Christopher J O'donnell

List of Publications by Year
in descending order

208	58,158	2538 96	1974 206
papers	citations	h-index	g-index

209	209	209	62849
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	2013 ACC/AHA Guideline on the Assessment ofÂCardiovascular Risk. Journal of the American College of Cardiology, 2014, 63, 2935-2959.	1.2	3,277
2	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
3	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
4	Metabolite profiles and the risk of developing diabetes. Nature Medicine, 2011, 17, 448-453.	15.2	2,586
5	Abdominal Visceral and Subcutaneous Adipose Tissue Compartments. Circulation, 2007, 116, 39-48.	1.6	2,349
6	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	9.4	2,054
7	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	6.3	1,937
8	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	13.7	1,855
9	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
10	Impact of High-Normal Blood Pressure on the Risk of Cardiovascular Disease. New England Journal of Medicine, 2001, 345, 1291-1297.	13.9	1,729
11	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Nature Genetics, 2011, 43, 333-338.	9.4	1,685
12	Common variants at 30 loci contribute to polygenic dyslipidemia. Nature Genetics, 2009, 41, 56-65.	9.4	1,234
13	Genome-wide association study of blood pressure and hypertension. Nature Genetics, 2009, 41, 677-687.	9.4	1,224
14	SNAP: a web-based tool for identification and annotation of proxy SNPs using HapMap. Bioinformatics, 2008, 24, 2938-2939.	1.8	1,201
15	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	9.4	1,104
16	Criteria for Evaluation of Novel Markers of Cardiovascular Risk. Circulation, 2009, 119, 2408-2416.	1.6	998
17	Genome-wide association of early-onset myocardial infarction with single nucleotide polymorphisms and copy number variants. Nature Genetics, 2009, 41, 334-341.	9.4	990
18	Loss-of-Function Mutations inAPOC3,Triglycerides, and Coronary Disease. New England Journal of Medicine, 2014, 371, 22-31.	13.9	936

#	Article	IF	Citations
19	Pericardial Fat, Visceral Abdominal Fat, Cardiovascular Disease Risk Factors, and Vascular Calcification in a Community-Based Sample. Circulation, 2008, 117, 605-613.	1.6	896
20	Genome-Wide Association Analysis Identifies Variants Associated with Nonalcoholic Fatty Liver Disease That Have Distinct Effects on Metabolic Traits. PLoS Genetics, 2011, 7, e1001324.	1.5	796
21	The Third Generation Cohort of the National Heart, Lung, and Blood Institute's Framingham Heart Study: Design, Recruitment, and Initial Examination. American Journal of Epidemiology, 2007, 165, 1328-1335.	1.6	752
22	Interleukin-6 receptor pathways in coronary heart disease: a collaborative meta-analysis of 82 studies. Lancet, The, 2012, 379, 1205-1213.	6.3	668
23	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	13.7	581
24	Association of pericardial fat, intrathoracic fat, and visceral abdominal fat with cardiovascular disease burden: the Framingham Heart Study. European Heart Journal, 2008, 30, 850-856.	1.0	526
25	Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. Circulation: Cardiovascular Genetics, 2009, 2, 73-80.	5.1	519
26	Metabolite Profiling Identifies Pathways Associated With Metabolic Risk in Humans. Circulation, 2012, 125, 2222-2231.	1.6	514
27	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	9.4	501
28	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. Nature Genetics, 2018, 50, 1514-1523.	9.4	497
29	A genome-wide meta-analysis identifies 22 loci associated with eight hematological parameters in the HaemGen consortium. Nature Genetics, 2009, 41, 1182-1190.	9.4	481
30	New susceptibility locus for coronary artery disease on chromosome 3q22.3. Nature Genetics, 2009, 41, 280-282.	9.4	440
31	Adiposity, Cardiometabolic Risk, and Vitamin D Status: The Framingham Heart Study. Diabetes, 2010, 59, 242-248.	0.3	437
32	Excess of rare variants in genes identified by genome-wide association study of hypertriglyceridemia. Nature Genetics, 2010, 42, 684-687.	9.4	414
33	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	9.4	403
34	2-Aminoadipic acid is a biomarker for diabetes risk. Journal of Clinical Investigation, 2013, 123, 4309-4317.	3.9	397
35	Inactivating Mutations in NPC1L1 and Protection from Coronary Heart Disease. New England Journal of Medicine, 2014, 371, 2072-2082.	13.9	386
36	Pericardial Fat Is Associated With Prevalent Atrial Fibrillation. Circulation: Arrhythmia and Electrophysiology, 2010, 3, 345-350.	2.1	364

