to the cytoplasm, promoting therapy resistance, and tumor progression in colorectal cancer. *International journal of cancer*.

Iturbe P, et al. (2024) Noncontiguous operon atlas for the *Staphylococcus aureus* genome. *microLife*, 5, uqae007.

Gretzinger J, et al. (2024) 9,000 years of genetic continuity in southernmost Africa demonstrated at Oakhurst rockshelter. *Nature ecology & evolution*, 8(11), 2121.

Xu X, et al. (2024) Nucleotidyltransferase toxin MenT extends aminoacyl acceptor ends of serine tRNAs to control *Mycobacterium tuberculosis* growth. *Nature communications*, 15(1), 9596.

Furuta T, et al. (2024) MCPtaggR: R package for accurate genotype calling in reduced representation sequencing data by eliminating error-prone markers based on genome comparison. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 31(1).