

Association analyses of East Asian individuals and trans individuals reveal new loci associated with cholesterol a

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Exome chip meta-analysis identifies novel loci and East Asian-specific coding variants that contribute to lipid levels and coronary artery disease. <i>Nature Genetics</i> , 2017, 49, 1722-1730.	9.4	129
2	Genetically Determined Plasma Lipid Levels and Risk of Diabetic Retinopathy: A Mendelian Randomization Study. <i>Diabetes</i> , 2017, 66, 3130-3141.	0.3	17
3	<i>Trans</i>-ancestry Fine Mapping and Molecular Assays Identify Regulatory Variants at the <i>ANGPTL8</i> HDL-C GWAS Locus. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3217-3227.	0.8	19
4	Penetrance of Polygenic Obesity Susceptibility Loci across the Body Mass Index Distribution. <i>American Journal of Human Genetics</i> , 2017, 101, 925-938.	2.6	103
5	Association of 48 type 2 diabetes susceptibility loci with fasting plasma glucose and lipid levels in Chinese Hans. <i>Diabetes Research and Clinical Practice</i> , 2018, 139, 114-121.	1.1	4
6	Cohort Profile: The Singapore Multi-Ethnic Cohort (MEC) study. <i>International Journal of Epidemiology</i> , 2018, 47, 699-699j.	0.9	67
7	Prediction of cholesterol ratios within a Korean population. <i>Royal Society Open Science</i> , 2018, 5, 171204.	1.1	0
8	WDR11-mediated Hedgehog signalling defects underlie a new ciliopathy related to Kallmann syndrome. <i>EMBO Reports</i> , 2018, 19, 269-289.	2.0	49
9	Genetic alterations in the NO-cGMP pathway and cardiovascular risk. <i>Nitric Oxide - Biology and Chemistry</i> , 2018, 76, 105-112.	1.2	34
10	The Role of RNA Editing in Cancer Development and Metabolic Disorders. <i>Frontiers in Endocrinology</i> , 2018, 9, 762.	1.5	70
11	Identification of 12 novel loci that confer susceptibility to early-onset dyslipidemia. <i>International Journal of Molecular Medicine</i> , 2018, 43, 57-82.	1.8	5
12	Genome-wide association meta-analysis yields 20 loci associated with gallstone disease. <i>Nature Communications</i> , 2018, 9, 5101.	5.8	73
13	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. <i>Nature Communications</i> , 2018, 9, 5052.	5.8	75
14	Characterization of LncRNA expression profile and identification of novel LncRNA biomarkers to diagnose coronary artery disease. <i>Atherosclerosis</i> , 2018, 275, 359-367.	0.4	99
15	GWAS Reveal Targets in Vessel Wall Pathways to Treat Coronary Artery Disease. <i>Frontiers in Cardiovascular Medicine</i> , 2018, 5, 72.	1.1	16
16	STEPS: an efficient prospective likelihood approach to genetic association analyses of secondary traits in extreme phenotype sequencing. <i>Biostatistics</i> , 2020, 21, 33-49.	0.9	4
17	Angiotensin-Like 3 (ANGPTL3) and Atherosclerosis: Lipid and Non-Lipid Related Effects. <i>Journal of Cardiovascular Development and Disease</i> , 2018, 5, 39.	0.8	36
18	Integrative genomics identifies new genes associated with severe COPD and emphysema. <i>Respiratory Research</i> , 2018, 19, 46.	1.4	20

