

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-Wurtemberg, 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 stereotypes 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.