

Themistocles L Assimes

List of Articles by Year in descending order

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226

PR articles

39,724

PR citations

5394

78

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2485

193

g-index

236

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44058

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6517

81

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65697

citing authors

#	ARTICLE	IF	CITATIONS
1	Premorbid predictors of death at initial presentation of coronary heart disease in the Women's Health Initiative study. <i>American Journal of Preventive Cardiology</i> , 2025, 21, 100931.	2.8	1
2	Associations between accurate measures of adiposity and fitness, blood proteins, and insulin sensitivity among South Asians and Europeans. <i>Frontiers in Endocrinology</i> , 2025, 15, .	3.9	1
3	Unveiling the Genetic Landscape of Coronary Artery Disease Through Common and Rare Structural Variants. <i>Journal of the American Heart Association</i> , 2025, 14, .	4.0	3
4	Plasma proteomic signatures for type 2 diabetes and related traits in the UK Biobank cohort. <i>Diabetes Research and Clinical Practice</i> , 2025, 224, 112194.	5.9	2
5	Bidirectional associations of zinc supplement intake with biological ageing interacted by metabolic equivalent of task: A large-scale population-based Biobank study. <i>Clinical Nutrition</i> , 2025, 50, 1-9.	5.3	0
6	Diet Quality and Epigenetic Aging in the Women's Health Initiative. <i>Journal of the Academy of Nutrition and Dietetics</i> , 2024, 124, 1419-1430.e3.	1.5	17
7	Multi-Ancestry Polygenic Risk Score for Coronary Heart Disease Based on an Ancestrally Diverse Genome-Wide Association Study and Population-Specific Optimization. <i>Circulation Genomic and Precision Medicine</i> , 2024, 17, .	2.9	23
8	Identifying therapeutic targets for cancer among 2074 circulating proteins and risk of nine cancers. <i>Nature Communications</i> , 2024, 15, .	13.7	22
9	Mendelian randomization analyses clarify the effects of height on cardiovascular diseases. <i>PLoS ONE</i> , 2024, 19, e0298786.	2.3	0
10	Diversity and scale: Genetic architecture of 2068 traits in the VA Million Veteran Program. <i>Science</i> , 2024, 385, .	36.2	250
11	Rare variant contribution to the heritability of coronary artery disease. <i>Nature Communications</i> , 2024, 15, .	13.7	9
12	Genome-wide association analyses identify distinct genetic architectures for age-related macular degeneration across ancestries. <i>Nature Genetics</i> , 2024, 56, 2659-2671.	25.2	24
13	Genetic evidence for causal relationships between age at natural menopause and the risk of ageing-associated adverse health outcomes. <i>International Journal of Epidemiology</i> , 2023, 52, 806-816.	4.9	9
14	Plasma proteomic signatures of a direct measure of insulin sensitivity in two population cohorts. <i>Diabetologia</i> , 2023, 66, 1643-1654.	7.6	12
15	Contemporary Polygenic Scores of Low-Density Lipoprotein Cholesterol and Coronary Artery Disease Predict Coronary Atherosclerosis in Adolescents and Young Adults. <i>Circulation Genomic and Precision Medicine</i> , 2023, 16, 480-482.	2.9	3
16	A multi-ancestry polygenic risk score improves risk prediction for coronary artery disease. <i>Nature Medicine</i> , 2023, 29, 1793-1803.	33.0	200
17	Proteomic analysis of 92 circulating proteins and their effects in cardiometabolic diseases. <i>Clinical Proteomics</i> , 2023, 20, .	2.8	5
18	Assessing efficiency of fine-mapping obesity-associated variants through leveraging ancestry architecture and functional annotation using PAGE and UKBB cohorts. <i>Human Genetics</i> , 2023, 142, 1477-1489.	2.9	1

