Themistocles L Assimes

List of Publications by Year in Descending Order

226 papers	34,638 citations	70 h-index	186 g-index
257 ext. papers	43,462 ext. citations	13.1 avg, IF	5.76 L-index

#	Paper	IF	Citations
226	ZEB2 Shapes the Epigenetic Landscape of Atherosclerosis.. *Circulation*, **2022**,	16.7	2
225	Coronary Artery Disease Risk of Familial Hypercholesterolemia Genetic Variants Independent of Clinically Observed Longitudinal Cholesterol Exposure.. *Circulation Genomic and Precision Medicine*, **2022**, CIRCGEN121003501	5.2	2
224	Rare coding variants in RCN3 are associated with blood pressure.. *BMC Genomics*, **2022**, 23, 148	4.5	
223	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential.. *Science Advances*, **2022**, 8, eabl6579	14.3	3
222	Gaseous air pollutants and DNA methylation in a methylome-wide association study of an ethnically and environmentally diverse population of U.S. adults.. *Environmental Research*, **2022**, 212, 113360	7.9	0
221	Genome-wide and phenome-wide analysis of ideal cardiovascular health in the VA Million Veteran Program. *PLoS ONE*, **2022**, 17, e0267900	3.7	
220	A multi-population phenome-wide association study of genetically-predicted height in the Million Veteran Program. *PLoS Genetics*, **2022**, 18, e1010193	6	0
219	Genetic Loci Associated With COVID-19 Positivity and Hospitalization in White, Black, and Hispanic Veterans of the VA Million Veteran Program.. *Frontiers in Genetics*, **2021**, 12, 777076	4.5	1
218	Multi-Trait Genome-Wide Association Study of Atherosclerosis Detects Novel Pleiotropic Loci.. *Frontiers in Genetics*, **2021**, 12, 787545	4.5	
217	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
216	Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. *Stroke*, **2021**, STROKEAHA120031792	6.7	2
215	Large-Scale Plasma Protein Profiling of Incident Myocardial Infarction, Ischemic Stroke, and Heart Failure. *Journal of the American Heart Association*, **2021**, 10, e023330	6	2
214	Mendelian Randomization Analysis of Hemostatic Factors and Their Contribution to Peripheral Artery Disease-Brief Report. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2021**, 41, 380-386	9.4	4
213	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. *Nature Communications*, **2021**, 12, 2182	17.4	5
212	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. *Aging Cell*, **2021**, 20, e13366	9.9	9
211	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. *Nature Communications*, **2021**, 12, 3987	17.4	3
210	Association Between Genetic Variation in Blood Pressure and Increased Lifetime Risk of Peripheral Artery Disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2021**, 41, 2027-2034	9.4	7

209	IL10RB as a key regulator of COVID-19 host susceptibility and severity **2021**,		2
208	Epigenome-wide association study of diet quality in the Women's Health Initiative and TwinsUK cohort. *International Journal of Epidemiology*, **2021**, 50, 675-684	7.8	8
207	Genetics of 35 blood and urine biomarkers in the UK Biobank. *Nature Genetics*, **2021**, 53, 185-194	36.3	78
206	Multi-trait association studies discover pleiotropic loci between Alzheimer's disease and cardiometabolic traits. *Alzheimerjs Research and Therapy*, **2021**, 13, 34	9	2
205	Epigenetically mediated electrocardiographic manifestations of sub-chronic exposures to ambient particulate matter air pollution in the Women's Health Initiative and Atherosclerosis Risk in Communities Study. *Environmental Research*, **2021**, 198, 111211	7.9	
204	DXA Versus Clinical Measures of Adiposity as Predictors of Cardiometabolic Diseases and All-Cause Mortality in Postmenopausal Women. *Mayo Clinic Proceedings*, **2021**, 96, 2831-2842	6.4	0
203	Alcohol use and cardiometabolic risk in the UK Biobank: A Mendelian randomization study. *PLoS ONE*, **2021**, 16, e0255801	3.7	4
