

Resource Summary Report

Generated by [kravitz2](#) on Sep 4, 2026

Bio-SamTools

RRID:SCR_024066

Type: Tool

Proper Citation

Bio-SamTools (RRID:SCR_024066)

Resource Information

URL: <https://metacpan.org/dist/Bio-SamTools>

Proper Citation: Bio-SamTools (RRID:SCR_024066)

Description: Software Perl interface to SamTools library for DNA sequencing.

Synonyms: libbio-samtools-perl

Resource Type: software application, software resource

Keywords: Perl interface, SamTools library, DNA sequencing,

Availability: Free, Available for download, Freely available,

Resource Name: Bio-SamTools

Resource ID: SCR_024066

Alternate URLs: <https://sources.debian.org/src/libbio-samtools-perl/>

License: perl_5

Record Creation Time: 20230824T050211+0000

Record Last Update: 20260904T000537+0000

Ratings and Alerts

No rating or validation information has been found for Bio-SamTools.

No alerts have been found for Bio-SamTools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Sandhu N, et al. (2024) Development of Novel KASP Markers for Improved Germination in Deep-Sown Direct Seeded Rice. Rice (New York, N.Y.), 17(1), 33.

Shanmugam V, et al. (2014) Whole genome sequencing reveals potential targets for therapy in patients with refractory KRAS mutated metastatic colorectal cancer. BMC medical genomics, 7, 36.

Collins JE, et al. (2012) Incorporating RNA-seq data into the zebrafish Ensembl genebuild. Genome research, 22(10), 2067.

Demeure MJ, et al. (2012) Cancer of the ampulla of Vater: analysis of the whole genome sequence exposes a potential therapeutic vulnerability. Genome medicine, 4(7), 56.

Weiss GJ, et al. (2012) Paired tumor and normal whole genome sequencing of metastatic olfactory neuroblastoma. PloS one, 7(5), e37029.