Alanna C Morrison

List of Publications by Year in Descending Order

226 papers	15,107 citations	57 h-index	120 g-index
257 ext. papers	20,101 ext. citations	10.6 avg, IF	5.01 L-index

#	Paper	IF	Citations
226	American Heart Association's Life's Simple 7: Lifestyle Recommendations, Polygenic Risk, and Lifetime Risk of Coronary Heart Disease.. *Circulation*, **2022**,	16.7	6
225	Rare coding variants in RCN3 are associated with blood pressure.. *BMC Genomics*, **2022**, 23, 148	4.5	
224	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus.. *Nature Communications*, **2022**, 13, 1222	17.4	0
223	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential.. *Science Advances*, **2022**, 8, eabl6579	14.3	3
222	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. *Molecular Psychiatry*, **2021**, 26, 2111-2125	15.1	3
221	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
220	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. *Stroke*, **2021**, STROKEAHA121037388	6.7	7
219	Mendelian Randomization Analysis of Hemostatic Factors and Their Contribution to Peripheral Artery Disease-Brief Report. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2021**, 41, 380-386	9.4	4
218	Association between ABO haplotypes and the risk of venous thrombosis: impact on disease risk estimation. *Blood*, **2021**, 137, 2394-2402	2.2	4
217	Multi-ancestry genome-wide gene-sleep interactions identify novel loci for blood pressure. *Molecular Psychiatry*, **2021**,	15.1	3
216	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. *Nature Communications*, **2021**, 12, 2182	17.4	5
215	CLUE: Exact maximal reduction of kinetic models by constrained lumping of differential equations. *Bioinformatics*, **2021**,	7.2	1
214	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. *American Journal of Human Genetics*, **2021**, 108, 874-893	11	5
213	FGL1 as a modulator of plasma D-dimer levels: Exome-wide marker analysis of plasma tPA, PAI-1, and D-dimer. *Journal of Thrombosis and Haemostasis*, **2021**, 19, 2019-2028	15.4	1
212	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. *Nature Communications*, **2021**, 12, 3505	17.4	5
211	Leveraging a health information exchange for analyses of COVID-19 outcomes including an example application using smoking history and mortality. *PLoS ONE*, **2021**, 16, e0247235	3.7	1
210	Maternal Hypertension-Related Genotypes and Congenital Heart Defects. *American Journal of Hypertension*, **2021**, 34, 82-91	2.3	1

209	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. *Nature*, **2021**, 590, 290-299	50.4	268
208	Supplemental Association of Clonal Hematopoiesis With Incident Heart Failure. *Journal of the American College of Cardiology*, **2021**, 78, 42-52	15.1	16
207	BinomiRare: A robust test for association of a rare genetic variant with a binary outcome for mixed models and any case-control proportion. *Human Genetics and Genomics Advances*, **2021**, 2,	0.8	1
206	Identification of novel and rare variants associated with handgrip strength using whole genome sequence data from the NHLBI Trans-Omics in Precision Medicine (TOPMed) Program. *PLoS ONE*, **2021**, 16, e0253611	3.7	1
205	Genetic susceptibility, obesity and lifetime risk of type 2 diabetes: The ARIC study and Rotterdam Study. *Diabetic Medicine*, **2021**, 38, e14639	3.5	2
204	The genomics of heart failure: design and rationale of the HERMES consortium. *ESC Heart Failure*, **2021**,	3.7	1
203	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	11	1
202	Rare and low-frequency exonic variants and gene-by-smoking interactions in pulmonary function. *Scientific Reports*, **2021**, 11, 19365	4.9	0
201	Epidemiologic and Genetic Associations of Erythropoietin With Blood Pressure, Hypertension, and Coronary Artery Disease. *Hypertension*, **2021**, 78, 1555-1566	8.5	0
200	Aptamer-Based Proteomic Platform Identifies Novel Protein Predictors of Incident Heart Failure and Echocardiographic Traits. *Circulation: Heart Failure*, **2020**, 13, e006749	7.6	8
199	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002772	5.2	8
198	Identifying blood pressure loci whose effects are modulated by multiple lifestyle exposures. *Genetic Epidemiology*, **2020**, 44, 629-641	2.6	1
197	Genetic loci associated with prevalent and incident myocardial infarction and coronary heart disease in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. *PLoS ONE*, **2020**, 15, e0230035	3.7	4
196	Burden of rare deleterious variants in WNT signaling genes among 511 myelomeningocele patients. *PLoS ONE*, **2020**, 15, e0239083	3.7	3
195	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. *Nature Communications*, **2020**, 11, 163	17.4	140
194	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. *Nature Communications*, **2020**, 11, 5182	17.4	6
193	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	11	8
192	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. *Nature Genetics*, **2020**, 52, 1314-1332	36.3	26

