

Resource Summary Report

Generated by T1D on Jul 31, 2026

methyKit

RRID:SCR_005177

Type: Tool

Proper Citation

methyKit (RRID:SCR_005177)

Resource Information

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

Proper Citation: methyKit (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: methyKit

Resource Type: software resource

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: methyKit

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 methyKit.

No alerts have been found for methyKit.

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 [T1D](#) .

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

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.

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.

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.

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).

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.

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

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*.

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.

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.

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

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

Yanai H, et al. (2025) DNA methylation drives hematopoietic stem cell aging phenotypes after proliferative stress. *GeroScience*, 47(2), 1873.

King SE, et al. (2025) Prenatal maternal stress in rats alters the epigenetic and transcriptomic landscape of the maternal-fetal interface across four generations. *Communications biology*, 8(1), 38.

Nohara K, et al. (2025) Acquired sperm hypomethylation by gestational arsenic exposure is re-established in both the paternal and maternal genomes of post-epigenetic reprogramming embryos. *Epigenetics & chromatin*, 18(1), 4.

McGregor BA, et al. (2025) Deciphering motor dysfunction and microglial activation in mThy1-?-synuclein mice: a comprehensive study of behavioral, gene expression, and methylation changes. *Frontiers in molecular neuroscience*, 18, 1544971.

Chen L, et al. (2025) The DNA demethylase TET1 modifies the impact of maternal folic acid status on embryonic brain development. *EMBO reports*, 26(1), 175.