Nilesh J Samani

List of Publications by Year
in descending order

313	71,139	1893	751
papers	citations	102 h-index	250 g-index

325	325	325	68017
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Elucidation of the genetic causes of bicuspid aortic valve disease. Cardiovascular Research, 2023, 119, 857-866.	3.8	11
2	Cis-epistasis at the LPA locus and risk of cardiovascular diseases. Cardiovascular Research, 2022, 118, 1088-1102.	3.8	14
3	Vascular histopathology and connective tissue ultrastructure in spontaneous coronary artery dissection: pathophysiological and clinical implications. Cardiovascular Research, 2022, 118, 1835-1848.	3.8	27
4	Multimarker profiling identifies protective and harmful immune processes in heart failure: findings from BIOSTAT-CHF. Cardiovascular Research, 2022, 118, 1964-1977.	3.8	10
5	Prevalence and Disease Spectrum of Extracoronary Arterial Abnormalities in Spontaneous Coronary Artery Dissection. JAMA Cardiology, 2022, 7, 159.	6.1	18
6	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	6.2	24
7	Measurement and initial characterization of leukocyte telomere length in 474,074 participants in UK Biobank. Nature Aging, 2022, 2, 170-179.	11.6	75
8	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus. Nature Communications, 2022, 13, 1222.	12.8	5
9	Clinical impact of changes in mitral regurgitation severity after medical therapy optimization in heart failure. Clinical Research in Cardiology, 2022, 111, 912-923.	3.3	10
10	Association of shorter leucocyte telomere length with risk of frailty. Journal of Cachexia, Sarcopenia and Muscle, 2022, 13, 1741-1751.	7.3	13
11	Biomarker changes as surrogate endpoints in earlyâ€phase trials in heart failure with reduced ejection fraction. ESC Heart Failure, 2022, 9, 2107-2118.	3.1	4
12	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
13	Heteroplasmic mitochondrial DNA variants in cardiovascular diseases. PLoS Genetics, 2022, 18, e1010068.	3.5	19
14	Long-term trends in the epidemiology of cardiovascular diseases in the UK: insights from the British Heart Foundation statistical compendium. Cardiovascular Research, 2022, 118, 2267-2280.	3.8	13
15	Clinical implications of low estimated protein intake in patients with heart failure. Journal of Cachexia, Sarcopenia and Muscle, 2022, , .	7.3	7
16	Investigation of a UK biobank cohort reveals causal associations of self-reported walking pace with telomere length. Communications Biology, 2022, 5, 381.	4.4	17
17	Effects of late, repetitive remote ischaemic conditioning on myocardial strain in patients with acute myocardial infarction. Basic Research in Cardiology, 2022, 117, 23.	5.9	3
18	Modifiable traits, healthy behaviours, and leukocyte telomere length: a population-based study in UK Biobank. The Lancet Healthy Longevity, 2022, 3, e321-e331.	4.6	27

