Resource Summary Report

Generated by dkNET on Apr 23, 2025

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

Funding:

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: 20250420T014256+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 990 mentions in open access literature.

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

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

Liang Y, et al. (2025) Comprehensive analysis of H3K27me3 LOCKs under different DNA methylation contexts reveal epigenetic redistribution in tumorigenesis. Epigenetics & chromatin, 18(1), 6.

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.

Chen L, et al. (2025) The DNA demethylase TET1 modifies the impact of maternal folic acid status on embryonic brain development. EMBO reports, 26(1), 175.

Perkins B, et al. (2025) Dnmt3a-dependent de novo DNA methylation enforces lineage commitment and preserves functionality of memory Th1 and Tfh cells. bioRxiv : the preprint server for biology.

Zhang W, et al. (2025) methylGrapher: genome-graph-based processing of DNA methylation data from whole genome bisulfite sequencing. Nucleic acids research, 53(3).

Nohara K, et al. (2025) Acquired sperm hypomethylation by gestational arsenic exposure is re-established in both the paternal and maternal genomes of post-epigenetic reprogramming embryos. Epigenetics & chromatin, 18(1), 4.

Lorzadeh A, et al. (2025) Motif distribution and DNA methylation underlie distinct Cdx2 binding during development and homeostasis. Nature communications, 16(1), 929.

Hure V, et al. (2025) Alternative silencing states of transposable elements in Arabidopsis associated with H3K27me3. Genome biology, 26(1), 11.

Liu Y, et al. (2025) iDog: a multi-omics resource for canids study. Nucleic acids research, 53(D1), D1039.

Demond H, et al. (2025) Transcriptome and DNA methylation profiling during the NSN to SN transition in mouse oocytes. BMC molecular and cell biology, 26(1), 2.

Fanourgakis G, et al. (2025) DNA methylation modulates nucleosome retention in sperm and H3K4 methylation deposition in early mouse embryos. Nature communications, 16(1), 465.

Lee D, et al. (2025) Increased local DNA methylation disorder in AMLs with DNMT3A-destabilizing variants and its clinical implication. Nature communications, 16(1), 560.

Sugrue VJ, et al. (2025) The androgen clock is an epigenetic predictor of long-term male hormone exposure. Proceedings of the National Academy of Sciences of the United States of America, 122(3), e2420087121.

Guo W, et al. (2025) High-throughput methylation sequencing reveals novel biomarkers for the early detection of renal cell carcinoma. BMC cancer, 25(1), 96.

Cao S, et al. (2024) Gapless genome assembly and epigenetic profiles reveal gene regulation of whole-genome triplication in lettuce. GigaScience, 13.

Chen SJ, et al. (2024) Epigenetically upregulated NSUN2 confers ferroptosis resistance in endometrial cancer via m5C modification of SLC7A11 mRNA. Redox biology, 69, 102975.

Edman S, et al. (2024) The 24-Hour Time Course of Integrated Molecular Responses to Resistance Exercise in Human Skeletal Muscle Implicates MYC as a Hypertrophic Regulator That is Sufficient for Growth. bioRxiv : the preprint server for biology.

Liang M, et al. (2024) Hypermethylated genome of a fish vertebrate iridovirus ISKNV plays important roles in viral infection. Communications biology, 7(1), 237.

Giaccari C, et al. (2024) A maternal-effect Padi6 variant causes nuclear and cytoplasmic abnormalities in oocytes, as well as failure of epigenetic reprogramming and zygotic genome activation in embryos. Genes & development, 38(3-4), 131.