Sandosh Padmanabhan

List of Publications by Year
in descending order

223	21,996	8181	11308
papers	citations	76 h-index	136 g-index

235	235	235	33013
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
2	Spironolactone versus placebo, bisoprolol, and doxazosin to determine the optimal treatment for drug-resistant hypertension (PATHWAY-2): a randomised, double-blind, crossover trial. Lancet, The, 2015, 386, 2059-2068.	13.7	904
3	Genetically Distinct Subsets within ANCA-Associated Vasculitis. New England Journal of Medicine, 2012, 367, 214-223.	27.0	820
4	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	2.2	567
5	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	21.4	552
6	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
7	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
8	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	6.0	528
9	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
10	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
11	Risk HLA-DQA1 and PLA₂R1 Alleles in Idiopathic Membranous Nephropathy. New England Journal of Medicine, 2011, 364, 616-626.	27.0	442
12	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
13	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.	1.6	403
14	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
15	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
16	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	27.8	320
17	Genome-Wide Association Study of Blood Pressure Extremes Identifies Variant near UMOD Associated with Hypertension. PLoS Genetics, 2010, 6, e1001177.	3.5	312
18	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	21.4	308

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19	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	11.4	298
20	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
21	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
22	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
23	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	21.4	279
24	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
25	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
26	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 410-425.	6.2	239
27	HLA Has Strongest Association with IgA Nephropathy in Genome-Wide Analysis. Journal of the American Society of Nephrology: JASN, 2010, 21, 1791-1797.	6.1	233
28	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	6.2	227
29	Genetic and Molecular Aspects of Hypertension. Circulation Research, 2015, 116, 937-959.	4.5	218
30	Endocrine and haemodynamic changes in resistant hypertension, and blood pressure responses to spironolactone or amiloride: the PATHWAY-2 mechanisms substudies. Lancet Diabetes and Endocrinology,the, 2018, 6, 464-475.	11.4	206
31	Variants in the fetal genome near FLT1 are associated with risk of preeclampsia. Nature Genetics, 2017, 49, 1255-1260.	21.4	205
32	Copy-Number Disorders Are a Common Cause of Congenital Kidney Malformations. American Journal of Human Genetics, 2012, 91, 987-997.	6.2	201
33	Cardiac Troponin T and Troponin I in the General Population. Circulation, 2019, 139, 2754-2764.	1.6	200
34	Association Between Genetic Variants on Chromosome 15q25 Locus and Objective Measures of Tobacco Exposure. Journal of the National Cancer Institute, 2012, 104, 740-748.	6.3	198
35	Obesity paradox in a cohort of 4880 consecutive patients undergoing percutaneous coronary intervention. European Heart Journal, 2010, 31, 222-226.	2.2	197
36	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193

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37	Gene-centric Association Signals for Lipids and Apolipoproteins Identified via the HumanCVD BeadChip. American Journal of Human Genetics, 2009, 85, 628-642.	6.2	183
38	Should Diabetes Be Considered a Coronary Heart Disease Risk Equivalent?: Results from 25 years of follow-up in the Renfrew and Paisley Survey. Diabetes Care, 2005, 28, 1588-1593.	8.6	181
39	Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. Biological Psychiatry, 2017, 81, 325-335.	1.3	175
40	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
41	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
42	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
43	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	6.2	159
44	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.	6.2	158
45	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
46	Molecular genetic contributions to socioeconomic status and intelligence. Intelligence, 2014, 44, 26-32.	3.0	156
47	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. Nature Communications, 2017, 8, 16015.	12.8	149
48	Genomewide Association Study Using a High-Density Single Nucleotide Polymorphism Array and Case-Control Design Identifies a Novel Essential Hypertension Susceptibility Locus in the Promoter Region of Endothelial NO Synthase. Hypertension, 2012, 59, 248-255.	2.7	144
49	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. PLoS Genetics, 2013, 9, e1003796.	3.5	142
50	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	2.9	141
51	Systems genetics identifies a convergent gene network for cognition and neurodevelopmental disease. Nature Neuroscience, 2016, 19, 223-232.	14.8	131
52	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
53	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
54	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	6.2	122