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19	Multi-ancestry genome-wide study identifies effector genes and druggable pathways for coronary artery calcification. <i>Nature Genetics</i> , 2023, 55, 1651-1664.	25.2	79
20	Genetic insights into resting heart rate and its role in cardiovascular disease. <i>Nature Communications</i> , 2023, 14, .	13.7	25
21	Plasma Protein Profiling of Incident Cardiovascular Diseases: A Multisample Evaluation. <i>Circulation Genomic and Precision Medicine</i> , 2023, 16, .	2.9	9
22	Whole-genome sequencing uncovers two loci for coronary artery calcification and identifies ARSE as a regulator of vascular calcification. <i>Nature Cardiovascular Research</i> , 2023, 2, 1159-1172.	8.4	17
23	Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. <i>Stroke</i> , 2022, 53, 875-885.	6.0	33
24	ZEB2 Shapes the Epigenetic Landscape of Atherosclerosis. <i>Circulation</i> , 2022, 145, 469-485.	18.1	66
25	APOL1 Risk Variants, Acute Kidney Injury, and Death in Participants With African Ancestry Hospitalized With COVID-19 From the Million Veteran Program. <i>JAMA Internal Medicine</i> , 2022, 182, 386.	10.5	57
26	Genetic Loci Associated With COVID-19 Positivity and Hospitalization in White, Black, and Hispanic Veterans of the VA Million Veteran Program. <i>Frontiers in Genetics</i> , 2022, 12, .	2.3	12
27	Multi-Trait Genome-Wide Association Study of Atherosclerosis Detects Novel Pleiotropic Loci. <i>Frontiers in Genetics</i> , 2022, 12, .	2.3	6
28	Coronary Artery Disease Risk of Familial Hypercholesterolemia Genetic Variants Independent of Clinically Observed Longitudinal Cholesterol Exposure. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, .	2.9	14
29	Rare coding variants in RCN3 are associated with blood pressure. <i>BMC Genomics</i> , 2022, 23, .	3.3	10
30	Interactions of physical activity, muscular fitness, adiposity, and genetic risk for NAFLD. <i>Hepatology Communications</i> , 2022, 6, 1516-1526.	4.5	13
31	Genetic Landscape of the ACE2 Coronavirus Receptor. <i>Circulation</i> , 2022, 145, 1398-1411.	18.1	34
32	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. <i>Science Advances</i> , 2022, 8, .	10.9	73
33	Gaseous air pollutants and DNA methylation in a methylome-wide association study of an ethnically and environmentally diverse population of U.S. adults. <i>Environmental Research</i> , 2022, 212, 113360.	7.8	15
34	Integration of rare expression outlier-associated variants improves polygenic risk prediction. <i>American Journal of Human Genetics</i> , 2022, 109, 1055-1064.	6.5	28
35	Genome-wide and phenome-wide analysis of ideal cardiovascular health in the VA Million Veteran Program. <i>PLoS ONE</i> , 2022, 17, e0267900.	2.3	6
36	High heritability of ascending aortic diameter and trans-ancestry prediction of thoracic aortic disease. <i>Nature Genetics</i> , 2022, 54, 772-782.	25.2	56

