

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

[methylKit](#)

RRID:SCR_005177

Type: Tool

Proper Citation

methylKit (RRID:SCR_005177)

Resource Information

URL: <https://code.google.com/p/methylkit/>

Proper Citation: methylKit (RRID:SCR_005177)

Description: An R package for DNA methylation analysis and annotation from high-throughput bisulfite sequencing., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: methylKit

Resource Type: software resource

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: methylKit

Resource ID: SCR_005177

Alternate IDs: OMICS_00606

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260725T190600+0000

Ratings and Alerts

No rating or validation information has been found for methylKit.

No alerts have been found for methylKit.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 617 mentions in open access literature.

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

Shi XY, et al. (2025) Mitofusin 1 Drives Preimplantation Development by Enhancing Chromatin Incorporation of Histone H3.3. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(18), e2414985.

Tran QT, et al. (2025) Validation of target-enriched enzymatic methylation sequencing for brain tumor classification from formalin-fixed paraffin embedded-derived DNA. *Brain pathology* (Zurich, Switzerland), 35(5), e70000.

Luo M, et al. (2025) The interplay between epigenomic and transcriptomic variation during ecotype divergence in stickleback. *BMC biology*, 23(1), 70.

Liu Y, et al. (2025) DNA Methylation and Transcriptome Profiling Reveal the Role of the Antioxidant Pathway and Lipid Metabolism in *Plectropomus leopardus* Skin Color Formation. *Antioxidants* (Basel, Switzerland), 14(1).

Misel-Wuchter KM, et al. (2025) Developmental epigenetic programming by Tet1/3 determines peripheral CD8 T cell fate. *EMBO reports*, 26(10), 2494.

Schwartz AV, et al. (2025) Catalytically distinct metabolic enzyme isocitrate dehydrogenase 1 mutants tune phenotype severity in tumor models. *The Journal of biological chemistry*, 301(5), 108477.

Saito T, et al. (2025) Altered spawning seasons of Atlantic salmon broodstock transcriptionally and epigenetically influence cell cycle and lipid-mediated regulations in their offspring. *PloS one*, 20(2), e0317770.

Ben Sassi M, et al. (2025) Improved tumor-type informed compared to tumor-informed mutation tracking for ctDNA detection and microscopic residual disease assessment in epithelial ovarian cancer. *Journal of experimental & clinical cancer research : CR*, 44(1), 174.

Huang H, et al. (2025) Decoding hepatobiliary-specific immune gene patterns in gastrointestinal cancers via gene ontology fingerprints, multi-omics, and experimental integration. *Precision clinical medicine*, 8(3), pbaf014.

Andersson S, et al. (2025) Old mitochondria regulate niche renewal via α -ketoglutarate metabolism in stem cells. *Nature metabolism*, 7(7), 1344.

Luviano-Aparicio N, et al. (2025) Introduction of epigenetic variation contribute to resistance against the human parasite *Schistosoma mansoni*. *Epigenetics & chromatin*, 18(1), 43.

Liu Y, et al. (2025) NANOME: A Nextflow pipeline for haplotype-aware allele-specific consensus DNA methylation detection by nanopore long-read sequencing. *bioRxiv : the preprint server for biology*.

Derbel H, et al. (2025) DiffMethylTools: a toolbox of the detection, annotation and visualization of differential DNA methylation. *bioRxiv : the preprint server for biology*.

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.

Jia H, et al. (2025) DNA methylation mediates the immunosuppressive tumour microenvironment in metastatic endometrial clear cell carcinoma. *EBioMedicine*, 120, 105954.

Han C, et al. (2025) An Isoform-Specific RUNX1C-BTG2 Axis Governs AML Quiescence and Chemoresistance. *Blood cancer discovery*, 6(5), 464.

Ho WZ, et al. (2025) Epigenetic Responses to Anthropogenic Versus Natural Sources of Oil Exposure Differ in Wild Arctic Seabird Populations. *Evolutionary applications*, 18(7), e70125.

He YJ, et al. (2025) Transcriptional and epigenetic dynamics of sex determining gene PdFERR and MADS-box related genes during flower development in *Populus deltoides*. *Frontiers in plant science*, 16, 1582915.

Kerns EV, et al. (2025) Variable performance of widely used bisulfite sequencing methods and read mapping software for DNA methylation. *bioRxiv : the preprint server for biology*.

Lyu L, et al. (2025) Whole-Genome DNA Methylation Analysis of Inoculation with *Trichothecium roseum* in Harvested Muskmelons. *Journal of fungi (Basel, Switzerland)*, 11(4).