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	Cardiovascular Risk Factors and MRI Markers of Cerebral Small Vessel Disease. Neurology, 2022, 98, .	1.1	26
2	Heteroplasmic mitochondrial DNA variants in cardiovascular diseases. PLoS Genetics, 2022, 18, e1010068.	3.5	19
3	Geneâ€“Environment Correlation over Time: A Longitudinal Analysis of Polygenic Risk Scores for Schizophrenia and Major Depression in Three British Cohorts Studies. Genes, 2022, 13, 1136.	2.4	1
4	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
5	Polygenic scores for schizophrenia and major depression are associated with psychosocial risk factors in children: evidence of geneâ€“environment correlation. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2022, 63, 1140-1152.	5.2	4
6	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
7	Prediction of Coronary Artery Disease and Major Adverse Cardiovascular Events Using Clinical and Genetic Risk Scores for Cardiovascular Risk Factors. Circulation Genomic and Precision Medicine, 2022, 15, .	3.6	1
8	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
9	A Method to Minimise the Impact of ECG Marker Inaccuracies on the Spatial QRS-T angle: Evaluation on 1,512 Manually Annotated ECGs. Biomedical Signal Processing and Control, 2021, 64, 102305.	5.7	6
10	Analysing electrocardiographic traits and predicting cardiac risk in UK biobank. JRSM Cardiovascular Disease, 2021, 10, 204800402110236.	0.7	2
11	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
12	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
13	An Academic Clinicianâ€™s Road Map to Hypertension Genomics. Hypertension, 2021, 77, 284-295.	2.7	9
14	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
15	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
16	The role of resistance to inhibitors of cholinesterase 8b in the control of heart rate. Physiological Genomics, 2021, 53, 150-159.	2.3	1
17	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
18	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

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19	Genome-wide association study of cardiac troponin I in the general population. Human Molecular Genetics, 2021, 30, 2027-2039.	2.9	11
20	Associations of Meat and Fish Consumption With Conventional and Radiomics Cardiovascular Magnetic Resonance Phenotypes in the UK Biobank. Frontiers in Cardiovascular Medicine, 2021, 8, 667849.	2.4	7
21	A Novel Two-Stage Heart Arrhythmia Ensemble Classifier. Computers, 2021, 10, 60.	3.3	7
22	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
23	Vitamin D and coronavirus disease 2019 (COVID-19): rapid evidence review. Aging Clinical and Experimental Research, 2021, 33, 2031-2041.	2.9	26
24	Genetically Determined Serum Calcium Levels and Markers of Ventricular Repolarization: A Mendelian Randomization Study in the UK Biobank. Circulation Genomic and Precision Medicine, 2021, 14, e003231.	3.6	11
25	Hypertension genetics past, present and future applications. Journal of Internal Medicine, 2021, 290, 1130-1152.	6.0	20
26	Prevalence of Hypertrophic Cardiomyopathy in the UK Biobank Population. JAMA Cardiology, 2021, 6, 852.	6.1	8
27	Genomic and pleiotropic analyses of resting QT interval identifies novel loci and overlap with atrial electrical disorders. Human Molecular Genetics, 2021, 30, 2513-2523.	2.9	5
28	Adverse Cardiovascular Outcomes and Antihypertensive Treatment: A Genomeâ€Wide Interaction Metaâ€Analysis in the International Consortium for Antihypertensive Pharmacogenomics Studies. Clinical Pharmacology and Therapeutics, 2021, 110, 723-732.	4.7	6
29	B-011-01 TRANS-ANCESTRY GWAS OF 252,730 INDIVIDUALS IDENTIFIES 114 NOVEL LOCI ASSOCIATED WITH THE QT INTERVAL. Heart Rhythm, 2021, 18, S473.	0.7	0
30	The Pharmacogenetics of Statin Therapy on Clinical Events: No Evidence that Genetic Variation Affects Statin Response on Myocardial Infarction. Frontiers in Pharmacology, 2021, 12, 679857.	3.5	2
31	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
32	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
33	Genetic variants in TRPM7 associated with unexplained stillbirth modify ion channel function. Human Molecular Genetics, 2020, 29, 1797-1807.	2.9	6
34	Molecular pathophysiology of systemic hypertension. , 2020, , 169-187.		2
35	Causal Inference for Genetic Obesity, Cardiometabolic Profile and COVID-19 Susceptibility: A Mendelian Randomization Study. Frontiers in Genetics, 2020, 11, 586308.	2.3	56
36	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

