Themistocles L Assimes

List of Publications by Year
in descending order

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		6592	1974
225	49,224	79	206
papers	citations	h-index	g-index

257	257	257	47177
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
2	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
3	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
4	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
5	A comprehensive 1000 Genomesâ€"based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	9.4	2,054
6	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
7	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
8	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Nature Genetics, 2011, 43, 333-338.	9.4	1,685
9	An epigenetic biomarker of aging for lifespan and healthspan. Aging, 2018, 10, 573-591.	1.4	1,552
10	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	9.4	1,439
11	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
12	DNA methylation GrimAge strongly predicts lifespan and healthspan. Aging, 2019, 11, 303-327.	1.4	1,128
13	Loss-of-Function Mutations inAPOC3,Triglycerides, and Coronary Disease. New England Journal of Medicine, 2014, 371, 22-31.	13.9	936
14	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, 949-960.	9.4	836
15	DNA methylation-based measures of biological age: meta-analysis predicting time to death. Aging, 2016, 8, 1844-1865.	1.4	786
16	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
17	Interleukin-6 receptor pathways in coronary heart disease: a collaborative meta-analysis of 82 studies. Lancet, The, 2012, 379, 1205-1213.	6.3	668
18	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	13.7	581

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19	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
20	Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391.	9.4	571
21	An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. Genome Biology, 2016, 17, 171.	3.8	535
22	Epigenetic clock analysis of diet, exercise, education, and lifestyle factors. Aging, 2017, 9, 419-446.	1.4	521
23	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. Nature Genetics, 2018, 50, 1514-1523.	9.4	497
24	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
25	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, 383-392.	6.3	466
26	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.	9.4	445
27	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	6.0	438
28	The glycolytic enzyme PKM2 bridges metabolic and inflammatory dysfunction in coronary artery disease. Journal of Experimental Medicine, 2016, 213, 337-354.	4.2	403
29	Clinical Interpretation and Implications of Whole-Genome Sequencing. JAMA - Journal of the American Medical Association, 2014, 311, 1035.	3.8	398
30	Inactivating Mutations in NPC1L1 and Protection from Coronary Heart Disease. New England Journal of Medicine, 2014, 371, 2072-2082.	13.9	386
31	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	13.7	383
32	Genetics of 35 blood and urine biomarkers in the UK Biobank. Nature Genetics, 2021, 53, 185-194.	9.4	377
33	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	1.5	371
34	Menopause accelerates biological aging. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9327-9332.	3.3	363
35	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	9.4	362
36	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353

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37	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.	1.5	331
38	Shared Genetic Susceptibility to Ischemic Stroke and Coronary Artery Disease. Stroke, 2014, 45, 24-36.	1.0	302
39	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. Diabetes, 2014, 63, 2158-2171.	0.3	297
40	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
41	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119.	9.4	260
42	DNA methylation age of blood predicts future onset of lung cancer in the women's health initiative. Aging, 2015, 7, 690-700.	1.4	254
43	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	3.8	251
44	Detailed Physiologic Characterization Reveals Diverse Mechanisms for Novel Genetic Loci Regulating Glucose and Insulin Metabolism in Humans. Diabetes, 2010, 59, 1266-1275.	0.3	237
45	A Bivariate Genome-Wide Approach to Metabolic Syndrome. Diabetes, 2011, 60, 1329-1339.	0.3	226
46	Genetically Determined Height and Coronary Artery Disease. New England Journal of Medicine, 2015, 372, 1608-1618.	13.9	220
47	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. Nature Genetics, 2017, 49, 1450-1457.	9.4	218
48	DNA methylation-based estimator of telomere length. Aging, 2019, 11, 5895-5923.	1.4	198
49	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	2.6	193
50	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, 5492-5504.	1.4	192
51	Integrative Genomics Reveals Novel Molecular Pathways and Gene Networks for Coronary Artery Disease. PLoS Genetics, 2014, 10, e1004502.	1.5	192
52	Abdominal Aortic Aneurysm Is Associated with a Variant in Low-Density Lipoprotein Receptor-Related Protein 1. American Journal of Human Genetics, 2011, 89, 619-627.	2.6	185
53	Genome-wide association study of peripheral artery disease in the Million Veteran Program. Nature Medicine, 2019, 25, 1274-1279.	15.2	177
54	Harmonizing Genetic Ancestry and Self-identified Race/Ethnicity in Genome-wide Association Studies. American Journal of Human Genetics, 2019, 105, 763-772.	2.6	169

