Resource Summary Report

Generated by dkNET on May 18, 2025

methylMnM

RRID:SCR_001289
Type: Tool

Proper Citation

methylMnM (RRID:SCR_001289)

Resource Information

URL: http://www.bioconductor.org/packages/release/bioc/html/methylMnM.html

Proper Citation: methylMnM (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: methylMnM

Synonyms: methylMnM - detect different methylation level (DMR)

Resource Type: software resource

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

Funding:

Availability: GNU General Public License, v3

Resource Name: methylMnM

Resource ID: SCR_001289

Alternate IDs: OMICS_02047

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250420T014025+0000

Ratings and Alerts

No rating or validation information has been found for methylMnM.

No alerts have been found for methylMnM.

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 dkNET.

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).

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

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-? 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.