Sekar Kathiresan

List of Publications by Year in Descending Order

168 papers	36,635 citations	75 h-index	177 g-index
177 ext. papers	49,028 ext. citations	21 avg, IF	6.58 L-index

#	Paper	IF	Citations
168	Association of Habitual Alcohol Intake With Risk of Cardiovascular Disease.. *JAMA Network Open*, **2022**, 5, e223849	10.4	10
167	Transethnic Transferability of a Genome-Wide Polygenic Score for Coronary Artery Disease. *Circulation Genomic and Precision Medicine*, **2021**, 14, e003092	5.2	5
166	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
165	Integrative analysis of the plasma proteome and polygenic risk of cardiometabolic diseases. *Nature Metabolism*, **2021**, 3, 1476-1483	14.6	6
164	Lp(a) (Lipoprotein[a]) Concentrations and Incident Atherosclerotic Cardiovascular Disease: New Insights From a Large National Biobank. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2021**, 41, 465-474	8.4	32
163	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. *Nature Communications*, **2021**, 12, 2182	17.4	5
162	In vivo CRISPR base editing of PCSK9 durably lowers cholesterol in primates. *Nature*, **2021**, 593, 429-434	50.4	96
161	Randomized prospective evaluation of genome sequencing versus standard-of-care as a first molecular diagnostic test. *Genetics in Medicine*, **2021**, 23, 1689-1696	8.1	3
160	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. *Aging Cell*, **2021**, 20, e13366	9.9	9
159	Association of Genetic Variation With Cirrhosis: A Multi-Trait Genome-Wide Association and Gene-Environment Interaction Study. *Gastroenterology*, **2021**, 160, 1620-1633.e13	13.3	20
158	Coronary Disease Association With ADAMTS7 Is Due to Protease Activity. *Circulation Research*, **2021**, 129, 458-470	15.7	6
157	Rare, Damaging DNA Variants in and Risk of Coronary Artery Disease: Insights From Functional Genomics and Large-Scale Sequencing Analyses. *Circulation Genomic and Precision Medicine*, **2021**, 14, e003399	5.2	2
156	Analysis of cardiac magnetic resonance imaging in 36,000 individuals yields genetic insights into dilated cardiomyopathy. *Nature Communications*, **2020**, 11, 2254	17.4	40
155	Limitations of Contemporary Guidelines for Managing Patients at High Genetic Risk of Coronary Artery Disease. *Journal of the American College of Cardiology*, **2020**, 75, 2769-2780	15.1	33
154	Association of Rare Pathogenic DNA Variants for Familial Hypercholesterolemia, Hereditary Breast and Ovarian Cancer Syndrome, and Lynch Syndrome With Disease Risk in Adults According to Family History. *JAMA Network Open*, **2020**, 3, e203959	10.4	31
153	EDEM3 Modulates Plasma Triglyceride Level through Its Regulation of LRP1 Expression. *IScience*, **2020**, 23, 100973	6.1	4
152	Non-parametric Polygenic Risk Prediction via Partitioned GWAS Summary Statistics. *American Journal of Human Genetics*, **2020**, 107, 46-59	11	16