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37	A multiancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation. <i>Nature Genetics</i> , 2022, 54, 761-771.	25.2	169
38	A multi-population phenome-wide association study of genetically-predicted height in the Million Veteran Program. <i>PLoS Genetics</i> , 2022, 18, e1010193.	3.2	21
39	Genetic interactions drive heterogeneity in causal variant effect sizes for gene expression and complex traits. <i>American Journal of Human Genetics</i> , 2022, 109, 1286-1297.	6.5	66
40	Association of Kidney Comorbidities and Acute Kidney Failure With Unfavorable Outcomes After COVID-19 in Individuals With the Sickle Cell Trait. <i>JAMA Internal Medicine</i> , 2022, 182, 796.	10.5	20
41	Use of Polygenic Risk Scores for Coronary Heart Disease in Ancestrally Diverse Populations. <i>Current Cardiology Reports</i> , 2022, 24, 1169-1177.	2.9	20
42	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. <i>Hypertension</i> , 2022, 79, 1656-1667.	6.6	26
43	Race and Ethnicity Stratification for Polygenic Risk Score Analyses May Mask Disparities in Hispanics. <i>Circulation</i> , 2022, 146, 265-267.	18.1	22
44	Broad clinical manifestations of polygenic risk for coronary artery disease in the Women's Health Initiative. <i>Communications Medicine</i> , 2022, 2, .	4.5	5
45	Large-scale genome-wide association study of coronary artery disease in genetically diverse populations. <i>Nature Medicine</i> , 2022, 28, 1679-1692.	33.0	302
46	A translational genomics approach identifies IL10RB as the top candidate gene target for COVID-19 susceptibility. <i>Npj Genomic Medicine</i> , 2022, 7, .	4.3	15
47	Fibromuscular Dysplasia and Abdominal Aortic Aneurysms Are Dimorphic Sex-Specific Diseases With Shared Complex Genetic Architecture. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, .	2.9	15
48	Genomics and phenomics of body mass index reveals a complex disease network. <i>Nature Communications</i> , 2022, 13, .	13.7	122
49	Mendelian Randomization Analysis of Hemostatic Factors and Their Contribution to Peripheral Artery Disease—Brief Report. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021, 41, 380-386.	6.0	28
50	Epigenome-wide association study of diet quality in the Women's Health Initiative and TwinsUK cohort. <i>International Journal of Epidemiology</i> , 2021, 50, 675-684.	4.9	27
51	Genetics of 35 blood and urine biomarkers in the UK Biobank. <i>Nature Genetics</i> , 2021, 53, 185-194.	25.2	680
52	Multi-trait association studies discover pleiotropic loci between Alzheimer's disease and cardiometabolic traits. <i>Alzheimer's Research and Therapy</i> , 2021, 13, .	6.6	31
53	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. <i>Nature Communications</i> , 2021, 12, .	13.7	24
54	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. <i>Aging Cell</i> , 2021, 20, .	6.8	121

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55	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021, 12, .	13.7	32
56	Association Between Genetic Variation in Blood Pressure and Increased Lifetime Risk of Peripheral Artery Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021, 41, 2027-2034.	6.0	33
57	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. <i>Environmental Research</i> , 2021, 198, 111211.	7.8	7
58	DXA Versus Clinical Measures of Adiposity as Predictors of Cardiometabolic Diseases and All-Cause Mortality in Postmenopausal Women. <i>Mayo Clinic Proceedings</i> , 2021, 96, 2831-2842.	3.7	5
59	Alcohol use and cardiometabolic risk in the UK Biobank: A Mendelian randomization study. <i>PLoS ONE</i> , 2021, 16, e0255801.	2.3	44
60	The Propagation of Racial Disparities in Cardiovascular Genomics Research. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, .	2.9	26
61	A Missense Variant in the IL-6 Receptor and Protection From Peripheral Artery Disease. <i>Circulation Research</i> , 2021, 129, 968-970.	13.2	27
62	Genetics of Smoking and Risk of Atherosclerotic Cardiovascular Diseases. <i>JAMA Network Open</i> , 2021, 4, e2034461.	6.6	76
63	Large-scale Plasma Protein Profiling of Incident Myocardial Infarction, Ischemic Stroke, and Heart Failure. <i>Journal of the American Heart Association</i> , 2021, 10, .	4.0	30
64	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	37.9	845
65	Associations between DNA methylation and BMI vary by metabolic health status: a potential link to disparate cardiovascular outcomes. <i>Clinical Epigenetics</i> , 2021, 13, .	3.9	21
66	Leukocyte Traits and Exposure to Ambient Particulate Matter Air Pollution in the Women's Health Initiative and Atherosclerosis Risk in Communities Study. <i>Environmental Health Perspectives</i> , 2020, 128, .	8.4	22
67	Cardioinformatics: the nexus of bioinformatics and precision cardiology. <i>Briefings in Bioinformatics</i> , 2020, 21, 2031-2051.	6.6	20
68	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. <i>Circulation</i> , 2020, 142, 1633-1646.	18.1	132
69	Comprehensive Investigation of Circulating Biomarkers and Their Causal Role in Atherosclerosis-Related Risk Factors and Clinical Events. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, .	2.9	27
70	Chromosome 1q21.2 and additional loci influence risk of spontaneous coronary artery dissection and myocardial infarction. <i>Nature Communications</i> , 2020, 11, .	13.7	85
71	Genetic determinants of increased body mass index mediate the effect of smoking on increased risk for type 2 diabetes but not coronary artery disease. <i>Human Molecular Genetics</i> , 2020, 29, 3327-3337.	2.9	10
72	Validating a non-invasive, ALT-based non-alcoholic fatty liver phenotype in the million veteran program. <i>PLoS ONE</i> , 2020, 15, e0237430.	2.3	25

