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

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

Funding: NHGRI R01 HG004719;
NHGRI RC2 HG005552

Availability: Free, Free for download, Freely Available

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

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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 271 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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

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

Keller V, et al. (2025) Genomic features of lichen-associated black fungi. IUBMB life, 77(1), e2934.

Cigler M, et al. (2025) Orpinolide disrupts a leukemic dependency on cholesterol transport by inhibiting OSBP. Nature chemical biology, 21(2), 193.

Desterke C, et al. (2025) Single-Cell RNA Sequencing Reveals LEF1-Driven Wnt Pathway Activation as a Shared Oncogenic Program in Hepatoblastoma and Medulloblastoma. Current oncology (Toronto, Ont.), 32(1).

Assis BA, et al. (2025) Genomic signatures of adaptation in native lizards exposed to human-introduced fire ants. Nature communications, 16(1), 89.

Makhani K, et al. (2025) Single-Cell Multi-Omics Profiling of Immune Cells Isolated from Atherosclerotic Plaques in Male ApoE Knockout Mice Exposed to Arsenic. Environmental health perspectives, 133(1), 17007.

Santamaria RM, et al. (2024) Comparative Transcriptome Analysis of Babesia bigemina Attenuated Vaccine and Virulent Strains of Mexican Origin. Vaccines, 12(3).

Amorim MT, et al. (2024) Detection of a Multiple Circulation Event of Dengue Virus 2 Strains in the Northern Region of Brazil. Tropical medicine and infectious disease, 9(1).

Nie XY, et al. (2024) Circadian regulation of stereotypic chromatin conformations at enhancers. bioRxiv : the preprint server for biology.

Mielnicka M, et al. (2024) Trim66's paternal deficiency causes intrauterine overgrowth. Life science alliance, 7(7).

Skojec C, et al. (2024) Long read genome assembly of Automeris io (Lepidoptera: Saturniidae) an emerging model for the evolution of deimatic displays. G3 (Bethesda, Md.), 14(3).

Dillon MN, et al. (2024) Is increased mutation driving genetic diversity in dogs within the Chornobyl exclusion zone? PloS one, 19(12), e0315244.

De Jode A, et al. (2024) Chromosome-scale Genome Assembly of the Rough Periwinkle Littorina saxatilis. Genome biology and evolution, 16(4).

Wang Y, et al. (2024) Genomic insights into the origin and evolution of spelt (Triticum spelta L.) as a valuable gene pool for modern wheat breeding. Plant communications, 5(5), 100883.

Ghareeb AFA, et al. (2024) Host transcriptome response to heat stress and Eimeria maxima infection in meat-type chickens. PloS one, 19(2), e0296350.

Tang Z, et al. (2024) Longitudinal integrative cell-free DNA analysis in gestational diabetes mellitus. Cell reports. Medicine, 5(8), 101660.

Mishra R, et al. (2024) LINC01432 binds to CELF2 in newly diagnosed multiple myeloma promoting short progression-free survival to standard therapy. bioRxiv : the preprint server for biology.

Niu J, et al. (2024) Tagging large CNV blocks in wheat boosts digitalization of germplasm resources by ultra-low-coverage sequencing. Genome biology, 25(1), 171.

Angelis N, et al. (2024) Loss of ARID3A perturbs intestinal epithelial proliferation-differentiation ratio and regeneration. The Journal of experimental medicine, 221(10).