

Epigenetic Epidemiology of Complex Diseases Using Two

Medical Epigenetics

1, 46-51

DOI: 10.1159/000354285

Citation Report

#	ARTICLE	IF	CITATIONS
1	Epigenetic signature of birth weight discordance in adult twins. BMC Genomics, 2014, 15, 1062.	2.8	48
2	Methylation as an epigenetic source of random genetic effects in the classical twin design. Advances in Genomics and Genetics, 2015, , 305.	0.8	1
3	Polymorphic Variation in the Epigenetic Gene DNMT3B Modulates the Environmental Impact on Cognitive Ability: A Twin Study. European Psychiatry, 2015, 30, 303-308.	0.2	10
4	Differentially Methylated Genomic Regions in Birthâ€Weight Discordant Twin Pairs. Annals of Human Genetics, 2016, 80, 81-87.	0.8	19
5	On the power of epigenome-wide association studies using a disease-discordant twin design. Bioinformatics, 2018, 34, 4073-4078.	4.1	31
6	Genome-wide profiling of DNA methylome and transcriptome in peripheral blood monocytes for major depression: A Monozygotic Discordant Twin Study. Translational Psychiatry, 2019, 9, 215.	4.8	49
7	DNA methylome profiling in identical twin pairs discordant for body mass index. International Journal of Obesity, 2019, 43, 2491-2499.	3.4	16
8	Differential long noncoding RNA profiling of BMI in twins. Epigenomics, 2020, 12, 1531-1541.	2.1	4