Resource Summary Report

Generated by NIF on Aug 19, 2026

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 resource, data analysis software, data processing software, software toolkit

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: 20260819T044031+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 33299 mentions in open access literature.

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

Patel UA, et al. (2026) CRISPR Screen Identifies HDAC3 as a Novel Radiosensitizing Target in Small Cell Lung Cancer. Molecular cancer therapeutics, 25(1), 183.

Dunn LN, et al. (2026) Altered hepatic metabolism in Down syndrome. Cell reports, 45(1), 116835.

Muppirala AN, et al. (2026) Tachykinin signaling defines distinct populations of glia in the enteric nervous system. Neuron.

Mol?? MA, et al. (2026) Modeling human embryo implantation in vitro. Cell, 189(1), 87.

Chang LJ, et al. (2026) Assessment of Circulating Tumor DNA for Early Detection of Hepatocellular Carcinoma in Alpha-Fetoprotein-Negative Patients With Cirrhotic Nodules. JGH open : an open access journal of gastroenterology and hepatology, 10(1), e70331.

Crnovrsanin N, et al. (2026) Combining cell-free DNA fragmentomes and total tumour volume improves prognostication and tumour response evaluation in patients with colorectal cancer liver metastases. EBioMedicine, 123, 106081.

Zeng TB, et al. (2026) SETDB1 enables development beyond cleavage stages by extinguishing the MERVL-driven two-cell totipotency transcriptional program in the mouse

embryo. eLife, 15.

Kamimae-Lanning AN, et al. (2026) Metabolite-induced DNA damage drives stochastic stem cell loss and clonal hematopoiesis. Cell stem cell, 33(4), 642.

Hayward MK, et al. (2026) Tissue tension fosters macrophage-driven lipid peroxidation-induced DNA damage. Cancer cell, 44(6), 1255.

Friske JD, et al. (2026) A Conserved Enhancer Locus in Extrachromosomal DNA and Homogeneously Staining Regions Activates MYC Transcription in Group 3 Medulloblastoma. Cancer research, 86(13), 3160.

Guillon M, et al. (2026) MECP2 mutations rewire human ESC fate and bias cortical lineage commitment. Stem cell reports, 21(5), 102895.

Ferreira S, et al. (2026) Inactivation of CDKN2AARF Promotes p53-Independent Remodeling of the PDAC Tumor Microenvironment. Cancer research, 86(13), 3109.

Budnik N, et al. (2026) Nucleoli-localized KANSL2 as an epigenetic regulator of ribosome biogenesis in glioblastoma cells. Communications biology, 9(1).

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect Cryptophyllium westwoodii provide insights into the evolution of leaf-like masquerade. GigaScience, 15.

Adami A, et al. (2026) Protocol for efficient CRISPRi-mediated silencing of retrotransposons in human pluripotent stem cells. STAR protocols, 7(1), 104398.

Sun W, et al. (2026) Reconstruction of T cell infiltration in an osteosarcoma PDX-organoid interactive biobank for personalized immunotherapy. Cell reports. Medicine, 7(3), 102644.

Shen N, et al. (2026) A genome-wide in vivo CRISPR screen identifies neuroprotective strategies in the mouse and human retina. Neuron.

Simmons SK, et al. (2026) Experimental and computational methods for allelic imbalance analysis from single-nucleus RNA-seq data. Genome biology, 27(1).

Fu ZH, et al. (2026) Synthetic rewriting of the IGH locus. Cell genomics, 6(6), 101252.

Chmelova L, et al. (2026) High-depth whole genome sequencing of premalignant breast lesions reveals rearrangement hotspots and personalized management opportunities. Nature communications, 17(1).