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19	Whole blood transcriptomic profiling identifies molecular pathways related to cardiovascular mortality in heart failure. European Journal of Heart Failure, 2022, 24, 1009-1019.	7.1	6
20	Exploring the Genetic Architecture of Spontaneous Coronary Artery Dissection Using Whole-Genome Sequencing. Circulation Genomic and Precision Medicine, 2022, 15, 101161CIRCGEN121003527.	3.6	14
21	Distinct pathophysiological pathways in women and men with heart failure. European Journal of Heart Failure, 2022, 24, 1532-1544.	7.1	10
22	Pregnancy and Spontaneous Coronary Artery Dissection: Lessons From Survivors and Nonsurvivors. Circulation, 2022, 146, 69-72.	1.6	7
23	Clinical implications of left atrial changes after optimization of medical therapy in patients with heart failure. European Journal of Heart Failure, 2022, 24, 2131-2139.	7.1	8
24	Is acute heart failure a distinctive disorder? An analysis from BIOSTATâ€CHF. European Journal of Heart Failure, 2021, 23, 43-57.	7.1	19
25	Professor Anthony H. Gershlick. European Heart Journal, 2021, 42, 1455-1457.	2.2	0
26	Polygenic risk scores in cardiovascular risk prediction: A cohort study and modelling analyses. PLoS Medicine, 2021, 18, e1003498.	8.4	95
27	The value of spot urinary creatinine as a marker of muscle wasting in patients with newâ€onset or worsening heart failure. Journal of Cachexia, Sarcopenia and Muscle, 2021, 12, 555-567.	7.3	15
28	Machine learning based on biomarker profiles identifies distinct subgroups of heart failure with preserved ejection fraction. European Journal of Heart Failure, 2021, 23, 983-991.	7.1	70
29	Quality of life in men and women with heart failure: association with outcome, and comparison between the Kansas City Cardiomyopathy Questionnaire and the EuroQol 5 dimensions questionnaire. European Journal of Heart Failure, 2021, 23, 567-577.	7.1	26
30	Differential miRNAs in acute spontaneous coronary artery dissection: Pathophysiological insights from a potential biomarker. EBioMedicine, 2021, 66, 103338.	6.1	10
31	Association between upâ€titration of medical therapy and total hospitalizations and mortality in patients with recent worsening heart failure across the ejection fraction spectrum. European Journal of Heart Failure, 2021, 23, 1170-1181.	7.1	11
32	Novel LOX Variants in Five Families with Aortic/Arterial Aneurysm and Dissection with Variable Connective Tissue Findings. International Journal of Molecular Sciences, 2021, 22, 7111.	4.1	7
33	Impact of mitral regurgitation in patients with worsening heart failure: insights from <scp>BIOSTATâ€CHF</scp>. European Journal of Heart Failure, 2021, 23, 1750-1758.	7.1	32
34	Shorter leukocyte telomere length is associated with adverse COVID-19 outcomes: A cohort study in UK Biobank. EBioMedicine, 2021, 70, 103485.	6.1	36
35	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	3.1	11
36	Leaders in Cardiovascular Research: Nilesh J. Samani. Cardiovascular Research, 2021, 117, e144-e146.	3.8	0

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37	Polygenic basis and biomedical consequences of telomere length variation. Nature Genetics, 2021, 53, 1425-1433.	21.4	145
38	128â€ƒClinical impact of changes in mitral regurgitation severity after optimization of medical therapy in heart failure: insights from BIOSTAT-CHF. European Heart Journal Supplements, 2021, 23, .	0.1	0
39	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	7.9	83
40	Plasma proteomic approach in patients withÂheart failure: insights into pathogenesis ofÂdisease progression and potential novel treatment targets. European Journal of Heart Failure, 2020, 22, 70-80.	7.1	28
41	Concentric vs. eccentric remodelling in heart failure with reduced ejection fraction: clinical characteristics, pathophysiology and response to treatment. European Journal of Heart Failure, 2020, 22, 1147-1155.	7.1	50
42	Evidence for Accelerated Biological Aging in Young Adults with Praderâ€“Willi Syndrome. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 2053-2059.	3.6	6
43	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	12.8	466
44	The role of cathepsin D in the pathophysiology of heart failure and its potentially beneficial properties: a translational approach. European Journal of Heart Failure, 2020, 22, 2102-2111.	7.1	24
45	Chronic infarct size after spontaneous coronary artery dissection: implications for pathophysiology and clinical management. European Heart Journal, 2020, 41, 2197-2205.	2.2	35
46	Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. Nature, 2020, 586, 769-775.	27.8	101
47	Association of Factor V Leiden With Subsequent Atherothrombotic Events. Circulation, 2020, 142, 546-555.	1.6	11
48	Novel loss of function mutation in NOTCH1 in a family with bicuspid aortic valve, ventricular septal defect, thoracic aortic aneurysm, and aortic valve stenosis. Molecular Genetics & Genomic Medicine, 2020, 8, e1437.	1.2	10
49	Genetic Associations With Plasma Angiotensin Converting Enzyme 2 Concentration. Circulation, 2020, 142, 1117-1119.	1.6	16
50	Spontaneous Coronary Artery Dissection. Circulation Genomic and Precision Medicine, 2020, 13, e003030.	3.6	43
51	HeterozygousABCG5Gene Deficiency and Risk of Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2020, 13, 417-423.	3.6	45
52	Enrichment of Rare Variants in Loeysâ€“Dietz Syndrome Genes in Spontaneous Coronary Artery Dissection but Not in Severe Fibromuscular Dysplasia. Circulation, 2020, 142, 1021-1024.	1.6	30
53	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. Circulation Genomic and Precision Medicine, 2020, 13, e002769.	3.6	5
54	Circulating plasma concentrations of angiotensin-converting enzyme 2 in men and women with heart failure and effects of reninâ€“angiotensinâ€“aldosterone inhibitors. European Heart Journal, 2020, 41, 1810-1817.	2.2	381

