Alexander P Reiner

List of Publications by Year in Descending Order

224 papers	16,277 citations	63 h-index	124 g-index
247 ext. papers	23,152 ext. citations	11.5 avg, IF	5.52 L-index

#	Paper	IF	Citations
224	Clonal hematopoiesis in sickle cell disease.. *Journal of Clinical Investigation*, **2022**,	15.9	7
223	Super interactive promoters provide insight into cell type-specific regulatory networks in blood lineage cell types.. *PLoS Genetics*, **2022**, 18, e1009984	6	0
222	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed.. *Cell Genomics*, **2022**, 2, 100084-100084		1
221	Upregulated heme biosynthesis increases obstructive sleep apnea severity: a pathway-based Mendelian randomization study.. *Scientific Reports*, **2022**, 12, 1472	4.9	0
220	From GWAS variant to function: A study of ~148,000 variants for blood cell traits.. *Human Genetics and Genomics Advances*, **2022**, 3, 100063	0.8	1
219	Rare coding variants in RCN3 are associated with blood pressure.. *BMC Genomics*, **2022**, 23, 148	4.5	
218	Intake and Sources of Dietary Fiber, Inflammation, and Cardiovascular Disease in Older US Adults.. *JAMA Network Open*, **2022**, 5, e225012	10.4	0
217	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations.. *Frontiers in Endocrinology*, **2022**, 13, 863893	5.7	
216	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
215	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. *Stroke*, **2021**, STROKEAHA121037388	6.7	7
214	Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. *Stroke*, **2021**, STROKEAHA120031792	6.7	2
213	Effect of Sickle Cell Trait and Genotype on the Association of Soluble uPAR with Kidney Function Measures in Black Americans. *Clinical Journal of the American Society of Nephrology: CJASN*, **2021**, 16, 287-289	6.9	2
212	Soluble Urokinase Plasminogen Activator Receptor: Genetic Variation and Cardiovascular Disease Risk in Blacks. *Circulation Genomic and Precision Medicine*, **2021**, CIRCGEN121003421	5.2	1
211	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. *American Journal of Human Genetics*, **2021**, 108, 564-582	11	7
210	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. *Nature Communications*, **2021**, 12, 2182	17.4	5
209	A System for Phenotype Harmonization in the National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Program. *American Journal of Epidemiology*, **2021**, 190, 1977-1992	3.8	3
208	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

207	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. *Aging Cell*, **2021**, 20, e13366	9.9	9
206	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
205	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. *Genome Biology*, **2021**, 22, 194	18.3	14
204	Multi-ethnic genome-wide association analyses of white blood cell and platelet traits in the Population Architecture using Genomics and Epidemiology (PAGE) study. *BMC Genomics*, **2021**, 22, 432	4.5	0
203	DNAm-based signatures of accelerated aging and mortality in blood are associated with low renal function. *Clinical Epigenetics*, **2021**, 13, 121	7.7	1
202	Soluble CD14 Levels in the Jackson Heart Study: Associations With Cardiovascular Disease Risk and Genetic Variants. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2021**, 41, e369-e378	9.4	0
201	Premature Menopause, Clonal Hematopoiesis, and Coronary Artery Disease in Postmenopausal Women. *Circulation*, **2021**, 143, 410-423	16.7	31
200	Mendelian randomization analysis with survival outcomes. *Genetic Epidemiology*, **2021**, 45, 16-23	2.6	0
199	Non-coding variants in MYH11, FZD3, and SORCS3 are associated with dementia in women. *Alzheimer's and Dementia*, **2021**, 17, 215-225	1.2	3
198	Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. *EBioMedicine*, **2021**, 63, 103157	8.8	3
197	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. *Nature*, **2021**, 590, 290-299	50.4	268
196	Supplemental Association of Clonal Hematopoiesis With Incident Heart Failure. *Journal of the American College of Cardiology*, **2021**, 78, 42-52	15.1	16
195	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
194	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
193	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. *Nature Communications*, **2021**, 12, 7173	17.4	1
192	Meta-analyses identify DNA methylation associated with kidney function and damage. *Nature Communications*, **2021**, 12, 7174	17.4	0
191	Comparison of Proteomic Assessment Methods in Multiple Cohort Studies. *Proteomics*, **2020**, 20, e1900278	4.8	27
190	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. *Nature Communications*, **2020**, 11, 2542	17.4	16

