

Resource Summary Report

Generated by [ASWG](#) on Sep 18, 2026

MethPipe

RRID:SCR_005168

Type: Tool

Proper Citation

MethPipe (RRID:SCR_005168)

Resource Information

URL: <http://smithlab.usc.edu/methpipe/>

Proper Citation: MethPipe (RRID:SCR_005168)

Description: A computational pipeline for analyzing bisulfite sequencing data.

Abbreviations: MethPipe

Resource Type: software resource

Defining Citation: [PMID:24324667](#)

Keywords: bio.tools

Resource Name: MethPipe

Resource ID: SCR_005168

Alternate IDs: biotools:methpipe, OMICS_00603

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

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260912T195622+0000

Ratings and Alerts

No rating or validation information has been found for MethPipe.

No alerts have been found for MethPipe.

Data and Source Information

Usage and Citation Metrics

We found 108 mentions in open access literature.

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

Wang C, et al. (2026) Demethylation-primed tandem CD19/CD20 CAR T cells in relapsed/refractory B-cell lymphoma: a phase I/II trial. *Nature communications*, 17(1).

Kafetzopoulos I, et al. (2026) DNMT1 loss leads to hypermethylation of a subset of late replicating domains by DNMT3A. *PLoS genetics*, 22(4), e1012098.

Li W, et al. (2026) DNA methylation clock in bull sperm cells reveals the epigenetic aging characteristics and impact on fertility. *Journal of animal science and biotechnology*, 17(1).

Zhang MS, et al. (2026) BCAT1-dependent HIF-1 α stabilization is a targetable metabolic vulnerability in hepatocellular carcinoma. *Cell reports. Medicine*, 7(5), 102784.

Brown ME, et al. (2025) Pancreatic islet β -cell subtypes are derived from biochemically-distinct and nutritionally-regulated islet progenitors. *Nature communications*, 16(1), 5758.

Cheng CCY, et al. (2025) Multi-omic analysis of hepatocellular carcinoma reveals aberrant cis-regulatory changes and dysregulated retrotransposons with prognostic potential. *Communications biology*, 8(1), 1792.

Ebert BC, et al. (2025) Establishment of neuronal and glial competence of neural stem cells requires distinct enzymatic activities of TET enzymes. *Stem cell reports*, 20(9), 102595.

De Vlaminck I, et al. (2025) Metagenomic Cell-free DNA Sequencing for Treatment Monitoring in Sepsis. *Research square*.

Zhou B, et al. (2025) Anticancer effects of zinc ion-mediated DNA demethylation in oesophageal squamous cell carcinoma. *Frontiers in pharmacology*, 16, 1559675.

Baffuto M, et al. (2025) Epigenetic mechanisms governing cell type specific somatic expansion and toxicity in Huntington's disease. *bioRxiv : the preprint server for biology*.

Guo L, et al. (2025) Duckweed: a starch-hyperaccumulating plant under cultivation with a combination of nutrient limitation and elevated CO₂. *Frontiers in plant science*, 16, 1531849.

Guerin LN, et al. (2025) Temporally discordant chromatin accessibility and DNA demethylation define short- and long-term enhancer regulation during cell fate specification. *Cell reports*, 44(5), 115680.

Wang J, et al. (2025) DNA methyltransferase 1 modulates mitochondrial function through bridging m⁵C RNA methylation. *Molecular cell*, 85(10), 1999.

Moqri M, et al. (2024) PRC2-AgeIndex as a universal biomarker of aging and rejuvenation. *Nature communications*, 15(1), 5956.

Ye X, et al. (2024) Enhancer-promoter activation by the Kaposi sarcoma-associated herpesvirus episome maintenance protein LANA. *Cell reports*, 43(3), 113888.

Murase Y, et al. (2024) In vitro reconstitution of epigenetic reprogramming in the human germ line. *Nature*, 631(8019), 170.

Buckley DN, et al. (2024) A comprehensive analysis of minimally differentially methylated regions common to pediatric and adult solid tumors. *NPJ precision oncology*, 8(1), 125.

Zhu Y, et al. (2024) DNA methylation profiling of CpG islands in trigeminal ganglion of rats with orofacial pain induced by experimental tooth movement. *BMC oral health*, 24(1), 1474.

Gu G, et al. (2024) Endocrine islet β -cell subtypes with differential function are derived from biochemically distinct embryonic endocrine islet progenitors that are regulated by maternal nutrients. *Research square*.

Chalkley ML, et al. (2024) Human TSC2 Mutant Cells Exhibit Aberrations in Early Neurodevelopment Accompanied by Changes in the DNA Methylome. *bioRxiv : the preprint server for biology*.