

CITATION REPORT

List of articles citing

Epigenome-wide association study of fasting blood lipids in the Genetics of Lipid-lowering Drugs and Diet Network study

DOI: 10.1161/circulationaha.114.009158
Circulation, 2014, 130, 565-72.

Source: <https://exaly.com/paper-pdf/59467929/citation-report.pdf>

Version: 2024-04-28

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
180	The Influences of Genetic and Environmental Factors on Methylome-wide Association Studies for Human Diseases. <i>Current Genetic Medicine Reports</i> , 2014 , 2, 261-270	2.2	16
179	PRKZ methylation is associated with sunlight exposure in a North American but not a Mediterranean population. 2014 , 31, 1034-40		10
178	Cardiovascular epigenome-wide association studies: is epigenetics falling short?. 2014 , 25, 474-5		8
177	Mechanisms and treatment of ischaemic stroke--insights from genetic associations. 2014 , 10, 723-30		41
176	Epigenetic mechanisms underlying the pathogenesis of neurogenetic diseases. 2014 , 11, 708-20		12
175	DNA methylation biomarkers: cancer and beyond. 2014 , 5, 821-64		180
174	Epigenetic Mechanisms of the Aging Human Retina. 2015 , 9, 51-79		25
173	Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. 2015 , 16, 290		70
172	Epigenome-wide study identifies novel methylation loci associated with body mass index and waist circumference. 2015 , 23, 1493-501		122
171	Lipid changes due to fenofibrate treatment are not associated with changes in DNA methylation patterns in the GOLDN study. <i>Frontiers in Genetics</i> , 2015 , 6, 304	4.5	19
170	Differential Gene Expression in Age-Related Macular Degeneration. 2014 , 5, a017210		14
169	DNA methylation of lipid-related genes affects blood lipid levels. 2015 , 8, 334-42		122
168	Recent developments on the role of epigenetics in obesity and metabolic disease. <i>Clinical Epigenetics</i> , 2015 , 7, 66	7.7	112
167	DNA methylation dynamics in human carotid plaques after cerebrovascular events. 2015 , 35, 1835-42		28
166	The DNA methylation drift of the atherosclerotic aorta increases with lesion progression. 2015 , 8, 7		73
165	Epigenome-wide association study (EWAS) of BMI, BMI change and waist circumference in African American adults identifies multiple replicated loci. 2015 , 24, 4464-79		219
164	Developmental bisphenol A (BPA) exposure leads to sex-specific modification of hepatic gene expression and epigenome at birth that may exacerbate high-fat diet-induced hepatic steatosis. 2015 , 284, 101-12		97

163	Clinical applications of epigenetics in cardiovascular disease: the long road ahead. 2015 , 165, 143-53		21
162	Cardiovascular Disorders and Epigenetics. 2016 , 243-256		
161	Estimation of Cell-Type Composition Including T and B Cell Subtypes for Whole Blood Methylation Microarray Data. <i>Frontiers in Genetics</i> , 2016 , 7, 23	4.5	14
160	Adjustment of Cell-Type Composition Minimizes Systematic Bias in Blood DNA Methylation Profiles Derived by DNA Collection Protocols. <i>PLoS ONE</i> , 2016 , 11, e0147519	3.7	17
159	Integrative Analysis of Multi-omics Data for Discovery and Functional Studies of Complex Human Diseases. 2016 , 93, 147-90		170
158	Triglycerides and Triglyceride-Rich Lipoproteins in the Causal Pathway of Cardiovascular Disease. 2016 , 118, 138-45		92
157	Epidemiology of cardiovascular disease: recent novel outlooks on risk factors and clinical approaches. 2016 , 14, 855-69		24
156	Epigenetics of Lipid Phenotypes. 2016 , 10, 1		16
155	Identification and validation of seven new loci showing differential DNA methylation related to serum lipid profile: an epigenome-wide approach. The REGICOR study. 2016 , 25, 4556-4565		55
154	The role of DNA methylation in dyslipidaemia: A systematic review. 2016 , 64, 178-191		28
153	Epigenome-wide association study of triglyceride postprandial responses to a high-fat dietary challenge. 2016 , 57, 2200-2207		24
152	Genome- and epigenome-wide association study of hypertriglyceridemic waist in Mexican American families. <i>Clinical Epigenetics</i> , 2016 , 8, 6	7.7	40
151	X chromosome-wide analysis identifies DNA methylation sites influenced by cigarette smoking. <i>Clinical Epigenetics</i> , 2016 , 8, 20	7.7	21
150	Interaction of methylation-related genetic variants with circulating fatty acids on plasma lipids: a meta-analysis of 7 studies and methylation analysis of 3 studies in the Cohorts for Heart and Aging Research in Genomic Epidemiology consortium. <i>American Journal of Clinical Nutrition</i> , 2016 , 103, 567-78	7	21
149	Epigenetic associations of type 2 diabetes and BMI in an Arab population. <i>Clinical Epigenetics</i> , 2016 , 8, 13	7.7	76
148	Epigenetic and genetic variations at the TNNT1 gene locus are associated with HDL-C levels and coronary artery disease. <i>Epigenomics</i> , 2016 , 8, 359-71	4.4	18
147	[Epigenetics in atherosclerosis]. 2016 , 28, 102-19		3
146	Recent Advances in Human Genetics and Epigenetics of Adiposity: Pathway to Precision Medicine?. 2017 , 152, 1695-1706		20