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55	The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443.	27.8	6,140
56	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
57	Clinical determinants and prognostic implications of renin and aldosterone in patients with symptomatic heart failure. ESC Heart Failure, 2020, 7, 953-963.	3.1	9
58	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. American Journal of Human Genetics, 2020, 106, 389-404.	6.2	118
59	Genetics of educational attainment and coronary risk in Mendelian randomization studies. European Heart Journal, 2020, 41, 894-895.	2.2	5
60	Geographical differences in heart failure characteristics and treatment across Europe: results from the BIOSTAT-CHF study. Clinical Research in Cardiology, 2020, 109, 967-977.	3.3	7
61	Exome Sequencing Analysis Identifies Rare Variants in ATM and RPL8 That Are Associated With Shorter Telomere Length. Frontiers in Genetics, 2020, 11, 337.	2.3	4
62	A network analysis to identify pathophysiological pathways distinguishing ischaemic from nonâ€ischaemic heart failure. European Journal of Heart Failure, 2020, 22, 821-833.	7.1	28
63	Metabolomics reveals a link between homocysteine and lipid metabolism and leukocyte telomere length: the ENGAGE consortium. Scientific Reports, 2019, 9, 11623.	3.3	13
64	A flexible and parallelizable approach to genomeâ€wide polygenic risk scores. Genetic Epidemiology, 2019, 43, 730-741.	1.3	32
65	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	12.0	75
66	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. Journal of the American College of Cardiology, 2019, 73, 3118-3131.	2.8	27
67	Identifying optimal doses of heart failure medications in men compared with women: a prospective, observational, cohort study. Lancet, The, 2019, 394, 1254-1263.	13.7	159
68	Genetically modulated educational attainment and coronary disease risk. European Heart Journal, 2019, 40, 2413-2420.	2.2	32
69	Genetic Risk Score for CoronaryÂDiseaseÂIdentifies Predispositions to Cardiovascular andÂNoncardiovascular Diseases. Journal of the American College of Cardiology, 2019, 73, 2932-2942.	2.8	58
70	HHIPL1 , a Gene at the 14q32 Coronary Artery Disease Locus, Positively Regulates Hedgehog Signaling and Promotes Atherosclerosis. Circulation, 2019, 140, 500-513.	1.6	24
71	The clinical significance of interleukinâ€6 in heart failure: results from the BIOSTATâ€CHF study. European Journal of Heart Failure, 2019, 21, 965-973.	7.1	172
72	Subsequent Event Risk in Individuals With Established Coronary Heart Disease. Circulation Genomic and Precision Medicine, 2019, 12, e002470.	3.6	17

