Alanna C Morrison

List of Publications by Year
in descending order

226 papers	23,559 citations	14655 66 h-index	10734 138 g-index
257 all docs	257 docs citations	257 times ranked	30822 citing authors

#	Article	IF	Citations
1	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	21.4	2,054
2	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
3	Genome-wide association study of blood pressure and hypertension. Nature Genetics, 2009, 41, 677-687.	21.4	1,224
4	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
5	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
6	Diagnostic Yield and Clinical Utility of Sequencing Familial Hypercholesterolemia Genes in Patients With Severe Hypercholesterolemia. Journal of the American College of Cardiology, 2016, 67, 2578-2589.	2.8	723
7	Meta-analyses of genome-wide association studies identify multiple loci associated with pulmonary function. Nature Genetics, 2010, 42, 45-52.	21.4	549
8	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
9	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	12.8	466
10	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
11	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
12	Inactivating Mutations in NPC1L1 and Protection from Coronary Heart Disease. New England Journal of Medicine, 2014, 371, 2072-2082.	27.0	386
13	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	7.1	376
14	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	21.4	367
15	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
16	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
17	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
18	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	6.2	326

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19	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. American Journal of Human Genetics, 2014, 94, 223-232.	6.2	287
20	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
21	Prediction of Coronary Heart Disease Risk using a Genetic Risk Score: The Atherosclerosis Risk in Communities Study. American Journal of Epidemiology, 2007, 166, 28-35.	3.4	249
22	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	27.8	248
23	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	21.4	223
24	ACAT: A Fast and Powerful p Value Combination Method for Rare-Variant Analysis in Sequencing Studies. American Journal of Human Genetics, 2019, 104, 410-421.	6.2	219
25	CD163+ macrophages promote angiogenesis and vascular permeability accompanied by inflammation in atherosclerosis. Journal of Clinical Investigation, 2018, 128, 1106-1124.	8.2	209
26	KLB is associated with alcohol drinking, and its gene product Î²-Klotho is necessary for FGF21 regulation of alcohol preference. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14372-14377.	7.1	208
27	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations. PLoS Genetics, 2019, 15, e1008500.	3.5	203
28	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. American Journal of Human Genetics, 2013, 93, 545-554.	6.2	189
29	Association of Genome-Wide Variation With the Risk of Incident Heart Failure in Adults of European and African Ancestry. Circulation: Cardiovascular Genetics, 2010, 3, 256-266.	5.1	176
30	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
31	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
32	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
33	Genome-Wide Association Studies Identify CHRNA5/3 and HTR4 in the Development of Airflow Obstruction. American Journal of Respiratory and Critical Care Medicine, 2012, 186, 622-632.	5.6	164
34	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	6.2	154
35	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. Journal of the American College of Cardiology, 2019, 73, 58-66.	2.8	147
36	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	21.4	146

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37	Plasma MCP-1 level and risk for peripheral arterial disease and incident coronary heart disease: Atherosclerosis Risk in Communities study. Atherosclerosis, 2005, 183, 301-307.	0.8	139
38	Genome-wide association analysis identifies multiple loci related to resting heart rate. Human Molecular Genetics, 2010, 19, 3885-3894.	2.9	133
39	Whole-genome sequenceâ€“based analysis of high-density lipoprotein cholesterol. Nature Genetics, 2013, 45, 899-901.	21.4	132
40	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	131
41	Genome-Wide Joint Meta-Analysis of SNP and SNP-by-Smoking Interaction Identifies Novel Loci for Pulmonary Function. PLoS Genetics, 2012, 8, e1003098.	3.5	130
42	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
43	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	12.8	119
44	Duffy antigen receptor for chemokines (Darc) polymorphism regulates circulating concentrations of monocyte chemoattractant protein-1 and other inflammatory mediators. Blood, 2010, 115, 5289-5299.	1.4	113
45	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
46	Gene-Age Interactions in Blood Pressure Regulation: A Large-Scale Investigation with the CHARGE, Global BPgen, and ICBP Consortia. American Journal of Human Genetics, 2014, 95, 24-38.	6.2	109
47	Cystatin C and Cardiovascular Disease. Journal of the American College of Cardiology, 2016, 68, 934-945.	2.8	109
48	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	1.1	107
49	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. Journal of Clinical Investigation, 2017, 127, 1798-1812.	8.2	106
50	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 260-274.	6.2	103
51	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. Circulation, 2019, 139, 620-635.	1.6	102
52	Association of Clonal Hematopoiesis With Incident HeartÂFailure. Journal of the American College of Cardiology, 2021, 78, 42-52.	2.8	101
53	Prospective Study of Epigenetic Age Acceleration and Incidence of Cardiovascular Disease Outcomes in the ARIC Study (Atherosclerosis Risk in Communities). Circulation Genomic and Precision Medicine, 2018, 11, e001937.	3.6	97
54	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