202	The Propagation of Racial Disparities in Cardiovascular Genomics Research. *Circulation Genomic and Precision Medicine*, **2021**, 14, e003178	5.2	1
201	A Missense Variant in the IL-6 Receptor and Protection From Peripheral Artery Disease. *Circulation Research*, **2021**, 129, 968-970	15.7	0
200	Genetics of Smoking and Risk of Atherosclerotic Cardiovascular Diseases: A Mendelian Randomization Study. *JAMA Network Open*, **2021**, 4, e2034461	10.4	11
199	Associations between DNA methylation and BMI vary by metabolic health status: a potential link to disparate cardiovascular outcomes.. *Clinical Epigenetics*, **2021**, 13, 230	7.7	0
198	Discovery of 318 new risk loci for type 2 diabetes and related vascular outcomes among 1.4 million participants in a multi-ancestry meta-analysis. *Nature Genetics*, **2020**, 52, 680-691	36.3	140
197	The Project Baseline Health Study: a step towards a broader mission to map human health. *Npj Digital Medicine*, **2020**, 3, 84	15.7	10
196	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study. *PLoS Genetics*, **2020**, 16, e1008684	6	5
195	Urinary Albumin, Sodium, and Potassium and Cardiovascular Outcomes in the UK Biobank: Observational and Mendelian Randomization Analyses. *Hypertension*, **2020**, 75, 714-722	8.5	12
194	PCSK9 loss of function is protective against extra-coronary atherosclerotic cardiovascular disease in a large multi-ethnic cohort. *PLoS ONE*, **2020**, 15, e0239752	3.7	2
193	Leukocyte Traits and Exposure to Ambient Particulate Matter Air Pollution in the Women's Health Initiative and Atherosclerosis Risk in Communities Study. *Environmental Health Perspectives*, **2020**, 128, 17004	8.4	11
192	Cardioinformatics: the nexus of bioinformatics and precision cardiology. *Briefings in Bioinformatics*, **2020**, 21, 2031-2051	13.4	8

191	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. *Circulation*, **2020**, 142, 1633-1646	16.7	24
190	Comprehensive Investigation of Circulating Biomarkers and Their Causal Role in Atherosclerosis-Related Risk Factors and Clinical Events. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002996	5.2	5
189	Chromosome 1q21.2 and additional loci influence risk of spontaneous coronary artery dissection and myocardial infarction. *Nature Communications*, **2020**, 11, 4432	17.4	22
188	Genetic determinants of increased body mass index mediate the effect of smoking on increased risk for type 2 diabetes but not coronary artery disease. *Human Molecular Genetics*, **2020**, 29, 3327-3337	5.6	2
187	Validating a non-invasive, ALT-based non-alcoholic fatty liver phenotype in the million veteran program. *PLoS ONE*, **2020**, 15, e0237430	3.7	5
186	Transcriptomic signatures across human tissues identify functional rare genetic variation. *Science*, **2020**, 369,	33.3	36
185	The relationship between circulating lipids and breast cancer risk: A Mendelian randomization study. *PLoS Medicine*, **2020**, 17, e1003302	11.6	16
184	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002769	5.2	1
183	Genotyping Array Design and Data Quality Control in the Million Veteran Program. *American Journal of Human Genetics*, **2020**, 106, 535-548	11	22
182	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. *International Journal of Epidemiology*, **2020**, 49, 1022-1031	7.8	15
181	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study **2020**, 16, e1008684		
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170	The relationship between circulating lipids and breast cancer risk: A Mendelian randomization study **2020**, 17, e1003302		
169	The relationship between circulating lipids and breast cancer risk: A Mendelian randomization study **2020**, 17, e1003302		
168	Harmonizing Genetic Ancestry and Self-identified Race/Ethnicity in Genome-wide Association Studies. *American Journal of Human Genetics*, **2019**, 105, 763-772	11	41
