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

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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:** 12
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 12 mentions in open access literature.

Listed below are recent publications. The full list is available at scicrunch.


Panopoulos AD, et al. (2017) Aberrant DNA Methylation in Human iPSCs Associates with