Mark J Caulfield

List of Publications by Year
in descending order

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Version: 2024-02-01

219 papers	69,778 citations	1980 101 h-index	1413 221 g-index
237 all docs	237 docs citations	237 times ranked	64615 citing authors

#	Article	IF	Citations
1	2013 ESH/ESC Guidelines for the management of arterial hypertension. European Heart Journal, 2013, 34, 2159-2219.	1.0	5,681
2	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
3	Prevention of coronary and stroke events with atorvastatin in hypertensive patients who have average or lower-than-average cholesterol concentrations, in the Anglo-Scandinavian Cardiac Outcomes Trialâ€"Lipid Lowering Arm (ASCOT-LLA): a multicentre randomised controlled trial. Lancet, The, 2003, 361, 1149-1158.	6.3	3,420
4	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
5	Effects of Torcetrapib in Patients at High Risk for Coronary Events. New England Journal of Medicine, 2007, 357, 2109-2122.	13.9	2,811
6	Prevention of cardiovascular events with an antihypertensive regimen of amlodipine adding perindopril as required versus atenolol adding bendroflumethiazide as required, in the Anglo-Scandinavian Cardiac Outcomes Trial-Blood Pressure Lowering Arm (ASCOT-BPLA): a multicentre randomised controlled trial. Lancet, The, 2005, 366, 895-906.	6.3	2,662
7	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
8	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
9	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
10	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
11	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
12	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. Nature Genetics, 2007, 39, 1329-1337.	9.4	1,298
13	Blood pressure and incidence of twelve cardiovascular diseases: lifetime risks, healthy life-years lost, and age-specific associations in 1Â·25 million people. Lancet, The, 2014, 383, 1899-1911.	6.3	1,239
14	Reappraisal of European guidelines on hypertension management: a European Society of Hypertension Task Force document. Journal of Hypertension, 2009, 27, 2121-2158.	0.3	1,236
15	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	9.4	1,179
16	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	9.4	1,104
17	Genetic mechanisms of critical illness in COVID-19. Nature, 2021, 591, 92-98.	13.7	1,014
18	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959

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19	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
20	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.	6.3	904
21	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	9.4	836
22	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	9.4	746
23	Genome-wide association analysis identifies 20 loci that influence adult height. Nature Genetics, 2008, 40, 575-583.	9.4	742
24	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	13.7	737
25	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	9.4	675
26	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. Nature Genetics, 2010, 42, 436-440.	9.4	581
27	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
28	Meta-Analysis of 28,141 Individuals Identifies Common Variants within Five New Loci That Influence Uric Acid Concentrations. PLoS Genetics, 2009, 5, e1000504.	1.5	572
29	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.	6.3	564
30	Linkage of the Angiotensinogen Gene to Essential Hypertension. New England Journal of Medicine, 1994, 330, 1629-1633.	13.9	544
31	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
32	Hypertension. Lancet, The, 2015, 386, 801-812.	6.3	539
33	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	9.4	501
34	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. Nature Genetics, 2011, 43, 984-989.	9.4	481
35	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
36	Bayesian refinement of association signals for 14 loci in 3 common diseases. Nature Genetics, 2012, 44, 1294-1301.	9.4	469

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37	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	1.5	453
38	Management of hypertension: summary of NICE guidance. BMJ: British Medical Journal, 2011, 343, d4891-d4891.	2.4	427
39	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	9.4	403
40	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
41	Reduction in Cardiovascular Events With Atorvastatin in 2,532 Patients With Type 2 Diabetes: Anglo-Scandinavian Cardiac Outcomes Trial-Lipid-Lowering Arm (ASCOT-LLA). Diabetes Care, 2005, 28, 1151-1157.	4.3	377
42	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	1.5	371
43	Dietary Nitrate Provides Sustained Blood Pressure Lowering in Hypertensive Patients. Hypertension, 2015, 65, 320-327.	1.3	367
44	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
45	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
46	Reappraisal of European guidelines on hypertension management: a European Society of Hypertension Task Force document. Blood Pressure, 2009, 18, 308-347.	0.7	351
47	Comprehensive Rare Variant Analysis via Whole-Genome Sequencing to Determine the Molecular Pathology of Inherited Retinal Disease. American Journal of Human Genetics, 2017, 100, 75-90.	2.6	343
48	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
49	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
50	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	9.4	328
51	Role of blood pressure and other variables in the differential cardiovascular event rates noted in the Anglo-Scandinavian Cardiac Outcomes Trial-Blood Pressure Lowering Arm (ASCOT-BPLA). Lancet, The, 2005, 366, 907-913.	6.3	314
52	Genome-Wide Association Study of Blood Pressure Extremes Identifies Variant near UMOD Associated with Hypertension. PLoS Genetics, 2010, 6, e1001177.	1.5	312
53	The 100â€‰000 Genomes Project: bringing whole genome sequencing to the NHS. BMJ: British Medical Journal, 2018, 361, k1687.	2.4	312
54	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	9.4	308

