

# Resource Summary Report

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## MethylViewer

RRID:SCR\_005448

Type: Tool

### Proper Citation

MethylViewer (RRID:SCR\_005448)

### Resource Information

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

**Proper Citation:** MethylViewer (RRID:SCR\_005448)

**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 [dkNET](#) .

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.