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73	Association of Chromosome 9p21 With Subsequent Coronary Heart Disease Events. Circulation Genomic and Precision Medicine, 2019, 12, e002471.	3.6	22
74	Spontaneous Coronary Artery Dissection. JACC: Cardiovascular Imaging, 2019, 12, 2475-2488.	5.3	88
75	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
76	Uncovering genetic mechanisms of kidney aging through transcriptomics, genomics, and epigenomics. Kidney International, 2019, 95, 624-635.	5.2	40
77	Clinical correlates and outcome associated with changes in 6â€minute walking distance in patients with heart failure: findings from the BIOSTATâ€CHF study. European Journal of Heart Failure, 2019, 21, 218-226.	7.1	25
78	Â£30 million award to transform cardiovascular research. Cardiovascular Research, 2019, 115, e7-e8.	3.8	0
79	Prognostic significance of changes in heart rate following uptitration of beta-blockers in patients with sub-optimally treated heart failure with reduced ejection fraction in sinus rhythm versus atrial fibrillation. Clinical Research in Cardiology, 2019, 108, 797-805.	3.3	10
80	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. Journal of the American College of Cardiology, 2019, 73, 58-66.	2.8	147
81	The narrow-sense and common single nucleotide polymorphism heritability of early repolarization. International Journal of Cardiology, 2019, 279, 135-140.	1.7	7
82	Long noncoding RNA NEXN-AS1 mitigates atherosclerosis by regulating the actin-binding protein NEXN. Journal of Clinical Investigation, 2019, 129, 1115-1128.	8.2	105
83	Network analysis of coronary artery disease risk genes elucidates disease mechanisms and druggable targets. Scientific Reports, 2018, 8, 3434.	3.3	43
84	Into the great wide openâ€"10 years of genome-wide association studies. Cardiovascular Research, 2018, 114, 1189-1191.	3.8	3
85	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
86	Biomarker-Guided Versus Guideline-Based Treatment of Patients With Heart Failure. Journal of the American College of Cardiology, 2018, 71, 386-398.	2.8	35
87	Proteomic diversity of highâ€density lipoprotein explains its association with clinical outcome in patients with heart failure. European Journal of Heart Failure, 2018, 20, 260-267.	7.1	30
88	Potassium and the use of reninâ€"angiotensinâ€"aldosterone system inhibitors in heart failure with reduced ejection fraction: data from BIOSTATâ€CHF. European Journal of Heart Failure, 2018, 20, 923-930.	7.1	57
89	Fibroblast growth factor 23 is related to profiles indicating volume overload, poor therapy optimization and prognosis in patients with new-onset and worsening heart failure. International Journal of Cardiology, 2018, 253, 84-90.	1.7	55
90	Evidence for reduced susceptibility to cardiac bradycardias in South Asians compared with Caucasians. Heart, 2018, 104, 1350-1355.	2.9	7

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91	Coronary angiography in worsening heart failure: determinants, findings and prognostic implications. Heart, 2018, 104, 606-613.	2.9	16
92	Using matrix assisted laser desorption ionisation mass spectrometry (MALDI-MS) profiling in order to predict clinical outcomes of patients with heart failure. Clinical Proteomics, 2018, 15, 35.	2.1	6
93	Novel endotypes in heart failure: effects on guideline-directed medical therapy. European Heart Journal, 2018, 39, 4269-4276.	2.2	44
94	Genomic Risk Prediction of Coronary Artery Disease in 480,000 Adults. Journal of the American College of Cardiology, 2018, 72, 1883-1893.	2.8	557
95	Adult height and risk of 50 diseases: a combined epidemiological and genetic analysis. BMC Medicine, 2018, 16, 187.	5.5	60
96	Non-cardiac comorbidities in heart failure with reduced, mid-range and preserved ejection fraction. International Journal of Cardiology, 2018, 271, 132-139.	1.7	140
97	JCAD , a Gene at the 10p11 Coronary Artery Disease Locus, Regulates Hippo Signaling in Endothelial Cells. Arteriosclerosis, Thrombosis, and Vascular Biology, 2018, 38, 1711-1722.	2.4	36
98	Daily remote ischaemic conditioning following acute myocardial infarction: a randomised controlled trial. Heart, 2018, 104, 1955-1962.	2.9	15
99	Waistâ€toâ€hip ratio and mortality in heart failure. European Journal of Heart Failure, 2018, 20, 1269-1277.	7.1	85
100	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. Genome Biology, 2018, 19, 87.	8.8	47
101	Identifying Pathophysiological Mechanisms in Heart Failure WithÂReduced Versus Preserved EjectionÂFraction. Journal of the American College of Cardiology, 2018, 72, 1081-1090.	2.8	199
102	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
103	Determinants of dayâ€“night difference in blood pressure, a comparison with determinants of daytime and night-time blood pressure. Journal of Human Hypertension, 2017, 31, 43-48.	2.2	9
104	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	21.4	492
105	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
106	Coronary Artery Diseaseâ€“Associated LIPA Coding Variant rs1051338 Reduces Lysosomal Acid Lipase Levels and Activity in Lysosomes. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 1050-1057.	2.4	32
107	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	7.1	376
108	Development and validation of multivariable models to predict mortality and hospitalization in patients with heart failure. European Journal of Heart Failure, 2017, 19, 627-634.	7.1	183

