

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

DMEAS

RRID:SCR_006679

Type: Tool

Proper Citation

DMEAS (RRID:SCR_006679)

Resource Information

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

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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: 20260905T132559+0000

Ratings and Alerts

No rating or validation information has been found for DMEAS.

No alerts have been found for DMEAS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Gautheron L, et al. (2026) Classification errors distort findings in automated speech processing: Examples and solutions from child-development research. Behavior research methods, 58(6).

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