

Resource Summary Report

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Bismark

RRID:SCR_005604

Type: Tool

Proper Citation

Bismark (RRID:SCR_005604)

Resource Information

URL: <http://www.bioinformatics.babraham.ac.uk/projects/bismark/>

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Description: Software tool to map bisulfite converted sequence reads and determine cytosine methylation states. Flexible aligner and methylation caller for Bisulfite-Seq applications. Used to map bisulfite treated sequencing reads to genome of interest and perform methylation calls in single step.

Abbreviations: Bismark

Resource Type: software resource

Defining Citation: [PMID:21493656](#), [DOI:10.1093/bioinformatics/btr167](#)

Keywords: Map bisulfite treated sequence reads, determine cytosine methylation states, genome, sequence reads, perform methylation calls, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: Bismark

Resource ID: SCR_005604

Alternate IDs: biotools:bismark, OMICS_00575

Alternate URLs: <https://github.com/FelixKrueger/Bismark>, <https://bio.tools/bismark>

Old URLs: <https://sources.debian.org/src/bismark/>

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260808T185836+0000

Ratings and Alerts

No rating or validation information has been found for Bismark.

No alerts have been found for Bismark.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1200 mentions in open access literature.

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

Acera-Mateos M, et al. (2026) Systematic evaluation of single-cell multimodal data integration enhances cell type resolution and discovery of clinically relevant states in complex tissues. *Genome biology*, 27(1).

Camacho O, et al. (2026) Convergence of aging- and rejuvenation-related epigenetic alterations on PRC2 targets. *Molecular systems biology*, 22(5), 787.

Lorzadeh A, et al. (2026) Epigenetic Gatekeeping of Intestinal Stem Cell Transformation. *bioRxiv : the preprint server for biology*.

Ding SC, et al. (2026) Adapting clinical chemistry plasma as a source for liquid biopsies. *eLife*, 14.

Giacca C, et al. (2026) Loss of maternal PADI6 disrupts DNA methylation and genomic imprinting maintenance in late preimplantation mouse embryos. *Epigenetics & chromatin*, 19(1).

Yu J, et al. (2026) Enriched methylomes of low-input and fragmented DNA using fragment ligation EXclusive methylation sequencing. *Nucleic acids research*, 54(9).

Hu Y, et al. (2026) Profiling the transcriptional regulatory network reveals putative shared regulatory elements within homoeologs in polyploid *Brassica napus*. *Genome biology*, 27(1).

Zhu J, et al. (2026) Long-distance transport of siRNAs with functional roles in pollen development. *Nature plants*, 12(2), 386.

Hao JP, et al. (2026) Tet2 deficiency orchestrates Alzheimer's pathogenesis through oxidative mtDNA-driven cGAS-STING activation. *Journal of neuroinflammation*, 23(1).

Zhang T, et al. (2026) Mucosal DNA methylation reveals immune-related methylation profile and correlates with crohn's disease status. *Scientific reports*, 16(1), 2848.

Collins CF, et al. (2026) Regulatory features determine the evolutionary fate of laterally acquired genes in plants. *Molecular biology and evolution*, 43(2).

Abu Manneh R, et al. (2026) Mitoeipigenetic Alterations in Early-Onset Parkinson's Disease. *International journal of molecular sciences*, 27(4).

Riek??tter J, et al. (2026) Insights into epigenetics suggest a role of DNA methylation in regulating Chinese yam tuber shape. *BMC plant biology*, 26(1).

Gao Z, et al. (2026) TCL1A mediates DNA methylation defects in recurrent hydatidiform mole with NLRP7 pathogenic variants. *Nature communications*, 17(1).

Shen Q, et al. (2026) High-throughput single-cell DNA methylation and chromatin accessibility co-profiling with SpliCOOL-seq. *Clinical and translational medicine*, 16(2), e70584.

Kojima K, et al. (2026) Establishment of DNA methylation during primate germ cell development. *Nature communications*, 17(1).

Kafetzopoulos I, et al. (2026) DNMT1 loss leads to hypermethylation of a subset of late replicating domains by DNMT3A. *PLoS genetics*, 22(4), e1012098.

Jia B, et al. (2026) Conserved Metanephric Kidney Development and Genome Methylation in Red-Eared Slider Turtle (*Trachemys scripta elegans*). *Journal of developmental biology*, 14(2).

Brown LG, et al. (2026) Systematic analysis of hippo pathway signaling identifies TEAD1 as a transcriptional regulator of neuroendocrine prostate cancer. *Neoplasia (New York, N.Y.)*, 78, 101321.

DiFrank AJ, et al. (2026) Putative Imprinting Control Regions with Aberrant Blood-Based DNA Methylation are Associated with Hepatocellular Carcinoma Risk. *Journal of hepatocellular carcinoma*, 13, 605131.