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55	Genetic Evidence for a Link Between Favorable Adiposity and Lower Risk of Type 2 Diabetes, Hypertension, and Heart Disease. Diabetes, 2016, 65, 2448-2460.	0.6	122
56	Resting Heart Rate Pattern During Follow-Up and Mortality in Hypertensive Patients. Hypertension, 2010, 55, 567-574.	2.7	118
57	Genetic basis of blood pressure and hypertension. Trends in Genetics, 2012, 28, 397-408.	6.7	117
58	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
59	Exploration of haplotype research consortium imputation for genome-wide association studies in 20,032 Generation Scotland participants. Genome Medicine, 2017, 9, 23.	8.2	110
60	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	12.8	108
61	Effect of Smoking on Blood Pressure and Resting Heart Rate. Circulation: Cardiovascular Genetics, 2015, 8, 832-841.	5.1	105
62	Genetic variation at the SLC23A1 locus is associated with circulating concentrations of l-ascorbic acid (vitamin C): evidence from 5 independent studies with >15,000 participants. American Journal of Clinical Nutrition, 2010, 92, 375-382.	4.7	102
63	Comparison between High-Sensitivity Cardiac Troponin T and Cardiac Troponin I in a Large General Population Cohort. Clinical Chemistry, 2018, 64, 1607-1616.	3.2	101
64	Genetic variation at CHRNA5-CHRNA3-CHRNB4 interacts with smoking status to influence body mass index. International Journal of Epidemiology, 2011, 40, 1617-1628.	1.9	100
65	Validation of Uromodulin as a Candidate Gene for Human Essential Hypertension. Hypertension, 2014, 63, 551-558.	2.7	100
66	Effect of amiloride, or amiloride plus hydrochlorothiazide, versus hydrochlorothiazide on glucose tolerance and blood pressure (PATHWAY-3): a parallel-group, double-blind randomised phase 4 trial. Lancet Diabetes and Endocrinology,the, 2016, 4, 136-147.	11.4	99
67	Genomics of hypertension: the road to precision medicine. Nature Reviews Cardiology, 2021, 18, 235-250.	13.7	99
68	Allopurinol and Cardiovascular Outcomes in Adults With Hypertension. Hypertension, 2016, 67, 535-540.	2.7	98
69	Monotherapy With Major Antihypertensive Drug Classes and Risk of Hospital Admissions for Mood Disorders. Hypertension, 2016, 68, 1132-1138.	2.7	97
70	Genomic Association Analysis of Common Variants Influencing Antihypertensive Response to Hydrochlorothiazide. Hypertension, 2013, 62, 391-397.	2.7	96
71	No Evidence of a Common DNA Variant Profile Specific to World Class Endurance Athletes. PLoS ONE, 2016, 11, e0147330.	2.5	96
72	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. International Journal of Epidemiology, 2016, 45, 1927-1937.	1.9	94

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73	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
74	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
75	Metabolomic Identification of a Novel Pathway of Blood Pressure Regulation Involving Hexadecanedioate. Hypertension, 2015, 66, 422-429.	2.7	90
76	Towards Precision Medicine for Hypertension: A Review of Genomic, Epigenomic, and Microbiomic Effects on Blood Pressure in Experimental Rat Models and Humans. Physiological Reviews, 2017, 97, 1469-1528.	28.8	85
77	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
78	Long-Term and Ultra Longâ€“Term Blood Pressure Variability During Follow-Up and Mortality in 14 522 Patients With Hypertension. Hypertension, 2013, 62, 698-705.	2.7	81
79	The Y Chromosome Effect on Blood Pressure in Two European Populations. Hypertension, 2002, 39, 353-356.	2.7	78
80	Combination Therapy Is Superior to Sequential Monotherapy for the Initial Treatment of Hypertension: A Doubleâ€Blind Randomized Controlled Trial. Journal of the American Heart Association, 2017, 6, .	3.7	74
81	Genetic dysregulation of endothelin-1 is implicated in coronary microvascular dysfunction. European Heart Journal, 2020, 41, 3239-3252.	2.2	73
82	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	12.8	71
83	Chronic pain, depression and cardiovascular disease linked through a shared genetic predisposition: Analysis of a family-based cohort and twin study. PLoS ONE, 2017, 12, e0170653.	2.5	71
84	The hidden hand of chloride in hypertension. Pflugers Archiv European Journal of Physiology, 2015, 467, 595-603.	2.8	68
85	Serum Chloride Is an Independent Predictor of Mortality in Hypertensive Patients. Hypertension, 2013, 62, 836-843.	2.7	67
86	Implications of discoveries from genome-wide association studies in current cardiovascular practice. World Journal of Cardiology, 2011, 3, 230.	1.5	62
87	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
88	Metabolomic study of carotidâ€“femoral pulse-wave velocity in women. Journal of Hypertension, 2015, 33, 791-796.	0.5	57
89	Genetics of hypertension: From experimental animals to humans. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2010, 1802, 1299-1308.	3.8	56
90	Elevated heart rate and cardiovascular outcomes in patients with coronary artery disease: Clinical evidence and pathophysiological mechanisms. Atherosclerosis, 2010, 212, 1-8.	0.8	53

