

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 12, 2026

MEDME

RRID:SCR_012995

Type: Tool

Proper Citation

MEDME (RRID:SCR_012995)

Resource Information

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

Proper Citation: MEDME (RRID:SCR_012995)

Description: Software that allows the prediction of absolute and relative methylation levels based on measures obtained by MeDIP-microarray experiments.

Abbreviations: MEDME

Resource Type: software resource

Resource Name: MEDME

Resource ID: SCR_012995

Alternate IDs: OMICS_00614

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260912T195757+0000

Ratings and Alerts

No rating or validation information has been found for MEDME.

No alerts have been found for MEDME.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Wu X, et al. (2024) 5-Aza-2'-Deoxycytidine Ameliorates Choroidal Neovascularization by Inhibiting the Wnt/??-Catenin Signaling Pathway. *Investigative ophthalmology & visual science*, 65(2), 23.

Le MNU, et al. (2023) ChIP-chip data for identifying target genes and consensus binding sequences of mutant p53 in MDA-MB-468 breast cancer cells. *Data in brief*, 50, 109499.

Martin LJ, et al. (2022) Aberrant DNA and RNA Methylation Occur in Spinal Cord and Skeletal Muscle of Human SOD1 Mouse Models of ALS and in Human ALS: Targeting DNA Methylation Is Therapeutic. *Cells*, 11(21).

Wang X, et al. (2021) Maternal folic acid impacts DNA methylation profile in male rat offspring implicated in neurodevelopment and learning/memory abilities. *Genes & nutrition*, 16(1), 1.

Noruzinia M, et al. (2021) Young Breast Cancer: Novel Gene Methylation in WBC. *Asian Pacific journal of cancer prevention : APJCP*, 22(8), 2371.

Huang Y, et al. (2019) Developmental features of DNA methylation in CpG islands of human gametes and preimplantation embryos. *Experimental and therapeutic medicine*, 17(6), 4447.

Wang J, et al. (2018) Integrated analysis of DNA methylation profiling and gene expression profiling identifies novel markers in lung cancer in Xuanwei, China. *PloS one*, 13(10), e0203155.

Kanherkar RR, et al. (2018) The Effect of Citalopram on Genome-Wide DNA Methylation of Human Cells. *International journal of genomics*, 2018, 8929057.

Ha A, et al. (2018) Comparative Efficacy of the New Optical Biometer on Intraocular Lens Power Calculation (AL-Scan versus IOLMaster). *Korean journal of ophthalmology : KJO*, 32(3), 241.

Xu J, et al. (2018) MeDEStrand: an improved method to infer genome-wide absolute methylation levels from DNA enrichment data. *BMC bioinformatics*, 19(1), 540.

Wang J, et al. (2016) DNA methylation is critical for tooth agenesis: implications for sporadic non-syndromic anodontia and hypodontia. *Scientific reports*, 6, 19162.

Chater-Diehl EJ, et al. (2016) Alteration of Gene Expression, DNA Methylation, and Histone Methylation in Free Radical Scavenging Networks in Adult Mouse Hippocampus following Fetal Alcohol Exposure. *PloS one*, 11(5), e0154836.

Xiao JL, et al. (2016) DNA methylation profiling in different phases of temporomandibular joint osteoarthritis in rats. *Archives of oral biology*, 68, 105.

Zhao M, et al. (2016) Increased 5-hydroxymethylcytosine in CD4(+) T cells in systemic lupus erythematosus. *Journal of autoimmunity*, 69, 64.

Song M, et al. (2016) Combined analysis of DNA methylome and transcriptome reveal novel candidate genes with susceptibility to bovine *Staphylococcus aureus* subclinical mastitis. *Scientific reports*, 6, 29390.

Yu B, et al. (2015) Epigenetic Alterations in Density Selected Human Spermatozoa for Assisted Reproduction. *PloS one*, 10(12), e0145585.

Melka MG, et al. (2015) Insights into the origin of DNA methylation differences between monozygotic twins discordant for schizophrenia. *Journal of molecular psychiatry*, 3(1), 7.

Yu M, et al. (2014) Folic acid stimulation of neural stem cell proliferation is associated with altered methylation profile of PI3K/Akt/CREB. *The Journal of nutritional biochemistry*, 25(4), 496.