191	A Mendelian randomization of B and total fibrinogen levels in relation to venous thromboembolism and ischemic stroke. *Blood*, **2020**, 136, 3062-3069	2.2	6
190	Identification of novel candidate risk genes for myelomeningocele within the glucose homeostasis/oxidative stress and folate/one-carbon metabolism networks. *Molecular Genetics & Genomic Medicine*, **2020**, 8, e1495	2.3	2
189	Efficient gene-environment interaction tests for large biobank-scale sequencing studies. *Genetic Epidemiology*, **2020**, 44, 908-923	2.6	5
188	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	36.3	33
187	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	11	22
186	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. *American Journal of Epidemiology*, **2019**, 188, 1033-1054	3.8	39
185	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. *Nature Communications*, **2019**, 10, 376	17.4	41
184	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	6.3	14
183	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. *Nature*, **2019**, 570, 71-76	50.4	129
182	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. *PLoS ONE*, **2019**, 14, e0216222	3.7	11
181	Metabolomic Pattern Predicts Incident Coronary Heart Disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2019**, 39, 1475-1482	9.4	23
180	Association of Variants with Blood Pressure in the Atherosclerosis Risk in Communities Study. *International Journal of Hypertension*, **2019**, 2019, 2137629	2.4	2
179	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	11	66
178	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. *Human Molecular Genetics*, **2019**, 28, 2615-2633	5.6	14
177	Dynamic Scan Procedure for Detecting Rare-Variant Association Regions in Whole-Genome Sequencing Studies. *American Journal of Human Genetics*, **2019**, 104, 802-814	11	13
176	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. *Nature Genetics*, **2019**, 51, 636-648	36.3	59
175	Metabolomics Identifies Novel Blood Biomarkers of Pulmonary Function and COPD in the General Population. *Metabolites*, **2019**, 9,	5.6	14
174	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. *Nature Human Behaviour*, **2019**, 3, 950-961	12.8	32

173	Pharmacogenomics of statin-related myopathy: Meta-analysis of rare variants from whole-exome sequencing. *PLoS ONE*, **2019**, 14, e0218115	3.7	12
172	Associations of autozygosity with a broad range of human phenotypes. *Nature Communications*, **2019**, 10, 4957	17.4	40
171	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. *Nature Communications*, **2019**, 10, 5121	17.4	31
170	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	6	90
169	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. *Circulation*, **2019**, 139, 620-635	16.7	51
168	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. *Journal of the American College of Cardiology*, **2019**, 73, 58-66	15.1	86
167	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	11	43
166	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. *Human Molecular Genetics*, **2019**, 28, 1212-1224	5.6	5
165	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. *Blood*, **2019**, 133, 967-977	2.2	17
164	Effects of Gender-Specific Differences, Inflammatory Response, and Genetic Variation on the Associations Among Depressive Symptoms and the Risk of Major Adverse Coronary Events in Patients With Acute Coronary Syndrome. *Biological Research for Nursing*, **2018**, 20, 168-176	2.6	3
163	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	5.2	45
162	Sequence-Based Analysis of Lipid-Related Metabolites in a Multiethnic Study. *Genetics*, **2018**, 209, 607-616	4	4
161	Genetic variants in microRNA genes and targets associated with cardiovascular disease risk factors in the African-American population. *Human Genetics*, **2018**, 137, 85-94	6.3	7
160	FastSKAT: Sequence kernel association tests for very large sets of markers. *Genetic Epidemiology*, **2018**, 42, 516-527	2.6	16
159	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	4.6	11
158	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. *Blood*, **2018**, 132, 1842-1850	2.2	11
157	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. *Nature Communications*, **2018**, 9, 2976	17.4	45
156	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. *PLoS ONE*, **2018**, 13, e0198166	3.7	31

