

Resource Summary Report

Generated by [kravitz2](#) on Jul 30, 2026

MEDIPS

RRID:SCR_012996

Type: Tool

Proper Citation

MEDIPS (RRID:SCR_012996)

Resource Information

URL: <http://www.bioconductor.org/packages/2.12/bioc/html/MEDIPS.html>

Proper Citation: MEDIPS (RRID:SCR_012996)

Description: Software developed for analyzing data derived from methylated DNA immunoprecipitation (MeDIP) experiments followed by sequencing (MeDIP-seq).

Abbreviations: MEDIPS

Synonyms: MeDIP-seq data analysis

Resource Type: software resource

Resource Name: MEDIPS

Resource ID: SCR_012996

Alternate IDs: OMICS_00613

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260725T190745+0000

Ratings and Alerts

No rating or validation information has been found for MEDIPS.

No alerts have been found for MEDIPS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 168 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Terp SK, et al. (2025) Genome-Wide cfDNA Methylation Profiling Reveals Robust Hypermethylation Signatures in Ovarian Cancer. *Cancers*, 17(12).

Zuccato JA, et al. (2025) Prediction of brain metastasis development with DNA methylation signatures. *Nature medicine*, 31(1), 116.

Pértille F, et al. (2025) Sex-Specific Methylomic and Transcriptomic Responses of the Avian Pineal Gland to Unpredictable Illumination Patterns. *Journal of pineal research*, 77(2), e70040.

Zhang R, et al. (2025) Dual mitotic bookmarking by GAF and H3K27ac orchestrates differential propagation of cell fate memory in neural development. *Nature communications*, 16(1), 7930.

Kim M, et al. (2025) Maternal dietary fish oil developmentally programs adipogenic development in the broiler chick embryo. *Poultry science*, 104(10), 105619.

Jones BC, et al. (2025) Epigenetic study of the long-term effects of gulf War illness. *Frontiers in genetics*, 16, 1553410.

Sokpor G, et al. (2024) H3 Acetylation-Induced Basal Progenitor Generation and Neocortex Expansion Depends on the Transcription Factor Pax6. *Biology*, 13(2).

El Zarif T, et al. (2024) Detecting Small Cell Transformation in Patients with Advanced EGFR Mutant Lung Adenocarcinoma through Epigenomic cfDNA Profiling. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(17), 3798.

Jovasevic V, et al. (2024) Formation of memory assemblies through the DNA-sensing TLR9 pathway. *Nature*, 628(8006), 145.

Lleshi E, et al. (2024) Prostate cancer detection through unbiased capture of methylated cell-free DNA. *iScience*, 27(7), 110330.

Conway AM, et al. (2024) A cfDNA methylation-based tissue-of-origin classifier for cancers of unknown primary. *Nature communications*, 15(1), 3292.

Ma K, et al. (2024) The Hypothalamic Epigenetic Landscape in Dietary Obesity. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 11(9), e2306379.

Nilsson EE, et al. (2024) Epigenetic biomarker for preeclampsia-associated preterm birth and potential preventative medicine. *Environmental epigenetics*, 10(1), dvae022.

Wang D, et al. (2024) DNA methylation patterns in the peripheral blood of Xinjiang brown cattle with variable somatic cell counts. *Frontiers in genetics*, 15, 1405478.

Christiansen C, et al. (2024) Enhanced resolution profiling in twins reveals differential methylation signatures of type 2 diabetes with links to its complications. *EBioMedicine*, 103, 105096.

Kaefer M, et al. (2023) Role of epigenetics in the etiology of hypospadias through penile foreskin DNA methylation alterations. *Scientific reports*, 13(1), 555.

Villicaña S, et al. (2023) Genetic impacts on DNA methylation help elucidate regulatory genomic processes. *Genome biology*, 24(1), 176.

Tatemoto P, et al. (2023) An enriched maternal environment and stereotypes of sows differentially affect the neuro-epigenome of brain regions related to emotionality in their piglets. *Epigenetics*, 18(1), 2196656.

Duncan GE, et al. (2023) Epigenome-wide association study of systemic effects of obesity susceptibility in human twins. *Epigenetics*, 18(1), 2268834.

Ye J, et al. (2023) Transition of allele-specific DNA hydroxymethylation at regulatory loci is associated with phenotypic variation in monozygotic twins discordant for psychiatric disorders. *BMC medicine*, 21(1), 491.