189	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
188	Cellular Adhesion Molecules in Young Adulthood and Cardiac Function in Later Life. *Journal of the American College of Cardiology*, **2020**, 75, 2156-2165	15.1	13
187	Soluble CD14 and Risk of Heart Failure and Its Subtypes in Older Adults. *Journal of Cardiac Failure*, **2020**, 26, 410-419	3.3	3
186	Multi-Ethnic Genome-Wide Association Study of Decomposed Cardioelectric Phenotypes Illustrates Strategies to Identify and Characterize Evidence of Shared Genetic Effects for Complex Traits. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002680	5.2	3
185	Association of Leukocyte Telomere Length With Mortality Among Adult Participants in 3 Longitudinal Studies. *JAMA Network Open*, **2020**, 3, e200023	10.4	24
184	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. *American Journal of Human Genetics*, **2020**, 106, 112-120	11	2
183	Interferon gamma-induced protein 10 (IP-10) and cardiovascular disease in African Americans. *PLoS ONE*, **2020**, 15, e0231013	3.7	4
182	The Polygenic and Monogenic Basis of Blood Traits and Diseases. *Cell*, **2020**, 182, 1214-1231.e11	56.2	96
181	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. *Nature*, **2020**, 586, 763-768	50.4	127
180	Coagulation factor VIII: Relationship to cardiovascular disease risk and whole genome sequence and epigenome-wide analysis in African Americans. *Journal of Thrombosis and Haemostasis*, **2020**, 18, 1335-1347	15.4	9
179	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. *Cell*, **2020**, 182, 1198-1213.e14	56.2	88
178	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. *Diabetes*, **2020**, 69, 2806-2818	0.9	10
177	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. *Nature Communications*, **2020**, 11, 6417	17.4	17
176	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. *Molecular Psychiatry*, **2020**, 25, 2392-2409	15.1	45
175	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
174	A large-scale exome array analysis of venous thromboembolism. *Genetic Epidemiology*, **2019**, 43, 449-457	2.6	11
173	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. *American Journal of Epidemiology*, **2019**, 188, 1033-1054	3.8	39
172	A fully adjusted two-stage procedure for rank-normalization in genetic association studies. *Genetic Epidemiology*, **2019**, 43, 263-275	2.6	29

171	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
170	Genetic analyses of diverse populations improves discovery for complex traits. *Nature*, **2019**, 570, 514-518	50.4	291
169	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. *American Journal of Human Genetics*, **2019**, 105, 15-28	11	12
168	A Cross-Sectional Analysis of Telomere Length and Sleep in the Women's Health Initiative. *American Journal of Epidemiology*, **2019**, 188, 1616-1626	3.8	2
167	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. *Nature*, **2019**, 570, 71-76	50.4	129
166	DNA methylation GrimAge strongly predicts lifespan and healthspan. *Aging*, **2019**, 11, 303-327	5.6	424
165	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
164	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
163	Genomic characterization of the RH locus detects complex and novel structural variation in multi-ethnic cohorts. *Genetics in Medicine*, **2019**, 21, 477-486	8.1	17
162	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. *Blood*, **2019**, 134, 1645-1657	2.2	63
161	Thirty-year risk of ischemic stroke in individuals with sickle cell trait and modification by chronic kidney disease: The atherosclerosis risk in communities (ARIC) study. *American Journal of Hematology*, **2019**, 94, 1306-1313	7.1	7
160	Statistical inference of genetic pathway analysis in high dimensions. *Biometrika*, **2019**, 106, 651	2	0
159	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. *Cell*, **2019**, 179, 984-1002.e36	56.2	76
158	Genome-wide association analysis of venous thromboembolism identifies new risk loci and genetic overlap with arterial vascular disease. *Nature Genetics*, **2019**, 51, 1574-1579	36.3	56
157	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
156	DNA methylation-based estimator of telomere length. *Aging*, **2019**, 11, 5895-5923	5.6	69
155	Epigenome-wide association study of leukocyte telomere length. *Aging*, **2019**, 11, 5876-5894	5.6	4
154	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44