155	CD163+ macrophages promote angiogenesis and vascular permeability accompanied by inflammation in atherosclerosis. *Journal of Clinical Investigation*, **2018**, 128, 1106-1124	15.9	126
154	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*, **2018**, 3, 4	4.8	16
153	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. *Nature Communications*, **2018**, 9, 5141	17.4	64
152	Large-scale whole-exome sequencing association studies identify rare functional variants influencing serum urate levels. *Nature Communications*, **2018**, 9, 4228	17.4	31
151	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	11	151
150	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
149	Contributions of rare coding variants in hypotension syndrome genes to population blood pressure variation. *Medicine (United States)*, **2018**, 97, e11865	1.8	5
148	Common Coding Variants in Are Associated With the Nav1.8 Late Current and Cardiac Conduction. *Circulation Genomic and Precision Medicine*, **2018**, 11, e001663	5.2	14
147	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	0.9	12
146	Reply to ‘Misestimation of heritability and prediction accuracy of male-pattern baldness’ *Nature Communications*, **2018**, 9, 2538	17.4	
145	Practical Approaches for Whole-Genome Sequence Analysis of Heart- and Blood-Related Traits. *American Journal of Human Genetics*, **2017**, 100, 205-215	11	29
144	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases: A Mendelian Randomization Study. *JAMA Oncology*, **2017**, 3, 636-651	13.4	236
143	Genome-wide association study of 1,5-anhydroglucitol identifies novel genetic loci linked to glucose metabolism. *Scientific Reports*, **2017**, 7, 2812	4.9	16
142	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. *Journal of the American Heart Association*, **2017**, 6,	6	65
141	Rare coding variants associated with blood pressure variation in 15 914 individuals of African ancestry. *Journal of Hypertension*, **2017**, 35, 1381-1389	1.9	7
140	Maternal gene-micronutrient interactions related to one-carbon metabolism and the risk of myelomeningocele among offspring. *Birth Defects Research*, **2017**, 109, 99-105	2.9	3
139	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. *Nature Genetics*, **2017**, 49, 1560-1563	36.3	68
138	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310

137	Mutations in folate transporter genes and risk for human myelomeningocele. *American Journal of Medical Genetics, Part A*, **2017**, 173, 2973-2984	2.5	13
136	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. *Circulation: Cardiovascular Genetics*, **2017**, 10,		33
135	Hypertension Susceptibility Loci are Associated with Anthracycline-related Cardiotoxicity in Long-term Childhood Cancer Survivors. *Scientific Reports*, **2017**, 7, 9698	4.9	18
134	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. *Hypertension*, **2017**,	8.5	85
133	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. *American Journal of Human Genetics*, **2017**, 101, 888-902	11	83
132	GWAS for male-pattern baldness identifies 71 susceptibility loci explaining 38% of the risk. *Nature Communications*, **2017**, 8, 1584	17.4	37
131	Whole-genome sequencing study of serum peptide levels: the Atherosclerosis Risk in Communities study. *Human Molecular Genetics*, **2017**, 26, 3442-3450	5.6	16
130	Genetic architecture of lipid traits in the Hispanic community health study/study of Latinos. *Lipids in Health and Disease*, **2017**, 16, 200	4.4	11
129	Gene-by-Psychosocial Factor Interactions Influence Diastolic Blood Pressure in European and African Ancestry Populations: Meta-Analysis of Four Cohort Studies. *International Journal of Environmental Research and Public Health*, **2017**, 14,	4.6	3
128	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. *Journal of Clinical Investigation*, **2017**, 127, 1798-1812	15.9	68
127	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. *PLoS Genetics*, **2017**, 13, e1006728	6	58
126	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. *PLoS ONE*, **2017**, 12, e0167742	3.7	21
125	Maternal hypertension and risk for hypospadias in offspring. *American Journal of Medical Genetics, Part A*, **2016**, 170, 3125-3132	2.5	7
124	KLB is associated with alcohol drinking, and its gene product β-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	11.5	150
123	Genetic association of the glycine cleavage system genes and myelomeningocele. *Birth Defects Research Part A: Clinical and Molecular Teratology*, **2016**, 106, 847-853		18
122	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. *Nature Genetics*, **2016**, 48, 1162-70	36.3	152
121	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184	36.3	251
120	Loss-of-function variants influence the human serum metabolome. *Science Advances*, **2016**, 2, e1600800	14.3	27

