# **Resource Summary Report**

Generated by NIF on May 16, 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 NIF.

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.

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

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

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.

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

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.

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.

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

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.

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.

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.

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.

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.

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.

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.