151	The mutational constraint spectrum quantified from variation in 141,456 humans. *Nature*, **2020**, 581, 434-443	50.4	2278
150	A structural variation reference for medical and population genetics. *Nature*, **2020**, 581, 444-451	50.4	223
149	Genetically Elevated LDL Associates with Lower Risk of Intracerebral Hemorrhage. *Annals of Neurology*, **2020**, 88, 56-66	9.4	12
148	Rare variants lowering the levels of coagulation factor X are protective against ischemic heart disease. *Haematologica*, **2020**, 105, e365-e369	6.6	7
147	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. *PLoS Genetics*, **2020**, 16, e1008629	6	49
146	Genetic Interleukin 6 Signaling Deficiency Attenuates Cardiovascular Risk in Clonal Hematopoiesis. *Circulation*, **2020**, 141, 124-131	16.7	120
145	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. *Circulation*, **2020**, 142, 1633-1646	16.7	24
144	Validation of a Genome-Wide Polygenic Score for Coronary Artery Disease in South Asians. *Journal of the American College of Cardiology*, **2020**, 76, 703-714	15.1	22
143	Interactomics Analyses of Wild-Type and Mutant A1CF Reveal Diverged Functions in Regulating Cellular Lipid Metabolism. *Journal of Proteome Research*, **2020**, 19, 3968-3980	5.6	
142	Mendelian Randomization Study of ACLY and Cardiovascular Disease. *New England Journal of Medicine*, **2020**, 383, e50	59.2	4
141	Heterozygous Gene Deficiency and Risk of Coronary Artery Disease. *Circulation Genomic and Precision Medicine*, **2020**, 13, 417-423	5.2	21
140	Genome-Wide Polygenic Score, Clinical Risk Factors, and Long-Term Trajectories of Coronary Artery Disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2020**, 40, 2738-2746	9.4	24
139	Polygenic background modifies penetrance of monogenic variants for tier 1 genomic conditions. *Nature Communications*, **2020**, 11, 3635	17.4	88
138	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. *Nature Communications*, **2020**, 11, 6417	17.4	17
137	Whole-Genome Sequencing to Characterize Monogenic and Polygenic Contributions in Patients Hospitalized With Early-Onset Myocardial Infarction. *Circulation*, **2019**, 139, 1593-1602	16.7	112
136	Single-Cell Analysis of the Normal Mouse Aorta Reveals Functionally Distinct Endothelial Cell Populations. *Circulation*, **2019**, 140, 147-163	16.7	104
135	Rare Protein-Truncating Variants in APOB, Lower Low-Density Lipoprotein Cholesterol, and Protection Against Coronary Heart Disease. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002376	5.2	30
134	Polygenic Prediction of Weight and Obesity Trajectories from Birth to Adulthood. *Cell*, **2019**, 177, 587-596.e9	36.2	265

133	Genetics of Common, Complex Coronary Artery Disease. *Cell*, **2019**, 177, 132-145	56.2	84
132	2018 Curt Stern Award Address. *American Journal of Human Genetics*, **2019**, 104, 384-388	11	
131	Biological and clinical insights from genetics of insomnia symptoms. *Nature Genetics*, **2019**, 51, 387-393	36.3	101
130	Association of Risk Alleles With Cardiovascular Disease in Blacks in the Million Veteran Program. *Circulation*, **2019**, 140, 1031-1040	16.7	18
129	Genome-wide association study of peripheral artery disease in the Million Veteran Program. *Nature Medicine*, **2019**, 25, 1274-1279	50.5	73
128	Clonal Hematopoiesis of Indeterminate Potential Reshapes Age-Related CVD: JACC Review Topic of the Week. *Journal of the American College of Cardiology*, **2019**, 74, 578-586	15.1	27
127	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
126	GPR146 Deficiency Protects against Hypercholesterolemia and Atherosclerosis. *Cell*, **2019**, 179, 1276-1288.e14	36.2	27
125	DNA Sequence Variation in Encoding the Activin Receptor-Like Kinase 7 Influences Body Fat Distribution and Protects Against Type 2 Diabetes. *Diabetes*, **2019**, 68, 226-234	0.9	12
124	Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. *Nature Communications*, **2018**, 9, 1613	17.4	55
123	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
122	Observational and Genetic Associations of Resting Heart Rate With Aortic Valve Calcium. *American Journal of Cardiology*, **2018**, 121, 1246-1252	3	2
121	Role of angiopoietin-like 3 (ANGPTL3) in regulating plasma level of low-density lipoprotein cholesterol. *Atherosclerosis*, **2018**, 268, 196-206	3.1	52
120	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. *Nature Communications*, **2018**, 9, 2606	17.4	53
119	Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations. *Nature Genetics*, **2018**, 50, 1219-1224	36.3	1073
118	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. *Nature Communications*, **2018**, 9, 3391	17.4	90
117	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. *Nature Communications*, **2018**, 9, 2252	17.4	71
116	Multi-ethnic genome-wide association study for atrial fibrillation. *Nature Genetics*, **2018**, 50, 1225-1233	36.3	277