119	The impact of multiple single day blood pressure readings on cardiovascular risk estimation: The Atherosclerosis Risk in Communities study. *European Journal of Preventive Cardiology*, **2016**, 23, 1529-36	3.9	2
118	Rare Exome Sequence Variants in CLCN6 Reduce Blood Pressure Levels and Hypertension Risk. *Circulation: Cardiovascular Genetics*, **2016**, 9, 64-70		35
117	Association of the IGF1 gene with fasting insulin levels. *European Journal of Human Genetics*, **2016**, 24, 1337-43	5.3	4
116	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nature Communications*, **2016**, 7, 10023	17.4	295
115	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. *Human Molecular Genetics*, **2016**, 25, 358-70	5.6	54
114	Discovery of Genetic Variation on Chromosome 5q22 Associated with Mortality in Heart Failure. *PLoS Genetics*, **2016**, 12, e1006034	6	26
113	Causal Role of Alcohol Consumption in an Improved Lipid Profile: The Atherosclerosis Risk in Communities (ARIC) Study. *PLoS ONE*, **2016**, 11, e0148765	3.7	45
112	Genome-Wide Association Study for Incident Myocardial Infarction and Coronary Heart Disease in Prospective Cohort Studies: The CHARGE Consortium. *PLoS ONE*, **2016**, 11, e0144997	3.7	53
111	An Empirical Comparison of Joint and Stratified Frameworks for Studying G E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Gene-Lifestyle Interactions Working Group. *Genetic Epidemiology*, **2016**, 40, 404-15	2.6	15
110	Whole genome sequence analysis of serum amino acid levels. *Genome Biology*, **2016**, 17, 237	18.3	12
109	Meta-analysis of 49 549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant in ANGPTL4 determining fasting TG levels. *Journal of Medical Genetics*, **2016**, 53, 441-9	5.8	27
108	Diagnostic Yield and Clinical Utility of Sequencing Familial Hypercholesterolemia Genes in Patients With Severe Hypercholesterolemia. *Journal of the American College of Cardiology*, **2016**, 67, 2578-89	15.1	458
107	Genetic loci associated with ideal cardiovascular health: A meta-analysis of genome-wide association studies. *American Heart Journal*, **2016**, 175, 112-20	4.9	17
106	Cystatin C and Cardiovascular Disease: A Mendelian Randomization Study. *Journal of the American College of Cardiology*, **2016**, 68, 934-45	15.1	65
105	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	30.4	119
104	Inherited coding variants at the CDKN2A locus influence susceptibility to acute lymphoblastic leukaemia in children. *Nature Communications*, **2015**, 6, 7553	17.4	51
103	Analysis of loss-of-function variants and 20 risk factor phenotypes in 8,554 individuals identifies loci influencing chronic disease. *Nature Genetics*, **2015**, 47, 640-2	36.3	39
102	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, 106-13		11