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73	Transcriptomic signatures across human tissues identify functional rare genetic variation. <i>Science</i> , 2020, 369, .	36.2	139
74	The relationship between circulating lipids and breast cancer risk: A Mendelian randomization study. <i>PLoS Medicine</i> , 2020, 17, e1003302.	8.1	105
75	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, .	2.9	10
76	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. <i>Nature Genetics</i> , 2020, 52, 680-691.	25.2	689
77	The Project Baseline Health Study: a step towards a broader mission to map human health. <i>Npj Digital Medicine</i> , 2020, 3, .	10.4	70
78	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study. <i>PLoS Genetics</i> , 2020, 16, e1008684.	3.2	32
79	Genotyping Array Design and Data Quality Control in the Million Veteran Program. <i>American Journal of Human Genetics</i> , 2020, 106, 535-548.	6.5	201
80	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. <i>International Journal of Epidemiology</i> , 2020, 49, 1022-1031.	4.9	46
81	Urinary Albumin, Sodium, and Potassium and Cardiovascular Outcomes in the UK Biobank. <i>Hypertension</i> , 2020, 75, 714-722.	6.6	46
82	PCSK9 loss of function is protective against extra-coronary atherosclerotic cardiovascular disease in a large multi-ethnic cohort. <i>PLoS ONE</i> , 2020, 15, e0239752.	2.3	16
83	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. <i>Circulation</i> , 2019, 140, 645-657.	18.1	201
84	Association of <i>APOL1</i> Risk Alleles With Cardiovascular Disease in Blacks in the Million Veteran Program. <i>Circulation</i> , 2019, 140, 1031-1040.	18.1	45
85	Genome-wide association study of peripheral artery disease in the Million Veteran Program. <i>Nature Medicine</i> , 2019, 25, 1274-1279.	33.0	280
86	Association Between Heart Failure and Postoperative Mortality Among Patients Undergoing Ambulatory Noncardiac Surgery. <i>JAMA Surgery</i> , 2019, 154, 907.	8.8	60
87	Genome-wide association analysis of venous thromboembolism identifies new risk loci and genetic overlap with arterial vascular disease. <i>Nature Genetics</i> , 2019, 51, 1574-1579.	25.2	222
88	Harmonizing Genetic Ancestry and Self-identified Race/Ethnicity in Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2019, 105, 763-772.	6.5	254
89	Leveraging linkage evidence to identify low-frequency and rare variants on 16p13 associated with blood pressure using TOPMed whole genome sequencing data. <i>Human Genetics</i> , 2019, 138, 199-210.	2.9	34
90	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. <i>Environment International</i> , 2019, 132, 104723.	10.2	78

