

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## BSMAP

RRID:SCR\_005671

Type: Tool

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### Proper Citation

BSMAP (RRID:SCR\_005671)

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### 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

**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:** 20260905T132539+0000

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### Ratings and Alerts

No rating or validation information has been found for BSMAP.

No alerts have been found for BSMAP.

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### Data and Source Information

## Usage and Citation Metrics

We found 355 mentions in open access literature.

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

Choy KY, et al. (2025) Hypomethylation of thrombospondin-1 promoter region is associated with reduced aqueous humor flow. *Communications biology*, 8(1), 1430.

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 L, et al. (2025) Duckweed: a starch-hyperaccumulating plant under cultivation with a combination of nutrient limitation and elevated CO<sub>2</sub>. *Frontiers in plant science*, 16, 1531849.

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.

Jang H, et al. (2025) Structure and evolution of the Forsythieae genome elucidated by chromosome-level genome comparison of *Abeliophyllum distichum* and *Forsythia ovata* (Oleaceae). *Communications biology*, 8(1), 254.

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).

Zhang Y, et al. (2025) Transgenerational inheritance of diabetes susceptibility in male offspring with maternal androgen exposure. *Cell discovery*, 11(1), 14.

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.

Usai G, et al. (2025) Haplotype-resolved genome assembly of *Ficus carica* L. reveals allele-specific expression in the fruit. *The Plant journal : for cell and molecular biology*, 121(4), e70012.

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.

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.

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.

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.

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.

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.

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.