101	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. *Nature Genetics*, **2015**, 47, 1294-1303	36.3	226
100	Integrative pathway genomics of lung function and airflow obstruction. *Human Molecular Genetics*, **2015**, 24, 6836-48	5.6	20
99	Association of Rare Loss-Of-Function Alleles in HAL, Serum Histidine: Levels and Incident Coronary Heart Disease. *Circulation: Cardiovascular Genetics*, **2015**, 8, 351-5		29
98	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. *Nature Genetics*, **2015**, 47, 1121-1130	36.3	1290
97	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. *Blood*, **2015**, 126, e19-29	2.2	45
96	Fine mapping the region reveals a common intronic insertion associated to HDL-C. *Npj Aging and Mechanisms of Disease*, **2015**, 1, 15011	5.5	5
95	Secondary findings and carrier test frequencies in a large multiethnic sample. *Genome Medicine*, **2015**, 7, 54	14.4	42
94	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. *Obstetrical and Gynecological Survey*, **2015**, 70, 758-762	2.4	
93	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. *Human Molecular Genetics*, **2015**, 24, 559-71	5.6	31
92	Rare coding variants and X-linked loci associated with age at menarche. *Nature Communications*, **2015**, 6, 7756	17.4	23
91	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications*, **2015**, 6, 5897	17.4	147
90	Population genomic analysis of 962 whole genome sequences of humans reveals natural selection in non-coding regions. *PLoS ONE*, **2015**, 10, e0121644	3.7	12
89	Direct Estimates of the Genomic Contributions to Blood Pressure Heritability within a Population-Based Cohort (ARIC). *PLoS ONE*, **2015**, 10, e0133031	3.7	32
88	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, 223-32	11	233
87	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, 452-7	6.7	18
86	Inactivating mutations in NPC1L1 and protection from coronary heart disease. *New England Journal of Medicine*, **2014**, 371, 2072-82	59.2	307
85	Genome-wide association analysis identifies six new loci associated with forced vital capacity. *Nature Genetics*, **2014**, 46, 669-77	36.3	104
84	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	11	80

83	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	11	52
82	Strategies to design and analyze targeted sequencing data: cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Targeted Sequencing Study. *Circulation: Cardiovascular Genetics*, **2014**, 7, 335-43		15
81	Sequencing of SCN5A identifies rare and common variants associated with cardiac conduction: Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. *Circulation: Cardiovascular Genetics*, **2014**, 7, 365-73		7
80	Large-scale genome-wide association studies and meta-analyses of longitudinal change in adult lung function. *PLoS ONE*, **2014**, 9, e100776	3.7	42
79	ADAM19 and HTR4 variants and pulmonary function: Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Targeted Sequencing Study. *Circulation: Cardiovascular Genetics*, **2014**, 7, 350-8		6
78	Genetic determinants influencing human serum metabolome among African Americans. *PLoS Genetics*, **2014**, 10, e1004212	6	57
77	Sequence variation in TMEM18 in association with body mass index: Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Targeted Sequencing Study. *Circulation: Cardiovascular Genetics*, **2014**, 7, 344-9		5
76	Association of levels of fasting glucose and insulin with rare variants at the chromosome 11p11.2-MADD locus: Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Targeted Sequencing Study. *Circulation: Cardiovascular Genetics*, **2014**, 7, 374-382		9
75	Pleiotropic genes for metabolic syndrome and inflammation. *Molecular Genetics and Metabolism*, **2014**, 112, 317-38	3.7	81
74	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	3.7	15
73	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, 545-54	11	145
72	Genome-wide association study of cardiac structure and systolic function in African Americans: the Candidate Gene Association Resource (CARe) study. *Circulation: Cardiovascular Genetics*, **2013**, 6, 37-46		40
71	Resequencing and clinical associations of the 9p21.3 region: a comprehensive investigation in the Framingham heart study. *Circulation*, **2013**, 127, 799-810	16.7	53
70	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
69	Whole-genome sequence-based analysis of high-density lipoprotein cholesterol. *Nature Genetics*, **2013**, 45, 899-901	36.3	117
68	Effects of rare and common blood pressure gene variants on essential hypertension: results from the Family Blood Pressure Program, CLUE, and Atherosclerosis Risk in Communities studies. *Circulation Research*, **2013**, 112, 318-26	15.7	20
67	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, 590-7	2.2	60
66	Genome-wide association study of gene by smoking interactions in coronary artery calcification. *PLoS ONE*, **2013**, 8, e74642	3.7	36