145	Epigenetic Patterns in Blood Associated With Lipid Traits Predict Incident Coronary Heart Disease Events and Are Enriched for Results From Genome-Wide Association Studies. 2017 , 10,		72
144	Epigenome-wide association study (EWAS) on lipids: the Rotterdam Study. <i>Clinical Epigenetics</i> , 2017 , 9, 15	7.7	71
143	Mitochondria and Epigenetics - Crosstalk in Homeostasis and Stress. 2017 , 27, 453-463		150
142	The State of Cardiovascular Genomics: Abundant Data, Limited Information. 2017 , 70, 696-698		
141	The epigenetic landscape of age-related diseases: the geroscience perspective. 2017 , 18, 549-559		46
140	Epigenomic and transcriptomic approaches in the post-genomic era: path to novel targets for diagnosis and therapy of the ischaemic heart? Position Paper of the European Society of Cardiology Working Group on Cellular Biology of the Heart. 2017 , 113, 725-736		85
139	CPT1A methylation is associated with plasma adiponectin. 2017 , 27, 225-233		16
138	Epigenome-Wide Association Study Identifies Methylation Sites Associated With Liver Enzymes and Hepatic Steatosis. 2017 , 153, 1096-1106.e2		38
137	Non-linear patterns in age-related DNA methylation may reflect CD4 T cell differentiation. <i>Epigenetics</i> , 2017 , 12, 492-503	5.7	16
136	Genome-Wide Analysis of DNA Methylation and Acute Coronary Syndrome. <i>Circulation Research</i> , 2017 , 120, 1754-1767	15.7	49
135	The integration of epigenetics and genetics in nutrition research for CVD risk factors. 2017 , 76, 333-346		11
134	The Epigenomic Analysis of Human Obesity. 2017 , 25, 1471-1481		27
133	DNA methylation as a marker of response in rheumatoid arthritis. <i>Pharmacogenomics</i> , 2017 , 18, 1323-1332		16
132	Blood triglyceride levels are associated with DNA methylation at the serine metabolism gene PHGDH. <i>Scientific Reports</i> , 2017 , 7, 11207	4.9	20
131	An epigenome-wide association study of inflammatory response to fenofibrate in the Genetics of Lipid Lowering Drugs and Diet Network. <i>Pharmacogenomics</i> , 2017 , 18, 1333-1341	2.6	6
130	Connecting the Dots Between Fatty Acids, Mitochondrial Function, and DNA Methylation in Atherosclerosis. <i>Current Atherosclerosis Reports</i> , 2017 , 19, 36	6	3
129	Translational Perspective on Epigenetics in Cardiovascular Disease. <i>Journal of the American College of Cardiology</i> , 2017 , 70, 590-606	15.1	51
128	Epigenetics in Cardiovascular Disease. 2017 , 135-157		2