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109	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.	7.4	148
110	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	2.8	214
111	Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363.	2.9	29
112	Protein-Truncating Variants at the Cholesteryl Ester Transfer Protein Gene and Risk for Coronary Heart Disease. Circulation Research, 2017, 121, 81-88.	4.5	68
113	Loss of Cardioprotective Effects at the ADAMTS7 Locus as a Result of Gene-Smoking Interactions. Circulation, 2017, 135, 2336-2353.	1.6	51
114	Risk Factors for Nonadherence to Antihypertensive Treatment. Hypertension, 2017, 69, 1113-1120.	2.7	150
115	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119.	21.4	260
116	Relations between lipoprotein(a) concentrations, LPA genetic variants, and the risk of mortality in patients with established coronary heart disease: a molecular and genetic association study. Lancet Diabetes and Endocrinology,the, 2017, 5, 534-543.	11.4	84
117	ANGPTL3 Deficiency and Protection Against Coronary Artery Disease. Journal of the American College of Cardiology, 2017, 69, 2054-2063.	2.8	348
118	Determinants and clinical outcome of uptitration of ACE-inhibitors and beta-blockers in patients with heart failure: a prospective European study. European Heart Journal, 2017, 38, 1883-1890.	2.2	299
119	Impact of Selection Bias on Estimation of Subsequent Event Risk. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	28
120	The PCSK9-LDL Receptor Axis andÂOutcomes in Heart Failure. Journal of the American College of Cardiology, 2017, 70, 2128-2136.	2.8	43
121	A genomic exploration identifies mechanisms that may explain adverse cardiovascular effects of COX-2 inhibitors. Scientific Reports, 2017, 7, 10252.	3.3	16
122	Large-Scale Analysis of Determinants, Stability, and Heritability of High-Density Lipoprotein Cholesterol Efflux Capacity. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 1956-1962.	2.4	33
123	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
124	Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391.	21.4	571
125	A miR-327â€“FGF10â€“FGFR2-mediated autocrine signaling mechanism controls white fat browning. Nature Communications, 2017, 8, 2079.	12.8	52
126	Comparison of exercise testing and CMR measured myocardial perfusion reserve for predicting outcome in asymptomatic aortic stenosis: the PRognostic Importance of MIcrovascular Dysfunction in Aortic Stenosis (PRIMID AS) Study. European Heart Journal, 2017, 38, 1222-1229.	2.2	72

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127	Switching harmful visceral fat to beneficial energy combustion improves metabolic dysfunctions. JCI Insight, 2017, 2, e89044.	5.0	28
128	Mineralocorticoid receptor antagonist pattern of use in heart failure with reduced ejection fraction: findings from <scp>BIOSTATâ€CHF</scp>. European Journal of Heart Failure, 2017, 19, 1284-1293.	7.1	79
129	Genomic correlates of glatiramer acetate adverse cardiovascular effects lead to a novel locus mediating coronary risk. PLoS ONE, 2017, 12, e0182999.	2.5	5
130	The Coronary Artery Disease-associated Coding Variant in Zinc Finger C3HC-type Containing 1 (ZC3HC1) Affects Cell Cycle Regulation. Journal of Biological Chemistry, 2016, 291, 16318-16327.	3.4	15
131	Genetic Variation Associated with Longer Telomere Length Increases Risk of Chronic Lymphocytic Leukemia. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1043-1049.	2.5	61
132	Coding Variation inANGPTL4,LPL,andSVEP1and the Risk of Coronary Disease. New England Journal of Medicine, 2016, 374, 1134-1144.	27.0	427
133	Cystatin C and Cardiovascular Disease. Journal of the American College of Cardiology, 2016, 68, 934-945.	2.8	109
134	Genomic prediction of coronary heart disease. European Heart Journal, 2016, 37, 3267-3278.	2.2	277
135	Analysis with the exome array identifies multiple new independent variants in lipid loci. Human Molecular Genetics, 2016, 25, 4094-4106.	2.9	19
136	KLB is associated with alcohol drinking, and its gene product Î²-Klotho is necessary for FGF21 regulation of alcohol preference. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14372-14377.	7.1	208
137	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
138	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
139	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
140	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. Science Translational Medicine, 2016, 8, 341ra76.	12.4	100
141	Endothelial PDGF-CC regulates angiogenesis-dependent thermogenesis in beige fat. Nature Communications, 2016, 7, 12152.	12.8	84
142	The PDGF-BB-SOX7 axis-modulated IL-33 in pericytes and stromal cells promotes metastasis through tumour-associated macrophages. Nature Communications, 2016, 7, 11385.	12.8	117
143	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
144	A systems <scp>BIOlogy</scp> Study to <scp>TAilored</scp> Treatment in Chronic Heart Failure: rationale, design, and baseline characteristics of <scp>BIOSTATâ€CHF</scp>. European Journal of Heart Failure, 2016, 18, 716-726.	7.1	149