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55	Age-Related Somatic Structural Changes in the Nuclear Genome of Human Blood Cells. American Journal of Human Genetics, 2012, 90, 217-228.	2.6	168
56	Homocysteine and Coronary Heart Disease: Meta-analysis of MTHFR Case-Control Studies, Avoiding Publication Bias. PLoS Medicine, 2012, 9, e1001177.	3.9	167
57	Susceptibility locus for clinical and subclinical coronary artery disease at chromosome 9p21 in the multi-ethnic ADVANCE study. Human Molecular Genetics, 2008, 17, 2320-2328.	1.4	166
58	Design of the Coronary ARtery DIsease Genome-Wide Replication And Meta-Analysis (CARDIoGRAM) Study. Circulation: Cardiovascular Genetics, 2010, 3, 475-483.	5.1	159
59	A Systems Biology Framework Identifies Molecular Underpinnings of Coronary Heart Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 1427-1434.	1.1	157
60	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	2.6	154
61	Genome-wide association analysis of venous thromboembolism identifies new risk loci and genetic overlap with arterial vascular disease. Nature Genetics, 2019, 51, 1574-1579.	9.4	152
62	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. Nature Communications, 2018, 9, 387.	5.8	151
63	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. Circulation, 2019, 140, 645-657.	1.6	151
64	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. Journal of the American College of Cardiology, 2019, 73, 58-66.	1.2	147
65	Characterizing the admixed African ancestry of African Americans. Genome Biology, 2009, 10, R141.	13.9	145
66	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.	1.4	135
67	Integrative functional genomics identifies regulatory mechanisms at coronary artery disease loci. Nature Communications, 2016, 7, 12092.	5.8	123
68	Genotyping Array Design and Data Quality Control in the Million Veteran Program. American Journal of Human Genetics, 2020, 106, 535-548.	2.6	118
69	Mendelian Randomization Studies Do Not Support a Causal Role for Reduced Circulating Adiponectin Levels in Insulin Resistance and Type 2 Diabetes. Diabetes, 2013, 62, 3589-3598.	0.3	116
70	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.	1.5	112
71	Coronary Heart Disease-Associated Variation in TCF21 Disrupts a miR-224 Binding Site and miRNA-Mediated Regulation. PLoS Genetics, 2014, 10, e1004263.	1.5	108
72	Epigenetic Aging and Immune Senescence in Women With Insomnia Symptoms: Findings From the Womenâ€™s Health Initiative Study. Biological Psychiatry, 2017, 81, 136-144.	0.7	108

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73	Genetics and Genomics for the Prevention and Treatment of Cardiovascular Disease: Update. Circulation, 2013, 128, 2813-2851.	1.6	100
74	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, 100-112.	5.1	98
75	Identification and validation of N-acetyltransferase 2 as an insulin sensitivity gene. Journal of Clinical Investigation, 2015, 125, 1739-1751.	3.9	94
76	Genetics: Implications for Prevention and Management of Coronary Artery Disease. Journal of the American College of Cardiology, 2016, 68, 2797-2818.	1.2	92
77	Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 2020, 369, .	6.0	89
78	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, 1552-1563.	1.2	84
79	Obesity, Physical Activity, and Their Interaction in Incident Atrial Fibrillation in Postmenopausal Women. Journal of the American Heart Association, 2014, 3, .	1.6	83
80	Polymorphisms in hypoxia inducible factor 1 and the initial clinical presentation of coronary disease. American Heart Journal, 2007, 154, 1035-1042.	1.2	82
81	Quantifying rare, deleterious variation in 12 human cytochrome P450 drug-metabolism genes in a large-scale exome dataset. Human Molecular Genetics, 2014, 23, 1957-1963.	1.4	82
82	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.	3.8	82
83	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.	0.5	80
84	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. Circulation, 2020, 142, 1633-1646.	1.6	78
85	Use of Medicare Data to Identify Coronary Heart Disease Outcomes in the Women's Health Initiative. Circulation: Cardiovascular Quality and Outcomes, 2014, 7, 157-162.	0.9	76
86	Leveraging Multi-ethnic Evidence for Risk Assessment of Quantitative Traits in Minority Populations. American Journal of Human Genetics, 2017, 101, 218-226.	2.6	75
87	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, 1712-1722.	1.1	72
88	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. Aging Cell, 2021, 20, e13366.	3.0	72
89	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.	1.1	71
90	Genetic Variants Associated With Glycine Metabolism and Their Role in Insulin Sensitivity and Type 2 Diabetes. Diabetes, 2013, 62, 2141-2150.	0.3	70