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91	Heavier smoking may lead to a relative increase in waist circumference: evidence for a causal relationship from a Mendelian randomisation meta-analysis. The CARTA consortium: TableÂ1. BMJ Open, 2015, 5, e008808.	1.9	53
92	Unsupervised Discovery and Comparison of Structural Families Across Multiple Samples in Untargeted Metabolomics. Analytical Chemistry, 2017, 89, 7569-7577.	6.5	52
93	Allopurinol Initiation and Change in Blood Pressure in Older Adults With Hypertension. Hypertension, 2014, 64, 1102-1107.	2.7	51
94	Genomics of Elite Sporting Performance. Advances in Genetics, 2013, 84, 123-149.	1.8	47
95	Blood Pressure Response to Patterns of Weather Fluctuations and Effect on Mortality. Hypertension, 2013, 62, 190-196.	2.7	47
96	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. Genome Biology, 2018, 19, 87.	8.8	47
97	Stratification by Smoking Status Reveals an Association of CHRNA5-A3-B4 Genotype with Body Mass Index in Never Smokers. PLoS Genetics, 2014, 10, e1004799.	3.5	45
98	Uromodulin, an Emerging Novel Pathway for Blood Pressure Regulation and Hypertension. Hypertension, 2014, 64, 918-923.	2.7	45
99	Genome-wide association study of antidepressant treatment resistance in a population-based cohort using health service prescription data and meta-analysis with GENDEP. Pharmacogenomics Journal, 2020, 20, 329-341.	2.0	45
100	Diastolic Blood Pressure J-Curve Phenomenon in a Tertiary-Care Hypertension Clinic. Hypertension, 2019, 74, 767-775.	2.7	41
101	Rationale and design of the Medical Research Council's Precision Medicine with Zibotentan in Microvascular Angina (PRIZE) trial. American Heart Journal, 2020, 229, 70-80.	2.7	40
102	Familial and Phenotypic Associations of the Aldosterone Renin Ratio. Journal of Clinical Endocrinology and Metabolism, 2009, 94, 4324-4333.	3.6	39
103	PTPRD gene associated with blood pressure response to atenolol and resistant hypertension. Journal of Hypertension, 2015, 33, 2278-2285.	0.5	38
104	Hypertension and genome-wide association studies: combining high fidelity phenotyping and hypercontrols. Journal of Hypertension, 2008, 26, 1275-1281.	0.5	37
105	Serum Uric Acid Level, Longitudinal Blood Pressure, Renal Function, and Long-Term Mortality in Treated Hypertensive Patients. Hypertension, 2013, 62, 105-111.	2.7	37
106	Resting Heart Rate and Outcomes in Patients with Cardiovascular Disease: Where Do We Currently Stand?. Cardiovascular Therapeutics, 2013, 31, 215-223.	2.5	37
107	Heritability analyses show visit-to-visit blood pressure variability reflects different pathological phenotypes in younger and older adults. Journal of Hypertension, 2013, 31, 2356-2361.	0.5	36
108	Common Polymorphisms in the CYP11B1 and CYP11B2 Genes: Evidence for a Digenic Influence on Hypertension. Hypertension, 2013, 61, 232-239.	2.7	35