167	Leveraging linkage evidence to identify low-frequency and rare variants on 16p13 associated with blood pressure using TOPMed whole genome sequencing data. *Human Genetics*, **2019**, 138, 199-210	6.3	14
166	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. *Environment International*, **2019**, 132, 104723	12.9	35
165	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. *Nature Communications*, **2019**, 10, 2581	17.4	31
164	DNA methylation GrimAge strongly predicts lifespan and healthspan. *Aging*, **2019**, 11, 303-327	5.6	424
163	HeartBioPortal. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002426	5.2	5
162	Identification of 22 novel loci associated with urinary biomarkers of albumin, sodium, and potassium excretion. *Kidney International*, **2019**, 95, 1197-1208	9.9	20
161	Association of Left Ventricular Ejection Fraction and Symptoms With Mortality After Elective Noncardiac Surgery Among Patients With Heart Failure. *JAMA - Journal of the American Medical Association*, **2019**, 321, 572-579	27.4	46
160	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. *Circulation*, **2019**, 140, 645-657	16.7	65
159	Association of Risk Alleles With Cardiovascular Disease in Blacks in the Million Veteran Program. *Circulation*, **2019**, 140, 1031-1040	16.7	18
158	Genome-wide association study of peripheral artery disease in the Million Veteran Program. *Nature Medicine*, **2019**, 25, 1274-1279	50.5	73
157	Association Between Heart Failure and Postoperative Mortality Among Patients Undergoing Ambulatory Noncardiac Surgery. *JAMA Surgery*, **2019**, 154, 907-914	5.4	9
156	Genome-wide association analysis of venous thromboembolism identifies new risk loci and genetic overlap with arterial vascular disease. *Nature Genetics*, **2019**, 51, 1574-1579	36.3	56

155	DNA methylation-based estimator of telomere length. *Aging*, **2019**, 11, 5895-5923	5.6	69
154	The role of epigenetic aging in education and racial/ethnic mortality disparities among older U.S. Women. *Psychoneuroendocrinology*, **2019**, 104, 18-24	5	26
153	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. *Journal of the American College of Cardiology*, **2019**, 73, 58-66	15.1	86
152	Breastfeeding Duration and the Risk of Coronary Artery Disease. *Journal of Womenjs Health*, **2019**, 28, 30-36	3	10
151	Melanoma risk prediction using a multilocus genetic risk score in the Women Health Initiative cohort. *Journal of the American Academy of Dermatology*, **2018**, 79, 36-41.e10	4.5	17
150	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. *Nature Communications*, **2018**, 9, 387	17.4	106
149	Genome-wide scan for circulating vascular adhesion protein-1 levels: MACROD2 as a potential transcriptional regulator of adipogenesis. *Journal of Diabetes Investigation*, **2018**, 9, 1067-1074	3.9	10
148	Hypermetabolic macrophages in rheumatoid arthritis and coronary artery disease due to glycogen synthase kinase 3b inactivation. *Annals of the Rheumatic Diseases*, **2018**, 77, 1053-1062	2.4	43
147	Evaluation of 71 Coronary Artery Disease Risk Variants in a Multiethnic Cohort. *Frontiers in Cardiovascular Medicine*, **2018**, 5, 19	5.4	8
146	Genome-Wide Association Studies of Coronary Artery Disease: Recent Progress and Challenges Ahead. *Current Atherosclerosis Reports*, **2018**, 20, 47	6	19
145	Discovery, fine-mapping, and conditional analyses of genetic variants associated with C-reactive protein in multiethnic populations using the Metabochip in the Population Architecture using Genomics and Epidemiology (PAGE) study. *Human Molecular Genetics*, **2018**, 27, 2940-2953	5.6	8
144	An epigenetic biomarker of aging for lifespan and healthspan. *Aging*, **2018**, 10, 573-591	5.6	658
143	Effects of Genetic Variants Associated with Familial Hypercholesterolemia on Low-Density Lipoprotein-Cholesterol Levels and Cardiovascular Outcomes in the Million Veteran Program. *Circulation Genomic and Precision Medicine*, **2018**, 11,	5.2	7