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55	SLC2A9 Is a High-Capacity Urate Transporter in Humans. PLoS Medicine, 2008, 5, e197.	3.9	305
56	Causal Associations of Adiposity and Body Fat Distribution With Coronary Heart Disease, Stroke Subtypes, and Type 2 Diabetes Mellitus. Circulation, 2017, 135, 2373-2388.	1.6	304
57	Cost-effectiveness of options for the diagnosis of high blood pressure in primary care: a modelling study. Lancet, The, 2011, 378, 1219-1230.	6.3	296
58	PanelApp crowdsources expert knowledge to establish consensus diagnostic gene panels. Nature Genetics, 2019, 51, 1560-1565.	9.4	294
59	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
60	KLHL3 mutations cause familial hyperkalemic hypertension by impairing ion transport in the distal nephron. Nature Genetics, 2012, 44, 456-460.	9.4	281
61	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
62	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
63	Genome-wide mapping of human loci for essential hypertension. Lancet, The, 2003, 361, 2118-2123.	6.3	247
64	Genetic loci influencing kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 373-375.	9.4	246
65	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 410-425.	2.6	239
66	Mutations in the TGF-Î² repressor SKI cause Shprintzen-Goldberg syndrome with aortic aneurysm. Nature Genetics, 2012, 44, 1249-1254.	9.4	237
67	Rationale, design, methods and baseline demography of participants of the Anglo-Scandinavian Cardiac Outcomes Trial. Journal of Hypertension, 2001, 19, 1139-1147.	0.3	234
68	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	2.6	227
69	Genetic and Molecular Aspects of Hypertension. Circulation Research, 2015, 116, 937-959.	2.0	218
70	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. Nature Communications, 2014, 5, 5068.	5.8	216
71	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.	5.5	206
72	Prevention of Coronary and Stroke Events with Atorvastatin in Hypertensive Patients who have Average or Lower-than-Average Cholesterol Concentrations, in the Anglo-Scandinavian Cardiac Outcomes Trial???Lipid Lowering Arm (ASCOT-LLA). Drugs, 2004, 64, 43-60.	4.9	189

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73	Gene-centric Association Signals for Lipids and Apolipoproteins Identified via the HumanCVD BeadChip. American Journal of Human Genetics, 2009, 85, 628-642.	2.6	183
74	Enhanced Vasodilator Activity of Nitrite in Hypertension. Hypertension, 2013, 61, 1091-1102.	1.3	183
75	Association of Hypertension Drug Target Genes With Blood Pressure and Hypertension in 86 588 Individuals. Hypertension, 2011, 57, 903-910.	1.3	181
76	Germline selection shapes human mitochondrial DNA diversity. Science, 2019, 364, .	6.0	178
77	Whole-genome sequencing reveals host factors underlying critical COVID-19. Nature, 2022, 607, 97-103.	13.7	174
78	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
79	Causal association between periodontitis and hypertension: evidence from Mendelian randomization and a randomized controlled trial of non-surgical periodontal therapy. European Heart Journal, 2019, 40, 3459-3470.	1.0	172
80	Genome-wide scan identifies CDH13 as a novel susceptibility locus contributing to blood pressure determination in two European populations. Human Molecular Genetics, 2009, 18, 2288-2296.	1.4	170
81	Genetic Predisposition to High Blood Pressure and Lifestyle Factors. Circulation, 2018, 137, 653-661.	1.6	169
82	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	1.4	168
83	Genome-wide association study of survival from sepsis due to pneumonia: an observational cohort study. Lancet Respiratory Medicine,the, 2015, 3, 53-60.	5.2	166
84	Genes for blood pressure: an opportunity to understand hypertension. European Heart Journal, 2013, 34, 951-961.	1.0	163
85	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	2.6	159
86	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
87	Potential synergy between lipid-lowering and blood-pressure-lowering in the Anglo-Scandinavian Cardiac Outcomes Trial. European Heart Journal, 2006, 27, 2982-2988.	1.0	146
88	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.	1.3	144
89	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	1.4	141
90	Functional analyses of coronary artery disease associated variation on chromosome 9p21 in vascular smooth muscle cells. Human Molecular Genetics, 2012, 21, 4021-4029.	1.4	136