127	Situaci3 actual en gen3tica cardiovascular: muchos datos, poca informaci3. 2017 , 70, 696-698		
126	Genome-wide identification of inter-individually variable DNA methylation sites improves the efficacy of epigenetic association studies. 2017 , 2, 11		39
125	DNA methylation and obesity traits: An epigenome-wide association study. The REGICOR study. <i>Epigenetics</i> , 2017 , 12, 909-916	5.7	53
124	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. 2017 , 14, e1002215		162
123	An epigenome-wide association study in whole blood of measures of adiposity among Ghanaians: the RODAM study. <i>Clinical Epigenetics</i> , 2017 , 9, 103	7.7	31
122	An exome-wide sequencing study of lipid response to high-fat meal and fenofibrate in Caucasians from the GOLDN cohort. 2018 , 59, 722-729		4
121	DNA methylation as a mediator of the association between prenatal adversity and risk factors for metabolic disease in adulthood. 2018 , 4, eaao4364		143
120	DNA methylation in human lipid metabolism and related diseases. 2018 , 29, 116-124		28
119	Role of genetic and environmental factors in DNA methylation of lipid metabolism. 2018 , 5, 9-15		15
118	Epigenome-wide association analysis revealed that SOCS3 methylation influences the effect of cumulative stress on obesity. 2018 , 131, 63-71		22
117	Epigenetics and precision medicine in cardiovascular patients: from basic concepts to the clinical arena. 2018 , 39, 4150-4158		49
116	Epigenetic reprogramming in metabolic disorders: nutritional factors and beyond. 2018 , 54, 1-10		58
115	Environmental and epigenetic regulation of postprandial lipemia. 2018 , 29, 30-35		6
114	Hypermethylation of MIR21 in CD4+ T cells from patients with relapsing-remitting multiple sclerosis associates with lower miRNA-21 levels and concomitant up-regulation of its target genes. 2018 , 24, 1288-1300		26
113	Array probe density and pathobiological relevant CpG calling bias in human disease and physiological DNA methylation profiling. 2018 , 17, 42-48		2
112	Genome-wide linkage scan for loci influencing plasma triglyceride levels. <i>BMC Proceedings</i> , 2018 , 12, 52	2.3	7
111	Incorporating methylation genome information improves prediction accuracy for drug treatment responses. <i>BMC Genetics</i> , 2018 , 19, 78	2.6	4
110	Application of novel and existing methods to identify genes with evidence of epigenetic association: results from GAW20. <i>BMC Genetics</i> , 2018 , 19, 72	2.6	1

109	Coping with family structure in genome-wide association studies: a comparative evaluation. <i>BMC Proceedings</i> , 2018 , 12, 42	2.3	1
108	Relating drug response to epigenetic and genetic markers using a region-based kernel score test. <i>BMC Proceedings</i> , 2018 , 12, 47	2.3	1
107	Application of Bayesian networks to GAW20 genetic and blood lipid data. <i>BMC Proceedings</i> , 2018 , 12, 19	2.3	3
106	Detecting responses to treatment with fenofibrate in pedigrees. <i>BMC Genetics</i> , 2018 , 19, 64	2.6	1
105	Identifying fenofibrate responsive CpG sites. <i>BMC Proceedings</i> , 2018 , 12, 43	2.3	3
104	Joint screening of ultrahigh dimensional variables for family-based genetic studies. <i>BMC Proceedings</i> , 2018 , 12, 24	2.3	1
103	An adaptive gene-based test for methylation data. <i>BMC Proceedings</i> , 2018 , 12, 60	2.3	1
102	Using penalized regression to predict phenotype from SNP data. <i>BMC Proceedings</i> , 2018 , 12, 38	2.3	7
101	Investigation of parent-of-origin effects induced by fenofibrate treatment on triglycerides levels. <i>BMC Genetics</i> , 2018 , 19, 83	2.6	2
100	Investigating potential causal relationships between SNPs, DNA methylation and HDL. <i>BMC Proceedings</i> , 2018 , 12, 20	2.3	2
99	CpG-set association assessment of lipid concentration changes and DNA methylation. <i>BMC Proceedings</i> , 2018 , 12, 30	2.3	2
98	Detection and analysis of CpG sites with multimodal DNA methylation level distributions and their relationships with SNPs. <i>BMC Proceedings</i> , 2018 , 12, 36	2.3	3
97	Analysis of genotype by methylation interactions through sparsity-inducing regularized regression. <i>BMC Proceedings</i> , 2018 , 12, 40	2.3	3
96	Epigenetics, heritability and longitudinal analysis. <i>BMC Genetics</i> , 2018 , 19, 77	2.6	5
95	Epigenetic prediction of complex traits and death. 2018 , 19, 136		77
94	Modification effect of fenofibrate therapy, a longitudinal epigenomic-wide methylation study of triglycerides levels in the GOLDN study. <i>BMC Genetics</i> , 2018 , 19, 75	2.6	2
93	Integrating epigenetic, genetic, and phenotypic data to uncover gene-region associations with triglycerides in the GOLDN study. <i>BMC Proceedings</i> , 2018 , 12, 57	2.3	2
92	Gene-methylation epistatic analyses via the W-test identifies enriched signals of neuronal genes in patients undergoing lipid-control treatment. <i>BMC Proceedings</i> , 2018 , 12, 53	2.3	4