142	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. *Nature Genetics*, **2018**, 50, 1514-1523	36.3	260
141	Coffee consumption is associated with DNA methylation levels of human blood. *European Journal of Human Genetics*, **2017**, 25, 608-616	5.3	21
140	Trans-ethnic fine-mapping of genetic loci for body mass index in the diverse ancestral populations of the Population Architecture using Genomics and Epidemiology (PAGE) Study reveals evidence for multiple signals at established loci. *Human Genetics*, **2017**, 136, 771-800	6.3	23
139	Leveraging information from genetic risk scores of coronary atherosclerosis. *Current Opinion in Lipidology*, **2017**, 28, 104-112	4.4	11
138	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. *Nature Genetics*, **2017**, 49, 1113-1119	36.3	184

137	Coronary Artery Disease and Myocardial Infarction **2017**, 127-163		
136	Association analyses of East Asian individuals and trans-ancestry analyses with European individuals reveal new loci associated with cholesterol and triglyceride levels. *Human Molecular Genetics*, **2017**, 26, 1770-1784	5.6	90
135	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
134	Epigenetic clock analysis of diet, exercise, education, and lifestyle factors. *Aging*, **2017**, 9, 419-446	5.6	317
133	Leveraging Multi-ethnic Evidence for Risk Assessment of Quantitative Traits in Minority Populations. *American Journal of Human Genetics*, **2017**, 101, 218-226	11	37
132	Association analyses based on false discovery rate implicate new loci for coronary artery disease. *Nature Genetics*, **2017**, 49, 1385-1391	36.3	361
131	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. *American Journal of Human Genetics*, **2017**, 101, 888-902	11	83
130	Epigenetic Aging and Immune Senescence in Women With Insomnia Symptoms: Findings From the Women's Health Initiative Study. *Biological Psychiatry*, **2017**, 81, 136-144	7.9	67
129	Impact of a Genetic Risk Score for Coronary Artery Disease on Reducing Cardiovascular Risk: A Pilot Randomized Controlled Study. *Frontiers in Cardiovascular Medicine*, **2017**, 4, 53	5.4	29
128	Leukocyte telomere length, T cell composition and DNA methylation age. *Aging*, **2017**, 9, 1983-1995	5.6	29
127	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. *Nature Genetics*, **2017**, 49, 1450-1457	36.3	136
126	Lean body mass and risk of incident atrial fibrillation in post-menopausal women. *European Heart Journal*, **2016**, 37, 1606-13	9.5	21
125	An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. *Genome Biology*, **2016**, 17, 171	18.3	357
124	Integrative functional genomics identifies regulatory mechanisms at coronary artery disease loci. *Nature Communications*, **2016**, 7, 12092	17.4	70
123	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184	36.3	251
122	Menopause accelerates biological aging. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 9327-32	11.5	248
121	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. *Scientific Reports*, **2016**, 6, 35278	4.9	18
120	Fine-mapping of lipid regions in global populations discovers ethnic-specific signals and refines previously identified lipid loci. *Human Molecular Genetics*, **2016**, 25, 5500-5512	5.6	22

119	Gene by Environment Investigation of Incident Lung Cancer Risk in African-Americans. *EBioMedicine* , **2016**, 4, 153-61	8.8	8
118	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. *Science*, **2016**, 351, 1166-71	33.3	325
117	The glycolytic enzyme PKM2 bridges metabolic and inflammatory dysfunction in coronary artery disease. *Journal of Experimental Medicine*, **2016**, 213, 337-54	16.6	268
116	Genetics of Coronary Artery Disease in Taiwan: A Cardiometabochip Study by the Taichi Consortium. *PLoS ONE*, **2016**, 11, e0138014	3.7	18
115	Associations between a Genetic Risk Score for Clinical CAD and Early Stage Lesions in the Coronary Artery and the Aorta. *PLoS ONE*, **2016**, 11, e0166994	3.7	2