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91	White Blood Cells and Blood Pressure. Circulation, 2020, 141, 1307-1317.	1.6	125
92	Endothelial C-type natriuretic peptide maintains vascular homeostasis. Journal of Clinical Investigation, 2014, 124, 4039-4051.	3.9	125
93	Association ofWNK1Gene Polymorphisms and Haplotypes With Ambulatory Blood Pressure in the General Population. Circulation, 2005, 112, 3423-3429.	1.6	124
94	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
95	Essential Hypertension in African Caribbeans Associates With a Variant of the Î² 2 -Adrenoceptor. Hypertension, 1997, 30, 773-776.	1.3	123
96	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	2.6	122
97	Ambulatory blood pressure monitoring predicts cardiovascular events in treated hypertensive patients â€“ an Anglo-Scandinavian cardiac outcomes trial substudy. Journal of Hypertension, 2009, 27, 876-885.	0.3	113
98	Pseudoexon Activation as a Novel Mechanism for Disease Resulting in Atypical Growth-Hormone Insensitivity. American Journal of Human Genetics, 2001, 69, 641-646.	2.6	110
99	Advances in Blood Pressure Genomics. Circulation Research, 2013, 112, 1365-1379.	2.0	106
100	Common Variants in Genes Underlying Monogenic Hypertension and Hypotension and Blood Pressure in the General Population. Hypertension, 2008, 51, 1658-1664.	1.3	104
101	NICE hypertension guideline 2011: evidence based evolution. BMJ, The, 2012, 344, e181-e181.	3.0	103
102	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.	5.5	99
103	The Anglo-Scandinavian Cardiac Outcomes Trial: blood pressure-lowering limb: effects in patients with type II diabetes. Journal of Hypertension, 2008, 26, 2103-2111.	0.3	98
104	Targeting 160 Candidate Genes for Blood Pressure Regulation with a Genome-Wide Genotyping Array. PLoS ONE, 2009, 4, e6034.	1.1	98
105	Genome-wide association study of genetic determinants of LDL-c response to atorvastatin therapy: importance of Lp(a). Journal of Lipid Research, 2012, 53, 1000-1011.	2.0	97
106	Common Variants in the ATP2B1 Gene Are Associated With Susceptibility to Hypertension. Hypertension, 2010, 56, 973-980.	1.3	96
107	ADAMTS7 Cleavage and Vascular Smooth Muscle Cell Migration Is Affected by a Coronary-Artery-Disease-Associated Variant. American Journal of Human Genetics, 2013, 92, 366-374.	2.6	95
108	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94