115	Phenotypic Refinement of Heart Failure in a National Biobank Facilitates Genetic Discovery. *Circulation*, **2018**,	16.7	51
114	Association Between Titin Loss-of-Function Variants and Early-Onset Atrial Fibrillation. *JAMA - Journal of the American Medical Association*, **2018**, 320, 2354-2364	27.4	75
113	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. *Nature Genetics*, **2018**, 50, 1514-1523	36.3	260
112	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
111	Genetic Association of Albuminuria with Cardiometabolic Disease and Blood Pressure. *American Journal of Human Genetics*, **2018**, 103, 461-473	11	62
110	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. *American Journal of Human Genetics*, **2018**, 102, 1204-1211	11	59
109	Polygenic Risk Score Identifies Subgroup With Higher Burden of Atherosclerosis and Greater Relative Benefit From Statin Therapy in the Primary Prevention Setting. *Circulation*, **2017**, 135, 2091-2101	16.7	244
108	Genetic invalidation of Lp-PLA as a therapeutic target: Large-scale study of five functional Lp-PLA-lowering alleles. *European Journal of Preventive Cardiology*, **2017**, 24, 492-504	3.9	16
107	Genetics of coronary artery disease: discovery, biology and clinical translation. *Nature Reviews Genetics*, **2017**, 18, 331-344	30.1	267
106	Association of Rare and Common Variation in the Lipoprotein Lipase Gene With Coronary Artery Disease. *JAMA - Journal of the American Medical Association*, **2017**, 317, 937-946	27.4	109
105	Genetic Association of Waist-to-Hip Ratio With Cardiometabolic Traits, Type 2 Diabetes, and Coronary Heart Disease. *JAMA - Journal of the American Medical Association*, **2017**, 317, 626-634	27.4	195
104	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. *Journal of the American College of Cardiology*, **2017**, 69, 823-836	15.1	146
103	Human knockouts and phenotypic analysis in a cohort with a high rate of consanguinity. *Nature*, **2017**, 544, 235-239	50.4	208
102	Genetic Variation at the Sulfonylurea Receptor, Type 2 Diabetes, and Coronary Heart Disease. *Diabetes*, **2017**, 66, 2310-2315	0.9	17
101	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. *Nature Genetics*, **2017**, 49, 946-952	36.3	176
100	Loss of Cardioprotective Effects at the Locus as a Result of Gene-Smoking Interactions. *Circulation*, **2017**, 135, 2336-2353	16.7	36
99	Clonal Hematopoiesis and Risk of Atherosclerotic Cardiovascular Disease. *New England Journal of Medicine*, **2017**, 377, 111-121	59.2	991
98	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. *Nature Genetics*, **2017**, 49, 1113-1119	36.3	184

