

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

[biobambam](#)

RRID:SCR_003308

Type: Tool

Proper Citation

biobambam (RRID:SCR_003308)

Resource Information

URL: <https://github.com/gt1/biobambam>

Proper Citation: biobambam (RRID:SCR_003308)

Description: Software tools for read pair collation based algorithms on BAM files including * bamcollate2: reads BAM and writes BAM reordered such that alignment or collated by query name * bammarkduplicates: reads BAM and writes BAM with duplicate alignments marked using the BAM flags field * bammaskflags: reads BAM and writes BAM while masking (removing) bits from the flags column * bamrecompress: reads BAM and writes BAM with a defined compression setting. This tool is capable of multi-threading. * bamsort: reads BAM and writes BAM resorted by coordinates or query name * bamtofastq: reads BAM and writes FastQ; output can be collated or uncollated by query name

Resource Type: data processing software, software application, software resource

Defining Citation: [DOI:10.1186/1751-0473-9-13](https://doi.org/10.1186/1751-0473-9-13)

Keywords: standalone software, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: biobambam

Resource ID: SCR_003308

Alternate IDs: biotools:biobambam, OMICS_04664

Alternate URLs: <https://bio.tools/biobambam>,
<https://sources.debian.org/src/biobambam2/>

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260905T133039+0000

Ratings and Alerts

No rating or validation information has been found for biobambam.

No alerts have been found for biobambam.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 65 mentions in open access literature.

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

Renner M, et al. (2026) Multi-layered molecular profiling informs the diagnosis and targeted therapy of desmoplastic small round cell tumor. *Nature communications*, 17(1).

Tamura Z, et al. (2026) Comparison of gene fusion detection algorithms reveals frequently overlooked driver fusions in hematologic malignancies. *NPJ precision oncology*, 10(1).

Friske JD, et al. (2026) A Conserved Enhancer Locus in Extrachromosomal DNA and Homogeneously Staining Regions Activates MYC Transcription in Group 3 Medulloblastoma. *Cancer research*, 86(13), 3160.

Chang HY, et al. (2026) Uniform Processing of Diverse Sequencing Data: A Cross-Population Comparison of Colon Cancer Genomic Landscapes from The Cancer Genome Atlas and a Chinese Cohort. *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*, 35(5), 762.

Roush SM, et al. (2026) Mutational profiling of HIV+ diffuse large B-cell lymphoma reveals distinct mutational features with evidence of genomic instability. *AIDS (London, England)*, 40(6), 719.

Hung LH, et al. (2025) Harmonizing and integrating the NCI Genomic Data Commons through accessible, interactive, and cloud-enabled workflows. *PloS one*, 20(3), e0318676.

Patte C, et al. (2025) Comprehensive molecular portrait reveals genetic diversity and distinct molecular subtypes of small intestinal neuroendocrine tumors. *Nature communications*, 16(1), 2197.

Arthur TD, et al. (2025) IFN γ activates an immune-like regulatory network in the cardiac vascular endothelium. *Journal of molecular and cellular cardiology plus*, 11, 100289.

Elliott MJ, et al. (2025) Ultrasensitive Detection and Monitoring of Circulating Tumor DNA Using Structural Variants in Early-Stage Breast Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(8), 1520.

Beck S, et al. (2025) Immunogenomic profiles of HIV-associated classic Hodgkin lymphoma from Malawi. *Blood global hematology*, 1(3).

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.

Trivedi M, et al. (2025) Historical Demography and Species Distribution Models Shed Light on Speciation in Primates of Northeast India. *Ecology and evolution*, 15(2), e70968.

Carrié H, et al. (2025) Comprehensive benchmarking of methods for mutation calling in circulating tumor DNA. *Nature communications*, 17(1), 1082.

Yoshizato T, et al. (2025) Stable clonal contribution of lineage-restricted stem cells to human hematopoiesis. *Nature genetics*, 57(12), 3088.

Umeda M, et al. (2025) Fusion oncoproteins and cooperating mutations define disease phenotypes in NUP98-rearranged leukemia. *medRxiv : the preprint server for health sciences*.

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

Smirnov P, et al. (2024) Multi-omic and single-cell profiling of chromothriptic medulloblastoma reveals genomic and transcriptomic consequences of genome instability. *Nature communications*, 15(1), 10183.

Fukumoto T, et al. (2024) Steroids-producing nodules: a two-layered adrenocortical nodular structure as a precursor lesion of cortisol-producing adenoma. *EBioMedicine*, 103, 105087.

Mentzer AJ, et al. (2024) High-resolution African HLA resource uncovers HLA-DRB1 expression effects underlying vaccine response. *Nature medicine*, 30(5), 1384.

Borowsky A, et al. (2024) Tumor microenvironmental determinants of high-risk DCIS progression. *Research square*.