

Resource Summary Report

Generated by [RRID](#) on Aug 11, 2026

DMRcate

RRID:SCR_028007

Type: Tool

Proper Citation

DMRcate (RRID:SCR_028007)

Resource Information

URL: <https://bioconductor.org/packages/release/bioc/html/DMRcate.html>

Proper Citation: DMRcate (RRID:SCR_028007)

Description: Software application for de novo identification and extraction of differentially methylated regions (DMRs) from the human genome using Whole Genome Bisulfite Sequencing (WGBS) and Illumina Infinium Array (450K and EPIC) data. Provides functionality for filtering probes possibly confounded by SNPs and cross-hybridisation. Includes GRanges generation and plotting functions.

Resource Type: software application, software resource

Keywords: de novo identification and extraction, differentially methylated regions, human genome,

Availability: Free, Available for download, Freely available

Resource Name: DMRcate

Resource ID: SCR_028007

License: GNU GPL v3

Record Creation Time: 20260224T055257+0000

Record Last Update: 20260810T040935+0000

Ratings and Alerts

No rating or validation information has been found for DMRcate.

No alerts have been found for DMRcate.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Bradic M, et al. (2022) DNA methylation predicts the outcome of COVID-19 patients with acute respiratory distress syndrome. Journal of translational medicine, 20(1), 526.

Ruzicka WB, et al. (2017) Variability of DNA Methylation within Schizophrenia Risk Loci across Subregions of Human Hippocampus. Genes, 8(5).