Patricia B Munroe

List of Publications by Year
in descending order

221	50,732	5268	1715
papers	citations	83 h-index	213 g-index

243	243	243	47500
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	27.8	3,249
3	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
4	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
5	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
6	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
7	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
8	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	21.4	1,572
9	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
10	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. Nature Genetics, 2007, 39, 1329-1337.	21.4	1,298
11	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	21.4	1,179
12	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	21.4	1,104
13	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
14	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.	21.4	836
15	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
16	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
17	Genome-wide association analysis identifies 20 loci that influence adult height. Nature Genetics, 2008, 40, 575-583.	21.4	742
18	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	27.8	737

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19	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
20	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. Nature Genetics, 2010, 42, 436-440.	21.4	581
21	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
22	Meta-Analysis of 28,141 Individuals Identifies Common Variants within Five New Loci That Influence Uric Acid Concentrations. PLoS Genetics, 2009, 5, e1000504.	3.5	572
23	Linkage of the Angiotensinogen Gene to Essential Hypertension. New England Journal of Medicine, 1994, 330, 1629-1633.	27.0	544
24	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
25	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	21.4	501
26	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
27	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
28	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	3.5	453
29	The Metabochip, a Custom Genotyping Array for Genetic Studies of Metabolic, Cardiovascular, and Anthropometric Traits. PLoS Genetics, 2012, 8, e1002793.	3.5	448
30	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	12.6	438
31	Artificial intelligence and machine learning to fight COVID-19. Physiological Genomics, 2020, 52, 200-202.	2.3	431
32	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
33	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
34	Genome-wide Association Study Identifies Genes for Biomarkers of Cardiovascular Disease: Serum Urate and Dyslipidemia. American Journal of Human Genetics, 2008, 82, 139-149.	6.2	397
35	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	3.5	371
36	Mutations in the gene encoding the human matrix Gla protein cause Keutel syndrome. Nature Genetics, 1999, 21, 142-144.	21.4	362

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37	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
38	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
39	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
40	Concept, Design and Implementation of a Cardiovascular Gene-Centric 50 K SNP Array for Large-Scale Genomic Association Studies. PLoS ONE, 2008, 3, e3583.	2.5	339
41	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	21.4	328
42	Genome-Wide Association Study of Blood Pressure Extremes Identifies Variant near UMOD Associated with Hypertension. PLoS Genetics, 2010, 6, e1001177.	3.5	312
43	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	21.4	308
44	SLC2A9 Is a High-Capacity Urate Transporter in Humans. PLoS Medicine, 2008, 5, e197.	8.4	305
45	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
46	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
47	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
48	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
49	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
50	Genome-wide mapping of human loci for essential hypertension. Lancet, The, 2003, 361, 2118-2123.	13.7	247
51	Genetic loci influencing kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 373-375.	21.4	246
52	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
53	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
54	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. Nature Communications, 2014, 5, 5068.	12.8	216

