biobambam
RRID:SCR_003308
Type: Tool

Proper Citation

biobambam (RRID:SCR_003308)

Resource Information

URL: https://github.com/gt1/biobambam
Proper Citation: biobambam (RRID:SCR_003308)

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

Keywords: standalone software, bio.tools

Availability: GNU General Public License, v3
Website Status: Last checked up

Resource Name: biobambam

Resource ID: SCR_003308
Alternate IDs: OMICS_04664, biotools:biobambam
Alternate URLs: https://bio.tools/biobambam
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 25 mentions in open access literature.

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


