Resource Summary Report

Generated by NIF on May 20, 2025

MethDB

RRID:SCR_003108
Type: Tool

Proper Citation

MethDB (RRID:SCR_003108)

Resource Information

URL: http://www.methdb.de

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Description: Database that provides a resource to store DNA methylation data and to make these data readily available to the public. Future development of the database will focus on environmental effects on DNA methylation. No restriction applies on the type of data, i.e. as well as global estimations (e.g. HPLC) as data from high resolution analysis (i.e. sequencing) can be stored. As much background information as possible should be provided by the users. This includes the origin of the sample, phenotype, expression of the related gene, etc..

Abbreviations: MethDB

Synonyms: DNA Methylation Database, MethDB - the database for DNA methylation and environmental epigenetic effects

Resource Type: service resource, database, data or information resource, storage service resource, data repository

Defining Citation: PMID:11125109, PMID:17965614, PMID:12163707

Keywords: methylation

Funding:

Availability: Acknowledgement requested

Resource Name: MethDB

Resource ID: SCR_003108

Alternate IDs: nif-0000-03119, OMICS_01840

Alternate URLs: http://www.methdb.net/

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250519T203232+0000

Ratings and Alerts

No rating or validation information has been found for MethDB.

No alerts have been found for MethDB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Xiao X, et al. (2017) Molecular mechanisms underlying noncoding risk variations in psychiatric genetic studies. Molecular psychiatry, 22(4), 497.

Han Y, et al. (2016) Integrating Epigenomics into the Understanding of Biomedical Insight. Bioinformatics and biology insights, 10, 267.

Liu Z, et al. (2015) Benchmark data for identifying DNA methylation sites via pseudo trinucleotide composition. Data in brief, 4, 87.

Bin Raies A, et al. (2015) DDMGD: the database of text-mined associations between genes methylated in diseases from different species. Nucleic acids research, 43(Database issue), D879.

Simeone P, et al. (2014) Epigenetic heredity of human height. Physiological reports, 2(6).

Yuen JW, et al. (2014) Epigenetic inactivation of inositol polyphosphate 4-phosphatase B (INPP4B), a regulator of PI3K/AKT signaling pathway in EBV-associated nasopharyngeal carcinoma. PloS one, 9(8), e105163.

Edwards SL, et al. (2013) Beyond GWASs: illuminating the dark road from association to

function. American journal of human genetics, 93(5), 779.

Milanowska K, et al. (2011) Databases and bioinformatics tools for the study of DNA repair. Molecular biology international, 2011, 475718.

Zhao Z, et al. (2010) Depletion of DNMT3A suppressed cell proliferation and restored PTEN in hepatocellular carcinoma cell. Journal of biomedicine & biotechnology, 2010, 737535.

Barekati Z, et al. (2010) Specificity of methylation assays in cancer research: a guideline for designing primers and probes. Obstetrics and gynecology international, 2010.

Rodriguez C, et al. (2010) CTCF is a DNA methylation-sensitive positive regulator of the INK/ARF locus. Biochemical and biophysical research communications, 392(2), 129.

Buard J, et al. (2009) Distinct histone modifications define initiation and repair of meiotic recombination in the mouse. The EMBO journal, 28(17), 2616.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.