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37	Repeatability of Cardiac Magnetic Resonance Radiomics: A Multi-Centre Multi-Vendor Test-Retest Study. Frontiers in Cardiovascular Medicine, 2020, 7, 586236.	2.4	17
38	The Effect of Blood Lipids on the LeftÂVentricle. Journal of the American College of Cardiology, 2020, 76, 2477-2488.	2.8	26
39	Machine learning-based classification and diagnosis of clinical cardiomyopathies. Physiological Genomics, 2020, 52, 391-400.	2.3	15
40	The effects of polygenic risk for psychiatric disorders and smoking behaviour on psychotic experiences in UK Biobank. Translational Psychiatry, 2020, 10, 330.	4.8	6
41	State of the Art Review on Genetics and Precision Medicine in Arrhythmogenic Cardiomyopathy. International Journal of Molecular Sciences, 2020, 21, 6615.	4.1	25
42	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2020, 13, 387-395.	3.6	16
43	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
44	Age, sex and disease-specific associations between resting heart rate and cardiovascularÂmortality in the UK BIOBANK. PLoS ONE, 2020, 15, e0233898.	2.5	22
45	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
46	Genetic Basis and Prognostic Value of Exercise QT Dynamics. Circulation Genomic and Precision Medicine, 2020, 13, e002774.	3.6	12
47	Artificial intelligence and machine learning to fight COVID-19. Physiological Genomics, 2020, 52, 200-202.	2.3	431
48	Common Genetic Variants Modulate the Electrocardiographic Tpeak-to-Tend Interval. American Journal of Human Genetics, 2020, 106, 764-778.	6.2	14
49	Meta-Analysis of Dilated Cardiomyopathy Using Cardiac RNA-Seq Transcriptomic Datasets. Genes, 2020, 11, 60.	2.4	30
50	Prognostic Significance of Left Ventricular Noncompaction. Circulation: Cardiovascular Imaging, 2020, 13, e009712.	2.6	74
51	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
52	Poor Bone Quality is Associated With Greater Arterial Stiffness: Insights From the UK Biobank. Journal of Bone and Mineral Research, 2020, 36, 90-99.	2.8	11
53	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
54	Over 1000 genetic loci influencing blood pressure with multiple systems and tissues implicated. Human Molecular Genetics, 2019, 28, R151-R161.	2.9	39

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55	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
56	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
57	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
58	Resting Heart Rate and Type 2 Diabetes. Journal of the American College of Cardiology, 2019, 74, 2175-2177.	2.8	4
59	Cardiovascular Predictive Value and Genetic Basis of Ventricular Repolarization Dynamics. Circulation: Arrhythmia and Electrophysiology, 2019, 12, e007549.	4.8	13
60	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
61	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
62	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
63	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
64	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
65	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
66	Genome-wide association study identifies loci for arterial stiffness index in 127,121 UK Biobank participants. Scientific Reports, 2019, 9, 9143.	3.3	28
67	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
68	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
69	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
70	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	21.4	328
71	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
72	The narrow-sense and common single nucleotide polymorphism heritability of early repolarization. International Journal of Cardiology, 2019, 279, 135-140.	1.7	7

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73	KCND3 potassium channel gene variant confers susceptibility to electrocardiographic early repolarization pattern. JCI Insight, 2019, 4, .	5.0	15
74	Electrolytes and electrophysiology: whatâ€™s next?. Aging, 2019, 11, 7329-7330.	3.1	1
75	Genetics and Genomics of Systemic Hypertension. , 2018, , 723-740.		0
76	Genetic variants in PPARGC1B and CNTN4 are associated with thromboxane A2 formation and with cardiovascular event free survival in the Anglo-Scandinavian Cardiac Outcomes Trial (ASCOT). Atherosclerosis, 2018, 269, 42-49.	0.8	7
77	Postmortem Genetic Testing for Cardiac Ion Channelopathies in Stillbirths. Circulation Genomic and Precision Medicine, 2018, 11, e001817.	3.6	18
78	Heritability of resting heart rate and association with mortality in middle-aged and elderly twins. Heart, 2018, 104, 6-7.	2.9	9
79	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
80	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
81	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
82	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	3.6	19
83	Thirty loci identified for heart rate response to exercise and recovery implicate autonomic nervous system. Nature Communications, 2018, 9, 1947.	12.8	70
84	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
85	Association Between Ambient Air Pollution and Cardiac Morpho-Functional Phenotypes. Circulation, 2018, 138, 2175-2186.	1.6	70
86	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
87	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. Genome Biology, 2018, 19, 87.	8.8	47
88	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
89	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
90	Quantifying the extent to which index event biases influence large genetic association studies. Human Molecular Genetics, 2017, 26, ddw433.	2.9	40

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91	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
92	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
93	A genome-wide interaction analysis of tricyclic/tetracyclic antidepressants and RR and QT intervals: a pharmacogenomics study from the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium. Journal of Medical Genetics, 2017, 54, 313-323.	3.2	9
94	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
95	Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363.	2.9	29
96	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
97	Multiancestry Study of Geneâ€“Lifestyle Interactions for Cardiovascular Traits in 610 475 Individuals From 124 Cohorts. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	55
98	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
99	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
100	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
101	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
102	Meta-analysis of genome-wide association studies of HDL cholesterol response to statins. Journal of Medical Genetics, 2016, 53, 835-845.	3.2	28
103	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
104	A genetic risk score is associated with statin-induced low-density lipoprotein cholesterol lowering. Pharmacogenomics, 2016, 17, 583-591.	1.3	9
105	Cystatin C and Cardiovascular Disease. Journal of the American College of Cardiology, 2016, 68, 934-945.	2.8	109
106	Analysis with the exome array identifies multiple new independent variants in lipid loci. Human Molecular Genetics, 2016, 25, 4094-4106.	2.9	19
107	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
108	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261

