Resource Summary Report

Generated by dkNET on May 18, 2025

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

Funding:

Resource Name: dmrFinder

Resource ID: SCR_012853

Alternate IDs: OMICS_00621

Record Creation Time: 20220129T080312+0000

Record Last Update: 20250420T014622+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 22 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.

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

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).

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.

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.

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.

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.

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.

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.

Reverdatto S, et al. (2022) Developmental and Injury-induced Changes in DNA Methylation in Regenerative versus Non-regenerative Regions of the Vertebrate Central Nervous System. BMC genomics, 23(1), 2.

Karlsson L, et al. (2021) A differential DNA methylome signature of pulmonary immune cells from individuals converting to latent tuberculosis infection. Scientific reports, 11(1), 19418.

Espeso-Gil S, et al. (2021) Environmental Enrichment Induces Epigenomic and Genome Organization Changes Relevant for Cognition. Frontiers in molecular neuroscience, 14, 664912.

Schachtschneider KM, et al. (2020) Altered Hippocampal Epigenetic Regulation Underlying Reduced Cognitive Development in Response to Early Life Environmental Insults. Genes, 11(2).

Amenyah SD, et al. (2020) Nutritional Epigenomics and Age-Related Disease. Current developments in nutrition, 4(7), nzaa097.

Hilliard AT, et al. (2019) Genome-wide effects of social status on DNA methylation in the brain of a cichlid fish, Astatotilapia burtoni. BMC genomics, 20(1), 699.

Yang Y, et al. (2019) UVB drives different stages of epigenome alterations during progression of skin cancer. Cancer letters, 449, 20.