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91	Genetic Predisposition to Higher Blood Pressure Increases Coronary Artery Disease Risk. Hypertension, 2013, 61, 995-1001.	1.3	70
92	Leveraging population admixture to characterize the heritability of complex traits. Nature Genetics, 2014, 46, 1356-1362.	9.4	69
93	A multiancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation. Nature Genetics, 2022, 54, 761-771.	9.4	68
94	Longâ€term use of antihypertensive drugs and risk of cancer. Pharmacoepidemiology and Drug Safety, 2008, 17, 1039-1049.	0.9	66
95	Long-Term Use of Angiotensin Receptor Blockers and the Risk of Cancer. PLoS ONE, 2012, 7, e50893.	1.1	65
96	Inhaled corticosteroid use in asthma and the prevention of myocardial infarction. American Journal of Medicine, 2003, 115, 377-381.	0.6	64
97	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.	1.5	63
98	The relationship between circulating lipids and breast cancer risk: A Mendelian randomization study. PLoS Medicine, 2020, 17, e1003302.	3.9	63
99	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. Nature Communications, 2019, 10, 2581.	5.8	62
100	Genetic Susceptibility to Peripheral Arterial Disease: A Dark Corner in Vascular Biology. Arteriosclerosis, Thrombosis, and Vascular Biology, 2007, 27, 2068-2078.	1.1	61
101	Multiple Nonglycemic Genomic Loci Are Newly Associated With Blood Level of Glycated Hemoglobin in East Asians. Diabetes, 2014, 63, 2551-2562.	0.3	61
102	Circulating chemokines accurately identify individuals with clinically significant atherosclerotic heart disease. Physiological Genomics, 2007, 31, 402-409.	1.0	60
103	Chromosome 1q21.2 and additional loci influence risk of spontaneous coronary artery dissection and myocardial infarction. Nature Communications, 2020, 11, 4432.	5.8	60
104	Association Between the Chromosome 9p21 Locus and Angiographic Coronary Artery Disease Burden. Journal of the American College of Cardiology, 2013, 61, 957-970.	1.2	58
105	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. Environment International, 2019, 132, 104723.	4.8	58
106	Common polymorphisms of ALOX5 and ALOX5AP and risk of coronary artery disease. Human Genetics, 2008, 123, 399-408.	1.8	54
107	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, 2225-2231.	1.1	53
108	Dissecting the Roles of MicroRNAs in Coronary Heart Disease via Integrative Genomic Analyses. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 1011-1021.	1.1	53

