Resource Summary Report

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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.

Abbreviations: SAMtools

Synonyms: samtools, Samtools, Sequence Alignment Map TOOLS, SAMtools, SAM tools

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

Defining Citation: PMID:19505943, PMID:21903627, DOI:10.1093/bioinformatics/btp352

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

Funding: Wellcome Trust ;
NHGRI U54 HG002750

Availability: Free, Available for download, Freely available

Resource Name: SAMTOOLS

Resource ID: SCR_002105

Alternate IDs: SCR_018682, biotools:samtools, OMICS_01074, nlx_154607, OMICS_00090

Alternate URLs: https://github.com/samtools/samtools, https://github.com/samtools/htslib, https://bio.tools/samtools, https://sources.debian.org/src/samtools/

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

License: MIT License

Record Creation Time: 20220129T080211+0000

Record Last Update: 20250524T055849+0000

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 25495 mentions in open access literature.

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

Ramponi V, et al. (2025) H4K20me3-Mediated Repression of Inflammatory Genes Is a Characteristic and Targetable Vulnerability of Persister Cancer Cells. Cancer research, 85(1), 32.

Wright SS, et al. (2025) Transplantation of gasdermin pores by extracellular vesicles propagates pyroptosis to bystander cells. Cell, 188(2), 280.

Battilani D, et al. (2025) Beyond population size: Whole-genome data reveal bottleneck legacies in the peninsular Italian wolf. The Journal of heredity, 116(1), 10.

Norton AM, et al. (2025) Deformed wing virus genotypes A and B do not elicit immunologically different responses in naïve honey bee hosts. Insect molecular biology, 34(1), 33.

Lee ES, et al. (2025) N-6-methyladenosine (m6A) promotes the nuclear retention of mRNAs with intact 5' splice site motifs. Life science alliance, 8(2).

Catacalos-Goad C, et al. (2025) Nucleotide-resolution Mapping of RNA N6-Methyladenosine (m6A) modifications and comprehensive analysis of global polyadenylation events in mRNA 3' end processing in malaria pathogen Plasmodium falciparum. bioRxiv : the preprint server for biology.

Xu H, et al. (2025) Landscape of human protein-coding somatic mutations across tissues and individuals. bioRxiv : the preprint server for biology.

Gad K, et al. (2025) Establishment of an Agrobacterium-mediated transformation system for the genetic engineering of Linum grandiflorum Desf. Physiologia plantarum, 177(1), e70059.

Fedkenheuer M, et al. (2025) A dual role of Cohesin in DNA DSB repair. Nature communications, 16(1), 843.

Torrado H, et al. (2025) Evolutionary Genomics of Two Co-occurring Congeneric Fore Reef Coral Species on Guam (Mariana Islands). Genome biology and evolution, 17(1).

Owens GL, et al. (2025) Shared Selection and Genetic Architecture Drive Strikingly Repeatable Evolution in Long-Term Experimental Hybrid Populations. Molecular biology and evolution, 42(1).

Mears HV, et al. (2025) Emergence of SARS-CoV-2 subgenomic RNAs that enhance viral fitness and immune evasion. PLoS biology, 23(1), e3002982.

Cerqueira de Araujo A, et al. (2025) Genome sequences of four Ixodes species expands understanding of tick evolution. BMC biology, 23(1), 17.

Han H, et al. (2025) Exome sequencing of 18,994 ethnically diverse patients with suspected rare Mendelian disorders. NPJ genomic medicine, 10(1), 6.

Gaston JM, et al. (2025) X-Mapper: fast and accurate sequence alignment via gapped x-mers. Genome biology, 26(1), 15.

Jakobsen MK, et al. (2025) Stochastic demethylation and redundant epigenetic suppressive mechanisms generate highly heterogeneous responses to pharmacological DNA methyltransferase inhibition. Journal of experimental & clinical cancer research : CR, 44(1), 21.

Schechter MS, et al. (2025) Ribosomal protein phylogeography offers quantitative insights into the efficacy of genome-resolved surveys of microbial communities. bioRxiv : the preprint server for biology.

Chen RW, et al. (2025) Native nucleosome-positioning elements for the investigation of nucleosome repositioning. bioRxiv : the preprint server for biology.

Lesturgie P, et al. (2025) Short-term evolutionary implications of an introgressed size-determining supergene in a vulnerable population. Nature communications, 16(1), 1096.

Liu C, et al. (2025) A chromosome-scale genome assembly of the pioneer plant Stylosanthes angustifolia: insights into genome evolution and drought adaptation. GigaScience, 14.