Nilesh J Samani

List of Publications by Year
in descending order

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313 papers	71,139 citations	1888 102 h-index	750 250 g-index
325 all docs	325 docs citations	325 times ranked	68017 citing authors

#	Article	IF	Citations
1	The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443.	13.7	6,140
2	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
3	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
4	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
5	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
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	Replication of Genome-Wide Association Signals in UK Samples Reveals Risk Loci for Type 2 Diabetes. Science, 2007, 316, 1336-1341.	6.0	2,040
8	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	6.3	1,937
9	Genomewide Association Analysis of Coronary Artery Disease. New England Journal of Medicine, 2007, 357, 443-453.	13.9	1,865
10	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
11	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
12	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Nature Genetics, 2011, 43, 333-338.	9.4	1,685
13	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	9.4	1,572
14	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	9.4	1,439
15	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
16	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	9.4	1,104
17	Human metabolic individuality in biomedical and pharmaceutical research. Nature, 2011, 477, 54-60.	13.7	916
18	The gene encoding 5-lipoxygenase activating protein confers risk of myocardial infarction and stroke. Nature Genetics, 2004, 36, 233-239.	9.4	859

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19	Identification of seven loci affecting mean telomere length and their association with disease. Nature Genetics, 2013, 45, 422-427.	9.4	808
20	DNA methylation and body-mass index: a genome-wide analysis. Lancet, The, 2014, 383, 1990-1998.	6.3	686
21	Telomere length, risk of coronary heart disease, and statin treatment in the West of Scotland Primary Prevention Study: a nested case-control study. Lancet, The, 2007, 369, 107-114.	6.3	671
22	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. Nature Genetics, 2010, 42, 436-440.	9.4	581
23	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	13.7	581
24	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
25	Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391.	9.4	571
26	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	1.0	567
27	Genomic Risk Prediction of Coronary Artery Disease in 480,000 Adults. Journal of the American College of Cardiology, 2018, 72, 1883-1893.	1.2	557
28	White Cell Telomere Length and Risk of Premature Myocardial Infarction. Arteriosclerosis, Thrombosis, and Vascular Biology, 2003, 23, 842-846.	1.1	544
29	Genetic Loci Associated With C-Reactive Protein Levels and Risk of Coronary Heart Disease. JAMA - Journal of the American Medical Association, 2009, 302, 37.	3.8	544
30	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
31	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	9.4	492
32	Identification of ADAMTS7 as a novel locus for coronary atherosclerosis and association of ABO with myocardial infarction in the presence of coronary atherosclerosis: two genome-wide association studies. Lancet, The, 2011, 377, 383-392.	6.3	466
33	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	5.8	466
34	New susceptibility locus for coronary artery disease on chromosome 3q22.3. Nature Genetics, 2009, 41, 280-282.	9.4	440
35	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	6.0	438
36	Genome-wide haplotype association study identifies the SLC22A3-LPAL2-LPA gene cluster as a risk locus for coronary artery disease. Nature Genetics, 2009, 41, 283-285.	9.4	427

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37	Coding Variation inANGPTL4,LPL,andSVEP1and the Risk of Coronary Disease. New England Journal of Medicine, 2016, 374, 1134-1144.	13.9	427
38	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	9.4	403
39	Genome-wide Association Study Identifies Genes for Biomarkers of Cardiovascular Disease: Serum Urate and Dyslipidemia. American Journal of Human Genetics, 2008, 82, 139-149.	2.6	397
40	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.3	387
41	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.	1.0	381
42	Meta-analysis of telomere length in 19â€‰713 subjects reveals high heritability, stronger maternal inheritance and a paternal age effect. European Journal of Human Genetics, 2013, 21, 1163-1168.	1.4	380
43	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	3.4	376
44	Genetic Variants Influencing Circulating Lipid Levels and Risk of Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 2264-2276.	1.1	369
45	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
46	Repeated Replication and a Prospective Meta-Analysis of the Association Between Chromosome 9p21.3 and Coronary Artery Disease. Circulation, 2008, 117, 1675-1684.	1.6	356
47	ANGPTL3 Deficiency and Protection Against Coronary Artery Disease. Journal of the American College of Cardiology, 2017, 69, 2054-2063.	1.2	348
48	Concept, Design and Implementation of a Cardiovascular Gene-Centric 50 K SNP Array for Large-Scale Genomic Association Studies. PLoS ONE, 2008, 3, e3583.	1.1	339
49	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	9.4	310
50	Shared Genetic Susceptibility to Ischemic Stroke and Coronary Artery Disease. Stroke, 2014, 45, 24-36.	1.0	302
51	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.	1.0	299
52	Common variants near TERC are associated with mean telomere length. Nature Genetics, 2010, 42, 197-199.	9.4	296
53	Genome-wide association study in Han Chinese identifies four new susceptibility loci for coronary artery disease. Nature Genetics, 2012, 44, 890-894.	9.4	295
54	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.	9.4	294

