Themistocles L Assimes

List of Publications by Citations

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	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
225	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
224	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
223	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
222	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
221	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. *Nature Genetics*, **2011**, 43, 333-8	36.3	1394
220	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
219	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. *Nature Genetics*, **2015**, 47, 1121-1130	36.3	1290
218	Large-scale association analysis identifies new risk loci for coronary artery disease. *Nature Genetics*, **2013**, 45, 25-33	36.3	1172
217	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
216	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. *Nature Genetics*, **2010**, 42, 949-60	36.3	724
215	Loss-of-function mutations in APOC3, triglycerides, and coronary disease. *New England Journal of Medicine*, **2014**, 371, 22-31	59.2	721
214	An epigenetic biomarker of aging for lifespan and healthspan. *Aging*, **2018**, 10, 573-591	5.6	658
213	Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature Genetics*, **2013**, 45, 1345-52	36.3	597
212	DNA methylation-based measures of biological age: meta-analysis predicting time to death. *Aging*, **2016**, 8, 1844-1865	5.6	531
211	Interleukin-6 receptor pathways in coronary heart disease: a collaborative meta-analysis of 82 studies. *Lancet, The*, **2012**, 379, 1205-13	40	522
210	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. *Nature*, **2015**, 518, 102-6	50.4	463

209	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
208	DNA methylation GrimAge strongly predicts lifespan and healthspan. *Aging*, **2019**, 11, 303-327	5.6	424
207	Identification of ADAMTS7 as a novel locus for coronary atherosclerosis and association of ABO with myocardial infarction in the presence of coronary atherosclerosis: two genome-wide association studies. *Lancet, The*, **2011**, 377, 383-92	40	399
206	Association analyses based on false discovery rate implicate new loci for coronary artery disease. *Nature Genetics*, **2017**, 49, 1385-1391	36.3	361
205	An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. *Genome Biology*, **2016**, 17, 171	18.3	357
204	Clinical interpretation and implications of whole-genome sequencing. *JAMA - Journal of the American Medical Association*, **2014**, 311, 1035-45	27.4	333
203	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. *Science*, **2016**, 351, 1166-71	33.3	325
202	Epigenetic clock analysis of diet, exercise, education, and lifestyle factors. *Aging*, **2017**, 9, 419-446	5.6	317
201	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
200	Inactivating mutations in NPC1L1 and protection from coronary heart disease. *New England Journal of Medicine*, **2014**, 371, 2072-82	59.2	307
199	FTO genotype is associated with phenotypic variability of body mass index. *Nature*, **2012**, 490, 267-72	50.4	304
198	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
197	The glycolytic enzyme PKM2 bridges metabolic and inflammatory dysfunction in coronary artery disease. *Journal of Experimental Medicine*, **2016**, 213, 337-54	16.6	268
196	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. *Nature Genetics*, **2018**, 50, 1514-1523	36.3	260
195	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
194	Menopause accelerates biological aging. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 9327-32	11.5	248
193	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
192	Impact of type 2 diabetes susceptibility variants on quantitative glycemic traits reveals mechanistic heterogeneity. *Diabetes*, **2014**, 63, 2158-71	0.9	235

191	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
190	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
189	Detailed physiologic characterization reveals diverse mechanisms for novel genetic Loci regulating glucose and insulin metabolism in humans. *Diabetes*, **2010**, 59, 1266-75	0.9	211
188	A bivariate genome-wide approach to metabolic syndrome: STAMPEED consortium. *Diabetes*, **2011**, 60, 1329-39	0.9	194
187	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
186	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. *Nature Genetics*, **2017**, 49, 1113-1119	36.3	184
185	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. *Genome Biology*, **2016**, 17, 255	18.3	171
184	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
183	Genetically determined height and coronary artery disease. *New England Journal of Medicine*, **2015**, 372, 1608-18	59.2	152
182	Integrative genomics reveals novel molecular pathways and gene networks for coronary artery disease. *PLoS Genetics*, **2014**, 10, e1004502	6	147
181	Susceptibility locus for clinical and subclinical coronary artery disease at chromosome 9p21 in the multi-ethnic ADVANCE study. *Human Molecular Genetics*, **2008**, 17, 2320-8	5.6	146
180	Abdominal aortic aneurysm is associated with a variant in low-density lipoprotein receptor-related protein 1. *American Journal of Human Genetics*, **2011**, 89, 619-27	11	145
179	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
178	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
177	Age-related somatic structural changes in the nuclear genome of human blood cells. *American Journal of Human Genetics*, **2012**, 90, 217-28	11	139
176	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
175	Design of the Coronary ARtery DIsease Genome-Wide Replication And Meta-Analysis (CARDIoGRAM) Study: A Genome-wide association meta-analysis involving more than 22 000 cases and 60 000 controls. *Circulation: Cardiovascular Genetics*, **2010**, 3, 475-83		135
174	Homocysteine and coronary heart disease: meta-analysis of MTHFR case-control studies, avoiding publication bias. *PLoS Medicine*, **2012**, 9, e1001177	11.6	135

