

Resource Summary Report

Generated by [NIF](#) on Aug 19, 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: 20260815T182452+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 175 mentions in open access literature.

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

Niu Z, et al. (2026) Histone modification clocks for robust cross-species biological age prediction and elucidating senescence regulation. *Proceedings of the National Academy of Sciences of the United States of America*, 123(11), e2533687123.

de Anca Prado V, et al. (2026) Benchmarking of methods to analyse data derived from GBS-MeDIP. *BMC bioinformatics*, 27(1), 17.

Richardson SA, et al. (2026) Cell-free DNA methylome and fragmentome analysis for relapse monitoring of Ewing sarcoma. *EMBO molecular medicine*, 18(4), 1342.

Kondrup K, et al. (2026) Genome-wide methylome profiling of cell-free DNA enables prognostication of patients with castration-resistant prostate cancer. *British journal of cancer*, 135(1), 127.

Kim DY, et al. (2026) Tissue-specific epigenetic regulation of fat metabolism in pigs through integrated analysis of DNA methylation and gene expression networks. *Journal of animal science and biotechnology*, 17(1).

Landry AP, et al. (2026) Spatially resolved single-cell analyses of human meningioma identify novel cell states influencing tumor microenvironment and progression. *Nature genetics*, 58(6), 1383.

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

P??rtile 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.

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

Androulidaki A, et al. (2025) Lack of caspase 8 directs neuronal progenitor-like reprogramming and small cell lung cancer progression. *Nature communications*, 16(1), 11280.

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).

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

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.

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

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

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

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