114	DNA methylation-based measures of biological age: meta-analysis predicting time to death. *Aging*, **2016**, 8, 1844-1865	5.6	531
113	The glycolytic enzyme PKM2 bridges metabolic and inflammatory dysfunction in coronary artery disease. *Journal of Cell Biology*, **2016**, 212, 2126OIA43	7.3	78
112	The associations of leptin, adiponectin and resistin with incident atrial fibrillation in women. *Heart*, **2016**, 102, 1354-62	5.1	22
111	Genetics: Implications for Prevention and Management of Coronary Artery Disease. *Journal of the American College of Cardiology*, **2016**, 68, 2797-2818	15.1	65
110	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. *Genome Biology*, **2016**, 17, 255	18.3	171
109	Genetic variants primarily associated with type 2 diabetes are related to coronary artery disease risk. *Atherosclerosis*, **2015**, 241, 419-26	3.1	23
108	Characterization of TCF21 Downstream Target Regions Identifies a Transcriptional Network Linking Multiple Independent Coronary Artery Disease Loci. *PLoS Genetics*, **2015**, 11, e1005202	6	36
107	Genetically determined height and coronary artery disease. *New England Journal of Medicine*, **2015**, 372, 1608-18	59.2	152
106	Susceptibility Loci for Clinical Coronary Artery Disease and Subclinical Coronary Atherosclerosis Throughout the Life-Course. *Circulation: Cardiovascular Genetics*, **2015**, 8, 803-11		22
105	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. *Nature Genetics*, **2015**, 47, 1121-1130	36.3	1290
104	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. *Nature*, **2015**, 518, 102-6	50.4	463
103	Detecting clinically meaningful biomarkers with repeated measurements: An illustration with electronic health records. *Biometrics*, **2015**, 71, 478-86	1.8	9
102	DNA methylation age of blood predicts future onset of lung cancer in the women's health initiative. *Aging*, **2015**, 7, 690-700	5.6	189

101	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. *PLoS Genetics*, **2015**, 11, e1005378	6	220
100	Effect of Common Genetic Variants of Growth Arrest-Specific 6 Gene on Insulin Resistance, Obesity and Type 2 Diabetes in an Asian Population. *PLoS ONE*, **2015**, 10, e0135681	3.7	5
99	Identification and validation of N-acetyltransferase 2 as an insulin sensitivity gene. *Journal of Clinical Investigation*, **2015**, 125, 1739-51	15.9	67
98	Systems Genetics Analysis of Genome-Wide Association Study Reveals Novel Associations Between Key Biological Processes and Coronary Artery Disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2015**, 35, 1712-22	9.4	55
97	Leukocyte Telomere Length and Risks of Incident Coronary Heart Disease and Mortality in a Racially Diverse Population of Postmenopausal Women. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2015**, 35, 2225-31	9.4	45
96	Dissecting the roles of microRNAs in coronary heart disease via integrative genomic analyses. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2015**, 35, 1011-21	9.4	46
95	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
94	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
93	Clinical interpretation and implications of whole-genome sequencing. *JAMA - Journal of the American Medical Association*, **2014**, 311, 1035-45	27.4	333
92	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal of Human Genetics*, **2014**, 94, 233-45	11	170
91	Dissecting the causal genetic mechanisms of coronary heart disease. *Current Atherosclerosis Reports* , **2014**, 16, 406	6	10
90	Shared genetic susceptibility to ischemic stroke and coronary artery disease: a genome-wide analysis of common variants. *Stroke*, **2014**, 45, 24-36	6.7	245
89	Quantifying rare, deleterious variation in 12 human cytochrome P450 drug-metabolism genes in a large-scale exome dataset. *Human Molecular Genetics*, **2014**, 23, 1957-63	5.6	68