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55	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
56	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
57	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
58	Genomic prediction of coronary heart disease. European Heart Journal, 2016, 37, 3267-3278.	1.0	277
59	A trans-acting locus regulates an anti-viral expression network and type 1 diabetes risk. Nature, 2010, 467, 460-464.	13.7	271
60	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
61	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119.	9.4	260
62	Mapping of a Major Locus that Determines Telomere Length in Humans. American Journal of Human Genetics, 2005, 76, 147-151.	2.6	243
63	Dysfunctional nitric oxide signalling increases risk of myocardial infarction. Nature, 2013, 504, 432-436.	13.7	230
64	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. Human Molecular Genetics, 2014, 23, 4420-4432.	1.4	227
65	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.	2.6	222
66	Genetically Determined Height and Coronary Artery Disease. New England Journal of Medicine, 2015, 372, 1608-1618.	13.9	220
67	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	1.2	214
68	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.	3.3	208
69	Identifying Pathophysiological Mechanisms in Heart Failure WithÂReduced Versus Preserved EjectionÂFraction. Journal of the American College of Cardiology, 2018, 72, 1081-1090.	1.2	199
70	Integrative Genomics Reveals Novel Molecular Pathways and Gene Networks for Coronary Artery Disease. PLoS Genetics, 2014, 10, e1004502.	1.5	192
71	Abdominal Aortic Aneurysm Is Associated with a Variant in Low-Density Lipoprotein Receptor-Related Protein 1. American Journal of Human Genetics, 2011, 89, 619-627.	2.6	185
72	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.	2.9	183

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73	Inheritance of coronary artery disease in men: an analysis of the role of the Y chromosome. Lancet, The, 2012, 379, 915-922.	6.3	179
74	The clinical significance of interleukinâ€6 in heart failure: results from the BIOSTATâ€CHF study. European Journal of Heart Failure, 2019, 21, 965-973.	2.9	172
75	Mendelian randomization studies in coronary artery disease. European Heart Journal, 2014, 35, 1917-1924.	1.0	169
76	Variants near TERT and TERC influencing telomere length are associated with high-grade glioma risk. Nature Genetics, 2014, 46, 731-735.	9.4	161
77	Design of the Coronary ARtery DIsease Genome-Wide Replication And Meta-Analysis (CARDIoGRAM) Study. Circulation: Cardiovascular Genetics, 2010, 3, 475-483.	5.1	159
78	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	2.6	159
79	Identifying optimal doses of heart failure medications in men compared with women: a prospective, observational, cohort study. Lancet, The, 2019, 394, 1254-1263.	6.3	159
80	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	2.6	158
81	Risk Factors for Nonadherence to Antihypertensive Treatment. Hypertension, 2017, 69, 1113-1120.	1.3	150
82	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.	2.9	149
83	A Genome-Wide Association Study Reveals Variants in ARL15 that Influence Adiponectin Levels. PLoS Genetics, 2009, 5, e1000768.	1.5	148
84	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.	3.8	148
85	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
86	Polygenic basis and biomedical consequences of telomere length variation. Nature Genetics, 2021, 53, 1425-1433.	9.4	145
87	Genetic Regulation of Serum Phytosterol Levels and Risk of Coronary Artery Disease. Circulation: Cardiovascular Genetics, 2010, 3, 331-339.	5.1	141
88	Genetic variation at chromosome 1p13.3 affects sortilin mRNA expression, cellular LDL-uptake and serum LDL levels which translates to the risk of coronary artery disease. Atherosclerosis, 2010, 208, 183-189.	0.4	141
89	Large Scale Association Analysis of Novel Genetic Loci for Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2009, 29, 774-780.	1.1	140
90	Non-cardiac comorbidities in heart failure with reduced, mid-range and preserved ejection fraction. International Journal of Cardiology, 2018, 271, 132-139.	0.8	140