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55	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. Nature Genetics, 2017, 49, 1560-1563.	21.4	93
56	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
57	Five common gene variants identify elevated genetic risk for coronary heart disease. Genetics in Medicine, 2007, 9, 682-689.	2.4	90
58	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	3.7	89
59	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	3.5	88
60	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. Stroke, 2022, 53, 788-797.	2.0	88
61	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976.	12.8	85
62	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
63	Genetic Determinants Influencing Human Serum Metabolome among African Americans. PLoS Genetics, 2014, 10, e1004212.	3.5	84
64	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
65	G-Protein Î²3 Subunit and Î±-Adducin Polymorphisms and Risk of Subclinical and Clinical Stroke. Stroke, 2001, 32, 822-829.	2.0	83
66	Genomic Variation Associated With Mortality Among Adults of European and African Ancestry With Heart Failure. Circulation: Cardiovascular Genetics, 2010, 3, 248-255.	5.1	80
67	ADD1460W Allele Associated With Cardiovascular Disease in Hypertensive Individuals. Hypertension, 2002, 39, 1053-1057.	2.7	79
68	Combined admixture mapping and association analysis identifies a novel blood pressure genetic locus on 5p13: contributions from the CARe consortium. Human Molecular Genetics, 2011, 20, 2285-2295.	2.9	77
69	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	12.0	75
70	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
71	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	2.9	73
72	Inherited coding variants at the CDKN2A locus influence susceptibility to acute lymphoblastic leukaemia in children. Nature Communications, 2015, 6, 7553.	12.8	72

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73	Common and rare von Willebrand factor (VWF) coding variants, VWF levels, and factor VIII levels in African Americans: the NHLBI Exome Sequencing Project. Blood, 2013, 122, 590-597.	1.4	70
74	Genome-Wide Association Study for Incident Myocardial Infarction and Coronary Heart Disease in Prospective Cohort Studies: The CHARGE Consortium. PLoS ONE, 2016, 11, e0144997.	2.5	69
75	Metabolomic Pattern Predicts Incident Coronary Heart Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 1475-1482.	2.4	65
76	Replication of the Wellcome Trust genome-wide association study of essential hypertension: the Family Blood Pressure Program. European Journal of Human Genetics, 2008, 16, 1507-1511.	2.8	64
77	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
78	American Heart Associationâ€™s Lifeâ€™s Simple 7: Lifestyle Recommendations, Polygenic Risk, and Lifetime Risk of Coronary Heart Disease. Circulation, 2022, 145, 808-818.	1.6	63
79	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
80	GWAS for male-pattern baldness identifies 71 susceptibility loci explaining 38% of the risk. Nature Communications, 2017, 8, 1584.	12.8	61
81	Resequencing and Clinical Associations of the 9p21.3 Region. Circulation, 2013, 127, 799-810.	1.6	58
82	Causal Role of Alcohol Consumption in an Improved Lipid Profile: The Atherosclerosis Risk in Communities (ARIC) Study. PLoS ONE, 2016, 11, e0148765.	2.5	57
83	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	1.4	55
84	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. PLoS ONE, 2014, 9, e100776.	2.5	52
85	Genome-Wide Association Study of Gene by Smoking Interactions in Coronary Artery Calcification. PLoS ONE, 2013, 8, e74642.	2.5	51
86	Practical Approaches for Whole-Genome Sequence Analysis of Heart- and Blood-Related Traits. American Journal of Human Genetics, 2017, 100, 205-215.	6.2	50
87	Analysis of loss-of-function variants and 20 risk factor phenotypes in 8,554 individuals identifies loci influencing chronic disease. Nature Genetics, 2015, 47, 640-642.	21.4	49
88	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	12.8	49
89	Diabetes Genes and Prostate Cancer in the Atherosclerosis Risk in Communities Study. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 558-565.	2.5	48
90	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48

