Resource Summary Report

Generated by RRID on Aug 2, 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: software resource, software application, 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: 20260801T190850+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 38 mentions in open access literature.

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

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

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.

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.

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

Wang B, et al. (2025) Near-complete genome assembly of allotetraploid Erianthus rockii reveals unique chromosome evolution and lineage-divergence trajectories in the Saccharum complex. Plant communications, 6(10), 101464.

Roush SM, et al. (2025) Shared genomic features of HIV+???diffuse large B-cell lymphoma in two African cohorts. Scientific reports, 15(1), 24599.

Boura I, et al. (2025) The genetic architecture of Parkinson's disease on the Island of Crete. NPJ Parkinson's disease, 11(1), 354.

Ryan K, et al. (2025) New Genome Assemblies for Poeciliidae: A Foundation for Adaptation Studies. Genome biology and evolution, 17(6).

Barre RS, et al. (2025) Bioluminescent reporter influenza A viruses to track viral infections. Microbiology spectrum, 13(11), e0215025.

Persaud N, et al. (2025) Clinical Significance of TERT Promoter Mutations in Neuroblastoma. JCO precision oncology, 9, e2500074.

Akopyan M, et al. (2025) Reference genome choice compromises population genetic analyses. Cell.

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. (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.

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.

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

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.

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