Resource Summary Report

Generated by dkNET on Apr 27, 2025

BSMAP

RRID:SCR_005671
Type: Tool

Proper Citation

BSMAP (RRID:SCR_005671)

Resource Information

URL: https://code.google.com/p/bsmap/

Proper Citation: BSMAP (RRID:SCR_005671)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on May 18,2023. Short reads mapping software for bisulfite sequencing reads.

Abbreviations: BSMAP

Synonyms: Bisulfite Sequence Mapping Program

Resource Type: software resource

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: BSMAP

Resource ID: SCR_005671

Alternate IDs: OMICS_00579

Record Creation Time: 20220129T080231+0000

Record Last Update: 20250420T014258+0000

Ratings and Alerts

No rating or validation information has been found for BSMAP.

No alerts have been found for BSMAP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 350 mentions in open access literature.

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

Grillo G, et al. (2025) ZBTB24 is a conserved multifaceted transcription factor at genes and centromeres that governs the DNA methylation state and expression of satellite repeats. Human molecular genetics, 34(2), 161.

Yu R, et al. (2025) Whole-Genome Methylation Sequencing Analysis and Functional Verification of LIM-Homeobox Family Genes in Cervical Cancer. International journal of general medicine, 18, 87.

Guo HY, et al. (2025) Gestational diabetes mellitus causes genome hyper-methylation of oocyte via increased EZH2. Nature communications, 16(1), 127.

Cassuto NG, et al. (2025) Genome-Wide microRNA Expression Profiling in Human Spermatozoa and Its Relation to Sperm Quality. Genes, 16(1).

Wen D, et al. (2025) Application of a new composite genetic marker semen-specific methylation-microhaplotype in the analysis of semen-vaginal fluid mixtures. Royal Society open science, 12(1), 241565.

Ahn SH, et al. (2025) Multi-omic insights into molecular mechanism and therapeutic targets in spinocerebellar ataxia type 7. Molecular therapy. Nucleic acids, 36(1), 102414.

Liu Y, et al. (2025) DNA Methylation and Transcriptome Profiling Reveal the Role of the Antioxidant Pathway and Lipid Metabolism in Plectropomus leopardus Skin Color Formation. Antioxidants (Basel, Switzerland), 14(1).

Ma Y, et al. (2025) Generation of live mice from haploid ESCs with germline-DMR deletions or switch. Cell discovery, 11(1), 5.

Graham MK, et al. (2024) The TERT Promoter is Polycomb-Repressed in Neuroblastoma Cells with Long Telomeres. Cancer research communications, 4(6), 1533.

Sun W, et al. (2024) Characteristics of duplicated gene expression and DNA methylation regulation in different tissues of allopolyploid Brassica napus. BMC plant biology, 24(1), 518.

Liu X, et al. (2024) Study on chromatin regulation patterns of expression vectors in the PhiC31 integration site. Epigenetics, 19(1), 2337085.

Ohtani H, et al. (2024) Efficient activation of hundreds of LTR12C elements reveals cis-regulatory function determined by distinct epigenetic mechanisms. Nucleic acids research, 52(14), 8205.

Wang W, et al. (2024) A DNA demethylase reduces seed size by decreasing the DNA methylation of AT-rich transposable elements in soybean. Communications biology, 7(1), 613.

Li Z, et al. (2024) Integrated analysis of DNA methylome and transcriptome revealing epigenetic regulation of CRIR1-promoted cold tolerance. BMC plant biology, 24(1), 631.

Zhao S, et al. (2024) Increased DNMT1 acetylation leads to global DNA methylation suppression in follicular granulosa cells during reproductive aging in mammals. BMC genomics, 25(1), 1030.

Shi W, et al. (2024) Epigenomic Landscape of Human Cumulus Cells in Premature Ovarian Insufficiency Using Single-Base Resolution Methylome and Hydroxymethylome. Journal of cellular and molecular medicine, 28(24), e70284.

Xiang X, et al. (2024) Japanese encephalitis virus-induced DNA methylation contributes to blood-brain barrier permeability by modulating tight junction protein expression. Journal of neuroinflammation, 21(1), 277.

Legault LM, et al. (2024) Sex-based disparities in DNA methylation and gene expression in late-gestation mouse placentas. Biology of sex differences, 15(1), 2.

Montaño J, et al. (2024) Transcriptional re-programming of liver-resident iNKT cells into T-regulatory type-1-like liver iNKT cells involves extensive gene de-methylation. Frontiers in immunology, 15, 1454314.

Du Y, et al. (2024) Methylation-regulated tumor suppressor gene PDE7B promotes HCC invasion and metastasis through the PI3K/AKT signaling pathway. BMC cancer, 24(1), 624.