biobambam

RRID:SCR_003308
Type: Tool

Proper Citation

biobambam (RRID:SCR_003308)

Resource Information

**URL:** https://github.com/gt1/biobambam

**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 Name:** biobambam

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

**Keywords:** standalone software

**Resource ID:** SCR_003308

**Availability:** GNU General Public License, v3

**Website Status:** Last checked up

**Alternate IDs:** OMICS_04664

**Mentions Count:** 13
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 13 mentions in open access literature.

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


Panopoulos AD, et al. (2017) Aberrant DNA Methylation in Human iPSCs Associates with MYC-Binding Motifs in a Clone-Specific Manner Independent of Genetics. Cell stem cell,