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109	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
110	Haplotypes of the WNK1 gene associate with blood pressure variation in a severely hypertensive population from the British Genetics of Hypertension study. Human Molecular Genetics, 2005, 14, 1805-1814.	1.4	91
111	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91
112	Evaluation of the Angiotensinogen Locus in Human Essential Hypertension. Hypertension, 1998, 31, 725-729.	1.3	89
113	Replication of the five novel loci for uric acid concentrations and potential mediating mechanisms. Human Molecular Genetics, 2010, 19, 387-395.	1.4	89
114	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
115	A deleterious gene-by-environment interaction imposed by calcium channel blockers in Marfan syndrome. ELife, 2015, 4, .	2.8	87
116	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
117	The Anglo-Scandinavian Cardiac Outcomes Trial lipid lowering arm: extended observations 2 years after trial closure. European Heart Journal, 2008, 29, 499-508.	1.0	83
118	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
119	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
120	Extracellular volume quantification in isolated hypertension - changes at the detectable limits?. Journal of Cardiovascular Magnetic Resonance, 2015, 17, 74.	1.6	79
121	Genetics of essential hypertension. Human Molecular Genetics, 2004, 13, 169R-175.	1.4	75
122	Nuclear-mitochondrial DNA segments resemble paternally inherited mitochondrial DNA in humans. Nature Communications, 2020, 11, 1740.	5.8	75
123	Predicting deleterious nsSNPs: an analysis of sequence and structural attributes. BMC Bioinformatics, 2006, 7, 217.	1.2	74
124	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, .	1.6	74
125	Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations. American Journal of Human Genetics, 2014, 95, 49-65.	2.6	73
126	Ethnic Differences in Blood Pressure Response to First and Second-Line Antihypertensive Therapies in Patients Randomized in the ASCOT Trial. American Journal of Hypertension, 2010, 23, 1023-1030.	1.0	72

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127	Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals. American Journal of Human Genetics, 2021, 108, 1350-1355.	2.6	72
128	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	0.7	69
129	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	1.1	64
130	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	5.8	59
131	A blood pressure-associated variant of theSLC39A8gene influences cellular cadmium accumulation and toxicity. Human Molecular Genetics, 2016, 25, 4117-4126.	1.4	53
132	Common Genetic Variation Near the Phospholamban Gene Is Associated with Cardiac Repolarisation: Meta-Analysis of Three Genome-Wide Association Studies. PLoS ONE, 2009, 4, e6138.	1.1	53
133	Coronary-Heart-Disease-Associated Genetic Variant at the COL4A1/COL4A2 Locus Affects COL4A1/COL4A2 Expression, Vascular Cell Survival, Atherosclerotic Plaque Stability and Risk of Myocardial Infarction. PLoS Genetics, 2016, 12, e1006127.	1.5	52
134	Two-dimensional genome-scan identifies novel epistatic loci for essential hypertension. Human Molecular Genetics, 2006, 15, 1365-1374.	1.4	50
135	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
136	Angiotensinogen in Human Essential Hypertension. Hypertension, 1996, 28, 1123-1125.	1.3	44
137	Polymorphisms in the WNK1 Gene Are Associated with Blood Pressure Variation and Urinary Potassium Excretion. PLoS ONE, 2009, 4, e5003.	1.1	43
138	Use of whole genome sequencing to determine genetic basis of suspected mitochondrial disorders: cohort study. BMJ, The, 2021, 375, e066288.	3.0	42
139	Joint UK societiesâ€™ 2014 consensus statement on renal denervation for resistant hypertension. Heart, 2015, 101, 10-16.	1.2	41
140	Over 1000 genetic loci influencing blood pressure with multiple systems and tissues implicated. Human Molecular Genetics, 2019, 28, R151-R161.	1.4	39
141	Population Genomics of Cardiometabolic Traits: Design of the University College London-London School of Hygiene and Tropical Medicine-Edinburgh-Bristol (UCLEB) Consortium. PLoS ONE, 2013, 8, e71345.	1.1	39
142	Genetics of Hypertension. Drugs, 1998, 56, 203-214.	4.9	38
143	Polymorphic Variation in the 11Î²-Hydroxylase Gene Associates With Reduced 11-Hydroxylase Efficiency. Hypertension, 2007, 49, 113-119.	1.3	37
144	Uncovering genetic mechanisms of hypertension through multi-omic analysis of the kidney. Nature Genetics, 2021, 53, 630-637.	9.4	37