153	Genome-wide Significance Thresholds for Admixture Mapping Studies. *American Journal of Human Genetics*, **2019**, 104, 454-465	11	11
152	A phenome-wide association study (PheWAS) in the Population Architecture using Genomics and Epidemiology (PAGE) study reveals potential pleiotropy in African Americans. *PLoS ONE*, **2019**, 14, e0226771	3.7	8
151	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
150	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
149	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
148	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. *Nature Genetics*, **2019**, 51, 237-244	36.3	516
147	Generalizing polygenic risk scores from Europeans to Hispanics/Latinos. *Genetic Epidemiology*, **2019** , 43, 50-62	2.6	48
146	Whole genome sequence association with E-selectin levels reveals loss-of-function variant in African Americans. *Human Molecular Genetics*, **2019**, 28, 515-523	5.6	10
145	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. *Biological Psychiatry*, **2019**, 85, 946-955	7.9	35
144	Genome-wide association study and meta-analysis identify loci associated with ventricular and supraventricular ectopy. *Scientific Reports*, **2018**, 8, 5675	4.9	1
143	Pre-pregnancy endothelial dysfunction and birth outcomes: The Coronary Artery Risk Development in Young Adults (CARDIA) Study. *Hypertension Research*, **2018**, 41, 282-289	4.7	9
142	Genetic variants in sex hormone pathways and the risk of type 2 diabetes among African American, Hispanic American, and European American postmenopausal women in the US. *Journal of Diabetes*, **2018**, 10, 524-533	3.8	3
141	Genome-wide association study of homocysteine in African Americans from the Jackson Heart Study, the Multi-Ethnic Study of Atherosclerosis, and the Coronary Artery Risk in Young Adults study. *Journal of Human Genetics*, **2018**, 63, 327-337	4.3	5
140	Generalization and fine mapping of red blood cell trait genetic associations to multi-ethnic populations: The PAGE Study. *American Journal of Hematology*, **2018**, 93, 1061	7.1	4
139	Discovery, fine-mapping, and conditional analyses of genetic variants associated with C-reactive protein in multiethnic populations using the Metabochip in the Population Architecture using Genomics and Epidemiology (PAGE) study. *Human Molecular Genetics*, **2018**, 27, 2940-2953	5.6	8
138	Common β-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. *PLoS Genetics*, **2018**, 14, e1007293	6	25
137	Epigenetic clock for skin and blood cells applied to Hutchinson Gilford Progeria Syndrome and studies. *Aging*, **2018**, 10, 1758-1775	5.6	187
136	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186

135	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. *Nature Genetics*, **2018**, 50, 524-537	36.3	536
134	An epigenetic biomarker of aging for lifespan and healthspan. *Aging*, **2018**, 10, 573-591	5.6	658
133	Nephropathy Risk Variants and Incident Cardiovascular Disease Events in Community-Dwelling Black Adults. *Circulation Genomic and Precision Medicine*, **2018**, 11, e002098	5.2	12
132	A common loss-of-function variant is associated with lower vitamin B concentration in African Americans. *Blood*, **2018**, 131, 2859-2863	2.2	4
131	Association of APOL1 With Heart Failure With Preserved Ejection Fraction in Postmenopausal African American Women. *JAMA Cardiology*, **2018**, 3, 712-720	16.2	12
130	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
129	A powerful statistical framework for generalization testing in GWAS, with application to the HCHS/SOL. *Genetic Epidemiology*, **2017**, 41, 251-258	2.6	24
128	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	5.8	5
127	Sickle Cell Trait and the Risk of ESRD in Blacks. *Journal of the American Society of Nephrology: JASN*, **2017**, 28, 2180-2187	12.7	53
126	Association of Sickle Cell Trait With Hemoglobin A1c in African Americans. *JAMA - Journal of the American Medical Association*, **2017**, 317, 507-515	27.4	81
125	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. *Journal of the American College of Cardiology*, **2017**, 69, 823-836	15.1	146
124	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. *Nature Genetics*, **2017**, 49, 946-952	36.3	176
123	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. *Lancet Diabetes and Endocrinology,the*, **2017**, 5, 97-105	18.1	225
122	Leisure-time physical activity and leukocyte telomere length among older women. *Experimental Gerontology*, **2017**, 95, 141-147	4.5	17
121	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. *Nature Communications*, **2017**, 8, 15805	17.4	50
120	Genome-wide association of white blood cell counts in Hispanic/Latino Americans: the Hispanic Community Health Study/Study of Latinos. *Human Molecular Genetics*, **2017**, 26, 1193-1204	5.6	23
119	The GH receptor exon 3 deletion is a marker of male-specific exceptional longevity associated with increased GH sensitivity and taller stature. *Science Advances*, **2017**, 3, e1602025	14.3	38
118	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. *Heart Rhythm*, **2017**, 14, 1675-1684	6.7	11

