# Resource Summary Report

Generated by dkNET on Apr 26, 2025

## 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

**Funding:**

**Resource Name:** MEDIPS

**Resource ID:** SCR_012996

**Alternate IDs:** OMICS_00613

**Record Creation Time:** 20220129T080313+0000

**Record Last Update:** 20250420T014628+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 163 mentions in open access literature.

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


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

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

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.

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.

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.

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.

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.

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

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

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

Nam AR, et al. (2023) The landscape of PBMC methylome in canine mammary tumors reveals the epigenetic regulation of immune marker genes and its potential application in predicting tumor malignancy. BMC genomics, 24(1), 403.

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.

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

Lees J, et al. (2023) The mitoepigenome responds to stress, suggesting novel mito-nuclear interactions in vertebrates. BMC genomics, 24(1), 561.

Wild MA, et al. (2023) Systemic epigenome-wide association study of elk treponeme-associated hoof disease. Scientific reports, 13(1), 15378.

Zhou BW, et al. (2023) Germline gene fusions across species reveal the chromosomal instability regions and cancer susceptibility. iScience, 26(12), 108431.

Guan X, et al. (2022) Prenatal inflammation exposure-programmed hypertension exhibits multi-generational inheritance via disrupting DNA methylome. Acta pharmacologica Sinica, 43(6), 1419.