

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/>

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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: 20260725T190604+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 [PRECISE-TBI](#) .

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.