

# Resource Summary Report

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## Bismark

RRID:SCR\_005604

Type: Tool

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### Proper Citation

Bismark (RRID:SCR\_005604)

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### Resource Information

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

**Proper Citation:** Bismark (RRID:SCR\_005604)

**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:** 20260905T132538+0000

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### Ratings and Alerts

No rating or validation information has been found for Bismark.

No alerts have been found for Bismark.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1200 mentions in open access literature.

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

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

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

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

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).

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

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).

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).

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

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

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.