91	Data for GAW20: genome-wide DNA sequence variation and epigenome-wide DNA methylation before and after fenofibrate treatment in a family study of metabolic phenotypes. <i>BMC Proceedings</i> , 2018 , 12, 35	2.3	10
90	Network analysis of drug effect on triglyceride-associated DNA methylation. <i>BMC Proceedings</i> , 2018 , 12, 27	2.3	5
89	Reliability of genomic predictions of complex human phenotypes. <i>BMC Proceedings</i> , 2018 , 12, 51	2.3	5
88	Assessment of fenofibrate-methylation interactions on triglycerides using longitudinal family data. <i>BMC Proceedings</i> , 2018 , 12, 48	2.3	2
87	Heritability and genetic associations of triglyceride and HDL-C levels using pedigree-based and empirical kinships. <i>BMC Proceedings</i> , 2018 , 12, 34	2.3	4
86	Joint analysis of genetic and epigenetic data using a conditional autoregressive model. <i>BMC Genetics</i> , 2018 , 19, 71	2.6	1
85	Disentangling associations between DNA methylation and blood lipids: a Mendelian randomization approach. <i>BMC Proceedings</i> , 2018 , 12, 23	2.3	10
84	Identification of epistatic interactions between the human RNA demethylases FTO and ALKBH5 with gene set enrichment analysis informed by differential methylation. <i>BMC Proceedings</i> , 2018 , 12, 59	2.3	6
83	Role of DNA De Novo (De)Methylation in the Kidney in Salt-Induced Hypertension. 2018 , 72, 1160-1171		15
82	Genome-wide analysis in multiple-case families: assessing the relationship between triglyceride and methylation. <i>BMC Proceedings</i> , 2018 , 12, 33	2.3	
81	The challenge of detecting genotype-by-methylation interaction: GAW20. <i>BMC Genetics</i> , 2018 , 19, 81	2.6	0
80	Simulation of a medication and methylation effects on triglycerides in the Genetic Analysis Workshop 20. <i>BMC Proceedings</i> , 2018 , 12, 25	2.3	4
79	Characterization of the contribution of shared environmental and genetic factors to metabolic syndrome methylation heritability and familial correlations. <i>BMC Genetics</i> , 2018 , 19, 69	2.6	2
78	Comparison of novel and existing methods for detecting differentially methylated regions. <i>BMC Genetics</i> , 2018 , 19, 84	2.6	7
77	Integrative methylation score to identify epigenetic modifications associated with lipid changes resulting from fenofibrate treatment in families. <i>BMC Proceedings</i> , 2018 , 12, 28	2.3	4
76	Using recursive feature elimination in random forest to account for correlated variables in high dimensional data. <i>BMC Genetics</i> , 2018 , 19, 65	2.6	83
75	Family-based genome-wide association of inflammation biomarkers and fenofibrate treatment response in the GOLDN study. <i>BMC Proceedings</i> , 2018 , 12, 41	2.3	1
74	Nutrieepigenetics and cardiovascular disease. <i>Current Opinion in Clinical Nutrition and Metabolic Care</i> , 2018 , 21, 252-259	3.8	19