117	HUGIn: Hi-C Unifying Genomic Interrogator. *Bioinformatics*, **2017**, 33, 3793-3795	7.2	41
116	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. *Nature Genetics*, **2017**, 49, 1113-1119	36.3	184
115	Genome-wide association study of iron traits and relation to diabetes in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL): potential genomic intersection of iron and glucose regulation?. *Human Molecular Genetics*, **2017**, 26, 1966-1978	5.6	16
114	Association of Accelerometer-Measured Physical Activity With Leukocyte Telomere Length Among Older Women. *Journals of Gerontology - Series A Biological Sciences and Medical Sciences*, **2017**, 72, 1532-1537	6.4	13
113	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. *American Journal of Human Genetics*, **2017**, 100, 51-63	11	30
112	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
111	Leukocyte telomere length and cardiovascular disease in African Americans: The Jackson Heart Study. *Atherosclerosis*, **2017**, 266, 41-47	3.1	19
110	Rare coding variants pinpoint genes that control human hematological traits. *PLoS Genetics*, **2017**, 13, e1006925	6	28
109	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. *BioData Mining*, **2017**, 10, 25	4.3	5
108	Genome-wide Association Study of Susceptibility to Particulate Matter-Associated QT Prolongation. *Environmental Health Perspectives*, **2017**, 125, 067002	8.4	5
107	D-Dimer in African Americans: Whole Genome Sequence Analysis and Relationship to Cardiovascular Disease Risk in the Jackson Heart Study. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2017**, 37, 2220-2227	9.4	22
106	Genome-Wide Association Study of Blood Pressure Traits by Hispanic/Latino Background: the Hispanic Community Health Study/Study of Latinos. *Scientific Reports*, **2017**, 7, 10348	4.9	13
105	Identifying gene-gene interactions that are highly associated with four quantitative lipid traits across multiple cohorts. *Human Genetics*, **2017**, 136, 165-178	6.3	8
104	African Ancestry-Specific Alleles and Kidney Disease Risk in Hispanics/Latinos. *Journal of the American Society of Nephrology: JASN*, **2017**, 28, 915-922	12.7	37
103	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
102	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
101	Genome-wide association study of red blood cell traits in Hispanics/Latinos: The Hispanic Community Health Study/Study of Latinos. *PLoS Genetics*, **2017**, 13, e1006760	6	38
100	Admixture mapping in the Hispanic Community Health Study/Study of Latinos reveals regions of genetic associations with blood pressure traits. *PLoS ONE*, **2017**, 12, e0188400	3.7	17

