Resource Summary Report

Generated by dkNET on May 2, 2025

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: software application, software resource, data processing software

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

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: 20250502T060549+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 26 mentions in open access literature.

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

Martins Rodrigues F, et al. (2025) Germline predisposition in multiple myeloma. iScience, 28(1), 111620.

Izydorczyk MB, et al. (2024) Single cell long read whole genome sequencing reveals somatic transposon activity in human brain. medRxiv : the preprint server for health sciences.

Helal AA, et al. (2024) Benchmarking long-read aligners and SV callers for structural variation detection in Oxford nanopore sequencing data. Scientific reports, 14(1), 6160.

Liau Y, et al. (2024) Low-pass nanopore sequencing for measurement of global methylation levels in plants. BMC genomics, 25(1), 1235.

Beiki H, et al. (2024) Enhanced bovine genome annotation through integration of transcriptomics and epi-transcriptomics datasets facilitates genomic biology. GigaScience, 13.

Simmons SK, et al. (2024) Experimental and Computational Methods for Allelic Imbalance Analysis from Single-Nucleus RNA-seq Data. bioRxiv : the preprint server for biology.

Varga GIB, et al. (2024) Archaeogenetic analysis revealed East Eurasian paternal origin to the Aba royal family of Hungary. iScience, 27(10), 110892.

Thung TY, et al. (2024) Genetic variation in individuals from a population of the minimalist bacteriophage Merri-merri-uth nyilam marra-natj driving evolution of the virus. mBio, 15(12), e0256424.

Chen Y, et al. (2024) An improved chromosome-level genome assembly of perennial ryegrass (Lolium perenne L.). GigaByte (Hong Kong, China), 2024, gigabyte112.

Rapado-González Ó, et al. (2023) Somatic mutations in tumor and plasma of locoregional recurrent and/or metastatic head and neck cancer using a next-generation sequencing panel: A preliminary study. Cancer medicine, 12(6), 6615.

Manley BF, et al. (2023) A highly contiguous genome assembly reveals sources of genomic novelty in the symbiotic fungus Rhizophagus irregularis. G3 (Bethesda, Md.), 13(6).

Lian Q, et al. (2023) Meiotic recombination is confirmed to be unusually high in the fission yeast Schizosaccharomyces pombe. iScience, 26(9), 107614.

Leiendecker L, et al. (2023) Human Papillomavirus 42 Drives Digital Papillary Adenocarcinoma and Elicits a Germ Cell-like Program Conserved in HPV-Positive Cancers. Cancer discovery, 13(1), 70.

Shi Y, et al. (2023) Characterization of genome-wide STR variation in 6487 human genomes. Nature communications, 14(1), 2092.

Kotwa JD, et al. (2023) Genomic and transcriptomic characterization of delta SARS-CoV-2 infection in free-ranging white-tailed deer (Odocoileus virginianus). iScience, 26(11), 108319.

de Manuel M, et al. (2022) A paternal bias in germline mutation is widespread in amniotes and can arise independently of cell division numbers. eLife, 11.

Wong TY, et al. (2022) Evaluating Antibody Mediated Protection against Alpha, Beta, and Delta SARS-CoV-2 Variants of Concern in K18-hACE2 Transgenic Mice. Journal of virology, 96(6), e0218421.

Maróti Z, et al. (2022) The genetic origin of Huns, Avars, and conquering Hungarians. Current biology : CB, 32(13), 2858.

Lesurf R, et al. (2022) Whole genome sequencing delineates regulatory, copy number, and cryptic splice variants in early onset cardiomyopathy. NPJ genomic medicine, 7(1), 18.

Tüns AI, et al. (2022) Detection and Validation of Circular DNA Fragments Using Nanopore Sequencing. Frontiers in genetics, 13, 867018.