Resource Summary Report

Generated by kravitz2 on Jul 29, 2026

mqtldb

RRID:SCR_018002
Type: Tool

Proper Citation

mqtldb (RRID:SCR_018002)

Resource Information

URL: http://www.mqtldb.org/

Proper Citation: mqtldb (RRID:SCR_018002)

Description: Data collection of large scale genome wide DNA methylation analysis of 1,000 mother-child pairs at serial time points across life course (ARIES).

Abbreviations: mqtldb

Synonyms: methylation quantitative trait loci database

Resource Type: data or information resource, database

Defining Citation: DOI:10.1186/s13059-016-0926-z

Keywords: Data, large scale, genome, DNA methylation, analysis, mother-child pair, serial time point, life course, aeries, methylation, quantitative trait loci, database

Resource Name: mqtldb

Resource ID: SCR_018002

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260729T044436+0000

Ratings and Alerts

No rating or validation information has been found for mqtldb.

No alerts have been found for mqtldb.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 36 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Zhao R, et al. (2025) Allele-specific methylation of SSTR4 associated with aging and cognitive functions in patients with schizophrenia. PloS one, 20(2), e0303038.

Jones MJ, et al. (2025) DNA methylation differences between cord and adult white blood cells reflect postnatal immune cell maturation. Communications biology, 8(1), 237.

Lovett A, et al. (2025) An Epigenomic Meta-Analysis of Differentially Methylated Sites in Pre- and Post-Metabolic/Bariatric Surgery Adult Female Patients. Epigenomes, 9(3).

Kupsco A, et al. (2025) Newborn mitochondrial DNA copy number is associated with changes to DNA methylation that persist into childhood and are associated with cognitive development. Clinical epigenetics, 17(1), 112.

Dueker ND, et al. (2025) Hypermethylation of PM20D1 Is Associated With Carotid Bifurcation Intima-Media Thickness in Dominican Republic Families. Journal of the American Heart Association, 14(2), e034033.

Grech GM, et al. (2025) Genomic Locus Tagged by Lung Function GWAS SNV rs12477314 (2q37.3) Acts as a Regulatory Region for a Systemic Inflammatory Phenotype. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 39(12), e70689.

Casazza W, et al. (2024) Sex-dependent placental methylation quantitative trait loci provide insight into the prenatal origins of childhood onset traits and conditions. iScience, 27(2), 109047.

Zhao R, et al. (2024) Methylation of SSTR4 promoter region in multiple mental health disorders. Frontiers in genetics, 15, 1431769.

Hjort L, et al. (2024) Epigenetics of the non-coding RNA nc886 across blood, adipose tissue and skeletal muscle in offspring exposed to diabetes in pregnancy. Clinical epigenetics, 16(1), 61.

Bruzzone SEP, et al. (2024) No association between peripheral serotonin-gene-related DNA methylation and brain serotonin neurotransmission in the healthy and depressed state. Clinical epigenetics, 16(1), 71.

Cheron J, et al. (2023) USP7/Maged1-mediated H2A??monoubiquitination in the paraventricular thalamus: an epigenetic mechanism involved in cocaine use disorder. Nature communications, 14(1), 8481.

Sarnowski C, et al. (2023) Multi-tissue epigenetic analysis identifies distinct associations underlying insulin resistance and Alzheimer's disease at CPT1A locus. Clinical

epigenetics, 15(1), 173.

Hebbar P, et al. (2023) Linkage analysis using whole exome sequencing data implicates SLC17A1, SLC17A3, TATDN2 and TMEM131L in type 1 diabetes in Kuwaiti families. Scientific reports, 13(1), 14978.

Nishitani S, et al. (2023) Cross-tissue correlations of genome-wide DNA methylation in Japanese live human brain and blood, saliva, and buccal epithelial tissues. Translational psychiatry, 13(1), 72.

Jiang W, et al. (2023) Mendelian Randomization Analysis Provides Insights into the Pathogenesis of Serum Levels of Branched-Chain Amino Acids in Cardiovascular Disease. Metabolites, 13(3).

Rijlaarsdam J, et al. (2022) Epigenetic profiling of social communication trajectories and co-occurring mental health problems: a prospective, methylome-wide association study. Development and psychopathology, 34(3), 854.

Caramaschi D, et al. (2022) Meta-analysis of epigenome-wide associations between DNA methylation at birth and childhood cognitive skills. Molecular psychiatry, 27(4), 2126.

Shirai Y, et al. (2021) Elucidation of disease etiology by trans-layer omics analysis. Inflammation and regeneration, 41(1), 6.

Barbu MC, et al. (2021) Epigenetic prediction of major depressive disorder. Molecular psychiatry, 26(9), 5112.

Breeze CE, et al. (2021) Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. Genome medicine, 13(1), 74.