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91	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. Nature Communications, 2019, 10, .	13.7	83
92	HeartBioPortal. Circulation Genomic and Precision Medicine, 2019, 12, .	2.9	8
93	Identification of 22 novel loci associated with urinary biomarkers of albumin, sodium, and potassium excretion. Kidney International, 2019, 95, 1197-1208.	5.3	43
94	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.	16.6	122
95	The role of epigenetic aging in education and racial/ethnic mortality disparities among older U.S. Women. Psychoneuroendocrinology, 2019, 104, 18-24.	2.7	67
96	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. Journal of the American College of Cardiology, 2019, 73, 58-66.	2.3	180
97	Breastfeeding Duration and the Risk of Coronary Artery Disease. Journal of Women's Health, 2019, 28, 30-36.	2.1	34
98	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.	1.8	23
99	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. Nature Communications, 2018, 9, .	13.7	187
100	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.	2.7	17
101	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.	6.9	103
102	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, .	2.9	20
103	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. Nature Genetics, 2018, 50, 1514-1523.	25.2	611
104	Evaluation of 71 Coronary Artery Disease Risk Variants in a Multiethnic Cohort. Frontiers in Cardiovascular Medicine, 2018, 5, .	2.5	19
105	Genome-Wide Association Studies of Coronary Artery Disease: Recent Progress and Challenges Ahead. Current Atherosclerosis Reports, 2018, 20, .	4.7	26
106	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.	2.9	20
107	Coffee consumption is associated with DNA methylation levels of human blood. European Journal of Human Genetics, 2017, 25, 608-616.	3.0	39
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.	2.9	36

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109	Leveraging information from genetic risk scores of coronary atherosclerosis. <i>Current Opinion in Lipidology</i> , 2017, 28, 104-112.	4.0	13
110	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. <i>Nature Genetics</i> , 2017, 49, 1113-1119.	25.2	306
111	Association analyses of East Asian individuals and trans-ancestry analyses with European individuals reveal new loci associated with cholesterol and triglyceride levels. <i>Human Molecular Genetics</i> , 2017, 26, 1770-1784.	2.9	154
112	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	25.2	543
113	Leveraging Multi-ethnic Evidence for Risk Assessment of Quantitative Traits in Minority Populations. <i>American Journal of Human Genetics</i> , 2017, 101, 218-226.	6.5	83
114	Association analyses based on false discovery rate implicate new loci for coronary artery disease. <i>Nature Genetics</i> , 2017, 49, 1385-1391.	25.2	679
115	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017, 101, 888-902.	6.5	198
116	Epigenetic Aging and Immune Senescence in Women With Insomnia Symptoms: Findings From the Women's Health Initiative Study. <i>Biological Psychiatry</i> , 2017, 81, 136-144.	5.4	148
117	Impact of a Genetic Risk Score for Coronary Artery Disease on Reducing Cardiovascular Risk: A Pilot Randomized Controlled Study. <i>Frontiers in Cardiovascular Medicine</i> , 2017, 4, .	2.5	53
118	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. <i>Nature Genetics</i> , 2017, 49, 1450-1457.	25.2	250
119	The associations of leptin, adiponectin and resistin with incident atrial fibrillation in women. <i>Heart</i> , 2016, 102, 1354-1362.	4.0	36
120	Genetics: Implications for Prevention and Management of Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2016, 68, 2797-2818.	2.3	104
121	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016, 17, .	8.1	317
122	An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. <i>Genome Biology</i> , 2016, 17, .	8.1	681
123	Integrative functional genomics identifies regulatory mechanisms at coronary artery disease loci. <i>Nature Communications</i> , 2016, 7, .	13.7	142
124	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016, 48, 1171-1184.	25.2	410
125	Menopause accelerates biological aging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9327-9332.	7.5	468
126	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. <i>Scientific Reports</i> , 2016, 6, .	3.4	30

