SAMTOOLS
RRID:SCR_002105
Type: Tool

Proper Citation

SAMTOOLS (RRID:SCR_002105)

Resource Information

URL: http://htslib.org/

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Description: Original SAMTOOLS package has been split into three separate repositories including Samtools, BCFtools and HTSlib. Samtools for manipulating next generation sequencing data used for reading, writing, editing, indexing, viewing nucleotide alignments in SAM, BAM, CRAM format. BCFtools used for reading, writing BCF2, VCF, gVCF files and calling, filtering, summarising SNP and short indel sequence variants. HTSlib used for reading, writing high throughput sequencing data.

Resource Type: Resource, data analysis software, data processing software, software application, sequence analysis software, software resource, software toolkit

References: PMID:19505943, PMID:21903627

Keywords: Samtools, BCFtools, HTSlib, next generation sequencing, nucleotide alignments, sequence variant, genomic, c, perl, read, alignment, nucleotide, sequence, data, process, sam, bam, cram, vcf, bcf, bio.tools

Parent Organization: Wellcome Trust Sanger Institute; Hinxton; United Kingdom

Funding Agency: NHGRI, Wellcome Trust

Related resources: Platypus, shovill, pysam

Availability: Free, Available for download, Freely available

Website Status: Last checked up
**Abbreviations:** SAMtools

**Resource Name:** SAMTOOLS

**Resource ID:** SCR_002105

**Alternate IDs:** nlx_154607, OMICS_01074, biotools: samtools, SCR_018682


**Old URLs:** http://samtools.sourceforge.net/

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**Ratings and Alerts**

No rating or validation information has been found for SAMTOOLS.

No alerts have been found for SAMTOOLS.

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**Data and Source Information**

**Source:** SciCrunch Registry

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**Usage and Citation Metrics**

We found 10402 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](http://FDI-Lab-SciCrunch.org).


Madden DE, et al. (2021) Taking the next-gen step: Comprehensive antimicrobial resistance detection from Burkholderia pseudomallei. EBioMedicine, 63, 103152.
Ji QM, et al. (2021) A chromosome-scale reference genome and genome-wide genetic variations elucidate adaptation in yak. Molecular ecology resources, 21(1), 201-211.


Felgner S, et al. (2020) Host-induced spermidine production in motiletriggers phagocytic