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109	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, 548-553.	1.5	48
110	The role of epigenetic aging in education and racial/ethnic mortality disparities among older U.S. Women. Psychoneuroendocrinology, 2019, 104, 18-24.	1.3	47
111	The Use of Perioperative Corticosteroids in Craniomaxillofacial Surgery. Plastic and Reconstructive Surgery, 1999, 103, 313-321.	0.7	44
112	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, 136-144.	0.4	44
113	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.	1.1	44
114	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.	1.1	44
115	Genetics of Smoking and Risk of Atherosclerotic Cardiovascular Diseases. JAMA Network Open, 2021, 4, e2034461.	2.8	42
116	Leukocyte telomere length, T cell composition and DNA methylation age. Aging, 2017, 9, 1983-1995.	1.4	42
117	Characterization of TCF21 Downstream Target Regions Identifies a Transcriptional Network Linking Multiple Independent Coronary Artery Disease Loci. PLoS Genetics, 2015, 11, e1005202.	1.5	41
118	Low lifetime recreational activity is a risk factor for peripheral arterial disease. Journal of Vascular Surgery, 2011, 54, 427-432.e4.	0.6	40
119	The Project Baseline Health Study: a step towards a broader mission to map human health. Npj Digital Medicine, 2020, 3, 84.	5.7	38
120	Susceptibility Loci for Clinical Coronary Artery Disease and Subclinical Coronary Atherosclerosis Throughout the Life-Course. Circulation: Cardiovascular Genetics, 2015, 8, 803-811.	5.1	36
121	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	4.7	36
122	Lean body mass and risk of incident atrial fibrillation in post-menopausal women. European Heart Journal, 2016, 37, 1606-1613.	1.0	34
123	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. International Journal of Epidemiology, 2020, 49, 1022-1031.	0.9	34
124	Association Between Heart Failure and Postoperative Mortality Among Patients Undergoing Ambulatory Noncardiac Surgery. JAMA Surgery, 2019, 154, 907.	2.2	33
125	Identification of 22 novel loci associated withÂurinary biomarkers of albumin, sodium, andÂpotassium excretion. Kidney International, 2019, 95, 1197-1208.	2.6	33
126	Genetics of Coronary Artery Disease in Taiwan: A Cardiometabochip Study by the Taichi Consortium. PLoS ONE, 2016, 11, e0138014.	1.1	33

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127	Sex differences in the prevalence of peripheral artery disease in patients undergoing coronary catheterization. Vascular Medicine, 2010, 15, 443-450.	0.8	32
128	The associations of leptin, adiponectin and resistin with incident atrial fibrillation in women. Heart, 2016, 102, 1354-1362.	1.2	31
129	Coffee consumption is associated with DNA methylation levels of human blood. European Journal of Human Genetics, 2017, 25, 608-616.	1.4	31
130	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.	1.8	31
131	Association of APOL1 Risk Alleles With Cardiovascular Disease in Blacks in the Million Veteran Program. Circulation, 2019, 140, 1031-1040.	1.6	31
132	ZEB2 Shapes the Epigenetic Landscape of Atherosclerosis. Circulation, 2022, 145, 469-485.	1.6	31
133	The shared allelic architecture of adiponectin levels and coronary artery disease. Atherosclerosis, 2013, 229, 145-148.	0.4	30
134	Genetic interactions drive heterogeneity in causal variant effect sizes for gene expression and complex traits. American Journal of Human Genetics, 2022, 109, 1286-1297.	2.6	30
135	Failure to replicate an association of SNPs in the oxidized LDL receptor gene (OLR1) with CAD. BMC Medical Genetics, 2008, 9, 23.	2.1	29
136	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.	1.4	29
137	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.	1.8	29
138	Urinary Albumin, Sodium, and Potassium and Cardiovascular Outcomes in the UK Biobank. Hypertension, 2020, 75, 714-722.	1.3	29
139	High heritability of ascending aortic diameter and trans-ancestry prediction of thoracic aortic disease. Nature Genetics, 2022, 54, 772-782.	9.4	29
140	Randomized Trial of Personal Genomics for Preventive Cardiology. Circulation: Cardiovascular Genetics, 2012, 5, 368-376.	5.1	28
141	Trans-ethnic fine mapping identifies a novel independent locus at the 3â€² end of CDKAL1 and novel variants of several susceptibility loci for type 2 diabetes in a Han Chinese population. Diabetologia, 2013, 56, 2619-2628.	2.9	27
142	Genetic variants primarily associated with type 2 diabetes are related to coronary artery disease risk. Atherosclerosis, 2015, 241, 419-426.	0.4	26
143	Breastfeeding Duration and the Risk of Coronary Artery Disease. Journal of Women's Health, 2019, 28, 30-36.	1.5	26
144	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. Scientific Reports, 2016, 6, 35278.	1.6	25

