

Resource Summary Report

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dmrFinder

RRID:SCR_012853

Type: Tool

Proper Citation

dmrFinder (RRID:SCR_012853)

Resource Information

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

Proper Citation: dmrFinder (RRID:SCR_012853)

Description: Function for differentially methylated regions (DMR) detection that is a part of the charm package in R/Bioconductor.

Abbreviations: dmrFinder

Resource Type: software resource

Resource Name: dmrFinder

Resource ID: SCR_012853

Alternate IDs: OMICS_00621

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260829T182423+0000

Ratings and Alerts

No rating or validation information has been found for dmrFinder.

No alerts have been found for dmrFinder.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 29 mentions in open access literature.

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

Sinke L, et al. (2026) DNA methylation of genes involved in lipid metabolism drives adiponectin levels and metabolic disease. *Diabetologia*, 69(1), 127.

Sinke L, et al. (2026) Epigenome-wide association study of circulating interleukin-6 connects DNA methylation to immunometabolic and inflammatory health. *Communications biology*, 9(1), 242.

Shibata T, et al. (2026) Disrupted epigenetic regulation in human senile lentigines revealed by characterizing gene expression and DNA methylation alterations. *Clinical epigenetics*, 18(1).

Fioriniello S, et al. (2025) Green forage impacts on the DNA methylation in the ruminal wall of Italian mediterranean dairy buffaloes. *Scientific reports*, 15(1), 8074.

Vicente CT, et al. (2025) Methylome analysis of FTLD patients with TDP-43 pathology identifies epigenetic signatures specific to pathological subtypes. *Molecular neurodegeneration*, 20(1), 80.

Hieromnimon M, et al. (2025) Single and multi-omic characterization of a porcine model of ethanol-induced hepatic fibrosis. *Epigenetics*, 20(1), 2471127.

Sinke L, et al. (2025) Tissue-specific methylomic responses to a lifestyle intervention in older adults associate with metabolic and physiological health improvements. *Aging cell*, 24(4), e14431.

Wen B, et al. (2024) Causal impact of DNA methylation on refracture in elderly individuals with osteoporosis - a prospective cohort study. *BMC musculoskeletal disorders*, 25(1), 432.

Cao S, et al. (2024) DNA methylation variations underlie lettuce domestication and divergence. *Genome biology*, 25(1), 158.

Schoofs K, et al. (2024) Therapy response monitoring in blood plasma from esophageal adenocarcinoma patients using cell-free DNA methylation profiling. *Scientific reports*, 14(1), 31112.

Stuart KC, et al. (2024) The genome of a globally invasive passerine, the common myna, *Acridotheres tristis*. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 31(2).

Li G, et al. (2024) Transformer-based AI technology improves early ovarian cancer diagnosis using cfDNA methylation markers. *Cell reports. Medicine*, 5(8), 101666.

Baetens M, et al. (2024) Advancing diagnosis and early risk assessment of preeclampsia through noninvasive cell-free DNA methylation profiling. *Clinical epigenetics*, 16(1), 182.

Yu Z, et al. (2024) DNA methylation profiling identifies TBKBP1 as potent amplifier of cytotoxic activity in CMV-specific human CD8+ T cells. *PLoS pathogens*, 20(9), e1012581.

Cox OH, et al. (2024) Implementation of the Methyl-Seq platform to identify tissue- and sex-specific DNA methylation differences in the rat epigenome. *Epigenetics*, 19(1), 2393945.

Jung YH, et al. (2023) Characterization of a strain-specific CD-1 reference genome reveals potential inter- and intra-strain functional variability. *BMC genomics*, 24(1), 437.

Hellbach F, et al. (2023) Pooled analysis of epigenome-wide association studies of food consumption in KORA, TwinsUK and LLS. *European journal of nutrition*, 62(3), 1357.

Schwartz U, et al. (2023) High-resolution transcriptomic and epigenetic profiling identifies novel regulators of COPD. *The EMBO journal*, 42(12), e111272.

Tian XP, et al. (2023) Diagnostic performance and prognostic value of circulating tumor DNA methylation marker in extranodal natural killer/T cell lymphoma. *Cell reports. Medicine*, 4(2), 100859.

Giurato G, et al. (2023) Genome-wide DNA methylation changes upon DOT1L inhibition in hormone-responsive breast cancer cells. *Frontiers in cell and developmental biology*, 11, 1308025.