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55	Genetic Evidence for a Normal-Weight â€œMetabolically Obeseâ€•Phenotype Linking Insulin Resistance, Hypertension, Coronary Artery Disease, and Type 2 Diabetes. Diabetes, 2014, 63, 4369-4377.	0.6	185
56	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
57	Spectrum of Mutations in the Batten Disease Gene, CLN3. American Journal of Human Genetics, 1997, 61, 310-316.	6.2	181
58	Association of Hypertension Drug Target Genes With Blood Pressure and Hypertension in 86 588 Individuals. Hypertension, 2011, 57, 903-910.	2.7	181
59	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
60	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.	2.9	170
61	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.	2.9	168
62	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	6.2	159
63	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
64	Investigating the Causal Relationship of C-Reactive Protein with 32 Complex Somatic and Psychiatric Outcomes: A Large-Scale Cross-Consortium Mendelian Randomization Study. PLoS Medicine, 2016, 13, e1001976.	8.4	150
65	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
66	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. PLoS Genetics, 2013, 9, e1003796.	3.5	142
67	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	2.9	141
68	Genome-Wide Analysis of Left Ventricular Image-Derived Phenotypes Identifies Fourteen Loci Associated With Cardiac Morphogenesis and Heart Failure Development. Circulation, 2019, 140, 1318-1330.	1.6	138
69	Identification of genomic loci associated with resting heart rate and shared genetic predictors with all-cause mortality. Nature Genetics, 2016, 48, 1557-1563.	21.4	131
70	Association of WNK1 Gene Polymorphisms and Haplotypes With Ambulatory Blood Pressure in the General Population. Circulation, 2005, 112, 3423-3429.	1.6	124
71	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
72	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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73	Vitamin D and high blood pressure: causal association or epiphenomenon?. European Journal of Epidemiology, 2014, 29, 1-14.	5.7	117
74	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
75	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
76	Pseudoexon Activation as a Novel Mechanism for Disease Resulting in Atypical Growth-Hormone Insensitivity. American Journal of Human Genetics, 2001, 69, 641-646.	6.2	110
77	Cystatin C and Cardiovascular Disease. Journal of the American College of Cardiology, 2016, 68, 934-945.	2.8	109
78	Advances in Blood Pressure Genomics. Circulation Research, 2013, 112, 1365-1379.	4.5	106
79	Reaching the End-Game for GWAS: Machine Learning Approaches for the Prioritization of Complex Disease Loci. Frontiers in Genetics, 2020, 11, 350.	2.3	106
80	Common Variation in the NOS1AP Gene Is Associated With Drug-Induced QT Prolongation and Ventricular Arrhythmia. Journal of the American College of Cardiology, 2012, 60, 841-850.	2.8	101
81	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
82	Targeting 160 Candidate Genes for Blood Pressure Regulation with a Genome-Wide Genotyping Array. PLoS ONE, 2009, 4, e6034.	2.5	98
83	Common Variants in the ATP2B1 Gene Are Associated With Susceptibility to Hypertension. Hypertension, 2010, 56, 973-980.	2.7	96
84	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
85	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.	2.2	93
86	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.	2.9	91
87	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
88	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
89	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
90	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85

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91	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
92	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
93	Genetics of essential hypertension. Human Molecular Genetics, 2004, 13, 169R-175.	2.9	75
94	Prognostic Significance of Left Ventricular Noncompaction. Circulation: Cardiovascular Imaging, 2020, 13, e009712.	2.6	74
95	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.	6.2	73
96	A model for Batten disease protein CLN3: Functional implications from homology and mutations. FEBS Letters, 1996, 399, 75-77.	2.8	71
97	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
98	Thirty loci identified for heart rate response to exercise and recovery implicate autonomic nervous system. Nature Communications, 2018, 9, 1947.	12.8	70
99	Association Between Ambient Air Pollution and Cardiac Morpho-Functional Phenotypes. Circulation, 2018, 138, 2175-2186.	1.6	70
100	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.	1.3	69
101	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
102	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	64
103	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62
104	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
105	Causal Inference for Genetic Obesity, Cardiometabolic Profile and COVID-19 Susceptibility: A Mendelian Randomization Study. Frontiers in Genetics, 2020, 11, 586308.	2.3	56
106	Multiancestry Study of Geneâ€“Lifestyle Interactions for Cardiovascular Traits in 610 475 Individuals From 124 Cohorts. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	55
107	Molecular basis of the neuronal ceroid lipofuscinoses: Mutations inCLN1,CLN2,CLN3, andCLN5. Human Mutation, 1999, 14, 199-215.	2.5	54
108	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.	2.5	53