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109	Glutathione S-transferase variants and hypertension. Journal of Hypertension, 2008, 26, 1343-1352.	0.5	34
110	Hematocrit Predicts Long-Term Mortality in a Nonlinear and Sex-Specific Manner in Hypertensive Adults. Hypertension, 2012, 60, 631-638.	2.7	34
111	Meta-analysis of 49â€…549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant inANGPTL4determining fasting TG levels. Journal of Medical Genetics, 2016, 53, 441-449.	3.2	34
112	Genome-Wide and Gene-Based Meta-Analyses Identify Novel Loci Influencing Blood Pressure Response to Hydrochlorothiazide. Hypertension, 2017, 69, 51-59.	2.7	34
113	Chromosome 2p Shows Significant Linkage to Antihypertensive Response in the British Genetics of Hypertension Study. Hypertension, 2006, 47, 603-608.	2.7	33
114	Genetic comorbidity between major depression and cardioâ€•metabolic traits, stratified by age at onset of major depression. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2020, 183, 309-330.	1.7	33
115	The effects of sex and method of blood pressure measurement on genetic associations with blood pressure in the PAMELA study. Journal of Hypertension, 2010, 28, 465-477.	0.5	32
116	Pharmacogenomic Association of Nonsynonymous SNPs in SIGLEC12 , A1BG , and the Selectin Region and Cardiovascular Outcomes. Hypertension, 2013, 62, 48-54.	2.7	32
117	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, 7756.	12.8	32
118	Shared Genetics and Couple-Associated Environment Are Major Contributors to the Risk of Both Clinical and Self-Declared Depression. EBioMedicine, 2016, 14, 161-167.	6.1	32
119	A Combined Pathway and Regional Heritability Analysis Indicates NETRIN1 Pathway Is Associated With Major Depressive Disorder. Biological Psychiatry, 2017, 81, 336-346.	1.3	32
120	Urinary antihypertensive drug metabolite screening using molecular networking coupled to high-resolution mass spectrometry fragmentation. Metabolomics, 2016, 12, 125.	3.0	30
121	Novel Urinary Peptidomic Classifier Predicts Incident Heart Failure. Journal of the American Heart Association, 2017, 6, .	3.7	30
122	TET2 and CSMD1 genes affect SBP response to hydrochlorothiazide in never-treated essential hypertensives. Journal of Hypertension, 2015, 33, 1301-1309.	0.5	29
123	Genomics and Precision Medicine for Clinicians and Scientists in Hypertension. Hypertension, 2017, 69, e10-e13.	2.7	29
124	Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363.	2.9	29
125	Risk of Neuropsychiatric Adverse Effects of Lipid-Lowering Drugs: A Mendelian Randomization Study. International Journal of Neuropsychopharmacology, 2018, 21, 1067-1075.	2.1	29
126	Genomics of Blood Pressure and Hypertension: Extending the Mosaic Theory Toward Stratification. Canadian Journal of Cardiology, 2020, 36, 694-705.	1.7	29

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127	Fibroblast Growth Factor 1 Gene and Hypertension. Circulation, 2007, 116, 1915-1924.	1.6	28
128	Four Genetic Loci Influencing Electrocardiographic Indices of Left Ventricular Hypertrophy. Circulation: Cardiovascular Genetics, 2011, 4, 626-635.	5.1	28
129	Gene-centric meta-analyses for central adiposity traits in up to 57 412 individuals of European descent confirm known loci and reveal several novel associations. Human Molecular Genetics, 2014, 23, 2498-2510.	2.9	28
130	Longitudinal Blood Pressure Control, Long-Term Mortality, and Predictive Utility of Serum Liver Enzymes and Bilirubin in Hypertensive Patients. Hypertension, 2015, 66, 37-43.	2.7	28
131	Discontinuation of beta-blockers in cardiovascular disease: UK primary care cohort study. International Journal of Cardiology, 2013, 167, 2695-2699.	1.7	27
132	Polygenic risk for alcohol dependence associates with alcohol consumption, cognitive function and social deprivation in a populationâ€based cohort. Addiction Biology, 2016, 21, 469-480.	2.6	27
133	Investigating shared aetiology between type 2 diabetes and major depressive disorder in a population based cohort. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 227-234.	1.7	27
134	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. Circulation Genomic and Precision Medicine, 2018, 11, e001758.	3.6	27
135	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
136	Gene and environmental interactions according to the components of lifestyle modifications in hypertension guidelines. Environmental Health and Preventive Medicine, 2019, 24, 19.	3.4	27
137	Acetaminophen Use and Risk of Myocardial Infarction and Stroke in a Hypertensive Cohort. Hypertension, 2015, 65, 1008-1014.	2.7	26
138	Genome-wide Regional Heritability Mapping Identifies a Locus Within the TOX2 Gene Associated With Major Depressive Disorder. Biological Psychiatry, 2017, 82, 312-321.	1.3	26
139	Artificial Intelligence in Hypertension. Circulation Research, 2021, 128, 1100-1118.	4.5	26
140	Family history of premature cardiovascular disease: blood pressure control and long-term mortality outcomes in hypertensive patients. European Heart Journal, 2014, 35, 563-570.	2.2	25
141	Genetics and Hypertension: Is It Time to Change My Practice?. Canadian Journal of Cardiology, 2012, 28, 296-304.	1.7	22
142	Exome-wide analysis of rare coding variation identifies novel associations with COPD and airflow limitation inMOCS3,IFIT3andSERPINA12. Thorax, 2016, 71, 501-509.	5.6	22
143	A PROgramme of Lifestyle Intervention in Families for Cardiovascular risk reduction (PROLIFIC Study): design and rationale of a family based randomized controlled trial in individuals with family history of premature coronary heart disease. BMC Public Health, 2017, 17, 10.	2.9	22
144	Rationale and design of the British Heart Foundation (BHF) Coronary Microvascular Angina (CorMicA) stratified medicine clinical trial. American Heart Journal, 2018, 201, 86-94.	2.7	22

