

Resource Summary Report

Generated by [ASWG](#) on Aug 18, 2026

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 toolkit, software resource

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: 20260815T182813+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 61 mentions in open access literature.

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

Furukawa T, et al. (2026) Patient-derived orthotopic xenograft models recapitulate the peritoneal dissemination of pancreatic cancer and delineate its transcriptional and regulatory programs. *Journal of experimental & clinical cancer research* : CR, 45(1).

Baeza M, et al. (2026) Transcriptomic Insights into Sre1-Related Regulatory Responses to Hypoxia, Cobalt Chloride, and Clotrimazole in *Phaffia rhodozyma*. *Journal of fungi (Basel, Switzerland)*, 12(3).

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.

Papp D, et al. (2025) 2b-RAD sequencing of *Malus florentina* populations reveals strong population structure and signals of balancing selection at disease resistance loci. *BMC plant biology*, 26(1), 95.

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.

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

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).

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

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

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

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

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

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.

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*.

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.