88	Leveraging population admixture to characterize the heritability of complex traits. *Nature Genetics*, **2014**, 46, 1356-62	36.3	45
87	Inactivating mutations in NPC1L1 and protection from coronary heart disease. *New England Journal of Medicine*, **2014**, 371, 2072-82	59.2	307
86	The relationship of lipoprotein(a), C-reactive protein and homocysteine with metabolic syndrome in South Asians. *Journal of Indian College of Cardiology*, **2014**, 4, 208-213	0.2	
85	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
84	Loss-of-function mutations in APOC3, triglycerides, and coronary disease. *New England Journal of Medicine*, **2014**, 371, 22-31	59.2	721

83	Impact of type 2 diabetes susceptibility variants on quantitative glycemic traits reveals mechanistic heterogeneity. *Diabetes*, **2014**, 63, 2158-71	0.9	235
82	Multiple nonglycemic genomic loci are newly associated with blood level of glycated hemoglobin in East Asians. *Diabetes*, **2014**, 63, 2551-62	0.9	46
81	The combination of 9p21.3 genotype and biomarker profile improves a peripheral artery disease risk prediction model. *Vascular Medicine*, **2014**, 19, 3-8	3.3	6
80	Obesity, physical activity, and their interaction in incident atrial fibrillation in postmenopausal women. *Journal of the American Heart Association*, **2014**, 3,	6	65
79	Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. *Human Molecular Genetics*, **2014**, 23, 5492-504	5.6	141
78	Simple, standardized incorporation of genetic risk into non-genetic risk prediction tools for complex traits: coronary heart disease as an example. *Frontiers in Genetics*, **2014**, 5, 254	4.5	39
77	Integrative genomics reveals novel molecular pathways and gene networks for coronary artery disease. *PLoS Genetics*, **2014**, 10, e1004502	6	147
76	Coronary heart disease-associated variation in TCF21 disrupts a miR-224 binding site and miRNA-mediated regulation. *PLoS Genetics*, **2014**, 10, e1004263	6	91
75	Study of exonic variation identifies incremental information regarding lipid-related and coronary heart disease genes. *Circulation Research*, **2014**, 115, 478-80	15.7	1
74	Near-term prediction of sudden cardiac death in older hemodialysis patients using electronic health records. *Clinical Journal of the American Society of Nephrology: CJASN*, **2014**, 9, 82-91	6.9	16
73	Use of Medicare data to identify coronary heart disease outcomes in the Women Health Initiative. *Circulation: Cardiovascular Quality and Outcomes*, **2014**, 7, 157-62	5.8	67
72	Insulin resistance: regression and clustering. *PLoS ONE*, **2014**, 9, e94129	3.7	2
71	The shared allelic architecture of adiponectin levels and coronary artery disease. *Atherosclerosis*, **2013**, 229, 145-8	3.1	25
70	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
69	Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature Genetics*, **2013**, 45, 1345-52	36.3	597
68	Genetic variants associated with glycine metabolism and their role in insulin sensitivity and type 2 diabetes. *Diabetes*, **2013**, 62, 2141-50	0.9	59
67	Trans-ethnic fine mapping identifies a novel independent locus at the 3 end of CDKAL1 and novel variants of several susceptibility loci for type 2 diabetes in a Han Chinese population. *Diabetologia*, **2013**, 56, 2619-28	10.3	25
66	Large-scale association analysis identifies new risk loci for coronary artery disease. *Nature Genetics*, **2013**, 45, 25-33	36.3	1172

65	Genetics and genomics for the prevention and treatment of cardiovascular disease: update: a scientific statement from the American Heart Association. *Circulation*, **2013**, 128, 2813-51	16.7	76
64	Association between the chromosome 9p21 locus and angiographic coronary artery disease burden: a collaborative meta-analysis. *Journal of the American College of Cardiology*, **2013**, 61, 957-70	15.1	56
63	Measurement of insulin-mediated glucose uptake: direct comparison of the modified insulin suppression test and the euglycemic, hyperinsulinemic clamp. *Metabolism: Clinical and Experimental* , **2013**, 62, 548-53	12.7	42
