

Resource Summary Report

Generated by SPARC SAWG on Sep 15, 2026

Bamtools

RRID:SCR_015987

Type: Tool

Proper Citation

Bamtools (RRID:SCR_015987)

Resource Information

URL: <https://github.com/pezmaster31/bamtools/wiki>

Proper Citation: Bamtools (RRID:SCR_015987)

Description: Software that provides both a C++ API and a command-line toolkit for reading, writing, and manipulating genome sequence alignment files in the BAM and SAM formats. It is used for research analysis and management of data produced by sequencing technologies.

Synonyms: API:Application Programming Interface, BAM:Binary Alignment Map, SAM:Sequence Alignment Map

Resource Type: data analysis software, data management software, data processing software, software application, software resource, software toolkit

Defining Citation: [PMID:21493652](https://pubmed.ncbi.nlm.nih.gov/21493652/), [DOI:10.1093/bioinformatics/btr174](https://doi.org/10.1093/bioinformatics/btr174)

Keywords: c++, api, sam, bam genome, sequence, alignment, data, analysis, management, command, manipulation, binary, map, bio.tools

Funding: NHGRI R01 HG004719;
NHGRI RC2 HG005552

Resource Name: Bamtools

Resource ID: SCR_015987

Alternate IDs: biotools:bamtools, OMICS_11315

Alternate URLs: <https://bio.tools/bamtools>, <https://sources.debian.org/src/bamtools/>

License: GNU General Public License (GPL), MIT licence

Record Creation Time: 20220129T080328+0000

Ratings and Alerts

No rating or validation information has been found for Bamtools.

No alerts have been found for Bamtools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 344 mentions in open access literature.

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

Abdelfattah N, et al. (2026) Male-biased Yap1-Cd276/B7-H3 axis for immune evasion in medulloblastoma. Cancer cell, 44(4), 760.

Wang Y, et al. (2026) Lamin A/C-regulated cysteine catabolic flux modulates stem cell fate through epigenome reprogramming. Nature metabolism, 8(2), 431.

Harrod A, et al. (2026) The SMARCA4 subunit of the SWI/SNF complex prevents genome instability at G quadruplexes. Genome biology, 27(1).

Jarrell AF, et al. (2026) Building genomic resources to facilitate the study and use of Solanum microdontum, a wild relative of cultivated potato. G3 (Bethesda, Md.), 16(1).

Eleftheraki A, et al. (2026) An RNA structural switch controlling bacterial toxin translation. Nucleic acids research, 54(6).

Davis E, et al. (2026) Ezh2 Control of Bivalent Genes Fine-Tunes Developmental Competence During Retinogenesis. Investigative ophthalmology & visual science, 67(6), 18.

Côrtés L, et al. (2026) Family-Based Study Reveals PDE11A/PDE11A-AS1 Variants in Testicular Germ Cell Tumor Predisposition. International journal of molecular sciences, 27(12).

Castelo-Martínez L, et al. (2026) Early-life rotavirus infection susceptibility and later gastrointestinal cancer protection: Reverse antagonistic pleiotropy and potential vaccine benefits. Current research in microbial sciences, 10, 100578.

Matsuyama S, et al. (2026) Prenatal corticosteroid exposure disrupts vascular-immune interactions and impairs steroidogenesis in the fetal testis. bioRxiv : the preprint server for biology.

Punga T, et al. (2026) The C16orf87 protein is a subunit of the MIER corepressor complex controlling embryonic development and cell migration. *Scientific reports*, 16(1).

Rossini R, et al. (2026) Loss of multilevel 3D genome organization during breast cancer progression. *Genome research*, 36(1), 20.

Lo BW, et al. (2026) Genomes of *Wiebesia* Fig Wasps Reveal the Adaptation and Codiversification in the Fig-Fig Wasp Mutualism. *Genome biology and evolution*, 18(4).

Lin F, et al. (2026) A chromosome-level genome assembly of the panda loach (*Yaoshania pachytilus*). *Scientific data*, 13(1).

Gouka L, et al. (2026) Genomic insights into adaptative traits of phyllosphere yeasts. *Environmental microbiome*, 21(1), 21.

Saber S, et al. (2026) Evolution of the rate, molecular spectrum, and fitness effects of mutation under minimal selection in *Caenorhabditis elegans*. *bioRxiv : the preprint server for biology*.

Setti A, et al. (2026) The role of low-complexity repeats in RNA-RNA interactions and a deep learning framework for duplex prediction. *Nature communications*, 17(1), 1637.

Forster PM, et al. (2026) Blimp-1 integrates alarmin signals in ILC2s and drives proinflammatory functions required for type 2 immunity. *The Journal of experimental medicine*, 223(5).

Xu C, et al. (2026) A Novel LMX1A Frameshift Variant Underlies Familial Phenotypic Heterogeneity in DFNA7. *Human mutation*, 2026, 9930672.

Power RI, et al. (2026) Population genomics reveals an ancient origin of heartworms in canids. *Communications biology*, 9(1), 68.

Denning-James KE, et al. (2025) Genome-wide association mapping dissects the selective breeding of determinacy and photoperiod sensitivity in common bean (*Phaseolus vulgaris* L.). *G3 (Bethesda, Md.)*, 15(6).