

Resource Summary Report

Generated by [ASWG](#) on Aug 3, 2026

MethylomeDB

RRID:SCR_005583

Type: Tool

Proper Citation

MethylomeDB (RRID:SCR_005583)

Resource Information

URL: <http://www.neuroepigenomics.org/methylomedb/>

Proper Citation: MethylomeDB (RRID:SCR_005583)

Description: A database containing genome-wide brain DNA methylation profiles for human and mouse brains. The DNA methylation profiles were generated by Methylation Mapping Analysis by Paired-end Sequencing (Methyl-MAPS) method and analyzed by Methyl-Analyzer software package. The methylation profiles cover over 80% CpG dinucleotides in human and mouse brains in single-CpG resolution. The integrated genome browser (modified from UCSC Genome Browser) allows users to browse DNA methylation profiles in specific genomic loci, to search specific methylation patterns, and to compare methylation patterns between individual samples. Two species were included in the Brain Methylome Database: human and mouse. Human postmortem brain samples were obtained from three distinct cortical regions, i.e., dorsal lateral prefrontal cortex (dlPFC), ventral prefrontal cortex (vPFC), and auditory cortex (AC). Human samples were selected from our postmortem brain collection with extensive neuropathological and psychopathological data, as well as brain toxicology reports. The Department of Psychiatry of Columbia University and the New York State Psychiatric Institute have assembled this brain collection, where a validated psychological autopsy method is used to generate Axis I and II DSM IV diagnoses and data are obtained on developmental history, history of psychiatric illness and treatment, and family history for each subject. The mouse sample (strain 129S6/SvEv) DNA was collected from the entire left cerebral hemisphere. The three human brain regions were selected because they have been implicated in the neuropathology of depression and schizophrenia. Within each cortical region, both disease and non-psychiatric samples have been profiled (matching subjects by age and sex in each group). Such careful matching of subjects allows one to perform a wide range of queries with the ability to characterize methylation features in non-psychiatric controls, as well as detect differentially methylated domains or features between disease and non-psychiatric samples. A total of 14 non-psychiatric, 9 schizophrenic, and 6 depression methylation profiles are included in the database.

Abbreviations: MethylomeDB

Synonyms: MethylomeDB - the Brain Methylome Database, Brain Methylome Database

Resource Type: database, data or information resource

Defining Citation: [PMID:22140101](#)

Keywords: brain, dna methylation, dorsal lateral prefrontal cortex, ventral prefrontal cortex, auditory cortex, bio.tools

Funding: NIH ;
NHGRI HG002915;
NIMH MH074118

Resource Name: MethylomeDB

Resource ID: SCR_005583

Alternate IDs: OMICS_01843, nlx_146210, biotools:methylomedb

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

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260803T040420+0000

Ratings and Alerts

No rating or validation information has been found for MethylomeDB.

No alerts have been found for MethylomeDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Pennington KL, et al. (2015) Epigenetic Mechanisms of the Aging Human Retina. Journal of experimental neuroscience, 9(Suppl 2), 51.