99	Leukocyte telomere length, T cell composition and DNA methylation age. *Aging*, **2017**, 9, 1983-1995	5.6	29
98	Replication of Genome-Wide Association Study Findings of Longevity in White, African American, and Hispanic Women: The Women's Health Initiative. *Journals of Gerontology - Series A Biological Sciences and Medical Sciences*, **2017**, 72, 1401-1406	6.4	10
97	Coronary Artery Calcium Score and Association with Recurrent Nephrolithiasis: The Multi-Ethnic Study of Atherosclerosis. *Journal of Urology*, **2016**, 195, 971-6	2.5	29
96	An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. *Genome Biology*, **2016**, 17, 171	18.3	357
95	Detection of non-CLL-like monoclonal B cell lymphocytosis increases dramatically in the very elderly, while detection of CLL-like populations varies by race: findings in a multiethnic population-based cohort of elderly women. *Annals of Hematology*, **2016**, 95, 1695-704	3	3
94	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
93	Association of Exome Sequences With Cardiovascular Traits Among Blacks in the Jackson Heart Study. *Circulation: Cardiovascular Genetics*, **2016**, 9, 368-74		7
92	Fine-mapping of lipid regions in global populations discovers ethnic-specific signals and refines previously identified lipid loci. *Human Molecular Genetics*, **2016**, 25, 5500-5512	5.6	22
91	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. *American Journal of Human Genetics*, **2016**, 99, 40-55	11	61
90	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. *American Journal of Human Genetics*, **2016**, 99, 22-39	11	42
89	Rare variant associations with waist-to-hip ratio in European-American and African-American women from the NHLBI-Exome Sequencing Project. *European Journal of Human Genetics*, **2016**, 24, 1181-7	5.3	2
88	The effect of phenotypic outliers and non-normality on rare-variant association testing. *European Journal of Human Genetics*, **2016**, 24, 1188-94	5.3	20
87	Tissue Factor Pathway Inhibitor, Activated Protein C Resistance, and Risk of Coronary Heart Disease Due To Combined Estrogen Plus Progestin Therapy. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2016**, 36, 418-24	9.4	4
86	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. *International Journal of Epidemiology*, **2016**, 45, 1927-1937	7.8	65
85	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. *Lancet Neurology, The*, **2016**, 15, 174-184	24.1	159
84	Testing the role of predicted gene knockouts in human anthropometric trait variation. *Human Molecular Genetics*, **2016**, 25, 2082-2092	5.6	7
83	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. *American Journal of Human Genetics*, **2016**, 98, 229-42	11	54
82	Shorter telomere length in Europeans than in Africans due to polygenetic adaptation. *Human Molecular Genetics*, **2016**, 25, 2324-2330	5.6	67

81	Model-free Estimation of Recent Genetic Relatedness. *American Journal of Human Genetics*, **2016**, 98, 127-48	11	164
80	Genetic Diversity and Association Studies in US Hispanic/Latino Populations: Applications in the Hispanic Community Health Study/Study of Latinos. *American Journal of Human Genetics*, **2016**, 98, 165-84	11	181
79	Lipids, obesity and gallbladder disease in women: insights from genetic studies using the cardiovascular gene-centric 50K SNP array. *European Journal of Human Genetics*, **2016**, 24, 106-12	5.3	20
78	DNA methylation-based measures of biological age: meta-analysis predicting time to death. *Aging*, **2016**, 8, 1844-1865	5.6	531
77	Association Between Absolute Neutrophil Count and Variation at TCIRG1: The NHLBI Exome Sequencing Project. *Genetic Epidemiology*, **2016**, 40, 470-4	2.6	8
76	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. *American Journal of Human Genetics*, **2016**, 99, 8-21	11	47
75	Low-frequency and common genetic variation in ischemic stroke: The METASTROKE collaboration. *Neurology*, **2016**, 86, 1217-26	6.5	98
74	Oxidative stress, inflammation, endothelial dysfunction and incidence of type 2 diabetes. *Cardiovascular Diabetology*, **2016**, 15, 51	8.7	138
73	Four Susceptibility Loci for Gallstone Disease Identified in a Meta-analysis of Genome-Wide Association Studies. *Gastroenterology*, **2016**, 151, 351-363.e28	13.3	54
72	Elevated D-dimer levels in African Americans with sickle cell trait. *Blood*, **2016**, 127, 2261-3	2.2	24
71	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. *American Journal of Human Genetics*, **2016**, 99, 636-646	11	44
70	Analysis of exome sequencing data sets reveals structural variation in the coding region of ABO in individuals of African ancestry. *Transfusion*, **2016**, 56, 2744-2749	2.9	2
69	Fine-mapping, novel loci identification, and SNP association transferability in a genome-wide association study of QRS duration in African Americans. *Human Molecular Genetics*, **2016**, 25, 4350-4368	5.6	20
68	Cystatin C and Cardiovascular Disease: A Mendelian Randomization Study. *Journal of the American College of Cardiology*, **2016**, 68, 934-45	15.1	65
67	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. *Nature Genetics*, **2016**, 48, 1303-1312	36.3	51
66	Guidelines for Large-Scale Sequence-Based Complex Trait Association Studies: Lessons Learned from the NHLBI Exome Sequencing Project. *American Journal of Human Genetics*, **2016**, 99, 791-801	11	67
65	Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GFI1B Splice Variants in Human Hematopoiesis. *American Journal of Human Genetics*, **2016**, 99, 481-8	11	31
64	Race and Melanocortin 1 Receptor Polymorphism R163Q Are Associated with Post-Burn Hypertrophic Scarring: A Prospective Cohort Study. *Journal of Investigative Dermatology*, **2015**, 135, 2394-2401	4.3	25