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37	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
38	Fatty liver is associated with dyslipidemia and dysglycemia independent of visceral fat: The Framingham heart study. Hepatology, 2010, 51, 1979-1987.	3.6	337
39	Neck Circumference as a Novel Measure of Cardiometabolic Risk: The Framingham Heart Study. Journal of Clinical Endocrinology and Metabolism, 2010, 95, 3701-3710.	1.8	337
40	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	9.4	328
41	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. Nature Genetics, 2009, 41, 1191-1198.	9.4	324
42	Abdominal Subcutaneous and Visceral Adipose Tissue and Insulin Resistance in the Framingham Heart Study. Obesity, 2010, 18, 2191-2198.	1.5	324
43	Actionable exomic incidental findings in 6503 participants: challenges of variant classification. Genome Research, 2015, 25, 305-315.	2.4	313
44	Shared Genetic Susceptibility to Ischemic Stroke and Coronary Artery Disease. Stroke, 2014, 45, 24-36.	1.0	302
45	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. American Journal of Human Genetics, 2014, 94, 223-232.	2.6	287
46	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
47	A Genome-wide Association Study of the Human Metabolome in a Community-Based Cohort. Cell Metabolism, 2013, 18, 130-143.	7.2	274
48	Genome-Wide Association Study for Coronary Artery Calcification With Follow-Up in Myocardial Infarction. Circulation, 2011, 124, 2855-2864.	1.6	269
49	Genomics of Cardiovascular Disease. New England Journal of Medicine, 2011, 365, 2098-2109.	13.9	248
50	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
51	NRXN3 Is a Novel Locus for Waist Circumference: A Genome-Wide Association Study from the CHARGE Consortium. PLoS Genetics, 2009, 5, e1000539.	1.5	230
52	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	9.4	223
53	Pericardial Fat, Intrathoracic Fat, and Measures of Left Ventricular Structure and Function. Circulation, 2009, 119, 1586-1591.	1.6	220
54	Genetically Determined Height and Coronary Artery Disease. New England Journal of Medicine, 2015, 372, 1608-1618.	13.9	220

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55	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. Nature Communications, 2014, 5, 5068.	5.8	216
56	A Genetic Risk Score Is Associated With Incident Cardiovascular Disease and Coronary Artery Calcium. Circulation: Cardiovascular Genetics, 2012, 5, 113-121.	5.1	196
57	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
58	Integrative Genomics Reveals Novel Molecular Pathways and Gene Networks for Coronary Artery Disease. PLoS Genetics, 2014, 10, e1004502.	1.5	192
59	Meta-analysis of genome-wide association studies from the CHARGE consortium identifies common variants associated with carotid intima media thickness and plaque. Nature Genetics, 2011, 43, 940-947.	9.4	191
60	Visceral fat is associated with lower brain volume in healthy middleâ€aged adults. Annals of Neurology, 2010, 68, 136-144.	2.8	189
61	Association of Low-Density Lipoprotein Cholesterolâ€“Related Genetic Variants With Aortic Valve Calcium and Incident Aortic Stenosis. JAMA - Journal of the American Medical Association, 2014, 312, 1764.	3.8	184
62	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. PLoS Genetics, 2012, 8, e1002490.	1.5	181
63	Genome-wide association study of peripheral artery disease in the Million Veteran Program. Nature Medicine, 2019, 25, 1274-1279.	15.2	177
64	Association of Genome-Wide Variation With the Risk of Incident Heart Failure in Adults of European and African Ancestry. Circulation: Cardiovascular Genetics, 2010, 3, 256-266.	5.1	176
65	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	5.8	173
66	Peri-aortic fat, cardiovascular disease risk factors, and aortic calcification: The Framingham Heart Study. Atherosclerosis, 2010, 210, 656-661.	0.4	170
67	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
68	Hepatic steatosis and cardiovascular disease outcomes: An analysis of the Framingham Heart Study. Journal of Hepatology, 2015, 63, 470-476.	1.8	165
69	Design of the Coronary ARtery DIsease Genome-Wide Replication And Meta-Analysis (CARDIoGRAM) Study. Circulation: Cardiovascular Genetics, 2010, 3, 475-483.	5.1	159
70	A Systems Biology Framework Identifies Molecular Underpinnings of Coronary Heart Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 1427-1434.	1.1	157
71	Distribution, Determinants, and Normal Reference Values of Thoracic and Abdominal Aortic Diameters by Computed Tomography (from the Framingham Heart Study). American Journal of Cardiology, 2013, 111, 1510-1516.	0.7	154
72	Patterns of Abdominal Fat Distribution. Diabetes Care, 2009, 32, 481-485.	4.3	152