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109	Two-dimensional genome-scan identifies novel epistatic loci for essential hypertension. Human Molecular Genetics, 2006, 15, 1365-1374.	2.9	50
110	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
111	Genomic Structure and Complete Nucleotide Sequence of the Batten Disease Gene,CLN3. Genomics, 1997, 40, 346-350.	2.9	47
112	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. Genome Biology, 2018, 19, 87.	8.8	47
113	Polymorphisms in the WNK1 Gene Are Associated with Blood Pressure Variation and Urinary Potassium Excretion. PLoS ONE, 2009, 4, e5003.	2.5	43
114	Quantifying the extent to which index event biases influence large genetic association studies. Human Molecular Genetics, 2017, 26, ddw433.	2.9	40
115	Over 1000 genetic loci influencing blood pressure with multiple systems and tissues implicated. Human Molecular Genetics, 2019, 28, R151-R161.	2.9	39
116	Polymorphic Variation in the 11Î²-Hydroxylase Gene Associates With Reduced 11-Hydroxylase Efficiency. Hypertension, 2007, 49, 113-119.	2.7	37
117	Gut microbiome-based supervised machine learning for clinical diagnosis of inflammatory bowel diseases. American Journal of Physiology - Renal Physiology, 2021, 320, G328-G337.	3.4	36
118	Common Polymorphisms in the CYP11B1 and CYP11B2 Genes: Evidence for a Digenic Influence on Hypertension. Hypertension, 2013, 61, 232-239.	2.7	35
119	Differentially expressed genes for atrial fibrillation identified by RNA sequencing from paired human left and right atrial appendages. Physiological Genomics, 2019, 51, 323-332.	2.3	35
120	Glutathione S-transferase variants and hypertension. Journal of Hypertension, 2008, 26, 1343-1352.	0.5	34
121	Genome-Wide Association Study on Plasma Levels of Midregional-Proadrenomedullin and C-Terminal-Pro-Endothelin-1. Hypertension, 2013, 61, 602-608.	2.7	34
122	Chromosome 2p Shows Significant Linkage to Antihypertensive Response in the British Genetics of Hypertension Study. Hypertension, 2006, 47, 603-608.	2.7	33
123	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.	2.9	31
124	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
125	Meta-Analysis of Dilated Cardiomyopathy Using Cardiac RNA-Seq Transcriptomic Datasets. Genes, 2020, 11, 60.	2.4	30
126	Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363.	2.9	29

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127	Long-term intra-individual reproducibility of heart rate dynamics during exercise and recovery in the UK Biobank cohort. PLoS ONE, 2017, 12, e0183732.	2.5	29
128	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.	2.8	29
129	Four Genetic Loci Influencing Electrocardiographic Indices of Left Ventricular Hypertrophy. Circulation: Cardiovascular Genetics, 2011, 4, 626-635.	5.1	28
130	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
131	Meta-analysis of genome-wide association studies of HDL cholesterol response to statins. Journal of Medical Genetics, 2016, 53, 835-845.	3.2	28
132	Genome-wide association study identifies loci for arterial stiffness index in 127,121 UK Biobank participants. Scientific Reports, 2019, 9, 9143.	3.3	28
133	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
134	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
135	Full-field ERG in patients with Batten/Spielmeyer-Vogt disease caused by mutations in the CLN3 gene. Ophthalmic Genetics, 2000, 21, 69-77.	1.2	26
136	The Effect of Blood Lipids on the LeftÂVentricle. Journal of the American College of Cardiology, 2020, 76, 2477-2488.	2.8	26
137	Vitamin D and coronavirus disease 2019 (COVID-19): rapid evidence review. Aging Clinical and Experimental Research, 2021, 33, 2031-2041.	2.9	26
138	Cardiovascular Risk Factors and MRI Markers of Cerebral Small Vessel Disease. Neurology, 2022, 98, .	1.1	26
139	State of the Art Review on Genetics and Precision Medicine in Arrhythmogenic Cardiomyopathy. International Journal of Molecular Sciences, 2020, 21, 6615.	4.1	25
140	Frequency, Penetrance, and Variable Expressivity of Dilated Cardiomyopathyâ€“Associated Putative Pathogenic Gene Variants in UK Biobank Participants. Circulation, 2022, 146, 110-124.	1.6	25
141	Bone marrow mononuclear cells reduce myocardial reperfusion injury by activating the PI3K/Akt survival pathway. Atherosclerosis, 2010, 213, 67-76.	0.8	24
142	Novel polymorphic AluYb8 insertion in the WNK1 gene is associated with blood pressure variation in Europeans. Human Mutation, 2011, 32, 806-814.	2.5	23
143	Genetics of hypertension. Current Opinion in Genetics and Development, 2000, 10, 325-329.	3.3	22
144	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.	6.2	22

