

Resource Summary Report

Generated by [RRID](#) on Aug 6, 2026

MethylViewer

RRID:SCR_005448

Type: Tool

Proper Citation

MethylViewer (RRID:SCR_005448)

Resource Information

URL: <http://dna.leeds.ac.uk/methylviewer/>

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Description: A simple integrated software tool for handling MAP (methyltransferase accessibility protocol) and MAP-IT (MAP individual templates) footprinting projects. It can process sequence data (*.txt, *.ab1 and *.scf) derived from the use of up to four different DNA methyltransferases.

Abbreviations: MethylViewer

Resource Type: software resource

Defining Citation: [PMID:20959287](#)

Keywords: primer design, bisulfite sequencing, bio.tools

Resource Name: MethylViewer

Resource ID: SCR_005448

Alternate IDs: OMICS_00608, biotools:methylviewer

Alternate URLs: <https://bio.tools/methylviewer>

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260801T190259+0000

Ratings and Alerts

No rating or validation information has been found for MethylViewer.

No alerts have been found for MethylViewer.

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 [RRID](#) .

Chaves R, et al. (2017) FA-SAT Is an Old Satellite DNA Frozen in Several Bilateria Genomes. *Genome biology and evolution*, 9(11), 3073.

Darst RP, et al. (2012) DNA methyltransferase accessibility protocol for individual templates by deep sequencing. *Methods in enzymology*, 513, 185.