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: 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,
