

# Resource Summary Report

Generated by ASWG on Aug 2, 2026

## DMEAS

RRID:SCR\_006679

Type: Tool

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### Proper Citation

DMEAS (RRID:SCR\_006679)

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### Resource Information

**URL:** <http://sourceforge.net/projects/dmeas/>

**Proper Citation:** DMEAS (RRID:SCR\_006679)

**Description:** A user-friendly DNA methylation analysis tool for DNA methylation pattern extraction, DNA methylation level estimation, DNA methylation entropy analysis and multi-sample comparison. It was developed in order to assess the DNA methylation variations for a given genomic locus or genome-wide methylation data.

**Abbreviations:** DMEAS

**Synonyms:** DNA Methylation Entropy Analysis Software, DMEAS - DNA Methylation Entropy Analysis Software

**Resource Type:** software resource

**Keywords:** c#

**Availability:** Creative Commons Attribution License

**Resource Name:** DMEAS

**Resource ID:** SCR\_006679

**Alternate IDs:** OMICS\_00598

**Record Creation Time:** 20220129T080237+0000

**Record Last Update:** 20260801T190314+0000

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### Ratings and Alerts

No rating or validation information has been found for DMEAS.

No alerts have been found for DMEAS.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Liau Y, et al. (2024) Low-pass nanopore sequencing for measurement of global methylation levels in plants. BMC genomics, 25(1), 1235.