

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

BWA-METH

RRID:SCR_025851

Type: Tool

Proper Citation

BWA-METH (RRID:SCR_025851)

Resource Information

URL: <https://github.com/brentp/bwa-meth>

Proper Citation: BWA-METH (RRID:SCR_025851)

Description: Software tool for fast and accurate alignment of BS-Seq reads using bwa-mem and 3-letter genome.

Synonyms: bwa-meth

Resource Type: image analysis software, data processing software, software application, software resource, source code, alignment software

Keywords: alignment of BS-Seq reads, alignment, BS-Seq reads, bwa-mem, 3-letter genome,

Availability: Free, Available for download, Freely available

Resource Name: BWA-METH

Resource ID: SCR_025851

License: MIT license

Record Creation Time: 20241005T053245+0000

Record Last Update: 20260815T042944+0000

Ratings and Alerts

No rating or validation information has been found for BWA-METH.

No alerts have been found for BWA-METH.

Data and Source Information

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

Zhao Q, et al. (2026) Investigating the contribution of rare non-coding variants in BRCA1, BRCA2 and PALB2 to hereditary breast cancer. NPJ breast cancer, 12(1).

Huang KK, et al. (2026) Mutational Signatures and Clonal Hematopoiesis in Intestinal Metaplasia across Countries with Varying Stomach Cancer Incidence. Cancer discovery, 16(3), 497.

Tollenaere A, et al. (2026) Mechanisms of gene regulation by SRCAP and H2A.Z. Nature communications, 17(1).

Michels S, et al. (2026) Multimodal analysis of cell-free DNA identifies epigenetic biomarkers for amyotrophic lateral sclerosis diagnosis and progression. bioRxiv : the preprint server for biology.

Michels S, et al. (2026) Multimodal analysis of cell-free DNA identifies epigenetic biomarkers for amyotrophic lateral sclerosis diagnosis and progression. The Journal of clinical investigation, 136(11).

Velez-Irizarry D, et al. (2025) scRNA seq of an F1 cross of Marek's disease resistant and susceptible chickens identifies allele specific expression signatures enriched in transcription modulators. Scientific reports, 15(1), 3689.

Pelosi JA, et al. (2025) The genome of the vining fern *Lygodium microphyllum* highlights genomic and functional differences between life phases of an invasive plant. Proceedings of the National Academy of Sciences of the United States of America, 122(39), e2504773122.

Pagano L, et al. (2025) Evaluation of Illumina and Oxford Nanopore Sequencing for the Study of DNA Methylation in Alzheimer's Disease and Frontotemporal Dementia. International journal of molecular sciences, 26(9).

Anderson EN, et al. (2025) De novo variants in KDM2A cause a syndromic neurodevelopmental disorder. medRxiv : the preprint server for health sciences.

Sen S, et al. (2025) Distinct structural and functional heterochromatin partitioning of lamin B1 and lamin B2 revealed using genome-wide nicking enzyme epitope targeted DNA sequencing. Nucleic acids research, 53(2).

Bensberg M, et al. (2025) Exposing the DNA methylation-responsive compartment of the leukaemic genome in T-ALL cell lines support its potential as a novel therapeutic target in T-ALL. Clinical epigenetics, 17(1), 114.

Rech GE, et al. (2025) Global DNA methylomes reveal oncogenic-associated 5-hydroxymethylated cytosine (5hmC) signatures in the cell-free DNA of cancer patients. medRxiv : the preprint server for health sciences.

Fonseca PAS, et al. (2025) Integration of epigenomic and genomic data to predict residual feed intake and the feed conversion ratio in dairy sheep via machine learning algorithms. BMC genomics, 26(1), 313.

Liu H, et al. (2025) High-Throughput Targeted Sequencing Identifies an HPV Methylation Panel for Detecting Cervical Lesion Progression. Journal of medical virology, 97(12), e70739.

Estève PO, et al. (2025) NPM1 mislocalization mediated by RNA Pol I inhibition alters chromatin landscape. bioRxiv : the preprint server for biology.

Venney CJ, et al. (2025) Captive rearing effects on the methylome of Atlantic salmon after oceanic migration: Sex-specificity and intergenerational stability. Molecular ecology resources, 25(5), e13766.

Gonzalez-Smith L, et al. (2025) Methyl-Micro-C: simultaneous characterization of chromatin accessibility, interactions, and DNA methylation. NAR genomics and bioinformatics, 7(2), lqaf060.

Guo X, et al. (2025) Methylation reference datasets from quartet DNA materials for benchmarking epigenome sequencing. Nature communications, 16(1), 9202.

Khulan B, et al. (2025) Normal bronchial field basal cells show persistent methylome-wide impact of tobacco smoking, including in known cancer genes. Epigenetics, 20(1), 2466382.

Rajaram N, et al. (2024) Allele-specific DNA demethylation editing leads to stable upregulation of allele-specific gene expression. iScience, 27(10), 111007.