97	Genetic Predisposition to Abdominal Obesity and Cardiometabolic Risk-Reply. *JAMA - Journal of the American Medical Association*, **2017**, 317, 2334-2335	27.4	0
96	ANGPTL3 Deficiency and Protection Against Coronary Artery Disease. *Journal of the American College of Cardiology*, **2017**, 69, 2054-2063	15.1	226
95	Large, Diverse Population Cohorts of hiPSCs and Derived Hepatocyte-like Cells Reveal Functional Genetic Variation at Blood Lipid-Associated Loci. *Cell Stem Cell*, **2017**, 20, 558-570.e10	18	102
94	Genetic Analysis of Venous Thromboembolism in UK Biobank Identifies the ZFPM2 Locus and Implicates Obesity as a Causal Risk Factor. *Circulation: Cardiovascular Genetics*, **2017**, 10,		52
93	Induced Pluripotent Stem Cell Differentiation Enables Functional Validation of GWAS Variants in Metabolic Disease. *Cell Stem Cell*, **2017**, 20, 547-557.e7	18	86
92	Is Coronary Atherosclerosis One Disease or Many? Setting Realistic Expectations for Precision Medicine. *Circulation*, **2017**, 135, 1005-1007	16.7	27
91	Genetic Risk, Lifestyle, and Coronary Artery Disease. *New England Journal of Medicine*, **2017**, 376, 1194-5	59.2	13
90	Evaluation of the Pooled Cohort Equations for Prediction of Cardiovascular Risk in a Contemporary Prospective Cohort. *American Journal of Cardiology*, **2017**, 119, 881-885	3	18
89	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
88	Exome chip meta-analysis identifies novel loci and East Asian-specific coding variants that contribute to lipid levels and coronary artery disease. *Nature Genetics*, **2017**, 49, 1722-1730	36.3	83
87	A human APOC3 missense variant and monoclonal antibody accelerate apoC-III clearance and lower triglyceride-rich lipoprotein levels. *Nature Medicine*, **2017**, 23, 1086-1094	50.5	63
86	Heart disease: Putative medicines that mimic mutations. *Nature*, **2017**, 548, 530-531	50.4	3
85	Genetic analysis in UK Biobank links insulin resistance and transendothelial migration pathways to coronary artery disease. *Nature Genetics*, **2017**, 49, 1392-1397	36.3	127
84	A Genetic Variant Associated with Five Vascular Diseases Is a Distal Regulator of Endothelin-1 Gene Expression. *Cell*, **2017**, 170, 522-533.e15	56.2	236
83	Mendelian Randomization. *JAMA - Journal of the American Medical Association*, **2017**, 318, 1925-1926	27.4	234
82	Cardiovascular endocrinology: Is ANGPTL3 the next PCSK9?. *Nature Reviews Endocrinology*, **2017**, 13, 503-504	15.2	14
81	Genetic Risk Prediction of Atrial Fibrillation. *Circulation*, **2017**, 135, 1311-1320	16.7	56
80	Leveraging human genetics to guide drug target discovery. *Trends in Cardiovascular Medicine*, **2017**, 27, 352-359	6.9	20

79	Heritability of Atrial Fibrillation. *Circulation: Cardiovascular Genetics*, **2017**, 10,		39
78	Phenotypic extremes in rare variant study designs. *European Journal of Human Genetics*, **2016**, 24, 924-30	5.3	43
77	Analysis of protein-coding genetic variation in 60,706 humans. *Nature*, **2016**, 536, 285-91	50.4	6940
76	Genetic variants in CETP increase risk of intracerebral hemorrhage. *Annals of Neurology*, **2016**, 80, 730-740	9.4	24
75	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
74	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. *Nature Genetics*, **2016**, 48, 1162-70	36.3	152
73	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
72	Association of Exome Sequences With Cardiovascular Traits Among Blacks in the Jackson Heart Study. *Circulation: Cardiovascular Genetics*, **2016**, 9, 368-74		7
71	Prospective functional classification of all possible missense variants in PPARG. *Nature Genetics*, **2016**, 48, 1570-1575	36.3	149
70	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. *Scientific Reports*, **2016**, 6, 35278	4.9	18
69	Aggregate penetrance of genomic variants for actionable disorders in European and African Americans. *Science Translational Medicine*, **2016**, 8, 364ra151	17.5	41
68	Gene-gene Interaction Analyses for Atrial Fibrillation. *Scientific Reports*, **2016**, 6, 35371	4.9	11
67	Genetic Risk, Adherence to a Healthy Lifestyle, and Coronary Disease. *New England Journal of Medicine*, **2016**, 375, 2349-2358	59.2	601
66	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. *Science Translational Medicine*, **2016**, 8, 341ra76	17.5	77
65	A null mutation in ANGPTL8 does not associate with either plasma glucose or type 2 diabetes in humans. *BMC Endocrine Disorders*, **2016**, 16, 7	3.3	8
64	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. *American Journal of Human Genetics*, **2016**, 99, 40-55	11	61
63	Surprises From Genetic Analyses of Lipid Risk Factors for Atherosclerosis. *Circulation Research*, **2016**, 118, 579-85	15.7	98
62	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. *Science*, **2016**, 351, 1166-71	33.3	325

