

Resource Summary Report

Generated by [RRID](#) on Sep 17, 2026

[MLML](#)

RRID:SCR_005449

Type: Tool

Proper Citation

MLML (RRID:SCR_005449)

Resource Information

URL: <http://smithlab.usc.edu/plone/software/mlml>

Proper Citation: MLML (RRID:SCR_005449)

Description: A software tool to simultaneously estimate hydroxymethylation (5hmC) and methylation (5mC) levels from BS-seq, oxBS-seq and TAB-seq experiments. It generates consistent estimates across experiment types.

Abbreviations: MLML

Resource Type: software resource

Resource Name: MLML

Resource ID: SCR_005449

Alternate IDs: OMICS_00609

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260912T195626+0000

Ratings and Alerts

No rating or validation information has been found for MLML.

No alerts have been found for MLML.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Xiang Z, et al. (2026) 5-Hydroxymethylcytosine Dynamics Reveals Coordinated Reprogramming of Parental Genomes and X Chromosome Dosage Balance in Mouse SCNT Embryos. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(6), e09682.

Hernández-Núñez I, et al. (2025) Active DNA demethylation is upstream of rod-photoreceptor fate determination and required for retinal development. *bioRxiv : the preprint server for biology*.

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*.

Hernández-Núñez I, et al. (2025) Active DNA demethylation upstream of rod-photoreceptor fate determination is required for retinal development. *PLoS biology*, 23(8), e3003332.

Liang D, et al. (2024) Distinct dynamics of parental 5-hydroxymethylcytosine during human preimplantation development regulate early lineage gene expression. *Nature cell biology*, 26(9), 1458.

Schutsky EK, et al. (2018) Nondestructive, base-resolution sequencing of 5-hydroxymethylcytosine using a DNA deaminase. *Nature biotechnology*.

Ivanov M, et al. (2016) Single base resolution analysis of 5-hydroxymethylcytosine in 188 human genes: implications for hepatic gene expression. *Nucleic acids research*, 44(14), 6756.