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73	Integrated genome-wide analysis of expression quantitative trait loci aids interpretation of genomic association studies. Genome Biology, 2017, 18, 16.	3.8	151
74	Cardiovascular Event Prediction and Risk Reclassification by Coronary, Aortic, and Valvular Calcification in the Framingham Heart Study. Journal of the American Heart Association, 2016, 5, .	1.6	150
75	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
76	Low Cardiac Index Is Associated With Incident Dementia and Alzheimer Disease. Circulation, 2015, 131, 1333-1339.	1.6	140
77	Causal Assessment of Serum Urate Levels inÂCardiometabolic Diseases Through a Mendelian Randomization Study. Journal of the American College of Cardiology, 2016, 67, 407-416.	1.2	138
78	Genome-wide identification of microRNA expression quantitative trait loci. Nature Communications, 2015, 6, 6601.	5.8	134
79	Mendelian Randomization. JAMA - Journal of the American Medical Association, 2009, 301, 2386.	3.8	133
80	Genome-wide association analysis identifies multiple loci related to resting heart rate. Human Molecular Genetics, 2010, 19, 3885-3894.	1.4	133
81	Genome-Wide Association Study of White Blood Cell Count in 16,388 African Americans: the Continental Origins and Genetic Epidemiology Network (COGENT). PLoS Genetics, 2011, 7, e1002108.	1.5	133
82	Whole-genome sequenceâ€“based analysis of high-density lipoprotein cholesterol. Nature Genetics, 2013, 45, 899-901.	9.4	132
83	Induced Pluripotent Stem Cell Differentiation Enables Functional Validation of GWAS Variants in Metabolic Disease. Cell Stem Cell, 2017, 20, 547-557.e7.	5.2	129
84	Multiethnic Meta-Analysis of Genome-Wide Association Studies in >100 000 Subjects Identifies 23 Fibrinogen-Associated Loci but No Strong Evidence of a Causal Association Between Circulating Fibrinogen and Cardiovascular Disease. Circulation, 2013, 128, 1310-1324.	1.6	128
85	Prescription Fill Patterns for Commonly Used Drugs During the COVID-19 Pandemic in the United States. JAMA - Journal of the American Medical Association, 2020, 323, 2524.	3.8	121
86	Distinct metabolomic signatures are associated with longevity in humans. Nature Communications, 2015, 6, 6791.	5.8	120
87	Whole- and refined-grain intakes are differentially associated with abdominal visceral and subcutaneous adiposity in healthy adults: the Framingham Heart Study. American Journal of Clinical Nutrition, 2010, 92, 1165-1171.	2.2	119
88	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	5.8	119
89	Guideline-Based Statin Eligibility, Coronary Artery Calcification, and Cardiovascular Events. JAMA - Journal of the American Medical Association, 2015, 314, 134.	3.8	118
90	Genotyping Array Design and Data Quality Control in the Million Veteran Program. American Journal of Human Genetics, 2020, 106, 535-548.	2.6	118

