

Resource Summary Report

Generated by [Kravitz](#) on Sep 13, 2026

MuLan-Methyl

RRID:SCR_023591

Type: Tool

Proper Citation

MuLan-Methyl (RRID:SCR_023591)

Resource Information

URL: <http://ab.cs.uni-tuebingen.de/software/mulan-methyl>

Proper Citation: MuLan-Methyl (RRID:SCR_023591)

Description: Web tool for predicting DNA methylation sites. Identifies methylation sites for three different types of DNA methylation, namely N6-adenine, N4-cytosine, and 5-hydroxymethylcytosine. MuLan-Methyl-Multiple transformer based language models for accurate DNA methylation prediction.

Resource Type: data access protocol, software resource, web service

Defining Citation: [DOI:10.1101/2023.01.04.522704](https://doi.org/10.1101/2023.01.04.522704)

Keywords: DNA methylation, Natural language processing, Model ensemble, Model explainability, Web server

Funding: German Network for Bioinformatics Infrastructure

Availability: Free, Freely available

Resource Name: MuLan-Methyl

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Alternate URLs: <https://plabase.cs.uni-tuebingen.de/mm/>

Record Creation Time: 20230523T050222+0000

Record Last Update: 20260912T200040+0000

Ratings and Alerts

No rating or validation information has been found for MuLan-Methyl.

No alerts have been found for MuLan-Methyl.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Zeng W, et al. (2022) MuLan-Methyl-multiple transformer-based language models for accurate DNA methylation prediction. GigaScience, 12.