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19	Genome-wide association study identifies novel recessive genetic variants for high TGs in an Arab population. <i>Journal of Lipid Research</i> , 2018, 59, 1951-1966.	2.0	24
20	<i>IGF1</i> Gene Is Associated With Triglyceride Levels In Subjects With Family History Of Hypertension From The SAPHIRe And TWB Projects. <i>International Journal of Medical Sciences</i> , 2018, 15, 1035-1042.	1.1	3
21	ZRANB3 is an African-specific type 2 diabetes locus associated with beta-cell mass and insulin response. <i>Nature Communications</i> , 2019, 10, 3195.	5.8	69
22	Identifying small-effect genetic associations overlooked by the conventional fixed-effect model in a large-scale meta-analysis of coronary artery disease. <i>Bioinformatics</i> , 2020, 36, 552-557.	1.8	2
23	Contributions of Interactions Between Lifestyle and Genetics on Coronary Artery Disease Risk. <i>Current Cardiology Reports</i> , 2019, 21, 89.	1.3	27
24	Associations with metabolites in Chinese suggest new metabolic roles in Alzheimer's and Parkinson's diseases. <i>Human Molecular Genetics</i> , 2019, 29, 189-201.	1.4	12
25	A genome-wide search for gene-by-obesity interaction loci of dyslipidemia in Koreans shows diverse genetic risk alleles. <i>Journal of Lipid Research</i> , 2019, 60, 2090-2101.	2.0	5
26	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. <i>Nature Communications</i> , 2019, 10, 5121.	5.8	62
27	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.	1.6	85
28	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	5.8	64
29	Identifying new associated pleiotropic SNPs with lipids by simultaneous test of multiple longitudinal traits: An Iranian family-based study. <i>Gene</i> , 2019, 692, 156-169.	1.0	4
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31	Identification of female-specific genetic variants for metabolic syndrome and its component traits to improve the prediction of metabolic syndrome in females. <i>BMC Medical Genetics</i> , 2019, 20, 99.	2.1	16
32	Combined analysis of keratinocyte cancers identifies novel genome-wide loci. <i>Human Molecular Genetics</i> , 2019, 28, 3148-3160.	1.4	46
33	Weighted gene co-expression network analysis to explain the relationship between plasma total carotenoids and lipid profile. <i>Genes and Nutrition</i> , 2019, 14, 16.	1.2	9
34	Allele-specific enhancers mediate associations between LCAT and ABCA1 polymorphisms and HDL metabolism. <i>PLoS ONE</i> , 2019, 14, e0215911.	1.1	3
35	Exome chip-driven association study of lipidemia in >14,000 Koreans and evaluation of genetic effect on identified variants between different ethnic groups. <i>Genetic Epidemiology</i> , 2019, 43, 617-628.	0.6	2
36	LncRNA ENST00000602558.1 regulates ABCG1 expression and cholesterol efflux from vascular smooth muscle cells through a p65-dependent pathway. <i>Atherosclerosis</i> , 2019, 285, 31-39.	0.4	26

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38	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648.	9.4	112
39	A Perception on Genome-Wide Genetic Analysis of Metabolic Traits in Arab Populations. <i>Frontiers in Endocrinology</i> , 2019, 10, 8.	1.5	14
40	Enhancer deletion and allelic effects define a regulatory molecular mechanism at the <i>VLDLR</i> cholesterol GWAS locus. <i>Human Molecular Genetics</i> , 2019, 28, 888-895.	1.4	5
41	The Korea Biobank Array: Design and Identification of Coding Variants Associated with Blood Biochemical Traits. <i>Scientific Reports</i> , 2019, 9, 1382.	1.6	179
42	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. <i>American Journal of Human Genetics</i> , 2019, 104, 112-138.	2.6	106
43	Generalizability and applicability of results obtained from populations of European descent regarding the effect direction and size of HDL-C level-associated genetic variants to the Hungarian general and Roma populations. <i>Gene</i> , 2019, 686, 187-193.	1.0	12
44	CoMM: a collaborative mixed model to dissecting genetic contributions to complex traits by leveraging regulatory information. <i>Bioinformatics</i> , 2019, 35, 1644-1652.	1.8	36
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48	Genome-wide association study of metabolic syndrome in Korean populations. <i>PLoS ONE</i> , 2020, 15, e0227357.	1.1	42
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50	Progressive effects of single-nucleotide polymorphisms on 16 phenotypic traits based on longitudinal data. <i>Genes and Genomics</i> , 2020, 42, 393-403.	0.5	3
51	Carotid Intima-Media Thickness. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2020, 40, 446-461.	1.1	25
52	TheAPOA5rs662799 Polymorphism Is a Determinant of Dyslipidemia in Vietnamese Primary School Children. <i>Lipids</i> , 2020, 55, 683-691.	0.7	2
53	Genetic susceptibility, dietary cholesterol intake, and plasma cholesterol levels in a Chinese population. <i>Journal of Lipid Research</i> , 2020, 61, 1504-1511.	2.0	3
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57	A gene-diet interaction-based score predicts response to dietary fat in the Women's Health Initiative. <i>American Journal of Clinical Nutrition</i> , 2020, 111, 893-902.	2.2	6
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60	Candidate Regulators of Dyslipidemia in Chromosome 1 Substitution Lines Using Liver Co-Expression Profiling Analysis. <i>Frontiers in Genetics</i> , 2020, 10, 1258.	1.1	1
61	Biological Role of Unsaturated Fatty Acid Desaturases in Health and Disease. <i>Nutrients</i> , 2020, 12, 356.	1.7	72
62	Genetic variants in the FAM3C gene are associated with lipid traits in Chinese children. <i>Pediatric Research</i> , 2021, 89, 673-678.	1.1	1
63	Network propagation of rare variants in Alzheimer's disease reveals tissue-specific hub genes and communities. <i>PLoS Computational Biology</i> , 2021, 17, e1008517.	1.5	1
64	Genome-wide identification of cis DNA methylation quantitative trait loci in three Southeast Asian Populations. <i>Human Molecular Genetics</i> , 2021, 30, 603-618.	1.4	5
65	Genetic risk scores for cardiometabolic traits in sub-Saharan African populations. <i>International Journal of Epidemiology</i> , 2021, 50, 1283-1296.	0.9	10
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71	The Genetic Basis of Hypertriglyceridemia. <i>Current Atherosclerosis Reports</i> , 2021, 23, 39.	2.0	17
72	Circulating ceramides as biomarkers of cardiovascular disease: Evidence from phenotypic and genomic studies. <i>Atherosclerosis</i> , 2021, 327, 18-30.	0.4	39
74	Evaluating marginal genetic correlation of associated loci for complex diseases and traits between European and East Asian populations. <i>Human Genetics</i> , 2021, 140, 1285-1297.	1.8	12
75	Impact of Amerind ancestry and FADS genetic variation on omega-3 deficiency and cardiometabolic traits in Hispanic populations. <i>Communications Biology</i> , 2021, 4, 918.	2.0	11

