

Resource Summary Report

Generated by [nidm-terms](#) on Sep 21, 2026

MethylCoder

RRID:SCR_012997

Type: Tool

Proper Citation

MethylCoder (RRID:SCR_012997)

Resource Information

URL: <https://github.com/brentp/methylcode>

Proper Citation: MethylCoder (RRID:SCR_012997)

Description: A single program that takes of bisulfite-treated reads and outputs per-base methylation data.

Abbreviations: MethylCoder

Resource Type: software resource

Defining Citation: [PMID:21724594](#)

Keywords: bio.tools

Resource Name: MethylCoder

Resource ID: SCR_012997

Alternate IDs: biotools:methylcoder, OMICS_00585

Alternate URLs: <https://bio.tools/methylcoder>

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260919T195236+0000

Ratings and Alerts

No rating or validation information has been found for MethylCoder.

No alerts have been found for MethylCoder.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Han Y, et al. (2016) Integrating Epigenomics into the Understanding of Biomedical Insight. Bioinformatics and biology insights, 10, 267.

Baheti S, et al. (2016) Targeted alignment and end repair elimination increase alignment and methylation measure accuracy for reduced representation bisulfite sequencing data. BMC genomics, 17, 149.

Karcher JR, et al. (2015) Genome-wide epigenetic and proteomic analysis reveals altered Notch signaling in EPC dysfunction. Physiological reports, 3(4).

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.