

Resource Summary Report

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Bamtools

RRID:SCR_015987

Type: Tool

Proper Citation

Bamtools (RRID:SCR_015987)

Resource Information

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

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

Defining Citation: [PMID:21493652](#), [DOI:10.1093/bioinformatics/btr174](#)

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

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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 324 mentions in open access literature.

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

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).

Lane KA, et al. (2025) PBRM1 directs PBAF to pericentromeres and protects centromere integrity. *Nature communications*, 16(1), 1980.

Kim J, et al. (2025) Combinational regenerative inductive effect of bio-adhesive hybrid hydrogels conjugated with hiPSC-derived myofibers and its derived EVs for volumetric muscle regeneration. *Bioactive materials*, 43, 579.

Silver LW, et al. (2025) Temporal Loss of Genome-Wide and Immunogenetic Diversity in a Near-Extinct Parrot. *Molecular ecology*, 34(9), e17746.

Gao W, et al. (2025) Chromosome-scale and haplotype-resolved genome assembly of *Populus trichocarpa*. *Horticulture research*, 12(4), uhaf012.

D'aes J, et al. (2025) Metagenomics-based tracing of genetically modified microorganism contaminations in commercial fermentation products. *Food chemistry. Molecular sciences*, 10, 100236.

Breitbart ST, et al. (2025) Anthropogenic Landscape Alteration, but Not Urbanization, Influences Non-Adaptive Evolution in Common Milkweed (*Asclepias syriaca* L.). *Ecology and evolution*, 15(4), e71250.

Robert MG, et al. (2025) Uncovering biomarkers for chronic toxoplasmosis detection highlights alternative pathways shaping parasite dormancy. *EMBO molecular medicine*, 17(7), 1686.

Sharma P, et al. (2025) Early methionine availability attenuates T cell exhaustion. *Nature immunology*, 26(8), 1384.

Ardura-Fabregat A, et al. (2025) Response of spatially defined microglia states with distinct chromatin accessibility in a mouse model of Alzheimer's disease. *Nature neuroscience*, 28(8), 1688.

Chen Y, et al. (2025) Non-disruptive 3D profiling of combinations of epigenetic marks in single cells. *bioRxiv : the preprint server for biology*.

Agrawal P, et al. (2025) Integrated in vivo functional screens and multiomics analyses identify α -2,3-sialylation as essential for melanoma maintenance. *Science advances*, 11(27), eadg3481.

Li B, et al. (2025) Zygotic activation of transposable elements during zebrafish early embryogenesis. *Nature communications*, 16(1), 3692.

Kerns EV, et al. (2025) Variable performance of widely used bisulfite sequencing methods and read mapping software for DNA methylation. *bioRxiv : the preprint server for biology*.

Cozzarolo CS, et al. (2025) Transcriptional profiles of the fish parasite *Neoechinorhynchus agilis* (Acanthocephala) emphasize energetic stress in males and high cell-division activity in females. *BMC genomics*, 26(1), 1090.

Kattner S, et al. (2025) Prevalence and microbiological profile of septic complications following ECMO decannulation: a prospective single-center study. *Scientific reports*, 15(1), 45668.

Turner AD, et al. (2025) ScillyHAB: A Multi-Disciplinary Survey of Harmful Marine Phytoplankton and Shellfish Toxins in the Isles of Scilly: Combining Citizen Science with State-of-the-Art Monitoring in an Isolated UK Island Territory. *Marine drugs*, 23(12).

Hsiung CC, et al. (2025) Engineered CRISPR-Cas12a for higher-order combinatorial chromatin perturbations. *Nature biotechnology*, 43(3), 369.

Zhang N, et al. (2025) Deciphering the molecular logic of WOX5 function in the root stem cell organizer. *The EMBO journal*, 44(1), 281.

Jensen EL, et al. (2025) Synteny Enabled Upgrade of the Galapagos Giant Tortoise Genome Improves Inferences of Runs of Homozygosity. *Ecology and evolution*, 15(4), e71358.