

Resource Summary Report

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methyIMnM

RRID:SCR_001289

Type: Tool

Proper Citation

methyIMnM (RRID:SCR_001289)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/methyIMnM.html>

Proper Citation: methyIMnM (RRID:SCR_001289)

Description: Software package to detect different methylation levels (DMR) that gives the exact p-value and q-value of MeDIP-seq and MRE-seq data for different samples comparison.

Abbreviations: methyIMnM

Synonyms: methyIMnM - detect different methylation level (DMR)

Resource Type: software resource

Keywords: dna methylation, sequencing, medip-seq, mre-seq

Availability: GNU General Public License, v3

Resource Name: methyIMnM

Resource ID: SCR_001289

Alternate IDs: OMICS_02047

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260725T190500+0000

Ratings and Alerts

No rating or validation information has been found for methyIMnM.

No alerts have been found for methyIMnM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Moody L, et al. (2019) Maternal Low-Fat Diet Programs the Hepatic Epigenome despite Exposure to an Obesogenic Postnatal Diet. *Nutrients*, 11(9).

Moody L, et al. (2019) Maternal and Post-weaning High-Fat Diets Produce Distinct DNA Methylation Patterns in Hepatic Metabolic Pathways within Specific Genomic Contexts. *International journal of molecular sciences*, 20(13).

Zhang C, et al. (2018) Long-Term In Vitro Expansion of Epithelial Stem Cells Enabled by Pharmacological Inhibition of PAK1-ROCK-Myosin II and TGF- β Signaling. *Cell reports*, 25(3), 598.

Keleher MR, et al. (2018) A high-fat diet alters genome-wide DNA methylation and gene expression in SM/J mice. *BMC genomics*, 19(1), 888.

Keleher MR, et al. (2018) Maternal high-fat diet associated with altered gene expression, DNA methylation, and obesity risk in mouse offspring. *PloS one*, 13(2), e0192606.

Li J, et al. (2017) Whole-Genome DNA Methylation Profiling Identifies Epigenetic Signatures of Uterine Carcinosarcoma. *Neoplasia (New York, N.Y.)*, 19(2), 100.

Hasbún R, et al. (2016) Differential Methylation of Genomic Regions Associated with Heteroblasty Detected by M&M Algorithm in the Nonmodel Species *Eucalyptus globulus* Labill. *International journal of genomics*, 2016, 4395153.

Lee HJ, et al. (2015) Developmental enhancers revealed by extensive DNA methylome maps of zebrafish early embryos. *Nature communications*, 6, 6315.

Nagarajan RP, et al. (2014) Recurrent epimutations activate gene body promoters in primary glioblastoma. *Genome research*, 24(5), 761.