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](http://www.fdi-lab.org).


- Panopoulous 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,
