**biobambam**

RRID:SCR_003308  
Type: Tool

### Proper Citation

biobambam (RRID:SCR_003308)

### Resource Information

**URL:** [https://github.com/gt1/biobambam](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 sorted 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:** GNU General Public License, v3

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**Alternate IDs:** biotools:biobambam, OMICS_04664

**Alternate URLs:** [https://bio.tools/biobambam](https://bio.tools/biobambam), [https://sources.debian.org/src/biobambam2/](https://sources.debian.org/src/biobambam2/)
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 45 mentions in open access literature.

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


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.


Valls-Margarit J, et al. (2022) GCAT|Panel, a comprehensive structural variant haplotype
map of the Iberian population from high-coverage whole-genome sequencing. Nucleic acids research, 50(5), 2464.


Srivastava A, et al. (2021) Whole Genome Sequencing Prioritizes CHEK2, EWSR1, and TIAM1 as Possible Predisposition Genes for Familial Non-Medullary Thyroid Cancer. Frontiers in endocrinology, 12, 600682.