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145	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
146	Remote ischaemic conditioning and remodelling following myocardial infarction: current evidence and future perspectives. Heart Failure Reviews, 2016, 21, 635-643.	3.9	6
147	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	12.6	438
148	Endocrine vasculatures are preferable targets of an antitumor ineffective low dose of anti-VEGF therapy. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4158-4163.	7.1	25
149	Causal Assessment of Serum Urate Levels inÂCardiometabolic Diseases Through a Mendelian Randomization Study. Journal of the American College of Cardiology, 2016, 67, 407-416.	2.8	138
150	Analysis of Gene-Gene Interactions among Common Variants in Candidate Cardiovascular Genes in Coronary Artery Disease. PLoS ONE, 2015, 10, e0117684.	2.5	8
151	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	3.5	77
152	Signatures of miR-181a on the Renal Transcriptome and Blood Pressure. Molecular Medicine, 2015, 21, 739-748.	4.4	48
153	DCAF4, a novel gene associated with leucocyte telomere length. Journal of Medical Genetics, 2015, 52, 157-162.	3.2	66
154	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
155	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
156	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. Diabetes, 2015, 64, 1841-1852.	0.6	63
157	Genetic variants primarily associated with type 2 diabetes are related to coronary artery disease risk. Atherosclerosis, 2015, 241, 419-426.	0.8	26
158	Runs of Homozygosity: Association with Coronary Artery Disease and Gene Expression in Monocytes and Macrophages. American Journal of Human Genetics, 2015, 97, 228-237.	6.2	37
159	Genetic Analysis of Leukocyte Type-I Interferon Production and Risk of Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 1456-1462.	2.4	11
160	Statin treatment: can genetics sharpen the focus?. Lancet, The, 2015, 385, 2227-2229.	13.7	10
161	Meta-analysis of 65,734 Individuals Identifies TSPAN15 and SLC44A2 as Two Susceptibility Loci for Venous Thromboembolism. American Journal of Human Genetics, 2015, 96, 532-542.	6.2	222
162	Cumulative effects of common genetic variants on risk of sudden cardiac death. IJC Heart and Vasculature, 2015, 7, 88-91.	1.1	7

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163	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	2.2	567
164	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	21.4	310
165	Renal Mechanisms of Association between Fibroblast Growth Factor 1 and Blood Pressure. Journal of the American Society of Nephrology: JASN, 2015, 26, 3151-3160.	6.1	20
166	Genetically Determined Height and Coronary Artery Disease. New England Journal of Medicine, 2015, 372, 1608-1618.	27.0	220
167	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nature Genetics, 2015, 47, 1282-1293.	21.4	294
168	VEGF-B-Neuropilin-1 signaling is spatiotemporally indispensable for vascular and neuronal development in zebrafish. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5944-53.	7.1	33
169	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	21.4	2,054
170	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	27.8	581
171	Prospective evaluation of two novel ECG-based restitution biomarkers for prediction of sudden cardiac death risk in ischaemic cardiomyopathy. Heart, 2014, 100, 1878-1885.	2.9	25
172	Mendelian randomization studies in coronary artery disease. European Heart Journal, 2014, 35, 1917-1924.	2.2	169
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