

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 19, 2026

CyMATE

RRID:SCR_005442

Type: Tool

Proper Citation

CyMATE (RRID:SCR_005442)

Resource Information

URL: <http://www.cymate.org/>

Proper Citation: CyMATE (RRID:SCR_005442)

Description: A web application that allows you to perform a quick and comprehensive methylation analysis of cytosine sites in DNA sequences.

Abbreviations: CyMATE

Synonyms: Cytosine Methylation Analysis Tool for Everyone

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Defining Citation: [PMID:17559516](#)

Resource Name: CyMATE

Resource ID: SCR_005442

Alternate IDs: OMICS_00597

Old URLs: <http://www.gmi.oeaw.ac.at/research-groups/cymate/cymate/>

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260912T200137+0000

Ratings and Alerts

No rating or validation information has been found for CyMATE.

No alerts have been found for CyMATE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 70 mentions in open access literature.

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

Jiang L, et al. (2026) RNA Interference Silences Genes at Post-Transcriptional Level Without Impacting Nascent RNA in Soybean Hairy Roots. *Plants* (Basel, Switzerland), 15(12).

Hanke A, et al. (2026) Exogenous 24nt siRNAs induce AGO4A-dependent silencing via promoter DNA methylation and H3K9me2 deposition. *Frontiers in plant science*, 17, 1826532.

Yan X, et al. (2025) CHH demethylation in the ZmGST2 promoter enhances maize drought tolerance by regulating ROS scavenging and root growth. *BMC plant biology*, 25(1), 1083.

Liang Z, et al. (2025) XYLEM NAC DOMAIN 1 (EjXND1) relieves cold-induced lignification by negatively regulating the EjHB1-EjPRX12 module in loquat fruit. *Journal of advanced research*, 73, 93.

Kellari LM, et al. (2025) Cross-kingdom RNAi induced by a beneficial endophytic fungus to its host requires transitivity and amplification of silencing signals. *Plant biology* (Stuttgart, Germany), 27(4), 504.

Zicola J, et al. (2025) Vegetative to generative1 (Vgt1) is an enhancer affecting flowering time and jasmonate signaling in maize by promoting the expression of Zea mays Related to APETALA 2.7. *Plant physiology*, 199(3).

Povilus RA, et al. (2025) Imprinting and DNA Methylation in Water Lily Endosperm: Implications for Seed Evolution. *Molecular biology and evolution*, 42(11).

Peng J, et al. (2025) LEC2 induces somatic cell reprogramming through epigenetic activation of plant cell totipotency regulators. *Nature communications*, 16(1), 4185.

Xu J, et al. (2024) Hypermethylation in the promoter regions of flavonoid pathway genes is associated with skin color fading during 'Daihong' apple fruit development. *Horticulture research*, 11(3), uhae031.

Matyášek R, et al. (2024) Transcriptional Silencing of 35S rDNA in *Tragopogon porrifolius* Correlates with Cytosine Methylation in Sequence-Specific Manner. *International journal of molecular sciences*, 25(14).

Niu X, et al. (2024) Regulatory mechanism of heat-active retrotransposons by the SET domain protein SUVH2. *Frontiers in plant science*, 15, 1355626.

Li H, et al. (2023) Methionine biosynthesis enzyme MoMet2 is required for rice blast fungus pathogenicity by promoting virulence gene expression via reducing 5mC modification. *PLoS genetics*, 19(9), e1010927.

Montacié C, et al. (2023) NICOTIANAMINE SYNTHASE activity affects nucleolar iron accumulation and impacts rDNA silencing and RNA methylation in *Arabidopsis*. *Journal of experimental botany*, 74(15), 4384.

Dalakouras A, et al. (2023) A beneficial fungal root endophyte triggers systemic RNA silencing and DNA methylation of a host reporter gene. *RNA biology*, 20(1), 20.

Yang A, et al. (2023) FZD7, Regulated by Non-CpG Methylation, Plays an Important Role in Immature Porcine Sertoli Cell Proliferation. *International journal of molecular sciences*, 24(7).

Williams BP, et al. (2022) Somatic DNA demethylation generates tissue-specific methylation states and impacts flowering time. *The Plant cell*, 34(4), 1189.

Mlinarec J, et al. (2022) Structure and Methylation of 35S rDNA in Allopolyploids *Anemone multifida* ($2n = 4x = 32$, BBDD) and *Anemone baldensis* ($2n = 6x = 48$, AABDD) and Their Parental Species Show Evidence of Nucleolar Dominance. *Frontiers in plant science*, 13, 908218.

Fei Y, et al. (2021) Non-perfectly matching small RNAs can induce stable and heritable epigenetic modifications and can be used as molecular markers to trace the origin and fate of silencing RNAs. *Nucleic acids research*, 49(4), 1900.

Wang H, et al. (2021) Response of Wheat DREB Transcription Factor to Osmotic Stress Based on DNA Methylation. *International journal of molecular sciences*, 22(14).

Wang Z, et al. (2021) ARGONAUTE 2 increases rice susceptibility to rice black-streaked dwarf virus infection by epigenetically regulating HEXOKINASE 1 expression. *Molecular plant pathology*, 22(9), 1029.