65	Association of SERPINA9 gene variants with carotid artery atherosclerosis: the Atherosclerosis Risk in Communities (ARIC) Carotid MRI Study. *International Journal of Molecular Epidemiology and Genetics*, **2013**, 4, 258-67	0.9	
64	Chromosome 9p21 single nucleotide polymorphisms are not associated with recurrent myocardial infarction in patients with established coronary artery disease. *Circulation Journal*, **2012**, 76, 950-6	2.9	23
63	Association of copper-zinc superoxide dismutase (SOD1) and manganese superoxide dismutase (SOD2) genes with nonsyndromic myelomeningocele. *Birth Defects Research Part A: Clinical and Molecular Teratology*, **2012**, 94, 762-9		15
62	Genome-wide joint meta-analysis of SNP and SNP-by-smoking interaction identifies novel loci for pulmonary function. *PLoS Genetics*, **2012**, 8, e1003098	6	108
61	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, 622-32	10.2	131
60	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, 1970-6	1.9	23
59	Folate metabolism gene 5,10-methylenetetrahydrofolate reductase (MTHFR) is associated with ADHD in myelomeningocele patients. *PLoS ONE*, **2012**, 7, e51330	3.7	11
58	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature* , **2011**, 478, 103-9	50.4	1564
57	Mining gold dust under the genome wide significance level: a two-stage approach to analysis of GWAS. *Genetic Epidemiology*, **2011**, 35, 111-8	2.6	41
56	Association of retinoic acid receptor genes with meningomyelocele. *Birth Defects Research Part A: Clinical and Molecular Teratology*, **2011**, 91, 39-43		12
55	Sodium intake and cardiovascular disease. *Annual Review of Public Health*, **2011**, 32, 71-90	20.6	33
54	Association between NEDD4L gene and sodium lithium countertransport. *American Journal of Hypertension*, **2011**, 24, 145-8	2.3	6
53	Association between SLC20A1 and sodium-lithium countertransport. *American Journal of Hypertension*, **2011**, 24, 1069-72	2.3	2
52	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, 2285-95	5.6	70
51	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. *Human Molecular Genetics*, **2011**, 20, 2273-84	5.6	146
50	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. *Nature Genetics*, **2011**, 43, 1005-11	36.3	338
49	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. *Nature Genetics*, **2011**, 43, 1082-90	36.3	313
48	Meta-analyses of genome-wide association studies identify multiple loci associated with pulmonary function. *Nature Genetics*, **2010**, 42, 45-52	36.3	467

47	Association of genome-wide variation with the risk of incident heart failure in adults of European and African ancestry: a prospective meta-analysis from the cohorts for heart and aging research in genomic epidemiology (CHARGE) consortium. *Circulation: Cardiovascular Genetics*, **2010**, 3, 256-66		147
46	Genomic variation associated with mortality among adults of European and African ancestry with heart failure: the cohorts for heart and aging research in genomic epidemiology consortium. *Circulation: Cardiovascular Genetics*, **2010**, 3, 248-55		66
45	Diabetes genes and prostate cancer in the Atherosclerosis Risk in Communities study. *Cancer Epidemiology Biomarkers and Prevention*, **2010**, 19, 558-65	4	42
44	Association of NOS3 Glu298Asp SNP with hypertension and possible effect modification of dietary fat intake in the ARIC study. *Hypertension Research*, **2010**, 33, 165-9	4.7	7
43	Genome-wide association analysis identifies multiple loci related to resting heart rate. *Human Molecular Genetics*, **2010**, 19, 3885-94	5.6	106
42	Duffy antigen receptor for chemokines (Darc) polymorphism regulates circulating concentrations of monocyte chemoattractant protein-1 and other inflammatory mediators. *Blood*, **2010**, 115, 5289-99	2.2	96
41	Allelic variations in angiogenic pathway genes are associated with preeclampsia. *American Journal of Obstetrics and Gynecology*, **2010**, 202, 445.e1-11	6.4	38
40	Genetic variation in solute carrier genes is associated with preeclampsia. *American Journal of Obstetrics and Gynecology*, **2010**, 203, 491.e1-491.e13	6.4	9
39	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, 689-94		30
38	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, 1705-18	1.7	17
37	Association of SLC34A2 variation and sodium-lithium countertransport activity in humans and baboons. *American Journal of Hypertension*, **2009**, 22, 288-93	2.3	5
36	GOSR2 Lys67Arg is associated with hypertension in whites. *American Journal of Hypertension*, **2009**, 22, 163-8	2.3	13
35	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.e1-11	6.4	38
34	Genome-wide association study of blood pressure and hypertension. *Nature Genetics*, **2009**, 41, 677-87	36.3	1065
33	Replication of the Wellcome Trust genome-wide association study of essential hypertension: the Family Blood Pressure Program. *European Journal of Human Genetics*, **2008**, 16, 1507-11	5.3	57
32	Single nucleotide polymorphisms associated with coronary heart disease predict incident ischemic stroke in the atherosclerosis risk in communities study. *Cerebrovascular Diseases*, **2008**, 26, 420-4	3.2	16
31	A whole-genome scan for stroke or myocardial infarction in family blood pressure program families. *Stroke*, **2008**, 39, 1115-20	6.7	9
30	Regional association-based fine-mapping for sodium-lithium countertransport on chromosome 10. *American Journal of Hypertension*, **2008**, 21, 117-21	2.3	4