173	A systems biology framework identifies molecular underpinnings of coronary heart disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2013**, 33, 1427-34	9.4	125
172	Characterizing the admixed African ancestry of African Americans. *Genome Biology*, **2009**, 10, R141	18.3	114
171	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. *Nature Communications*, **2018**, 9, 387	17.4	106
170	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
169	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
168	Coronary heart disease-associated variation in TCF21 disrupts a miR-224 binding site and miRNA-mediated regulation. *PLoS Genetics*, **2014**, 10, e1004263	6	91
167	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
166	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
165	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
164	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. *American Journal of Human Genetics*, **2017**, 101, 888-902	11	83
163	The glycolytic enzyme PKM2 bridges metabolic and inflammatory dysfunction in coronary artery disease. *Journal of Cell Biology*, **2016**, 212, 2126OIA43	7.3	78
162	Genetics of 35 blood and urine biomarkers in the UK Biobank. *Nature Genetics*, **2021**, 53, 185-194	36.3	78
161	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
160	Lack of association between the Trp719Arg polymorphism in kinesin-like protein-6 and coronary artery disease in 19 case-control studies. *Journal of the American College of Cardiology*, **2010**, 56, 1552-63	15.1	75
159	Genome-wide association study of peripheral artery disease in the Million Veteran Program. *Nature Medicine*, **2019**, 25, 1274-1279	50.5	73
158	Polymorphisms in hypoxia inducible factor 1 and the initial clinical presentation of coronary disease. *American Heart Journal*, **2007**, 154, 1035-42	4.9	72
157	Integrative functional genomics identifies regulatory mechanisms at coronary artery disease loci. *Nature Communications*, **2016**, 7, 12092	17.4	70
156	DNA methylation-based estimator of telomere length. *Aging*, **2019**, 11, 5895-5923	5.6	69

155	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
154	Epigenetic Aging and Immune Senescence in Women With Insomnia Symptoms: Findings From the Women Health Initiative Study. *Biological Psychiatry*, **2017**, 81, 136-144	7.9	67
153	Identification and validation of N-acetyltransferase 2 as an insulin sensitivity gene. *Journal of Clinical Investigation*, **2015**, 125, 1739-51	15.9	67
152	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
151	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. *Circulation*, **2019**, 140, 645-657	16.7	65
150	Obesity, physical activity, and their interaction in incident atrial fibrillation in postmenopausal women. *Journal of the American Heart Association*, **2014**, 3,	6	65
149	Genetics: Implications for Prevention and Management of Coronary Artery Disease. *Journal of the American College of Cardiology*, **2016**, 68, 2797-2818	15.1	65
148	Genetic variants associated with glycine metabolism and their role in insulin sensitivity and type 2 diabetes. *Diabetes*, **2013**, 62, 2141-50	0.9	59
147	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
146	Long-term use of antihypertensive drugs and risk of cancer. *Pharmacoepidemiology and Drug Safety*, **2008**, 17, 1039-49	2.6	58
145	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
144	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
143	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
142	Genetic predisposition to higher blood pressure increases coronary artery disease risk. *Hypertension*, **2013**, 61, 995-1001	8.5	55
141	Inhaled corticosteroid use in asthma and the prevention of myocardial infarction. *American Journal of Medicine*, **2003**, 115, 377-81	2.4	53
140	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
139	Long-term use of angiotensin receptor blockers and the risk of cancer. *PLoS ONE*, **2012**, 7, e50893	3.7	50
138	Circulating chemokines accurately identify individuals with clinically significant atherosclerotic heart disease. *Physiological Genomics*, **2007**, 31, 402-9	3.6	50