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91	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
92	Lifelong Reduction of LDL-Cholesterol Related to a Common Variant in the LDL-Receptor Gene Decreases the Risk of Coronary Artery Diseaseâ€"A Mendelian Randomisation Study. PLoS ONE, 2008, 3, e2986.	1.1	137
93	A Genome-Wide Association Study Identifies LIPA as a Susceptibility Gene for Coronary Artery Disease. Circulation: Cardiovascular Genetics, 2011, 4, 403-412.	5.1	130
94	Genetic determinants of diastolic and pulse pressure map to different loci in Lyon hypertensive rats. Nature Genetics, 1993, 3, 354-357.	9.4	126
95	A Genome-Wide Association Study for Coronary Artery Disease Identifies a Novel Susceptibility Locus in the Major Histocompatibility Complex. Circulation: Cardiovascular Genetics, 2012, 5, 217-225.	5.1	125
96	Association ofWNK1Gene Polymorphisms and Haplotypes With Ambulatory Blood Pressure in the General Population. Circulation, 2005, 112, 3423-3429.	1.6	124
97	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	1.3	123
98	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.	2.6	123
99	Beyond â€œmisunderstandingâ€: Written information and decisions about taking part in a genetic epidemiology study. Social Science and Medicine, 2007, 65, 2212-2222.	1.8	120
100	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. American Journal of Human Genetics, 2020, 106, 389-404.	2.6	118
101	The PDGF-BB-SOX7 axis-modulated IL-33 in pericytes and stromal cells promotes metastasis through tumour-associated macrophages. Nature Communications, 2016, 7, 11385.	5.8	117
102	Biological ageing and cardiovascular disease. Heart, 2008, 94, 537-539.	1.2	115
103	Secretory Phospholipase A2-IIA and Cardiovascular Disease. Journal of the American College of Cardiology, 2013, 62, 1966-1976.	1.2	115
104	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
105	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	3.3	110
106	Cystatin C and Cardiovascular Disease. Journal of the American College of Cardiology, 2016, 68, 934-945.	1.2	109
107	A Genomewide Linkage Study of 1,933 Families Affected by Premature Coronary Artery Disease: The British Heart Foundation (BHF) Family Heart Study. American Journal of Human Genetics, 2005, 77, 1011-1020.	2.6	105
108	Long noncoding RNA NEXN-AS1 mitigates atherosclerosis by regulating the actin-binding protein NEXN. Journal of Clinical Investigation, 2019, 129, 1115-1128.	3.9	105

