Resource Summary Report

Generated by dkNET on Apr 22, 2025

MethLAB

RRID:SCR_010957
Type: Tool

Proper Citation

MethLAB (RRID:SCR_010957)

Resource Information

URL: http://genetics.emory.edu/research/?assetID=2087

Proper Citation: MethLAB (RRID:SCR_010957)

Description: A GUI software package for analysis of DNA methylation microarray data.

Abbreviations: MethLAB

Resource Type: software resource

Funding:

Resource Name: MethLAB

Resource ID: SCR_010957

Alternate IDs: OMICS_00797

Record Creation Time: 20220129T080301+0000

Record Last Update: 20250420T014516+0000

Ratings and Alerts

No rating or validation information has been found for MethLAB.

No alerts have been found for MethLAB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Hohos NM, et al. (2018) CD4+ and CD8+ T-Cell-Specific DNA Cytosine Methylation Differences Associated With Obesity. Obesity (Silver Spring, Md.), 26(8), 1312.

Badraiq H, et al. (2017) Effects of maternal obesity on Wharton's Jelly mesenchymal stromal cells. Scientific reports, 7(1), 17595.

Jeyapalan JN, et al. (2016) DNA methylation analysis of paediatric low-grade astrocytomas identifies a tumour-specific hypomethylation signature in pilocytic astrocytomas. Acta neuropathologica communications, 4(1), 54.

Argos M, et al. (2015) Gene-specific differential DNA methylation and chronic arsenic exposure in an epigenome-wide association study of adults in Bangladesh. Environmental health perspectives, 123(1), 64.

Dogan MV, et al. (2015) Ethnicity and Smoking-Associated DNA Methylation Changes at HIV Co-Receptor GPR15. Frontiers in psychiatry, 6, 132.

Beach SR, et al. (2015) Higher levels of protective parenting are associated with better young adult health: exploration of mediation through epigenetic influences on pro-inflammatory processes. Frontiers in psychology, 6, 676.

Philibert RA, et al. (2014) A pilot examination of the genome-wide DNA methylation signatures of subjects entering and exiting short-term alcohol dependence treatment programs. Epigenetics, 9(9), 1212.

Parets SE, et al. (2013) Fetal DNA Methylation Associates with Early Spontaneous Preterm Birth and Gestational Age. PloS one, 8(6), e67489.