137	Genetic susceptibility to peripheral arterial disease: a dark corner in vascular biology. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2007**, 27, 2068-78	9.4	49
136	Common polymorphisms of ALOX5 and ALOX5AP and risk of coronary artery disease. *Human Genetics*, **2008**, 123, 399-408	6.3	47
135	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
134	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
133	Multiple nonglycemic genomic loci are newly associated with blood level of glycated hemoglobin in East Asians. *Diabetes*, **2014**, 63, 2551-62	0.9	46
132	Leveraging population admixture to characterize the heritability of complex traits. *Nature Genetics*, **2014**, 46, 1356-62	36.3	45
131	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
130	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
129	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
128	Harmonizing Genetic Ancestry and Self-identified Race/Ethnicity in Genome-wide Association Studies. *American Journal of Human Genetics*, **2019**, 105, 763-772	11	41
127	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
126	A near null variant of 12/15-LOX encoded by a novel SNP in ALOX15 and the risk of coronary artery disease. *Atherosclerosis*, **2008**, 198, 136-44	3.1	39
125	Leveraging Multi-ethnic Evidence for Risk Assessment of Quantitative Traits in Minority Populations. *American Journal of Human Genetics*, **2017**, 101, 218-226	11	37
124	The use of perioperative corticosteroids in craniomaxillofacial surgery. *Plastic and Reconstructive Surgery*, **1999**, 103, 313-21; quiz 322	2.7	37
123	Characterization of TCF21 Downstream Target Regions Identifies a Transcriptional Network Linking Multiple Independent Coronary Artery Disease Loci. *PLoS Genetics*, **2015**, 11, e1005202	6	36
122	Transcriptomic signatures across human tissues identify functional rare genetic variation. *Science*, **2020**, 369,	33.3	36
121	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. *Environment International*, **2019**, 132, 104723	12.9	35
120	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

119	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. *Nature Communications*, **2019**, 10, 2581	17.4	31
118	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
117	Leukocyte telomere length, T cell composition and DNA methylation age. *Aging*, **2017**, 9, 1983-1995	5.6	29
116	Sex differences in the prevalence of peripheral artery disease in patients undergoing coronary catheterization. *Vascular Medicine*, **2010**, 15, 443-50	3.3	26
115	The role of epigenetic aging in education and racial/ethnic mortality disparities among older U.S. Women. *Psychoneuroendocrinology*, **2019**, 104, 18-24	5	26
114	The shared allelic architecture of adiponectin levels and coronary artery disease. *Atherosclerosis*, **2013**, 229, 145-8	3.1	25
113	Trans-ethnic fine mapping identifies a novel independent locus at the 3Q 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
112	Genetics of 38 blood and urine biomarkers in the UK Biobank		25
111	Failure to replicate an association of SNPs in the oxidized LDL receptor gene (OLR1) with CAD. *BMC Medical Genetics*, **2008**, 9, 23	2.1	24
110	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
109	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. *Circulation*, **2020**, 142, 1633-1646	16.7	24
108	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
107	Genetic variants primarily associated with type 2 diabetes are related to coronary artery disease risk. *Atherosclerosis*, **2015**, 241, 419-26	3.1	23
106	Randomized trial of personal genomics for preventive cardiology: design and challenges. *Circulation: Cardiovascular Genetics*, **2012**, 5, 368-76		23
105	Susceptibility Loci for Clinical Coronary Artery Disease and Subclinical Coronary Atherosclerosis Throughout the Life-Course. *Circulation: Cardiovascular Genetics*, **2015**, 8, 803-11		22
104	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
103	Chromosome 1q21.2 and additional loci influence risk of spontaneous coronary artery dissection and myocardial infarction. *Nature Communications*, **2020**, 11, 4432	17.4	22
102	The associations of leptin, adiponectin and resistin with incident atrial fibrillation in women. *Heart*, **2016**, 102, 1354-62	5.1	22