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109	Common Variants in Genes Underlying Monogenic Hypertension and Hypotension and Blood Pressure in the General Population. Hypertension, 2008, 51, 1658-1664.	1.3	104
110	Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. Nature, 2020, 586, 769-775.	13.7	101
111	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. Science Translational Medicine, 2016, 8, 341ra76.	5.8	100
112	Leukocyte telomere length associates with prospective mortality independent of immune-related parameters and known genetic markers. International Journal of Epidemiology, 2014, 43, 878-886.	0.9	95
113	Polygenic risk scores in cardiovascular risk prediction: A cohort study and modelling analyses. PLoS Medicine, 2021, 18, e1003498.	3.9	95
114	Comparative analysis of genome-wide association studies signals for lipids, diabetes, and coronary heart disease: Cardiovascular Biomarker Genetics Collaboration. European Heart Journal, 2012, 33, 393-407.	1.0	93
115	A gene differentially expressed in the kidney of the spontaneously hypertensive rat cosegregates with increased blood pressure.. Journal of Clinical Investigation, 1993, 92, 1099-1103.	3.9	91
116	Genetics of myocardial infarction: a progress report. European Heart Journal, 2010, 31, 918-925.	1.0	90
117	Transcription profiling in human platelets reveals LRRFIP1 as a novel protein regulating platelet function. Blood, 2010, 116, 4646-4656.	0.6	90
118	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
119	Spontaneous Coronary Artery Dissection. JACC: Cardiovascular Imaging, 2019, 12, 2475-2488.	2.3	88
120	Exome Sequencing and Directed Clinical Phenotyping Diagnose Cholesterol Ester Storage Disease Presenting as Autosomal Recessive Hypercholesterolemia. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 2909-2914.	1.1	87
121	Genetic Associations for Activated Partial Thromboplastin Time and Prothrombin Time, their Gene Expression Profiles, and Risk of Coronary Artery Disease. American Journal of Human Genetics, 2012, 91, 152-162.	2.6	85
122	Waistâ€toâ€hip ratio and mortality in heart failure. European Journal of Heart Failure, 2018, 20, 1269-1277.	2.9	85
123	Lack of Association Between the Trp719Arg Polymorphism in Kinesin-Like Protein-6 and Coronary Artery Disease in 19 Case-Control Studies. Journal of the American College of Cardiology, 2010, 56, 1552-1563.	1.2	84
124	Endothelial PDGF-CC regulates angiogenesis-dependent thermogenesis in beige fat. Nature Communications, 2016, 7, 12152.	5.8	84
125	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.	5.5	84
126	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	4.1	83

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127	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	2.6	82
128	The novel genetic variant predisposing to coronary artery disease in the region of the PSRC1 and CELSR2 genes on chromosome 1 associates with serum cholesterol. Journal of Molecular Medicine, 2008, 86, 1233-1241.	1.7	80
129	Coronary Artery Diseaseâ€"Associated Locus on Chromosome 9p21 and Early Markers of Atherosclerosis. Arteriosclerosis, Thrombosis, and Vascular Biology, 2008, 28, 1679-1683.	1.1	80
130	Elevated C-Reactive Protein in Atherosclerosis â€" Chicken or Egg?. New England Journal of Medicine, 2008, 359, 1953-1955.	13.9	80
131	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.	2.9	79
132	The impact of newly identified loci on coronary heart disease, stroke and total mortality in the MORGAM prospective cohorts. Genetic Epidemiology, 2009, 33, 237-246.	0.6	77
133	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	1.5	77
134	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	6.2	75
135	Measurement and initial characterization of leukocyte telomere length in 474,074 participants in UK Biobank. Nature Aging, 2022, 2, 170-179.	5.3	75
136	Insertion/deletion polymorphism in the angiotensin-converting enzyme gene and risk of restenosis after coronary angioplasty. Lancet, The, 1995, 345, 1013-1016.	6.3	72
137	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.	1.0	72
138	Genetic Predisposition to Higher Blood Pressure Increases Coronary Artery Disease Risk. Hypertension, 2013, 61, 995-1001.	1.3	70
139	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.	2.9	70
140	Protein-Truncating Variants at the Cholesteryl Ester Transfer Protein Gene and Risk for Coronary Heart Disease. Circulation Research, 2017, 121, 81-88.	2.0	68
141	DCAF4, a novel gene associated with leucocyte telomere length. Journal of Medical Genetics, 2015, 52, 157-162.	1.5	66
142	The Relationship Between Plasma Angiopoietin-like Protein 4 Levels, Angiopoietin-like Protein 4 Genotype, and Coronary Heart Disease Risk. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 2277-2282.	1.1	64
143	Genetic Architecture of Ambulatory Blood Pressure in the General Population. Hypertension, 2010, 56, 1069-1076.	1.3	64
144	Glycoprotein IIIa polymorphism and risk of myocardial infarction. Cardiovascular Research, 1997, 33, 693-697.	1.8	63