61	Causal Assessment of Serum Urate Levels in Cardiometabolic Diseases Through a Mendelian Randomization Study. *Journal of the American College of Cardiology*, **2016**, 67, 407-416	15.1	101
60	Recurring exon deletions in the HP (haptoglobin) gene contribute to lower blood cholesterol levels. *Nature Genetics*, **2016**, 48, 359-66	36.3	61
59	Risk prediction by genetic risk scores for coronary heart disease is independent of self-reported family history. *European Heart Journal*, **2016**, 37, 561-7	9.5	152
58	The future of low-density lipoprotein cholesterol lowering therapy: An end to statin exceptionalism?. *European Journal of Preventive Cardiology*, **2016**, 23, 1062-4	3.9	5
57	Whole exome sequencing combined with integrated variant annotation prediction identifies a causative myosin essential light chain variant in hypertrophic cardiomyopathy. *Journal of Cardiology* , **2016**, 67, 133-9	3	11
56	An eMERGE Clinical Center at Partners Personalized Medicine. *Journal of Personalized Medicine*, **2016**, 6,	3.6	22
55	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. *American Journal of Human Genetics*, **2016**, 99, 8-21	11	47
54	Phenotypic Characterization of Genetically Lowered Human Lipoprotein(a) Levels. *Journal of the American College of Cardiology*, **2016**, 68, 2761-2772	15.1	127
53	Diagnostic Yield and Clinical Utility of Sequencing Familial Hypercholesterolemia Genes in Patients With Severe Hypercholesterolemia. *Journal of the American College of Cardiology*, **2016**, 67, 2578-89	15.1	458
52	PCSK9 Inhibitors. *Cell*, **2016**, 165, 1037	56.2	18
51	Targeted exonic sequencing of GWAS loci in the high extremes of the plasma lipids distribution. *Atherosclerosis*, **2016**, 250, 63-8	3.1	9
50	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,	6	101
49	JCL roundtable: Lessons from genetic variants altering lipoprotein metabolism. *Journal of Clinical Lipidology*, **2016**, 10, 448-57	4.9	1
48	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. *Nature Neuroscience*, **2016**, 19, 1563-1565	25.5	63
47	Loss of Function of GALNT2 Lowers High-Density Lipoproteins in Humans, Nonhuman Primates, and Rodents. *Cell Metabolism*, **2016**, 24, 234-45	24.6	78
46	Systematic cell-based phenotyping of missense alleles empowers rare variant association studies: a case for LDLR and myocardial infarction. *PLoS Genetics*, **2015**, 11, e1004855	6	32
45	Genetic variants primarily associated with type 2 diabetes are related to coronary artery disease risk. *Atherosclerosis*, **2015**, 241, 419-26	3.1	23
44	Genetic risk, coronary heart disease events, and the clinical benefit of statin therapy: an analysis of primary and secondary prevention trials. *Lancet, The*, **2015**, 385, 2264-2271	40	371

43	Myocardial Infarction-Associated SNP at 6p24 Interferes With MEF2 Binding and Associates With PHACTR1 Expression Levels in Human Coronary Arteries. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2015**, 35, 1472-1479	9.4	62
42	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. *American Journal of Human Genetics*, **2015**, 97, 576-92	11	649
41	Genome-wide identification of microRNAs regulating cholesterol and triglyceride homeostasis. *Nature Medicine*, **2015**, 21, 1290-7	50.5	160
40	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. *Nature Genetics*, **2015**, 47, 1121-1130	36.3	1290
39	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. *Nature*, **2015**, 518, 102-6	50.4	463
38	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. *Lancet, The*, **2015**, 385, 351-61	40	409
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	6	220
36	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. *Human Molecular Genetics*, **2015**, 24, 559-71	5.6	31
35	Novel genetic markers associate with atrial fibrillation risk in Europeans and Japanese. *Journal of the American College of Cardiology*, **2014**, 63, 1200-1210	15.1	102
34	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, 223-32	11	233
33	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
32	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
31	Multiple associated variants increase the heritability explained for plasma lipids and coronary artery disease. *Circulation: Cardiovascular Genetics*, **2014**, 7, 583-7		23
30	Twelve-single nucleotide polymorphism genetic risk score identifies individuals at increased risk for future atrial fibrillation and stroke. *Stroke*, **2014**, 45, 2856-2862	6.7	72
29	Meta-analysis of gene-level tests for rare variant association. *Nature Genetics*, **2014**, 46, 200-4	36.3	142
28	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. *Nature Genetics*, **2014**, 46, 357-63	36.3	351
27	Loss-of-function mutations in APOC3, triglycerides, and coronary disease. *New England Journal of Medicine*, **2014**, 371, 22-31	59.2	721
26	Distribution and medical impact of loss-of-function variants in the Finnish founder population. *PLoS Genetics*, **2014**, 10, e1004494	6	243