73	The Role of Epigenetic Modifications in Cardiometabolic Diseases. 2018 , 347-364		2
72	Remnant-Like Particle Cholesterol, Low-Density Lipoprotein Triglycerides, and Incident Cardiovascular Disease. <i>Journal of the American College of Cardiology</i> , 2018 , 72, 156-169	15.1	71
71	Metabolic and inflammatory biomarkers are associated with epigenetic aging acceleration estimates in the GOLDN study. <i>Clinical Epigenetics</i> , 2018 , 10, 56	7.7	43
70	Genetic and Epigenetic Regulations of Post-prandial Lipemia. <i>Current Genetic Medicine Reports</i> , 2018 , 6, 124-131	2.2	
69	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. <i>Circulation</i> , 2019 , 140, 645-657	16.7	65
68	DNA methylation modules associate with incident cardiovascular disease and cumulative risk factor exposure. <i>Clinical Epigenetics</i> , 2019 , 11, 142	7.7	20
67	Body Mass Index Drives Changes in DNA Methylation: A Longitudinal Study. <i>Circulation Research</i> , 2019 , 125, 824-833	15.7	22
66	Epigenetics of Aging and Age-Related Disorders. 2019 , 871-883		1
65	Metabolic and Immunological Shifts during Mid-to-Late Gestation Influence Maternal Blood Methylation of and. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	6
64	DNA methylation markers in obesity, metabolic syndrome, and weight loss. <i>Epigenetics</i> , 2019 , 14, 421-444	5.7	55
63	An Exome-Wide Sequencing Study of the GOLDN Cohort Reveals Novel Associations of Coding Variants and Fasting Plasma Lipids. <i>Frontiers in Genetics</i> , 2019 , 10, 158	4.5	1
62	Dissecting features of epigenetic variants underlying cardiometabolic risk using full-resolution epigenome profiling in regulatory elements. <i>Nature Communications</i> , 2019 , 10, 1209	17.4	9
61	Bioinformatic and Biostatistic Methods for DNA Methylation Analysis of Obesity. 2019 , 165-179		
60	Differential methylation pattern in patients with coronary artery disease: pilot study. <i>Molecular Biology Reports</i> , 2019 , 46, 541-550	2.8	6
59	Multiple metals exposure and chromosome damage: Exploring the mediation effects of microRNAs and their potentials in lung carcinogenesis. <i>Environment International</i> , 2019 , 122, 291-300	12.9	12
58	Precision Medicine in Weight Loss and Healthy Living. <i>Progress in Cardiovascular Diseases</i> , 2019 , 62, 15-28	8.5	20
57	Methylation in CPT1A, Lipoproteins, and Epigenetics. 2019 , 387-403		
56	DNA Methylation Analysis Identifies Differentially Methylated Sites Associated with Early-Onset Intracranial Atherosclerotic Stenosis. <i>Journal of Atherosclerosis and Thrombosis</i> , 2020 , 27, 71-99	4	2