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145	Scaling national and international improvement in virtual gene panel curation via a collaborative approach to discordance resolution. American Journal of Human Genetics, 2021, 108, 1551-1557.	2.6	36
146	Common Polymorphisms in the CYP11B1 and CYP11B2 Genes: Evidence for a Digenic Influence on Hypertension. Hypertension, 2013, 61, 232-239.	1.3	35
147	Mendelian randomisation analyses find pulmonary factors mediate the effect of height on coronary artery disease. Communications Biology, 2019, 2, 119.	2.0	35
148	Glutathione S-transferase variants and hypertension. Journal of Hypertension, 2008, 26, 1343-1352.	0.3	34
149	Chromosome 2p Shows Significant Linkage to Antihypertensive Response in the British Genetics of Hypertension Study. Hypertension, 2006, 47, 603-608.	1.3	33
150	Impact of amlodipine-based therapy among older and younger patients in the Anglo-Scandinavian Cardiac Outcomes Trialâ^'Blood Pressure Lowering Arm (ASCOT-BPLA). Journal of Hypertension, 2011, 29, 583-591.	0.3	32
151	Identification and validation of a novel pathogenic variant in <scp>GDF2</scp> (<scp>BMP9</scp>) responsible for hereditary hemorrhagic telangiectasia and pulmonary arteriovenous malformations. American Journal of Medical Genetics, Part A, 2022, 188, 959-964.	0.7	32
152	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	1.4	31
153	Exploring hypertension genomeâ€wide association studies findings and impact on pathophysiology, pathways, and pharmacogenetics. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2015, 7, 73-90.	6.6	30
154	Renal artery sympathetic denervation: observations from the UK experience. Clinical Research in Cardiology, 2016, 105, 544-552.	1.5	30
155	Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363.	1.4	29
156	Genome-wide association meta-analysis of 30,000 samples identifies seven novel loci for quantitative ECG traits. European Journal of Human Genetics, 2019, 27, 952-962.	1.4	29
157	Meta-analysis of genome-wide association studies of HDL cholesterol response to statins. Journal of Medical Genetics, 2016, 53, 835-845.	1.5	28
158	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. Journal of the American College of Cardiology, 2019, 73, 3118-3131.	1.2	27
159	Biallelic Mutation of ARHGEF18, Involved in the Determination of Epithelial Apicobasal Polarity, Causes Adult-Onset Retinal Degeneration. American Journal of Human Genetics, 2017, 100, 334-342.	2.6	26
160	Possible association but no linkage of the HSD11B2 gene encoding the kidney isozyme of 11Î²-hydroxysteroid dehydrogenase to hypertension in Black people. Clinical Endocrinology, 2001, 55, 249-252.	1.2	24
161	Impact of atorvastatin among older and younger patients in the Anglo-Scandinavian Cardiac Outcomes Trial Lipid-Lowering Arm. Journal of Hypertension, 2011, 29, 592-599.	0.3	24
162	Novel polymorphic AluYb8 insertion in the WNK1 gene is associated with blood pressure variation in Europeans. Human Mutation, 2011, 32, 806-814.	1.1	23

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163	The role of pharmacogenomics in contemporary cardiovascular therapy: a position statement from the European Society of Cardiology Working Group on Cardiovascular Pharmacotherapy. European Heart Journal - Cardiovascular Pharmacotherapy, 2022, 8, 85-99.	1.4	23
164	Genetics of hypertension. Current Opinion in Genetics and Development, 2000, 10, 325-329.	1.5	22
165	Linkage Analysis Using Co-Phenotypes in the BRIGHT Study Reveals Novel Potential Susceptibility Loci for Hypertension. American Journal of Human Genetics, 2006, 79, 323-331.	2.6	22
166	Increased Support for Linkage of a Novel Locus on Chromosome 5q13 for Essential Hypertension in the British Genetics of Hypertension Study. Hypertension, 2006, 48, 105-111.	1.3	22
167	Increased NBCn1 expression, Na ⁺ /HCO ₃ ⁻ co-transport and intracellular pH in human vascular smooth muscle cells with a risk allele for hypertension. Human Molecular Genetics, 2017, 26, ddx015.	1.4	21
168	The biological impact of blood pressure-associated genetic variants in the natriuretic peptide receptor C gene on human vascular smooth muscle. Human Molecular Genetics, 2018, 27, 199-210.	1.4	21
169	Hypertension genomics and cardiovascular prevention. Annals of Translational Medicine, 2018, 6, 291-291.	0.7	21
170	Haplotypes of the ??2-adrenergic receptor gene are associated with essential hypertension in a Singaporean Chinese population. Journal of Hypertension, 2004, 22, 2111-2116.	0.3	20
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172	Heteroplasmic mitochondrial DNA variants in cardiovascular diseases. PLoS Genetics, 2022, 18, e1010068.	1.5	19
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