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91	Cardiovascular Risk Factors. Insights From Framingham Heart Study. Revista Espanola De Cardiologia (English Ed), 2008, 61, 299-310.	0.4	112
92	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	0.5	107
93	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. PLoS Genetics, 2015, 11, e1005035.	1.5	107
94	Prevalence and Prognostic Implications of Coronary Artery Calcification in Low-Risk Women. JAMA - Journal of the American Medical Association, 2016, 316, 2126.	3.8	107
95	Multiple Loci Are Associated with White Blood Cell Phenotypes. PLoS Genetics, 2011, 7, e1002113.	1.5	106
96	Gene Expression Signatures of Coronary Heart Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 1418-1426.	1.1	105
97	Integrative network analysis reveals molecular mechanisms of blood pressure regulation. Molecular Systems Biology, 2015, 11, 799.	3.2	102
98	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. Circulation, 2019, 139, 620-635.	1.6	102
99	Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. Nature, 2020, 586, 769-775.	13.7	101
100	Common genetic variation at the IL1RL1 locus regulates IL-33/ST2 signaling. Journal of Clinical Investigation, 2013, 123, 4208-4218.	3.9	101
101	Genetics and Genomics for the Prevention and Treatment of Cardiovascular Disease: Update. Circulation, 2013, 128, 2813-2851.	1.6	100
102	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
103	Association of Lifestyle Factors With Abdominal Subcutaneous and Visceral Adiposity. Diabetes Care, 2009, 32, 505-510.	4.3	96
104	Rural-Urban Differences in Cardiovascular Mortality in the US, 1999-2017. JAMA - Journal of the American Medical Association, 2020, 323, 1852.	3.8	94
105	HDAC9 is implicated in atherosclerotic aortic calcification and affects vascular smooth muscle cell phenotype. Nature Genetics, 2019, 51, 1580-1587.	9.4	92
106	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. Blood, 2012, 120, 4873-4881.	0.6	90
107	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	1.6	89
108	An Increased Burden of Common and Rare Lipid-Associated Risk Alleles Contributes to the Phenotypic Spectrum of Hypertriglyceridemia. Arteriosclerosis, Thrombosis, and Vascular Biology, 2011, 31, 1916-1926.	1.1	84

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109	Periaortic Fat Deposition Is Associated With Peripheral Arterial Disease. Circulation: Cardiovascular Imaging, 2010, 3, 515-519.	1.3	83
110	Genetic association analysis highlights new loci that modulate hematological trait variation in Caucasians and African Americans. Human Genetics, 2011, 129, 307-317.	1.8	81
111	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. Circulation, 2020, 142, 1633-1646.	1.6	78
112	Genetics of coronary artery calcification among African Americans, a meta-analysis. BMC Medical Genetics, 2013, 14, 75.	2.1	73
113	Prevalence, Distribution, and Risk Factor Correlates of High Pericardial and Intrathoracic Fat Depots in the Framingham Heart Study. Circulation: Cardiovascular Imaging, 2010, 3, 559-566.	1.3	71
114	Cross-Sectional Relations of Arterial Stiffness, Pressure Pulsatility, Wave Reflection, and Arterial Calcification. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 2495-2500.	1.1	70
115	An exome array study of the plasma metabolome. Nature Communications, 2016, 7, 12360.	5.8	69
116	High-throughput multimodal automated phenotyping (MAP) with application to PheWAS. Journal of the American Medical Informatics Association: JAMIA, 2019, 26, 1255-1262.	2.2	69
117	Pericardial Fat Volume Correlates With Inflammatory Markers: The Framingham Heart Study. Obesity, 2010, 18, 1039-1045.	1.5	68
118	Cross-Sectional Associations Bet ween Abdominal and Thoracic Adipose Tissue Compartments and Adiponectin and Resistin in the Framingham Heart Study. Diabetes Care, 2009, 32, 903-908.	4.3	66
119	Integromic Analysis of Genetic Variation and Gene Expression Identifies Networks for Cardiovascular Disease Phenotypes. Circulation, 2015, 131, 536-549.	1.6	65
120	PRIMe: a method for characterization and evaluation of pleiotropic regions from multiple genome-wide association studies. Bioinformatics, 2011, 27, 1201-1206.	1.8	63
121	Predicting Stroke Through Genetic Risk Functions. Stroke, 2014, 45, 403-412.	1.0	62
122	Genetic analysis for a shared biological basis between migraine and coronary artery disease. Neurology: Genetics, 2015, 1, e10.	0.9	61
123	Posttraumatic Stress Disorder and Cardiovascular Disease. JAMA Cardiology, 2021, 6, 1207.	3.0	61
124	Genetic Predictors of Fibrin D-Dimer Levels in Healthy Adults. Circulation, 2011, 123, 1864-1872.	1.6	60
125	Periaortic Adipose Tissue and Aortic Dimensions in the Framingham Heart Study. Journal of the American Heart Association, 2012, 1, e000885.	1.6	60
126	Chromosome 1q21.2 and additional loci influence risk of spontaneous coronary artery dissection and myocardial infarction. Nature Communications, 2020, 11, 4432.	5.8	60