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91	A Genome-wide Association Study Discovers 46 Loci of the Human Metabolome in the Hispanic Community Health Study/Study of Latinos. American Journal of Human Genetics, 2020, 107, 849-863.	6.2	48
92	Secondary findings and carrier test frequencies in a large multiethnic sample. Genome Medicine, 2015, 7, 54.	8.2	47
93	Direct Estimates of the Genomic Contributions to Blood Pressure Heritability within a Population-Based Cohort (ARIC). PLoS ONE, 2015, 10, e0133031.	2.5	47
94	Sodium Intake and Cardiovascular Disease. Annual Review of Public Health, 2011, 32, 71-90.	17.4	46
95	Mining gold dust under the genome wide significance level: a twoâ€stage approach to analysis of GWAS. Genetic Epidemiology, 2011, 35, 111-118.	1.3	46
96	Genome-Wide Association Study of Cardiac Structure and Systolic Function in African Americans. Circulation: Cardiovascular Genetics, 2013, 6, 37-46.	5.1	46
97	Loss-of-function variants influence the human serum metabolome. Science Advances, 2016, 2, e1600800.	10.3	46
98	Allelic variations in angiogenic pathway genes are associated with preeclampsia. American Journal of Obstetrics and Gynecology, 2010, 202, 445.e1-445.e11.	1.3	45
99	Rare Exome Sequence Variants in CLCN6 Reduce Blood Pressure Levels and Hypertension Risk. Circulation: Cardiovascular Genetics, 2016, 9, 64-70.	5.1	44
100	Impact of Rare and Common Genetic Variants on Diabetes Diagnosis by Hemoglobin A1c in Multi-Ancestry Cohorts: The Trans-Omics for Precision Medicine Program. American Journal of Human Genetics, 2019, 105, 706-718.	6.2	44
101	Large-scale whole-exome sequencing association studies identify rare functional variants influencing serum urate levels. Nature Communications, 2018, 9, 4228.	12.8	43
102	Dynamic Scan Procedure for Detecting Rare-Variant Association Regions in Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 802-814.	6.2	43
103	LPL polymorphism predicts stroke risk in men. Genetic Epidemiology, 2002, 22, 233-242.	1.3	42
104	Genetic association study of putative functional single nucleotide polymorphisms of genes in folate metabolism and spina bifida. American Journal of Obstetrics and Gynecology, 2009, 201, 394.e1-394.e11.	1.3	42
105	Association of Rare Loss-Of-Function Alleles in HAL , Serum Histidine. Circulation: Cardiovascular Genetics, 2015, 8, 351-355.	5.1	41
106	Use of Wrapper Algorithms Coupled with a Random Forests Classifier for Variable Selection in Large-Scale Genomic Association Studies. Journal of Computational Biology, 2009, 16, 1705-1718.	1.6	40
107	Parental History of Stroke Predicts Subclinical But Not Clinical Stroke. Stroke, 2000, 31, 2098-2102.	2.0	36
108	Association of folate receptor (folr1, folr2, folr3) and reduced folate carrier (slc19a1) genes with meningomyelocele. Birth Defects Research Part A: Clinical and Molecular Teratology, 2010, 88, 689-694.	1.6	36