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76	Both variants of A1CF and BAZ1B genes are associated with gout susceptibility: a replication study and meta-analysis in a Japanese population. <i>Human Cell</i> , 2021, 34, 293-299.	1.2	2
82	Hepatic lipase (LIPC) sequencing in individuals with extremely high and low high-density lipoprotein cholesterol levels. <i>PLoS ONE</i> , 2020, 15, e0243919.	1.1	3
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95	A common variant in 11q23.3 associated with hyperlipidemia is mediated by the binding and regulation of GATA4. <i>Npj Genomic Medicine</i> , 2022, 7, 4.	1.7	7
97	High-density lipoprotein, low-density lipoprotein and triglyceride levels and upper gastrointestinal cancers risk: a trans-ancestry Mendelian randomization study. <i>European Journal of Clinical Nutrition</i> , 2022, , .	1.3	4
98	Comprehensive Statistical and Bioinformatics Analysis in the Deciphering of Putative Mechanisms by Which Lipid-Associated GWAS Loci Contribute to Coronary Artery Disease. <i>Biomedicine</i> , 2022, 10, 259.	1.4	7
99	OUP accepted manuscript. <i>Briefings in Bioinformatics</i> , 2022, , .	3.2	3
100	Interpreting Clinical Trials With Omega-3 Supplements in the Context of Ancestry and FADS Genetic Variation. <i>Frontiers in Nutrition</i> , 2021, 8, 808054.	1.6	12
101	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	13.7	353
102	Mendelian randomization study of circulating lipids and biliary tract cancer among East Asians. <i>BMC Cancer</i> , 2022, 22, 273.	1.1	3
103	Gene-based association tests using GWAS summary statistics and incorporating eQTL. <i>Scientific Reports</i> , 2022, 12, 3553.	1.6	1
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111	Longitudinal relationships of polycyclic aromatic hydrocarbons exposure and genetic susceptibility with blood lipid profiles. <i>Environment International</i> , 2022, 164, 107259.	4.8	13
113	The human ATP-binding cassette (ABC) transporter superfamily. <i>Human Mutation</i> , 2022, 43, 1162-1182.	1.1	45
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116	Genetic evidence for a causal relationship between type 2 diabetes and peripheral artery disease in both Europeans and East Asians. <i>BMC Medicine</i> , 2022, 20, .	2.3	6
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122	Implicating genes, pleiotropy, and sexual dimorphism at blood lipid loci through multi-ancestry meta-analysis. <i>Genome Biology</i> , 2022, 23, .	3.8	17
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124	Lack of GPR180 ameliorates hepatic lipid depot via downregulation of mTORC1 signaling. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
125	Quantifying portable genetic effects and improving cross-ancestry genetic prediction with GWAS summary statistics. <i>Nature Communications</i> , 2023, 14, .	5.8	13
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