

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

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: 20260803T040324+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 30156 mentions in open access literature.

Listed below are recent publications. The full list is available at [ASWG](#) .

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.

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.

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

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

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

Nitsch S, et al. (2026) H4K16 acylations destabilize chromatin architecture and facilitate transcriptional response during metabolic perturbations. Molecular cell, 86(1), 24.

Yang Q, et al. (2026) Molecular mechanism of resistance to lonafarnib conferred by mutations in the cysteine-rich region of respiratory syncytial virus fusion glycoprotein and discovery of a lonafarnib-derived antiviral PROTAC. *Journal of virology*, 100(1), e0148725.

Yang W, et al. (2026) Multi-omics reveals co-regulation of hepatic bile acid metabolism in laying hens by host genetics and the cecal *Anaerostipes*. *Poultry science*, 105(3), 106388.

Morrissey RL, et al. (2026) Elucidating cooperative genetic events in DCIS progression in mutant p53-driven breast cancer. *Proceedings of the National Academy of Sciences of the United States of America*, 123(2), e2526544123.

Liu X, et al. (2026) Investigation into the Pancreatic Pathogenesis of SFTSV across Multiple Levels. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(1), e15862.

Taylor RS, et al. (2026) Accurate Runs of Homozygosity Estimation From Low Coverage Genome Sequences in Non-Model Species. *Molecular ecology resources*, 26(1), e70083.

Ang??lica Maya M, et al. (2026) Adenovirus Genotypes Associated With Severe Acute Respiratory Infections Outbreak in Children, in Antioquia, Colombia, 2022-2023. *The Pediatric infectious disease journal*, 45(2), 112.

Pena-Ortiz MA, et al. (2026) Astrocytic Chromatin Remodeler ATRX Gates Hippocampal Memory Consolidation Through Metabolic and Synaptic Regulation. *Glia*, 74(1), e70098.

Burns R, et al. (2026) Diploid origins and early genome stabilization in the allotetraploid *Arabidopsis suecica*. *The New phytologist*, 249(1), 524.

Maurstad MF, et al. (2026) The green lacewing venom system and the complex mechanisms underlying its evolution. *Molecular biology and evolution*, 43(1).

Sankar V, et al. (2026) Genetic elements promote retention of extrachromosomal DNA in cancer cells. *Nature*, 649(8095), 152.

Lima Cunha W, et al. (2026) Molecular mechanisms associated with rootstock-scion interactions in rubber trees. *The plant genome*, 19(1), e70147.

Kosmopoulos JC, et al. (2026) Ecosystem health shapes viral ecology in peatland soils. *Nature microbiology*, 11(1), 142.

Zhang X, et al. (2026) Genetic and Functional Evidence Links Germline Biallelic Inactivating Variants in *WWOX* to Histological Mixed-Type Thyroid Cancer. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(1), e07602.