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109	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. Human Molecular Genetics, 2015, 24, 559-571.	2.9	36
110	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
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	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. Blood, 2019, 133, 967-977.	1.4	34
113	Discovery of Genetic Variation on Chromosome 5q22 Associated with Mortality in Heart Failure. PLoS Genetics, 2016, 12, e1006034.	3.5	34
114	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, 7756.	12.8	32
115	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	12.8	32
116	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
117	Variants in CXADR and F2RL1 are associated with blood pressure and obesity in African-Americans in regions identified through admixture mapping. Journal of Hypertension, 2012, 30, 1970-1976.	0.5	30
118	Metabolomics Identifies Novel Blood Biomarkers of Pulmonary Function and COPD in the General Population. Metabolites, 2019, 9, 61.	2.9	30
119	Leveraging linkage evidence to identify low-frequency and rare variants on 16p13 associated with blood pressure using TOPMed whole genome sequencing data. Human Genetics, 2019, 138, 199-210.	3.8	29
120	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. PLoS ONE, 2017, 12, e0167742.	2.5	29
121	Integrative pathway genomics of lung function and airflow obstruction. Human Molecular Genetics, 2015, 24, 6836-6848.	2.9	28
122	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	6.2	28
123	Characteristics of a spina bifida population including North American Caucasian and Hispanic individuals. Birth Defects Research Part A: Clinical and Molecular Teratology, 2008, 82, 692-700.	1.6	27
124	A multi-ethnic polygenic risk score is associated with hypertension prevalence and progression throughout adulthood. Nature Communications, 2022, 13, .	12.8	27
125	Genome-wide association study of 1,5-anhydroglucitol identifies novel genetic loci linked to glucose metabolism. Scientific Reports, 2017, 7, 2812.	3.3	26
126	Common Coding Variants in SCN10A Are Associated With the Nav1.8 Late Current and Cardiac Conduction. Circulation Genomic and Precision Medicine, 2018, 11, e001663.	3.6	26

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127	FastSKAT: Sequence kernel association tests for very large sets of markers. Genetic Epidemiology, 2018, 42, 516-527.	1.3	26
128	Aptamer-Based Proteomic Platform Identifies Novel Protein Predictors of Incident Heart Failure and Echocardiographic Traits. Circulation: Heart Failure, 2020, 13, e006749.	3.9	26
129	Genetic loci associated with ideal cardiovascular health: A meta-analysis of genome-wide association studies. American Heart Journal, 2016, 175, 112-120.	2.7	25
130	Whole-genome sequencing study of serum peptide levels: the Atherosclerosis Risk in Communities study. Human Molecular Genetics, 2017, 26, 3442-3450.	2.9	25
131	A Mendelian randomization of Î³â€² and total fibrinogen levels in relation to venous thromboembolism and ischemic stroke. Blood, 2020, 136, 3062-3069.	1.4	25
132	Chromosome 9p21 Single Nucleotide Polymorphisms Are Not Associated With Recurrent Myocardial Infarction in Patients With Established Coronary Artery Disease. Circulation Journal, 2012, 76, 950-956.	1.6	24
133	Effects of Rare and Common Blood Pressure Gene Variants on Essential Hypertension. Circulation Research, 2013, 112, 318-326.	4.5	24
134	Targeted sequencing in candidate genes for atrial fibrillation: The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Targeted Sequencing Study. Heart Rhythm, 2014, 11, 452-457.	0.7	24
135	Rare coding variants in 35 genes associate with circulating lipid levelsâ€”A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	6.2	24
136	Hypertension Susceptibility Loci are Associated with Anthracycline-related Cardiotoxicity in Long-term Childhood Cancer Survivors. Scientific Reports, 2017, 7, 9698.	3.3	23
137	The impact of data quality on the identification of complex disease genes: experience from the Family Blood Pressure Program. European Journal of Human Genetics, 2006, 14, 469-477.	2.8	19
138	ESR1 polymorphism is associated with plasma lipid and apolipoprotein levels in Caucasians of the Rochester Family Heart Study*. Journal of Lipid Research, 2008, 49, 1701-1706.	4.2	19
139	Genetic association of the glycine cleavage system genes and myelomeningocele. Birth Defects Research Part A: Clinical and Molecular Teratology, 2016, 106, 847-853.	1.6	19
140	Association between ABO haplotypes and the risk of venous thrombosis: impact on disease risk estimation. Blood, 2021, 137, 2394-2402.	1.4	19
141	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	1.8	19
142	Sequence Analysis of Six Blood Pressure Candidate Regions in 4,178 Individuals: The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Targeted Sequencing Study. PLoS ONE, 2014, 9, e109155.	2.5	19
143	Association of copperâ€zinc superoxide dismutase (SOD1) and manganese superoxide dismutase (SOD2) genes with nonsyndromic myelomeningocele. Birth Defects Research Part A: Clinical and Molecular Teratology, 2012, 94, 762-769.	1.6	18
144	Strategies to Design and Analyze Targeted Sequencing Data. Circulation: Cardiovascular Genetics, 2014, 7, 335-343.	5.1	18