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109	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
110	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
111	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
112	Common Polymorphisms at the CYP17A1 Locus Associate With Steroid Phenotype. Hypertension, 2016, 67, 724-732.	2.7	14
113	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	12.6	438
114	Testing the role of predicted gene knockouts in human anthropometric trait variation. Human Molecular Genetics, 2016, 25, 2082-2092.	2.9	10
115	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
116	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
117	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
118	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
119	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
120	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
121	Genome-wide association studies and contribution to cardiovascular physiology. Physiological Genomics, 2015, 47, 365-375.	2.3	11
122	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	64
123	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. Nature Communications, 2014, 5, 5068.	12.8	216
124	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
125	Two Further Blood Pressure Loci Identified in Ion Channel Genes With a Genecentric Approach. Circulation: Cardiovascular Genetics, 2014, 7, 873-879.	5.1	7
126	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

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127	Vitamin D and high blood pressure: causal association or epiphenomenon?. European Journal of Epidemiology, 2014, 29, 1-14.	5.7	117
128	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
129	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
130	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
131	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
132	Protein interaction networks associated with cardiovascular disease and cancer: exploring the effect of bias on shared network properties. International Journal of Data Mining and Bioinformatics, 2014, 9, 339.	0.1	2
133	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
134	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
135	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	2.9	141
136	Common Polymorphisms in the CYP11B1 and CYP11B2 Genes: Evidence for a Digenic Influence on Hypertension. Hypertension, 2013, 61, 232-239.	2.7	35
137	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
138	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
139	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
140	Genome-Wide Analysis of Blood Pressure Variability and Ischemic Stroke. Stroke, 2013, 44, 2703-2709.	2.0	17
141	Genome-Wide Association Study on Plasma Levels of Midregional-Proadrenomedullin and C-Terminal-Pro-Endothelin-1. Hypertension, 2013, 61, 602-608.	2.7	34
142	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. PLoS Genetics, 2013, 9, e1003796.	3.5	142
143	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
144	Advances in Blood Pressure Genomics. Circulation Research, 2013, 112, 1365-1379.	4.5	106

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145	The Metabochip, a Custom Genotyping Array for Genetic Studies of Metabolic, Cardiovascular, and Anthropometric Traits. PLoS Genetics, 2012, 8, e1002793.	3.5	448
146	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
147	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
148	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
149	Integrated Computational and Experimental Analysis of the Neuroendocrine Transcriptome in Genetic Hypertension Identifies Novel Control Points for the Cardiometabolic Syndrome. Circulation: Cardiovascular Genetics, 2012, 5, 430-440.	5.1	6
150	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
151	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
152	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
153	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
154	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	21.4	501
155	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
156	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	6.2	159
157	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
158	Association of Hypertension Drug Target Genes With Blood Pressure and Hypertension in 86 588 Individuals. Hypertension, 2011, 57, 903-910.	2.7	181
159	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
160	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
161	Four Genetic Loci Influencing Electrocardiographic Indices of Left Ventricular Hypertrophy. Circulation: Cardiovascular Genetics, 2011, 4, 626-635.	5.1	28
162	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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163	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	27.8	3,249
164	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
165	Genetic loci influencing kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 373-375.	21.4	246
166	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. Nature Genetics, 2010, 42, 436-440.	21.4	581
167	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
168	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
169	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	21.4	308
170	Genome-Wide Association Studies Will Unlock the Genetic Basis of Hypertension. Hypertension, 2010, 56, 1017-1020.	2.7	19
171	Common Variants in the ATP2B1 Gene Are Associated With Susceptibility to Hypertension. Hypertension, 2010, 56, 973-980.	2.7	96
172	Genome-Wide Association Study of Blood Pressure Extremes Identifies Variant near UMOD Associated with Hypertension. PLoS Genetics, 2010, 6, e1001177.	3.5	312
173	Bone marrow mononuclear cells reduce myocardial reperfusion injury by activating the PI3K/Akt survival pathway. Atherosclerosis, 2010, 213, 67-76.	0.8	24
174	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	3.5	453
175	Polymorphisms in the WNK1 Gene Are Associated with Blood Pressure Variation and Urinary Potassium Excretion. PLoS ONE, 2009, 4, e5003.	2.5	43
176	Targeting 160 Candidate Genes for Blood Pressure Regulation with a Genome-Wide Genotyping Array. PLoS ONE, 2009, 4, e6034.	2.5	98
177	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
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