

Resource Summary Report

Generated by T1D on Jul 31, 2026

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](https://pubmed.ncbi.nlm.nih.gov/21493656/), [DOI:10.1093/bioinformatics/btr167](https://doi.org/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: 20260725T190609+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 1123 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Parra-Torres M, et al. (2026) Aberrant NSUN1 activity connects m5C-RNA modification to TDP-43 neurotoxicity in ALS/FTD. Life science alliance, 9(1).

Chandramohan D, et al. (2025) Dual role of Oct4 and Sox2 in controlling the developmental capacity and timing of tissue morphogenesis in the embryonic lineage. Developmental cell.

Kim SR, et al. (2025) Molecular Classification of Endometrial Cancers Using an Integrative DNA Sequencing Panel. Journal of surgical oncology, 131(4), 734.

Saito T, et al. (2025) Altered spawning seasons of Atlantic salmon broodstock transcriptionally and epigenetically influence cell cycle and lipid-mediated regulations in their offspring. PloS one, 20(2), e0317770.

Wei TL, et al. (2025) CHH hypermethylation contributes to the early ripening of grapes revealed by DNA methylome landscape of 'Kyoho' and its bud mutant. Horticulture research, 12(1), uhae285.

Rohm D, et al. (2025) Activation of the imprinted Prader-Willi syndrome locus by CRISPR-based epigenome editing. Cell genomics, 5(2), 100770.

Pappas F, et al. (2025) Sperm DNA methylation landscape and its links to male fertility in a non-model teleost using EM-seq. Heredity, 134(5), 293.

Acera-Mateos M, et al. (2025) Systematic evaluation of single-cell multimodal data integration for comprehensive human reference atlas. bioRxiv : the preprint server for biology.

Misel-Wuchter KM, et al. (2025) Developmental epigenetic programming by Tet1/3 determines peripheral CD8 T cell fate. EMBO reports, 26(10), 2494.

Townsend J, et al. (2025) Epigenetic remodeling of sheep oocytes and embryos induced by maternal methionine supplementation. Epigenetics, 20(1), 2567459.

McCallion O, et al. (2025) HLA matching or CRISPR editing of HLA class I/II enables engraftment and effective function of allogeneic human regulatory T cell therapy in a

humanized mouse transplantation model. *Nature communications*, 16(1), 9090.

Shao X, et al. (2025) CpG methylation changes associated with hyperglycemia in type 1 diabetes occur at angiogenic glomerular and retinal gene loci. *Scientific reports*, 15(1), 15999.

Nabila A, et al. (2025) Adverse gestational environment configures a subpopulation of ventral dentate granule cells for recruitment to drive innate anxiety. *Cell reports*, 44(9), 116219.

Gittens OE, et al. (2025) Examination of DNA Methylation Patterns in Children Born Premature with Prenatal Tobacco Smoke Exposure. *Toxics*, 13(9).

Oh SJ, et al. (2025) Epigenetic landscape of hormone-independent sexual dimorphism and characterization of canine XIST. *Scientific reports*, 15(1), 35431.

Dong S, et al. (2025) Bryophytes hold a larger gene family space than vascular plants. *Nature genetics*, 57(10), 2562.

Brennan RS, et al. (2025) Complementary genetic and epigenetic changes facilitate rapid adaptation to multiple global change stressors. *Proceedings of the National Academy of Sciences of the United States of America*, 122(29), e2422782122.

Liu Y, et al. (2025) NANOME: A Nextflow pipeline for haplotype-aware allele-specific consensus DNA methylation detection by nanopore long-read sequencing. *bioRxiv : the preprint server for biology*.

Benedetti C, et al. (2025) Single-cell multiomic analysis reveals methylome and transcriptome deviations following oocyte maturation in vitro. *Reproduction (Cambridge, England)*, 170(2).

Berger MMJ, et al. (2025) Grapevine cell response to carbon deficiency requires transcriptome and methylome reprogramming. *Horticulture research*, 12(1), uhae277.