29	ESR1 polymorphism is associated with plasma lipid and apolipoprotein levels in Caucasians of the Rochester Family Heart Study. *Journal of Lipid Research*, **2008**, 49, 1701-6	6.3	15
28	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		25
27	Comprehensive linkage and linkage heterogeneity analysis of 4344 sibling pairs affected with hypertension from the Family Blood Pressure Program. *Genetic Epidemiology*, **2007**, 31, 195-210	2.6	6
26	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	3.8	222
25	Five common gene variants identify elevated genetic risk for coronary heart disease. *Genetics in Medicine*, **2007**, 9, 682-9	8.1	79
24	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, 469-77	5.3	18
23	Plasma MCP-1 level and risk for peripheral arterial disease and incident coronary heart disease: Atherosclerosis Risk in Communities study. *Atherosclerosis*, **2005**, 183, 301-7	3.1	117
22	Genome-wide linkage study of erythrocyte sodium-lithium countertransport. *American Journal of Hypertension*, **2005**, 18, 653-6	2.3	11
21	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	2.3	6
20	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, 834-8	2.3	12
19	Evaluating the context-dependent effect of family history of stroke in a genome scan for hypertension. *Stroke*, **2003**, 34, 1170-5	6.7	12
18	LPL polymorphism predicts stroke risk in men. *Genetic Epidemiology*, **2002**, 22, 233-42	2.6	38
17	ADD1 460W allele associated with cardiovascular disease in hypertensive individuals. *Hypertension*, **2002**, 39, 1053-7	8.5	67
16	Linkage disequilibrium structure and its impact on the localization of a candidate functional mutation. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S620-5	2.6	5
15	G-protein beta3 subunit and alpha-adducin polymorphisms and risk of subclinical and clinical stroke. *Stroke*, **2001**, 32, 822-9	6.7	78
14	Parental history of stroke predicts subclinical but not clinical stroke: the Atherosclerosis Risk in Communities Study. *Stroke*, **2000**, 31, 2098-102	6.7	29
13	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*,3, 4	4.8	6
12	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*,3, 4	4.8	1

11	Genome-wide association study provides new insights into the genetic architecture and pathogenesis of heart failure	2
10	FastSKAT: Sequence kernel association tests for very large sets of markers	1
9	Novel blood pressure locus and gene discovery using GWAS and expression datasets from blood and the kidney	1
8	Genetic analysis of over one million people identifies 535 novel loci for blood pressure	4
7	Rare Non-coding Variation Identified by Large Scale Whole Genome Sequencing Reveals Unexplained Heritability of Type 2 Diabetes	2
6	Rare coding variants in 35 genes associate with circulating lipid levels a multi-ancestry analysis of 170,000 exomes	2
5	Genetic discovery and translational decision support from exome sequencing of 20,791 type 2 diabetes cases and 24,440 controls from five ancestries	2
4	Efficient variant set mixed model association tests for continuous and binary traits in large-scale whole genome sequencing studies	2
3	Multi-ancestry analysis of gene-sleep interactions in 126,926 individuals identifies multiple novel blood lipid loci that contribute to our understanding of sleep-associated adverse blood lipid profile	1
2	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program	68
1	Discovery and systematic characterization of risk variants and genes for coronary artery disease in over a million participants	5