25	Genetics and causality of triglyceride-rich lipoproteins in atherosclerotic cardiovascular disease. *Journal of the American College of Cardiology*, **2014**, 64, 2525-40	15.1	149
24	Association of sickle cell trait with chronic kidney disease and albuminuria in African Americans. *JAMA - Journal of the American Medical Association*, **2014**, 312, 2115-25	27.4	126
23	Association of low-density lipoprotein cholesterol-related genetic variants with aortic valve calcium and incident aortic stenosis. *JAMA - Journal of the American Medical Association*, **2014**, 312, 1764-71	27.4	134
22	Clonal Hematopoiesis with Somatic Mutations Is a Common, Age-Related Condition Associated with Adverse Outcomes. *Blood*, **2014**, 124, 840-840	2.2	0
21	Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature Genetics*, **2013**, 45, 1345-52	36.3	597
20	Dysfunctional nitric oxide signalling increases risk of myocardial infarction. *Nature*, **2013**, 504, 432-6	50.4	185
19	Genetic predisposition to higher blood pressure increases coronary artery disease risk. *Hypertension*, **2013**, 61, 995-1001	8.5	55
18	Genetics of human cardiovascular disease. *Cell*, **2012**, 148, 1242-57	56.2	296
17	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
16	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. *Nature Genetics*, **2011**, 43, 333-8	36.3	1394
15	DASH: a method for identical-by-descent haplotype mapping uncovers association with recent variation. *American Journal of Human Genetics*, **2011**, 88, 706-717	11	60
14	The mouse QTL map helps interpret human genome-wide association studies for HDL cholesterol. *Journal of Lipid Research*, **2011**, 52, 1139-1149	6.3	20
13	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
12	Polymorphisms at newly identified lipid-associated loci are associated with blood lipids and cardiovascular disease in an Asian Malay population. *Journal of Lipid Research*, **2009**, 50, 514-520	6.3	41
11	Common variants at 30 loci contribute to polygenic dyslipidemia. *Nature Genetics*, **2009**, 41, 56-65	36.3	1095
10	Six new loci associated with blood low-density lipoprotein cholesterol, high-density lipoprotein cholesterol or triglycerides in humans. *Nature Genetics*, **2008**, 40, 189-97	36.3	1108
9	Polymorphisms associated with cholesterol and risk of cardiovascular events. *New England Journal of Medicine*, **2008**, 358, 1240-9	59.2	534
8	Defining the spectrum of alleles that contribute to blood lipid concentrations in humans. *Current Opinion in Lipidology*, **2008**, 19, 122-7	4.4	40

7	Factor V Leiden Is Associated with Premature Myocardial Infarction.. *Blood*, **2008**, 112, 1817-1817	2.2	
6	Case records of the Massachusetts General Hospital. Case 14-2005. A 38-year-old man with fever and blurred vision. *New England Journal of Medicine*, **2005**, 352, 2003-12	59.2	10
5	Cardiac troponin T elevation after coronary artery bypass grafting is associated with increased one-year mortality. *American Journal of Cardiology*, **2004**, 94, 879-81	3	66
4	Off-pump coronary bypass grafting is associated with less myocardial injury than coronary bypass surgery with cardiopulmonary bypass. *Heart Surgery Forum*, **2003**, 6, E174-8	0.7	5
3	Argatroban. *Journal of Thrombosis and Thrombolysis*, **2002**, 13, 41-7	5.1	43
2	Lipid nanoparticles incorporating a GalNAc ligand enable in vivo liver ANGPTL3 editing in wild-type and somatic LDLR knockout non-human primates		1
1	Discovery and systematic characterization of risk variants and genes for coronary artery disease in over a million participants		5