Resource Summary Report

Generated by SPARC SAWG on Sep 16, 2026

mosdepth

RRID:SCR_018929
Type: Tool

Proper Citation

mosdepth (RRID:SCR_018929)

Resource Information

URL: https://github.com/brentp/mosdepth

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Description: Software command line tool for rapidly calculating genome wide sequencing coverage. Measures depth from BAM or CRAM files at either each nucleotide position in genome or for sets of genomic regions. Used for fast BAM/CRAM depth calculation for WGS, exome, or targeted sequencing quick coverage calculation for genomes and exomes.

Resource Type: data processing software, software application, software resource

Defining Citation: PMID:29096012

Keywords: Calculating genome, wide sequencing coverage, depth measurement, BAM file, CRAM file, nucleotide position, genome, genomic region set, WGS exom, targeted sequencing, coverage calculation, exom, bio.tools

Funding: NCI U24 CA209999;
NHGRI R01 HG006693;
NHGRI R01 HG009141;
NIGMS R01 GM124355

Availability: Free, Available for download, Freely available

Resource Name: mosdepth

Resource ID: SCR_018929

Alternate IDs: OMICS_20873, biotools:mosdepth

Alternate URLs: https://bio.tools/mosdepth, https://sources.debian.org/src/mosdepth/

License: MIT license

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260912T200108+0000

Ratings and Alerts

No rating or validation information has been found for mosdepth.

No alerts have been found for mosdepth.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 56 mentions in open access literature.

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

Kamitaki N, et al. (2026) Human and bacterial genetic variation shape oral microbiomes and health. Nature, 651(8105), 429.

Dunham TJ, et al. (2026) Optimized library preparation, sequencing, and data analysis protocols for the generation of orbivirus consensus sequences. BMC genomics, 27(1), 48.

Valentín López JC, et al. (2026) Evolution of AR and Non-AR Alterations in ctDNA of Patients with Metastatic Prostate Cancer Treated in the Phase III Alliance A031201 Trial. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(12), 2413.

Thygesen VFDF, et al. (2026) The genomic history of Streptococcus mutans from the Mesolithic until modern times. Genome biology, 27(1).

Castro EM, et al. (2026) A bireporter recombinant SARS-CoV-2 Omicron BA.5 for in vitro and in vivo studies. bioRxiv : the preprint server for biology.

Kim SK, et al. (2026) Integrative analysis of in silico predictions and clinical evidence to delineate the capability of HiFi long-read sequencing in paralogous genes. NPJ genomic medicine, 11(1).

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

El-Wahab TEA, et al. (2026) Whole-genome sequencing of Apis mellifera lamarckii: first comprehensive genomic atlas of Egyptian honeybees reveals pathogen resistance mechanisms and local adaptation signatures. BMC genomics, 27(1).

Kamitaki N, et al. (2026) The DNA virome varies with human genes and environments. Nature, 653(8116), 1099.

Fu L, et al. (2026) Completely resolved structural variants by optical genome mapping with adaptive sampling from CNV discovery. NPJ genomic medicine, 11(1).

Roush SM, et al. (2026) Mutational profiling of HIV+ diffuse large B-cell lymphoma reveals distinct mutational features with evidence of genomic instability. AIDS (London, England), 40(6), 719.

Mortazavi M, et al. (2026) Long-read genome sequencing improves detection and functional interpretation of structural and repeat variants in autism. Cell genomics, 6(5), 101186.

Lehmann AE, et al. (2026) Aneuploidy promotes transient stress adaptation and metabolic flexibility in the human fungal pathogen Aspergillus fumigatus. Current biology : CB, 36(13), 3258.

Kim JA, et al. (2025) Systematic genetic assessment of hearing loss using whole-genome sequencing identifies pathogenic variants. Experimental & molecular medicine, 57(4), 775.

Mostafa A, et al. (2025) A live attenuated NS1-deficient vaccine candidate for cattle-origin influenza A (H5N1) clade 2.3.4.4.b viruses. NPJ vaccines, 10(1), 151.

Beck S, et al. (2025) Immunogenomic profiles of HIV-associated classic Hodgkin lymphoma from Malawi. Blood global hematology, 1(3).

Adami A, et al. (2025) LINE-1 retrotransposons mediate cis-acting transcriptional control in human pluripotent stem cells and regulate early brain development. Cell genomics, 100979.

Izydorczyk MB, et al. (2025) Single cell long read whole genome sequencing reveals somatic transposon activity in human brain. Communications biology, 8(1), 1627.

Gandotra N, et al. (2025) CFTR haplotype phasing using long-read genome sequencing from ultralow input DNA. Genetics in medicine open, 3, 101962.

Cuenca-Guardiola J, et al. (2025) Advanced analysis of retrotransposon variation in the human genome with nanopore sequencing using RetroInspector. Scientific reports, 15(1), 14489.