101	Genotyping Array Design and Data Quality Control in the Million Veteran Program. *American Journal of Human Genetics*, **2020**, 106, 535-548	11	22
100	Lean body mass and risk of incident atrial fibrillation in post-menopausal women. *European Heart Journal*, **2016**, 37, 1606-13	9.5	21
99	Coffee consumption is associated with DNA methylation levels of human blood. *European Journal of Human Genetics*, **2017**, 25, 608-616	5.3	21
98	Identification of 22 novel loci associated with urinary biomarkers of albumin, sodium, and potassium excretion. *Kidney International*, **2019**, 95, 1197-1208	9.9	20
97	Genome-Wide Association Studies of Coronary Artery Disease: Recent Progress and Challenges Ahead. *Current Atherosclerosis Reports*, **2018**, 20, 47	6	19
96	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. *Scientific Reports*, **2016**, 6, 35278	4.9	18
95	Association of Risk Alleles With Cardiovascular Disease in Blacks in the Million Veteran Program. *Circulation*, **2019**, 140, 1031-1040	16.7	18
94	Genetics of Coronary Artery Disease in Taiwan: A Cardiometabochip Study by the Taichi Consortium. *PLoS ONE*, **2016**, 11, e0138014	3.7	18
93	Melanoma risk prediction using a multilocus genetic risk score in the Women's Health Initiative cohort. *Journal of the American Academy of Dermatology*, **2018**, 79, 36-41.e10	4.5	17
92	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
91	The relationship between circulating lipids and breast cancer risk: A Mendelian randomization study. *PLoS Medicine*, **2020**, 17, e1003302	11.6	16
90	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
89	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
88	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
87	Discovery of 318 novel loci for type-2 diabetes and related micro- and macrovascular outcomes among 1.4 million participants in a multi-ethnic meta-analysis		13
86	Diverse transcriptomic signatures across human tissues identify functional rare genetic variation		13
85	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
84	Leveraging information from genetic risk scores of coronary atherosclerosis. *Current Opinion in Lipidology*, **2017**, 28, 104-112	4.4	11

83	An "almost exhaustive" search-based sequential permutation method for detecting epistasis in disease association studies. *Genetic Epidemiology*, **2010**, 34, 434-43	2.6	11
82	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
81	Genetics of Smoking and Risk of Atherosclerotic Cardiovascular Diseases: A Mendelian Randomization Study. *JAMA Network Open*, **2021**, 4, e2034461	10.4	11
80	The Project Baseline Health Study: a step towards a broader mission to map human health. *Npj Digital Medicine*, **2020**, 3, 84	15.7	10
79	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
78	Dissecting the causal genetic mechanisms of coronary heart disease. *Current Atherosclerosis Reports* , **2014**, 16, 406	6	10
77	Heritability of left ventricular mass in Japanese families living in Hawaii: the SAPPHIRe Study. *Journal of Hypertension*, **2007**, 25, 985-92	1.9	10
76	Breastfeeding Duration and the Risk of Coronary Artery Disease. *Journal of Womenjs Health*, **2019**, 28, 30-36	3	10
75	Association Between Heart Failure and Postoperative Mortality Among Patients Undergoing Ambulatory Noncardiac Surgery. *JAMA Surgery*, **2019**, 154, 907-914	5.4	9
74	Detecting clinically meaningful biomarkers with repeated measurements: An illustration with electronic health records. *Biometrics*, **2015**, 71, 478-86	1.8	9
73	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. *Aging Cell*, **2021**, 20, e13366	9.9	9
72	Gene by Environment Investigation of Incident Lung Cancer Risk in African-Americans. *EBioMedicine* , **2016**, 4, 153-61	8.8	8
71	Evaluation of 71 Coronary Artery Disease Risk Variants in a Multiethnic Cohort. *Frontiers in Cardiovascular Medicine*, **2018**, 5, 19	5.4	8
70	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
69	Cardioinformatics: the nexus of bioinformatics and precision cardiology. *Briefings in Bioinformatics*, **2020**, 21, 2031-2051	13.4	8
68	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
67	Immortal person time bias in pharmacoepidemiological studies of antihypertensive drugs. *American Journal of Cardiology*, **2011**, 108, 902-3	3	7
66	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

65	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
64	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
63	Age at incident treatment of hypertension and risk of cancer: a population study. *Cancer Causes and Control*, **2009**, 20, 1811-20	2.8	6
62	HeartBioPortal. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002426	5.2	5
61	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
60	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
59	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
58	Validating a non-invasive, ALT-based non-alcoholic fatty liver phenotype in the million veteran program. *PLoS ONE*, **2020**, 15, e0237430	3.7	5
57	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. *Nature Communications*, **2021**, 12, 2182	17.4	5
56	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
55	Measuring genetic variation in the multi-ethnic Million Veteran Program (MVP)		4
54	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
53	Alcohol use and cardiometabolic risk in the UK Biobank: A Mendelian randomization study. *PLoS ONE*, **2021**, 16, e0255801	3.7	4
52	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. *Nature Communications*, **2021**, 12, 3987	17.4	3
51	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential.. *Science Advances*, **2022**, 8, eabl6579	14.3	3
50	ZEB2 Shapes the Epigenetic Landscape of Atherosclerosis.. *Circulation*, **2022**,	16.7	2
49	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
48	Insulin resistance: regression and clustering. *PLoS ONE*, **2014**, 9, e94129	3.7	2

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