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145	Variants for HDL-C, LDL-C, and Triglycerides Identified from Admixture Mapping and Fine-Mapping Analysis in African American Families. Circulation: Cardiovascular Genetics, 2015, 8, 106-113.	5.1	18
146	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
147	Genetic architecture of lipid traits in the Hispanic community health study/study of Latinos. Lipids in Health and Disease, 2017, 16, 200.	3.0	18
148	RNA sequence analysis of inducible pluripotent stem cell-derived cardiomyocytes reveals altered expression of DNA damage and cell cycle genes in response to doxorubicin. Toxicology and Applied Pharmacology, 2018, 356, 44-53.	2.8	18
149	Pharmacogenomics of statin-related myopathy: Meta-analysis of rare variants from whole-exome sequencing. PLoS ONE, 2019, 14, e0218115.	2.5	18
150	Single Nucleotide Polymorphisms Associated with Coronary Heart Disease Predict Incident Ischemic Stroke in the Atherosclerosis Risk in Communities Study. Cerebrovascular Diseases, 2008, 26, 420-424.	1.7	17
151	Whole genome sequence analysis of serum amino acid levels. Genome Biology, 2016, 17, 237.	8.8	17
152	Mutations in folate transporter genes and risk for human myelomeningocele. American Journal of Medical Genetics, Part A, 2017, 173, 2973-2984.	1.2	17
153	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. PLoS ONE, 2019, 14, e0216222.	2.5	17
154	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
155	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	12.8	17
156	GEM: scalable and flexible geneâ€“environment interaction analysis in millions of samples. Bioinformatics, 2021, 37, 3514-3520.	4.1	17
157	Genome-Wide Association Study of Serum Fructosamine and Glycated Albumin in Adults Without Diagnosed Diabetes: Results From the Atherosclerosis Risk in Communities Study. Diabetes, 2018, 67, 1684-1696.	0.6	16
158	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. Blood, 2018, 132, 1842-1850.	1.4	16
159	Rare coding variants associated with blood pressure variation in 15â€Š914 individuals of African ancestry. Journal of Hypertension, 2017, 35, 1381-1389.	0.5	15
160	Efficient geneâ€“environment interaction tests for large biobankâ€scale sequencing studies. Genetic Epidemiology, 2020, 44, 908-923.	1.3	15
161	Evaluating the Context-Dependent Effect of Family History of Stroke in a Genome Scan for Hypertension. Stroke, 2003, 34, 1170-1175.	2.0	14
162	GOSR2 Lys67Arg Is Associated With Hypertension in Whites. American Journal of Hypertension, 2009, 22, 163-168.	2.0	14

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163	Mendelian Randomization Analysis of Hemostatic Factors and Their Contribution to Peripheral Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2020, 41, 380-386.	2.4	14
164	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 1836-1851.	6.2	14
165	Folate Metabolism Gene 5,10-Methylenetetrahydrofolate Reductase (MTHFR) Is Associated with ADHD in Myelomeningocele Patients. PLoS ONE, 2012, 7, e51330.	2.5	14
166	Monogenic and Polygenic Contributions to QTc Prolongation in the Population. Circulation, 2022, 145, 1524-1533.	1.6	14
167	Genome scan for hypertension in nonobese African Americans: the National Heart, Lung, and Blood Institute Family Blood Pressure Program. American Journal of Hypertension, 2004, 17, 834-838.	2.0	13
168	Association of retinoic acid receptor genes with meningomyelocele. Birth Defects Research Part A: Clinical and Molecular Teratology, 2011, 91, 39-43.	1.6	13
169	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
170	Population Genomic Analysis of 962 Whole Genome Sequences of Humans Reveals Natural Selection in Non-Coding Regions. PLoS ONE, 2015, 10, e0121644.	2.5	13
171	Association of NOS3 Glu298Asp SNP with hypertension and possible effect modification of dietary fat intake in the ARIC study. Hypertension Research, 2010, 33, 165-169.	2.7	12
172	Association of Levels of Fasting Glucose and Insulin With Rare Variants at the Chromosome 11p11.2-MADD Locus. Circulation: Cardiovascular Genetics, 2014, 7, 374-382.	5.1	12
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