## **Resource Summary Report**

Generated by <u>NIF</u> on May 2, 2025

# **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

Funding:

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: 20250420T014252+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 <u>NIF</u>.

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.