55	Epigenome-wide association study of DNA methylation and microRNA expression highlights novel pathways for human complex traits. <i>Epigenetics</i> , 2020 , 15, 183-198	5.7	5
54	Cardioinformatics: the nexus of bioinformatics and precision cardiology. <i>Briefings in Bioinformatics</i> , 2020 , 21, 2031-2051	13.4	8
53	Pubertal maturation and weight status are associated with dyslipidemia among children and adolescents in Northwest China. <i>Scientific Reports</i> , 2020 , 10, 16344	4.9	1
52	Early pregnancy dyslipidemia is associated with placental DNA methylation at loci relevant for cardiometabolic diseases. <i>Epigenomics</i> , 2020 , 12, 921-934	4.4	6
51	Gypenosides improves nonalcoholic fatty liver disease induced by high-fat diet induced through regulating LPS/TLR4 signaling pathway. <i>Cell Cycle</i> , 2020 , 19, 3042-3053	4.7	1
50	Carbohydrate and fat intake associated with risk of metabolic diseases through epigenetics of CPT1A. <i>American Journal of Clinical Nutrition</i> , 2020 , 112, 1200-1211	7	15
49	Methylome-wide association study of central adiposity implicates genes involved in immune and endocrine systems. <i>Epigenomics</i> , 2020 , 12, 1483-1499	4.4	4
48	NRF2 loss recapitulates heritable impacts of paternal cigarette smoke exposure. <i>PLoS Genetics</i> , 2020 , 16, e1008756	6	6
47	Bayesian network analysis of plasma microRNA sequencing data in patients with venous thrombosis. <i>European Heart Journal Supplements</i> , 2020 , 22, C34-C45	1.5	4
46	Exercise, redox homeostasis and the epigenetic landscape. <i>Redox Biology</i> , 2020 , 35, 101477	11.3	17
45	Epigenetics of aging and disease: a brief overview. <i>Aging Clinical and Experimental Research</i> , 2021 , 33, 737-745	4.8	29
44	Effect of gene DNA methylations on the lipid-lowering efficacy of simvastatin. <i>Pharmacogenomics</i> , 2021 , 22, 27-39	2.6	0
43	DNA methylation and lipid metabolism: an EWAS of 226 metabolic measures. <i>Clinical Epigenetics</i> , 2021 , 13, 7	7.7	11
42	DNA methylation of blood cells is associated with prevalent type 2 diabetes in a meta-analysis of four European cohorts. <i>Clinical Epigenetics</i> , 2021 , 13, 40	7.7	8
41	The Therapeutic Potential of Epigenome-Modifying Drugs in Cardiometabolic Disease. <i>Current Genetic Medicine Reports</i> , 2021 , 9, 22-36	2.2	
40	DNA Methylation and Blood Pressure Phenotypes: A Review of the Literature. <i>American Journal of Hypertension</i> , 2021 , 34, 267-273	2.3	3
39	Detecting differentially methylated regions with multiple distinct associations. <i>Epigenomics</i> , 2021 , 13, 451-464	4.4	2
38	Cardiovascular disease risk and pathophysiology in South Asians: can longitudinal multi-omics shed light?. <i>Wellcome Open Research</i> , 2020 , 5, 255	4.8	0

37	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021 , 12, 3987	17.4	3
36	Hepatic-Metabolite-Based Intermittent Fasting Enables a Sustained Reduction in Insulin Resistance in Type 2 Diabetes and Metabolic Syndrome. <i>Hormone and Metabolic Research</i> , 2021 , 53, 529-540	3.1	2
35	Disentangling the epigenetic landscape in cardiovascular patients: a path toward personalized medicine. <i>Minerva Cardiology and Angiology</i> , 2021 , 69, 331-345	2.4	1
34	Epigenome-wide analysis of DNA methylation and coronary heart disease: a nested case-control study. <i>ELife</i> , 2021 , 10,	8.9	0
33	Lipid Phenotypes and DNA Methylation: a Review of the Literature. <i>Current Atherosclerosis Reports</i> , 2021 , 23, 71	6	3
32	Peripheral blood DNA and RNA biomarkers of cardiovascular disease in clinical practice. 2021 , 261-281		
31	Epigenetic Basis of Oxidative Stress in Diabetic Coronary Atherosclerosis: A Shift in Focus from Genetic Prerogative. 2019 , 419-455		1
30	DNA methylation modules associate with incident cardiovascular disease and cumulative risk factor exposure.		1
29	The circulating lipidome is largely defined by sex descriptors in the GOLDN, GeneBank and the ADNI studies.		1
28	Association of DNA Methylation at CPT1A Locus with Metabolic Syndrome in the Genetics of Lipid Lowering Drugs and Diet Network (GOLDN) Study. <i>PLoS ONE</i> , 2016 , 11, e0145789	3.7	40
27	Heritable DNA Methylation in CD4+ Cells among Complex Families Displays Genetic and Non-Genetic Effects. <i>PLoS ONE</i> , 2016 , 11, e0165488	3.7	18
26	Energizing Genetics and Epi-genetics: Role in the Regulation of Mitochondrial Function. <i>Current Genomics</i> , 2014 , 15, 436-56	2.6	9
25	A 6-CpG Validated Methylation Risk Score Model for Metabolic Syndrome: The HyperGEN and GOLDN Studies.		
24	DNA methylation signatures of incident coronary heart disease: findings from epigenome-wide association studies. <i>Clinical Epigenetics</i> , 2021 , 13, 186	7.7	2
23	Methylation in CPT1A, Lipoproteins, and Epigenetics. 2017 , 1-17		
22	Epigenetics, the Vascular Wall, and Atherosclerosis. 2019 , 302-313		
21	Methylome-Wide Association Study of Central Adiposity Implicate Genes Involved in Immune and Endocrine Systems.		
20	Involvement of Epigenetic Control and Non-coding RNAs in Cardiovascular System. <i>Advances in Experimental Medicine and Biology</i> , 2020 , 1229, 121-132	3.6	