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127	Visceral and Subcutaneous Adiposity and Brachial Artery Vasodilator Function. Obesity, 2009, 17, 2054-2059.	1.5	59
128	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. European Heart Journal, 2018, 39, 3961-3969.	1.0	59
129	Resequencing and Clinical Associations of the 9p21.3 Region. Circulation, 2013, 127, 799-810.	1.6	58
130	Cholesteryl ester transfer protein (CETP) as a drug target for cardiovascular disease. Nature Communications, 2021, 12, 5640.	5.8	57
131	Association of Visceral and Subcutaneous Adiposity with Kidney Function. Clinical Journal of the American Society of Nephrology: CJASN, 2008, 3, 1786-1791.	2.2	56
132	Association of Fat Density With Subclinical Atherosclerosis. Journal of the American Heart Association, 2014, 3, .	1.6	55
133	Astronaut Cardiovascular Health and Risk Modification (Astro-CHARM) Coronary Calcium Atherosclerotic Cardiovascular Disease Risk Calculator. Circulation, 2018, 138, 1819-1827.	1.6	54
134	Cross-classification of JNC VI Blood Pressure Stages and Risk Groups in the Framingham Heart Study. Archives of Internal Medicine, 1999, 159, 2206.	4.3	53
135	Phosphodiesterase 1 regulation is a key mechanism in vascular aging. Clinical Science, 2015, 129, 1061-1075.	1.8	53
136	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
137	Genetic analysis in European ancestry individuals identifies 517 loci associated with liver enzymes. Nature Communications, 2021, 12, 2579.	5.8	51
138	Relation of Subcutaneous and Visceral Adipose Tissue to Coronary and Abdominal Aortic Calcium (from the Framingham Heart Study). American Journal of Cardiology, 2009, 104, 543-547.	0.7	49
139	Genetic associations with expression for genes implicated in GWAS studies for atherosclerotic cardiovascular disease and blood phenotypes. Human Molecular Genetics, 2014, 23, 782-795.	1.4	49
140	Synthesis of 53 tissue and cell line expression QTL datasets reveals master eQTLs. BMC Genomics, 2014, 15, 532.	1.2	49
141	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	5.8	49
142	Relation of Visceral Adiposity to Circulating Natriuretic Peptides in Ambulatory Individuals. American Journal of Cardiology, 2011, 108, 979-984.	0.7	48
143	Identification of the BCAR1-CFDP1-TMEM170A Locus as a Determinant of Carotid Intima-Media Thickness and Coronary Artery Disease Risk. Circulation: Cardiovascular Genetics, 2012, 5, 656-665.	5.1	47
144	Serum Sortilin Associates With Aortic Calcification and Cardiovascular Risk in Men. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 1005-1011.	1.1	44

