

Resource Summary Report

Generated by [NIF](#) on Sep 2, 2026

eDMR

RRID:SCR_006960

Type: Tool

Proper Citation

eDMR (RRID:SCR_006960)

Resource Information

URL: <https://code.google.com/p/edmr/>

Proper Citation: eDMR (RRID:SCR_006960)

Description: Comprehensive differentially methylated regions (DMR) analysis based on bimodal normal distribution model and weighted cost function for regional methylation analysis optimization.

Abbreviations: eDMR

Resource Type: software resource

Keywords: bio.tools

Availability: MIT License

Resource Name: eDMR

Resource ID: SCR_006960

Alternate IDs: biotools:edmr, OMICS_00622

Alternate URLs: <https://bio.tools/edmr>

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260829T182245+0000

Ratings and Alerts

No rating or validation information has been found for eDMR.

No alerts have been found for eDMR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Qin X, et al. (2025) Short-Chain Fatty Acids Are Potential Biomarkers of Immune Regulation in Diabetic Retinopathy. *Investigative ophthalmology & visual science*, 66(6), 23.

Nohara K, et al. (2025) Acquired sperm hypomethylation by gestational arsenic exposure is re-established in both the paternal and maternal genomes of post-epigenetic reprogramming embryos. *Epigenetics & chromatin*, 18(1), 4.

Geng R, et al. (2023) Sub-micron spin-based magnetic field imaging with an organic light emitting diode. *Nature communications*, 14(1), 1441.

Laplana M, et al. (2022) Differentially methylated regions within lung cancer risk loci are enriched in deregulated enhancers. *Epigenetics*, 17(2), 117.

Liu Y, et al. (2021) Dynamic changes of genomic methylation profiles at different growth stages in Chinese Tan sheep. *Journal of animal science and biotechnology*, 12(1), 118.

Liu H, et al. (2021) DNA methylation atlas of the mouse brain at single-cell resolution. *Nature*, 598(7879), 120.

Sureshchandra S, et al. (2021) Phenotypic and Epigenetic Adaptations of Cord Blood CD4+ T Cells to Maternal Obesity. *Frontiers in immunology*, 12, 617592.

Nohara K, et al. (2020) Gestational arsenic exposure induces site-specific DNA hypomethylation in active retrotransposon subfamilies in offspring sperm in mice. *Epigenetics & chromatin*, 13(1), 53.

He A, et al. (2020) Analysis of DNA methylation differences in gonads of the large yellow croaker. *Gene*, 749, 144754.

Fan X, et al. (2020) Genetic and Global Epigenetic Modification, Which Determines the Phenotype of Transgenic Rice? *International journal of molecular sciences*, 21(5).

Okamura K, et al. (2019) DNA methylation changes involved in the tumor increase in F2 males born to gestationally arsenite-exposed F1 male mice. *Cancer science*, 110(8), 2629.

Shi TT, et al. (2019) Identifying and Validating Genes with DNA Methylation Data in the Context of Biological Network for Chinese Patients with Graves' Orbitopathy. *International journal of endocrinology*, 2019, 6212681.

Xin Z, et al. (2019) A Pathway Analysis Based on Genome-Wide DNA Methylation of Chinese Patients with Graves' Orbitopathy. *BioMed research international*, 2019, 9565794.

Razzak J, et al. (2019) Global, regional and national burden of emergency medical diseases using specific emergency disease indicators: analysis of the 2015 Global Burden of Disease Study. *BMJ global health*, 4(2), e000733.

Dong L, et al. (2019) Genome-wide Analysis Reveals DNA Methylation Alterations in Obesity Associated with High Risk of Colorectal Cancer. *Scientific reports*, 9(1), 5100.

Matsushita J, et al. (2018) The DNA methylation profile of liver tumors in C3H mice and identification of differentially methylated regions involved in the regulation of tumorigenic genes. *BMC cancer*, 18(1), 317.

Frolinger T, et al. (2018) Epigenetic modifications by polyphenolic compounds alter gene expression in the hippocampus. *Biology open*, 7(10).

Ho TT, et al. (2017) Autophagy maintains the metabolism and function of young and old stem cells. *Nature*, 543(7644), 205.

Yu F, et al. (2017) Systemic analysis of osteoblast-specific DNA methylation marks reveals novel epigenetic basis of osteoblast differentiation. *Bone reports*, 6, 109.