19	Cardiovascular disease risk and pathophysiology in South Asians: can longitudinal multi-omics shed light?. <i>Wellcome Open Research</i> , 2020 , 5, 255	4.8	○
18	Persistent Variations of Blood DNA Methylation Associated with Treatment Exposures and Risk for Cardiometabolic Outcomes among Long-term Survivors of Childhood Cancer: A Report from the St. Jude Lifetime Cohort.		○
17	Genomics of Postprandial Lipidomics in the Genetics of Lipid-Lowering Drugs and Diet Network Study. <i>Nutrients</i> , 2021 , 13,	6.7	○
16	A 6-CpG validated methylation risk score model for metabolic syndrome: The HyperGEN and GOLDN studies. <i>PLoS ONE</i> , 2021 , 16, e0259836	3.7	○
15	Genomic Surveillance in Public Health. 2022 , 189-201		
14	Using Machine Learning to Predict Obesity Based on Genome-Wide and Epigenome-Wide Gene-Gene and Gene-Diet Interactions.. <i>Frontiers in Genetics</i> , 2021 , 12, 783845	4.5	2
13	Table_1.DOCX. 2019 ,		
12	The Role of Dynamic Epigenetic Changes in Modulating Homeostasis after Exposure to Low-dose Environmental Chemicals. 2022 , 213-228		
11	A systematic review and metaanalysis of observational studies on the effects of epigenetic factors on serum triglycerides.. <i>Archives of Endocrinology and Metabolism</i> , 2022 ,	2.2	
10	Association of Cardiovascular Health Through Young Adulthood With Genome-Wide DNA Methylation Patterns in Midlife: The CARDIA Study. <i>Circulation</i> , 2022 , 146, 94-109	16.7	○
9	Studying Epigenetics of Cardiovascular Diseases on Chip Guide. <i>Neurology International</i> , 2022 , 12, 218-234		
8	Gestational Nutrition as a Predisposing Factor to Obesity Onset in Offspring: Role for Involvement of Epigenetic Mechanism. 2022 , 37, 1-7		1
7	The epigenetics of aging. 2023 , 333-358		○
6	The Interplay of Epigenetic, Genetic, and Traditional Risk Factors on Blood Pressure: Findings from the Health and Retirement Study. 2022 , 13, 1959		○
5	Epigenetics and Gut Microbiota Crosstalk: A potential Factor in Pathogenesis of Cardiovascular Disorders. 2022 , 9, 798		○
4	Epigenetics of aging. 2023 , 213-234		○
3	The impact of alcoholic drinks and dietary factors on epigenetic markers associated with triglyceride levels. 14,		○
2	DNA methylation in peripheral blood leukocytes for the association with glucose metabolism and invasive breast cancer. 2023 , 15,		○

- 1 DNA Methylation Near CPT1A and Changes in Triglyceride-rich Lipoproteins in Response to Weight-loss Diet Interventions.

o