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145	Association Between the Coronary Artery Disease Risk Locus on Chromosome 9p21.3 and Abdominal Aortic Aneurysm. Circulation: Cardiovascular Genetics, 2008, 1, 39-42.	5.1	63
146	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. Diabetes, 2015, 64, 1841-1852.	0.3	63
147	Genetic Variation Associated with Longer Telomere Length Increases Risk of Chronic Lymphocytic Leukemia. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1043-1049.	1.1	61
148	Adult height and risk of 50 diseases: a combined epidemiological and genetic analysis. BMC Medicine, 2018, 16, 187.	2.3	60
149	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	5.8	59
150	Analysis of Quantitative Trait Loci for Blood Pressure on Rat Chromosomes 2 and 13. Hypertension, 1996, 28, 1118-1122.	1.3	59
151	A regulatory SNP of the BICD1 gene contributes to telomere length variation in humans. Human Molecular Genetics, 2008, 17, 2518-2523.	1.4	58
152	Association Between the Chromosome 9p21 Locus and Angiographic Coronary Artery Disease Burden. Journal of the American College of Cardiology, 2013, 61, 957-970.	1.2	58
153	Genetic Risk Score for CoronaryÂDiseaseÂIdentifies Predispositions to Cardiovascular andÂNoncardiovascular Diseases. Journal of the American College of Cardiology, 2019, 73, 2932-2942.	1.2	58
154	Genetic Dissection of Region Around the Sa Gene on Rat Chromosome 1. Hypertension, 2001, 38, 216-221.	1.3	57
155	Male-Specific Region of the Y Chromosome and Cardiovascular Risk. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 1722-1727.	1.1	57
156	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.	2.9	57
157	Successful Isolation of a Rat Chromosome 1 Blood Pressure Quantitative Trait Locus in Reciprocal Congenic Strains. Hypertension, 1998, 32, 639-646.	1.3	55
158	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.	0.8	55
159	Genome-Wide Haplotype Analysis of Cis Expression Quantitative Trait Loci in Monocytes. PLoS Genetics, 2013, 9, e1003240.	1.5	53
160	The personal genomeâ€”the future of personalised medicine?. Lancet, The, 2010, 375, 1497-1498.	6.3	52
161	Modulation of age-related insulin sensitivity by VEGF-dependent vascular plasticity in adipose tissues. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14906-14911.	3.3	52
162	A miR-327â€“FGF10â€“FGFR2-mediated autocrine signaling mechanism controls white fat browning. Nature Communications, 2017, 8, 2079.	5.8	52

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163	Loss of Cardioprotective Effects at the ADAMTS7 Locus as a Result of Gene-Smoking Interactions. Circulation, 2017, 135, 2336-2353.	1.6	51
164	A Widespread Abnormality of Renin Gene Expression in the Spontaneously Hypertensive Rat: Modulation in Some Tissues with the Development of Hypertension. Clinical Science, 1989, 77, 629-636.	1.8	50
165	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.	2.9	50
166	Signatures of miR-181a on the Renal Transcriptome and Blood Pressure. Molecular Medicine, 2015, 21, 739-748.	1.9	48
167	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. Genome Biology, 2018, 19, 87.	3.8	47
168	HeterozygousABCG5Gene Deficiency and Risk of Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2020, 13, 417-423.	1.6	45
169	Novel endotypes in heart failure: effects on guideline-directed medical therapy. European Heart Journal, 2018, 39, 4269-4276.	1.0	44
170	The PCSK9-LDL Receptor Axis andÂOutcomes in Heart Failure. Journal of the American College of Cardiology, 2017, 70, 2128-2136.	1.2	43
171	Network analysis of coronary artery disease risk genes elucidates disease mechanisms and druggable targets. Scientific Reports, 2018, 8, 3434.	1.6	43
172	Spontaneous Coronary Artery Dissection. Circulation Genomic and Precision Medicine, 2020, 13, e003030.	1.6	43
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