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145	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	1.7	22
146	Pharmacogenomics and Stratified Medicine. , 2014, , 3-25.		21
147	Mendelian randomization to assess causality between uromodulin, blood pressure and chronic kidney disease. Kidney International, 2021, 100, 1282-1291.	5.2	20
148	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	3.6	19
149	Impact of major depression on cardiovascular outcomes for individuals with hypertension: prospective survival analysis in UK Biobank. BMJ Open, 2019, 9, e024433.	1.9	19
150	Association between ADRA1A gene and the metabolic syndrome: candidate genes and functional counterpart in the PAMELA population. Journal of Hypertension, 2011, 29, 1121-1127.	0.5	18
151	Acetaminophen use and change in blood pressure in a hypertensive population. Journal of Hypertension, 2013, 31, 1485-1490.	0.5	18
152	An Empirical Comparison of Joint and Stratified Frameworks for Studying G Ã— E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Geneâ€Lifestyle Interactions Working Group. Genetic Epidemiology, 2016, 40, 404-415.	1.3	18
153	Cardiovascular and Renal Risk Factors and Complications Associated With COVID-19. CJC Open, 2021, 3, 1257-1272.	1.5	18
154	Contrasting mortality risks among subgroups of treated hypertensive patients developing new-onset diabetes. European Heart Journal, 2016, 37, 968-974.	2.2	17
155	Genomics of hypertension. Pharmacological Research, 2017, 121, 219-229.	7.1	17
156	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
157	Genomic approaches to coronary artery disease. Indian Journal of Medical Research, 2010, 132, 567-78.	1.0	17
158	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2020, 13, 387-395.	3.6	16
159	Genomic Determinants of Hypertension With a Focus on Metabolomics and the Gut Microbiome. American Journal of Hypertension, 2020, 33, 473-481.	2.0	16
160	The relationship between antihypertensive medications and mood disorders: analysis of linked healthcare data for 1.8 million patients. Psychological Medicine, 2021, 51, 1183-1191.	4.5	16
161	Efficacy of a family-based cardiovascular risk reduction intervention in individuals with a family history of premature coronary heart disease in India (PROLIFIC): an open-label, single-centre, cluster randomised controlled trial. The Lancet Global Health, 2021, 9, e1442-e1450.	6.3	16
162	Vascular dysfunction and increased cardiovascular risk in hypospadias. European Heart Journal, 2022, 43, 1832-1845.	2.2	16

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163	Prospects for Genetic Risk Prediction in Hypertension. Hypertension, 2013, 61, 961-963.	2.7	15
164	KCND3 potassium channel gene variant confers susceptibility to electrocardiographic early repolarization pattern. JCI Insight, 2019, 4, .	5.0	15
165	Genetic and environmental determinants of stressful life events and their overlap with depression and neuroticism. Wellcome Open Research, 2018, 3, 11.	1.8	15
166	The genetics of cardiovascular disease. Trends in Endocrinology and Metabolism, 2008, 19, 309-316.	7.1	14
167	Pharmacokinetic Pharmacogenomics. , 2014, , 341-364.		14
168	Gene Variants at Loci Related to Blood Pressure Account for Variation in Response to Antihypertensive Drugs Between Black and White Individuals. Hypertension, 2019, 74, 614-622.	2.7	14
169	Variation in the SLC23A1 gene does not influence cardiometabolic outcomes to the extent expected given its association with l-ascorbic acid. American Journal of Clinical Nutrition, 2015, 101, 202-209.	4.7	13
170	Mechanistic interactions of uromodulin with the thick ascending limb: perspectives in physiology and hypertension. Journal of Hypertension, 2021, 39, 1490-1504.	0.5	13
171	N-glycosylation of immunoglobulin G predicts incident hypertension. Journal of Hypertension, 2021, 39, 2527-2533.	0.5	13
172	The Pharmacogenomics of Anti-Hypertensive Therapy. Pharmaceuticals, 2010, 3, 1779-1791.	3.8	12
173	Recent Findings in the Genetics of Blood Pressure: How to Apply in Practice or Is a Moonshot Required?. Current Hypertension Reports, 2018, 20, 54.	3.5	12
174	Development, Evaluation, and Comparison of Land Use Regression Modeling Methods to Estimate Residential Exposure to Nitrogen Dioxide in a Cohort Study. Environmental Science & Technology, 2016, 50, 11085-11093.	10.0	11
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