63	Mendelian randomization of blood lipids for coronary heart disease. *European Heart Journal*, **2015**, 36, 539-50	9.5	417
62	Leveraging Multi-ethnic Evidence for Mapping Complex Traits in Minority Populations: An Empirical Bayes Approach. *American Journal of Human Genetics*, **2015**, 96, 740-52	11	11
61	Gene-centric approach identifies new and known loci for FVIII activity and VWF antigen levels in European Americans and African Americans. *American Journal of Hematology*, **2015**, 90, 534-40	7.1	15
60	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
59	Plasma Levels of Soluble Interleukin-2 Receptor Associations With Clinical Cardiovascular Events and Genome-Wide Association Scan. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2015**, 35, 2246-53	9.4	30
58	Genetic meta-analysis of 15,901 African Americans identifies variation in EXOC3L1 is associated with HDL concentration. *Journal of Lipid Research*, **2015**, 56, 1781-6	6.3	8
57	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. *Nature*, **2015**, 518, 102-6	50.4	463
56	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. *Lancet, The*, **2015**, 385, 351-61	40	409
55	A genetic risk score comprising known venous thromboembolism loci is associated with chronic venous disease in a multi-ethnic cohort. *Thrombosis Research*, **2015**, 136, 966-73	8.2	8
54	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
53	Genetic Determinants of Pelvic Organ Prolapse among African American and Hispanic Women in the Women's Health Initiative. *PLoS ONE*, **2015**, 10, e0141647	3.7	15
52	DCAF4, a novel gene associated with leucocyte telomere length. *Journal of Medical Genetics*, **2015**, 52, 157-62	5.8	48
51	Leukocyte Telomere Length and Risks of Incident Coronary Heart Disease and Mortality in a Racially Diverse Population of Postmenopausal Women. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2015**, 35, 2225-31	9.4	45
50	Rare coding variants and X-linked loci associated with age at menarche. *Nature Communications*, **2015**, 6, 7756	17.4	23
49	Adiposity patterns and the risk for ESRD in postmenopausal women. *Clinical Journal of the American Society of Nephrology: CJASN*, **2015**, 10, 241-50	6.9	21
48	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
47	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal of Human Genetics*, **2014**, 94, 233-45	11	170
46	Leveraging population admixture to characterize the heritability of complex traits. *Nature Genetics*, **2014**, 46, 1356-62	36.3	45

