

Resource Summary Report

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[biobambam](#)

RRID:SCR_003308

Type: Tool

Proper Citation

biobambam (RRID:SCR_003308)

Resource Information

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

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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: software application, software resource, data processing software

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: 20260727T040324+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 58 mentions in open access literature.

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

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.

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.

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

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.

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

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 chromothrptic medulloblastoma reveals genomic and transcriptomic consequences of genome instability. Nature communications, 15(1), 10183.

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

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.

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

Neumann J, et al. (2023) Disrupted Ca²⁺ homeostasis and immunodeficiency in patients with functional IP3 receptor subtype 3 defects. *Cellular & molecular immunology*, 20(1), 11.

Giannakopoulou E, et al. (2023) A T cell receptor targeting a recurrent driver mutation in FLT3 mediates elimination of primary human acute myeloid leukemia in vivo. *Nature cancer*, 4(10), 1474.

Claeys A, et al. (2023) Benchmark of tools for in silico prediction of MHC class I and class II genotypes from NGS data. *BMC genomics*, 24(1), 247.

Napolitano S, et al. (2023) Antitumor Efficacy of Dual Blockade with Encorafenib + Cetuximab in Combination with Chemotherapy in Human BRAFV600E-Mutant Colorectal Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 29(12), 2299.

Shiraishi Y, et al. (2023) Precise characterization of somatic complex structural variations from tumor/control paired long-read sequencing data with nanomonsv. *Nucleic acids research*, 51(14), e74.

Gilly A, et al. (2022) Gene-based whole genome sequencing meta-analysis of 250 circulating proteins in three isolated European populations. *Molecular metabolism*, 61, 101509.

Criscione SW, et al. (2022) The landscape of therapeutic vulnerabilities in EGFR inhibitor osimertinib drug tolerant persister cells. *NPJ precision oncology*, 6(1), 95.