62	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
61	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
60	A systems biology framework identifies molecular underpinnings of coronary heart disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2013**, 33, 1427-34	9.4	125
59	Genetic predisposition to higher blood pressure increases coronary artery disease risk. *Hypertension*, **2013**, 61, 995-1001	8.5	55
58	Disease-related growth factor and embryonic signaling pathways modulate an enhancer of TCF21 expression at the 6q23.2 coronary heart disease locus. *PLoS Genetics*, **2013**, 9, e1003652	6	52
57	Trans-ethnic fine-mapping of lipid loci identifies population-specific signals and allelic heterogeneity that increases the trait variance explained. *PLoS Genetics*, **2013**, 9, e1003379	6	94
56	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. *PLoS Genetics*, **2013**, 9, e1003500	6	277
55	Mendelian randomization studies do not support a causal role for reduced circulating adiponectin levels in insulin resistance and type 2 diabetes. *Diabetes*, **2013**, 62, 3589-98	0.9	95
54	Interleukin-6 receptor pathways in coronary heart disease: a collaborative meta-analysis of 82 studies. *Lancet, The*, **2012**, 379, 1205-13	40	522
53	Association between chromosome 9p21 variants and the ankle-brachial index identified by a meta-analysis of 21 genome-wide association studies. *Circulation: Cardiovascular Genetics*, **2012**, 5, 100-12		84
52	Central obesity is important but not essential component of the metabolic syndrome for predicting diabetes mellitus in a hypertensive family-based cohort. Results from the Stanford Asia-pacific program for hypertension and insulin resistance (SAPPHIRe) Taiwan follow-up study. *Cardiovascular Diabetology*, **2012**, 11, 43	8.7	15
51	FTO genotype is associated with phenotypic variability of body mass index. *Nature*, **2012**, 490, 267-72	50.4	304
50	Evaluation of the metabochip genotyping array in African Americans and implications for fine mapping of GWAS-identified loci: the PAGE study. *PLoS ONE*, **2012**, 7, e35651	3.7	59
49	Long-term use of angiotensin receptor blockers and the risk of cancer. *PLoS ONE*, **2012**, 7, e50893	3.7	50
48	Randomized trial of personal genomics for preventive cardiology: design and challenges. *Circulation: Cardiovascular Genetics*, **2012**, 5, 368-76		23

47	Age-related somatic structural changes in the nuclear genome of human blood cells. *American Journal of Human Genetics*, **2012**, 90, 217-28	11	139
46	Homocysteine and coronary heart disease: meta-analysis of MTHFR case-control studies, avoiding publication bias. *PLoS Medicine*, **2012**, 9, e1001177	11.6	135
45	Low lifetime recreational activity is a risk factor for peripheral arterial disease. *Journal of Vascular Surgery*, **2011**, 54, 427-32, 432.e1-4	3.5	32
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10	Measuring genetic variation in the multi-ethnic Million Veteran Program (MVP)		4
9	Integration of rare large-effect expression variants improves polygenic risk prediction		1
8	An epigenetic biomarker of aging for lifespan and healthspan		2
7	Genetic analyses in UK Biobank identifies 78 novel loci associated with urinary biomarkers providing new insights into the biology of kidney function and chronic disease		1
6	Genetics of 38 blood and urine biomarkers in the UK Biobank		25
5	Diverse transcriptomic signatures across human tissues identify functional rare genetic variation		13
4	Assessing a causal relationship between circulating lipids and breast cancer risk: Mendelian randomization study		1
3	GWAS of epigenetic ageing rates in blood reveals a critical role forTERT		1
2	A trans-ancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation		5
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