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127	Genetic cardiovascular risk prediction: are we already there?. <i>European Heart Journal</i> , 2016, 37, 3279-3281.	2.2	6
128	Fine-mapping of lipid regions in global populations discovers ethnic-specific signals and refines previously identified lipid loci. <i>Human Molecular Genetics</i> , 2016, 25, 5500-5512.	2.9	32
129	Gene by Environment Investigation of Incident Lung Cancer Risk in African-Americans. <i>EBioMedicine</i> , 2016, 4, 153-161.	9.7	17
130	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. <i>Science</i> , 2016, 351, 1166-1171.	36.2	506
131	The glycolytic enzyme PKM2 bridges metabolic and inflammatory dysfunction in coronary artery disease. <i>Journal of Experimental Medicine</i> , 2016, 213, 337-354.	9.2	518
132	Lean body mass and risk of incident atrial fibrillation in post-menopausal women. <i>European Heart Journal</i> , 2016, 37, 1606-1613.	2.2	35
133	Genetics of Coronary Artery Disease in Taiwan: A Cardiometabochip Study by the Taichi Consortium. <i>PLoS ONE</i> , 2016, 11, e0138014.	2.3	36
134	Associations between a Genetic Risk Score for Clinical CAD and Early Stage Lesions in the Coronary Artery and the Aorta. <i>PLoS ONE</i> , 2016, 11, e0166994.	2.3	2
135	Detecting Clinically Meaningful Biomarkers with Repeated Measurements: An Illustration with Electronic Health Records. <i>Biometrics</i> , 2015, 71, 478-486.	1.6	13
136	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	3.2	393
137	Effect of Common Genetic Variants of Growth Arrest-Specific 6 Gene on Insulin Resistance, Obesity and Type 2 Diabetes in an Asian Population. <i>PLoS ONE</i> , 2015, 10, e0135681.	2.3	8
138	Identification and validation of N-acetyltransferase 2 as an insulin sensitivity gene. <i>Journal of Clinical Investigation</i> , 2015, 125, 1739-1751.	10.6	111
139	Systems Genetics Analysis of Genome-Wide Association Study Reveals Novel Associations Between Key Biological Processes and Coronary Artery Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 1712-1722.	6.0	79
140	Leukocyte Telomere Length and Risks of Incident Coronary Heart Disease and Mortality in a Racially Diverse Population of Postmenopausal Women. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 2225-2231.	6.0	58
141	Dissecting the Roles of MicroRNAs in Coronary Heart Disease via Integrative Genomic Analyses. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 1011-1021.	6.0	56
142	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	37.9	1,561
143	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	37.9	4,431
144	Genetic variants primarily associated with type 2 diabetes are related to coronary artery disease risk. <i>Atherosclerosis</i> , 2015, 241, 419-426.	1.5	28

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145	Characterization of TCF21 Downstream Target Regions Identifies a Transcriptional Network Linking Multiple Independent Coronary Artery Disease Loci. <i>PLoS Genetics</i> , 2015, 11, e1005202.	3.2	44
146	Genetically Determined Height and Coronary Artery Disease. <i>New England Journal of Medicine</i> , 2015, 372, 1608-1618.	34.6	244
147	Susceptibility Loci for Clinical Coronary Artery Disease and Subclinical Coronary Atherosclerosis Throughout the Life-Course. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 803-811.	3.8	36
148	A comprehensive 1000 Genomesâ€‘based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015, 47, 1121-1130.	25.2	2,461
149	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. <i>Diabetes</i> , 2014, 63, 2158-2171.	4.2	333
150	Multiple Nonglycemic Genomic Loci Are Newly Associated With Blood Level of Glycated Hemoglobin in East Asians. <i>Diabetes</i> , 2014, 63, 2551-2562.	4.2	65
151	The combination of 9p21.3 genotype and biomarker profile improves a peripheral artery disease risk prediction model. <i>Vascular Medicine</i> , 2014, 19, 3-8.	2.4	8
152	Obesity, Physical Activity, and Their Interaction in Incident Atrial Fibrillation in Postmenopausal Women. <i>Journal of the American Heart Association</i> , 2014, 3, .	4.0	98
153	Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. <i>Human Molecular Genetics</i> , 2014, 23, 5492-5504.	2.9	209
154	Simple, standardized incorporation of genetic risk into non-genetic risk prediction tools for complex traits: coronary heart disease as an example. <i>Frontiers in Genetics</i> , 2014, 5, .	2.3	47
155	Integrative Genomics Reveals Novel Molecular Pathways and Gene Networks for Coronary Artery Disease. <i>PLoS Genetics</i> , 2014, 10, e1004502.	3.2	199
156	Coronary Heart Disease-Associated Variation in TCF21 Disrupts a miR-224 Binding Site and miRNA-Mediated Regulation. <i>PLoS Genetics</i> , 2014, 10, e1004263.	3.2	114
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