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145	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.	2.7	22
146	Genetic invalidation of Lp-PLA2 as a therapeutic target: Large-scale study of five functional Lp-PLA2-lowering alleles. European Journal of Preventive Cardiology, 2017, 24, 492-504.	1.8	22
147	Age, sex and disease-specific associations between resting heart rate and cardiovascularÂmortality in the UK BIOBANK. PLoS ONE, 2020, 15, e0233898.	2.5	22
148	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.	2.9	21
149	Genomeâ€Wide Metaâ€Analysis of Blood Pressure Response to Î² ₁ â€Blockers: Results From ICAPS (International Consortium of Antihypertensive Pharmacogenomics Studies). Journal of the American Heart Association, 2019, 8, e013115.	3.7	21
150	Hypertension genetics past, present and future applications. Journal of Internal Medicine, 2021, 290, 1130-1152.	6.0	20
151	Genome-Wide Association Studies Will Unlock the Genetic Basis of Hypertension. Hypertension, 2010, 56, 1017-1020.	2.7	19
152	Analysis with the exome array identifies multiple new independent variants in lipid loci. Human Molecular Genetics, 2016, 25, 4094-4106.	2.9	19
153	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	3.6	19
154	Heteroplasmic mitochondrial DNA variants in cardiovascular diseases. PLoS Genetics, 2022, 18, e1010068.	3.5	19
155	Genome-wide association analysis reveals insights into the genetic architecture of right ventricular structure and function. Nature Genetics, 2022, 54, 783-791.	21.4	19
156	Structure of the CLN3 Gene and Predicted Structure, Location and Function of CLN3 Protein. Neuropediatrics, 1997, 28, 12-14.	0.6	18
157	Postmortem Genetic Testing for Cardiac Ion Channelopathies in Stillbirths. Circulation Genomic and Precision Medicine, 2018, 11, e001817.	3.6	18
158	Genetic association analysis of inositol polyphosphate phosphatase-like 1 (INPPL1, SHIP2) variants with essential hypertension. Journal of Medical Genetics, 2007, 44, 603-605.	3.2	17
159	Genome-Wide Analysis of Blood Pressure Variability and Ischemic Stroke. Stroke, 2013, 44, 2703-2709.	2.0	17
160	Emerging applications of genome-editing technology to examine functionality of GWAS-associated variants for complex traits. Physiological Genomics, 2018, 50, 510-522.	2.3	17
161	Repeatability of Cardiac Magnetic Resonance Radiomics: A Multi-Centre Multi-Vendor Test-Retest Study. Frontiers in Cardiovascular Medicine, 2020, 7, 586236.	2.4	17
162	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

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163	Adverse cardiovascular magnetic resonance phenotypes are associated with greater likelihood of incident coronavirus disease 2019: findings from the UK Biobank. Aging Clinical and Experimental Research, 2021, 33, 1133-1144.	2.9	17
164	Absence of linkage of the epithelial sodium channel to hypertension in black Caribbeans. American Journal of Hypertension, 1998, 11, 942-945.	2.0	16
165	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2020, 13, 387-395.	3.6	16
166	Machine learning-based classification and diagnosis of clinical cardiomyopathies. Physiological Genomics, 2020, 52, 391-400.	2.3	15
167	No Clinically Relevant Effect of Heart Rate Increase and Heart Rate Recovery During Exercise on Cardiovascular Disease: A Mendelian Randomization Analysis. Frontiers in Genetics, 2021, 12, 569323.	2.3	15
168	KCND3 potassium channel gene variant confers susceptibility to electrocardiographic early repolarization pattern. JCI Insight, 2019, 4, .	5.0	15
169	Common Polymorphisms at the CYP17A1 Locus Associate With Steroid Phenotype. Hypertension, 2016, 67, 724-732.	2.7	14
170	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
171	Common Genetic Variants Modulate the Electrocardiographic Tpeak-to-Tend Interval. American Journal of Human Genetics, 2020, 106, 764-778.	6.2	14
172	The role of GRIP1 and ephrin B3 in blood pressure control and vascular smooth muscle cell contractility. Scientific Reports, 2016, 6, 38976.	3.3	13
173	Cardiovascular Predictive Value and Genetic Basis of Ventricular Repolarization Dynamics. Circulation: Arrhythmia and Electrophysiology, 2019, 12, e007549.	4.8	13
174	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
175	Women With Diabetes Are at Increased Relative Risk of Heart Failure Compared to Men: Insights From UK Biobank. Frontiers in Cardiovascular Medicine, 2021, 8, 658726.	2.4	13
176	Strategy for Mutation Detection in CLN3: Characterisation of Two Finnish Mutations. Neuropediatrics, 1997, 28, 15-17.	0.6	12
177	The genetic architecture of blood pressure variation. Current Cardiovascular Risk Reports, 2009, 3, 418-425.	2.0	12
178	Genetic Basis and Prognostic Value of Exercise QT Dynamics. Circulation Genomic and Precision Medicine, 2020, 13, e002774.	3.6	12
179	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	2.7	12
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