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145	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.	2.2	24
146	Genome-Wide Association Studies of Coronary Artery Disease: Recent Progress and Challenges Ahead. Current Atherosclerosis Reports, 2018, 20, 47.	2.0	24
147	Association Between Genetic Variation in Blood Pressure and Increased Lifetime Risk of Peripheral Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 2027-2034.	1.1	24
148	Alcohol use and cardiometabolic risk in the UK Biobank: A Mendelian randomization study. PLoS ONE, 2021, 16, e0255801.	1.1	24
149	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.	0.6	22
150	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.	2.7	20
151	Genetic Landscape of the ACE2 Coronavirus Receptor. Circulation, 2022, 145, 1398-1411.	1.6	20
152	Epigenome-wide association study of diet quality in the Womenâ€™s Health Initiative and TwinsUK cohort. International Journal of Epidemiology, 2021, 50, 675-684.	0.9	19
153	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. Nature Communications, 2021, 12, 3987.	5.8	18
154	Leukocyte Traits and Exposure to Ambient Particulate Matter Air Pollution in the Womenâ€™s Health Initiative and Atherosclerosis Risk in Communities Study. Environmental Health Perspectives, 2020, 128, 17004.	2.8	17
155	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.	1.5	17
156	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	5.8	17
157	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.	1.4	16
158	Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. Stroke, 2021, , STROKEAHA120031792.	1.0	16
159	Heritability of left ventricular mass in Japanese families living in Hawaii: the SAPPHIRe Study. Journal of Hypertension, 2007, 25, 985-992.	0.3	15
160	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, .	1.6	15
161	Cardioinformatics: the nexus of bioinformatics and precision cardiology. Briefings in Bioinformatics, 2020, 21, 2031-2051.	3.2	15
162	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.	1.6	15

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163	Validating a non-invasive, ALT-based non-alcoholic fatty liver phenotype in the million veteran program. PLoS ONE, 2020, 15, e0237430.	1.1	15
164	Multi-trait association studies discover pleiotropic loci between Alzheimerâ€™s disease and cardiometabolic traits. Alzheimer's Research and Therapy, 2021, 13, 34.	3.0	15
165	Mendelian Randomization Analysis of Hemostatic Factors and Their Contribution to Peripheral Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2020, 41, 380-386.	1.1	14
166	The Propagation of Racial Disparities in Cardiovascular Genomics Research. Circulation Genomic and Precision Medicine, 2021, 14, e003178.	1.6	14
167	Largeâ€Scale Plasma Protein Profiling of Incident Myocardial Infarction, Ischemic Stroke, and Heart Failure. Journal of the American Heart Association, 2021, 10, e023330.	1.6	14
168	Leveraging information from genetic risk scores of coronary atherosclerosis. Current Opinion in Lipidology, 2017, 28, 104-112.	1.2	13
169	Genomeâ€wide scan for circulating vascular adhesion proteinâ€1 levels: <scp>MACROD</scp>2 as a potential transcriptional regulator of adipogenesis. Journal of Diabetes Investigation, 2018, 9, 1067-1074.	1.1	13
170	Evaluation of 71 Coronary Artery Disease Risk Variants in a Multiethnic Cohort. Frontiers in Cardiovascular Medicine, 2018, 5, 19.	1.1	13
171	An â€œalmost exhaustiveâ€•searchâ€based sequential permutation method for detecting epistasis in disease association studies. Genetic Epidemiology, 2010, 34, 434-443.	0.6	12
172	Detecting Clinically Meaningful Biomarkers with Repeated Measurements: An Illustration with Electronic Health Records. Biometrics, 2015, 71, 478-486.	0.8	12
173	Gene by Environment Investigation of Incident Lung Cancer Risk in African-Americans. EBioMedicine, 2016, 4, 153-161.	2.7	12
174	A multi-population phenome-wide association study of genetically-predicted height in the Million Veteran Program. PLoS Genetics, 2022, 18, e1010193.	1.5	12
175	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	1.3	12
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