SAMTOOLS
RRID:SCR_002105
Type: Tool

Proper Citation

SAMTOOLS (RRID:SCR_002105)

Resource Information

URL: http://samtools.sourceforge.net/

Description: Software tool for manipulating alignments in SAM format for storing nucleotide sequence alignment, including sorting, merging, indexing and generating alignments in per position format. Parts that are relevant to genetic analysis include SNP and indel callings.

Resource Name: SAMTOOLS

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

Keywords: gene, genomic, c, c++, java, perl, python, ruby, common, lisp, haskell, read, alignment, nucleotide, sequence, data, process

Resource ID: SCR_002105

Parent Organization: SourceForge

Funding Agency: NHGRI, Wellcome Trust

Related resources: Platypus, shovill

References: PMID:19505943

Availability: Free, Available for download, Freely available

Website Status: Last checked up
Alternate IDs: nlx_154607, OMICS_01074
Alternate URLs: http://sourceforge.net/projects/samtools/
Abbreviations: SAMtools
Mentions Count: 7681

Ratings and Alerts
No rating or validation information has been found for SAMTOOLS.
No alerts have been found for SAMTOOLS.

Data and Source Information
Source: SciCrunch Registry

Usage and Citation Metrics
We found 7681 mentions in open access literature.

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


Bekkevold D, et al. (2020) Northern European(L.) populations are genetically divergent across geographical regions and environmental gradients. Evolutionary applications, 13(2), 400-416.