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145	Future Translational Applications From the Contemporary Genomics Era. Circulation, 2015, 131, 1715-1736.	1.6	38
146	Association of Maternal Prepregnancy Dyslipidemia With Adult Offspring Dyslipidemia in Excess of Anthropometric, Lifestyle, and Genetic Factors in the Framingham Heart Study. JAMA Cardiology, 2016, 1, 26.	3.0	38
147	Association of genomic loci from a cardiovascular gene SNP array with fibrinogen levels in European Americans and African-Americans from six cohort studies: the Candidate Gene Association Resource (CARe). Blood, 2011, 117, 268-275.	0.6	36
148	Relations of Long-Term and Contemporary Lipid Levels and Lipid Genetic Risk Scores With Coronary Artery Calcium in the Framingham Heart Study. Journal of the American College of Cardiology, 2012, 60, 2364-2371.	1.2	36
149	A systematic heritability analysis of the human whole blood transcriptome. Human Genetics, 2015, 134, 343-358.	1.8	35
150	Development of the Initial Surveys for the All of Us Research Program. Epidemiology, 2019, 30, 597-608.	1.2	35
151	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. Blood, 2019, 133, 967-977.	0.6	34
152	Association of FADS1/2 Locus Variants and Polyunsaturated Fatty Acids With Aortic Stenosis. JAMA Cardiology, 2020, 5, 694.	3.0	32
153	Overlap Between Common Genetic Polymorphisms Underpinning Kidney Traits and Cardiovascular Disease Phenotypes: The CKDGen Consortium. American Journal of Kidney Diseases, 2013, 61, 889-898.	2.1	31
154	Variants in the CNR1 and the FAAH Genes and Adiposity Traits in the Community. Obesity, 2009, 17, 755-760.	1.5	29
155	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. PLoS ONE, 2017, 12, e0167742.	1.1	29
156	Meta-analysis of genome-wide association studies of HDL cholesterol response to statins. Journal of Medical Genetics, 2016, 53, 835-845.	1.5	28
157	Maintenance of Ideal Cardiovascular Health and Coronary Artery Calcium Progression in Low-Risk Men and Women in the Framingham Heart Study. Circulation: Cardiovascular Imaging, 2018, 11, e006209.	1.3	28
158	Increased Aortic Diameters on Multidetector Computed Tomographic Scan Are Independent Predictors of Incident Adverse Cardiovascular Events. Circulation: Cardiovascular Imaging, 2017, 10, .	1.3	27
159	Genetic loci associated with ideal cardiovascular health: A meta-analysis of genome-wide association studies. American Heart Journal, 2016, 175, 112-120.	1.2	25
160	Association of Triglyceride-Related Genetic Variants With MitralÂAnnularÂCalcification. Journal of the American College of Cardiology, 2017, 69, 2941-2948.	1.2	25
161	Association of Genome-Wide Variation With Highly Sensitive Cardiac Troponin-T Levels in European Americans and Blacks. Circulation: Cardiovascular Genetics, 2013, 6, 82-88.	5.1	24
162	Novel Thrombotic Function of a Human SNP in STXBP5 Revealed by CRISPR/Cas9 Gene Editing in Mice. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 264-270.	1.1	24

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163	Consent for genetic research in the Framingham Heart Study. American Journal of Medical Genetics, Part A, 2010, 152A, 1250-1256.	0.7	23
164	Genome-Wide Association Study of Retinopathy in Individuals without Diabetes. PLoS ONE, 2013, 8, e54232.	1.1	22
165	Guideline-Based Statin Eligibility, Cancer Events, and Noncardiovascular Mortality in the Framingham Heart Study. Journal of Clinical Oncology, 2017, 35, 2927-2933.	0.8	22
166	Radiomics of Coronary Artery Calcium in the Framingham Heart Study. Radiology: Cardiothoracic Imaging, 2020, 2, e190119.	0.9	22
167	Metabolite Signatures of Metabolic Risk Factors and their Longitudinal Changes. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 1779-1789.	1.8	20
168	Genotype-driven identification of a molecular network predictive of advanced coronary calcium in ClinSeqÂ® and Framingham Heart Study cohorts. BMC Systems Biology, 2017, 11, 99.	3.0	20
169	Allele-specific variation atAPOEincreases nonalcoholic fatty liver disease and obesity but decreases risk of Alzheimerâ€™s disease and myocardial infarction. Human Molecular Genetics, 2021, 30, 1443-1456.	1.4	20
170	A gene-centric association scan for Coagulation Factor VII levels in European and African Americans: the Candidate Gene Association Resource (CARe) Consortium. Human Molecular Genetics, 2011, 20, 3525-3534.	1.4	19
171	Association of Multiorgan Computed Tomographic Phenomap With Adverse Cardiovascular Health Outcomes. JAMA Cardiology, 2017, 2, 1236.	3.0	19
172	Plasma Protein Profile of Carotid Artery Atherosclerosis and Atherosclerotic Outcomes. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 1777-1788.	1.1	18
173	Genetic and Clinical Correlates of Early-Outgrowth Colony-Forming Units. Circulation: Cardiovascular Genetics, 2011, 4, 296-304.	5.1	17
174	Using Family-Based Imputation in Genome-Wide Association Studies with Large Complex Pedigrees: The Framingham Heart Study. PLoS ONE, 2012, 7, e51589.	1.1	17
175	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. PLoS ONE, 2019, 14, e0216222.	1.1	17
176	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
177	Phenome-wide association of 1809 phenotypes and COVID-19 disease progression in the Veterans Health Administration Million Veteran Program. PLoS ONE, 2021, 16, e0251651.	1.1	17
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