45	Large multiethnic Candidate Gene Study for C-reactive protein levels: identification of a novel association at CD36 in African Americans. *Human Genetics*, **2014**, 133, 985-95	6.3	25
44	Rare and low-frequency coding variants in CXCR2 and other genes are associated with hematological traits. *Nature Genetics*, **2014**, 46, 629-34	36.3	92
43	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. *BMJ, The*, **2014**, 349, g4164	5.9	406
42	Trans-ethnic meta-analysis of white blood cell phenotypes. *Human Molecular Genetics*, **2014**, 23, 6944-60	5.6	45
41	Causal effects of body mass index on cardiometabolic traits and events: a Mendelian randomization analysis. *American Journal of Human Genetics*, **2014**, 94, 198-208	11	156
40	Loss-of-function mutations in APOC3, triglycerides, and coronary disease. *New England Journal of Medicine*, **2014**, 371, 22-31	59.2	721
39	A genetic association study of D-dimer levels with 50K SNPs from a candidate gene chip in four ethnic groups. *Thrombosis Research*, **2014**, 134, 462-7	8.2	5
38	Whole-exome imputation of sequence variants identified two novel alleles associated with adult body height in African Americans. *Human Molecular Genetics*, **2014**, 23, 6607-15	5.6	11
37	Distribution and medical impact of loss-of-function variants in the Finnish founder population. *PLoS Genetics*, **2014**, 10, e1004494	6	243
36	Association of sickle cell trait with chronic kidney disease and albuminuria in African Americans. *JAMA - Journal of the American Medical Association*, **2014**, 312, 2115-25	27.4	126
35	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. *American Journal of Human Genetics*, **2014**, 94, 349-60	11	131
34	Pleiotropic genes for metabolic syndrome and inflammation. *Molecular Genetics and Metabolism*, **2014**, 112, 317-38	3.7	81
33	Prospective associations of coronary heart disease loci in African Americans using the MetaboChip: the PAGE study. *PLoS ONE*, **2014**, 9, e113203	3.7	17
32	Imputation of coding variants in African Americans: better performance using data from the exome sequencing project. *Bioinformatics*, **2013**, 29, 2744-9	7.2	30
31	Soluble CD14: genomewide association analysis and relationship to cardiovascular risk and mortality in older adults. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2013**, 33, 158-64	9.4	92
30	Genome-wide association analysis of red blood cell traits in African Americans: the COGENT Network. *Human Molecular Genetics*, **2013**, 22, 2529-38	5.6	48
29	Genome-wide and gene-centric analyses of circulating myeloperoxidase levels in the charge and care consortia. *Human Molecular Genetics*, **2013**, 22, 3381-93	5.6	18
28	Genetic risk factors for ischaemic stroke and its subtypes (the METASTROKE collaboration): a meta-analysis of genome-wide association studies. *Lancet Neurology, The*, **2012**, 11, 951-62	24.1	359

27	Genome-wide association and population genetic analysis of C-reactive protein in African American and Hispanic American women. *American Journal of Human Genetics*, **2012**, 91, 502-12	11	90
26	Imputation of exome sequence variants into population- based samples and blood-cell-trait-associated loci in African Americans: NHLBI GO Exome Sequencing Project. *American Journal of Human Genetics*, **2012**, 91, 794-808	11	103
25	Large-scale gene-centric meta-analysis across 32 studies identifies multiple lipid loci. *American Journal of Human Genetics*, **2012**, 91, 823-38	11	189
24	Gene-centric meta-analysis of lipid traits in African, East Asian and Hispanic populations. *PLoS ONE*, **2012**, 7, e50198	3.7	37
23	Kidney stones and subclinical atherosclerosis in young adults: the CARDIA study. *Journal of Urology*, **2011**, 185, 920-5	2.5	90
22	Genetic association analysis highlights new loci that modulate hematological trait variation in Caucasians and African Americans. *Human Genetics*, **2011**, 129, 307-17	6.3	74
21	Genome-wide association study of white blood cell count in 16,388 African Americans: the continental origins and genetic epidemiology network (COGENT). *PLoS Genetics*, **2011**, 7, e1002108	6	111
20	Genome-wide association study of coronary heart disease and its risk factors in 8,090 African Americans: the NHLBI CARe Project. *PLoS Genetics*, **2011**, 7, e1001300	6	249
19	Common coding variants of the HNF1A gene are associated with multiple cardiovascular risk phenotypes in community-based samples of younger and older European-American adults: the Coronary Artery Risk Development in Young Adults Study and The Cardiovascular Health Study. *Circulation: Cardiovascular Genetics*, **2009**, 2, 244-54		36
18	Inflammation and thrombosis biomarkers and incident frailty in postmenopausal women. *American Journal of Medicine*, **2009**, 122, 947-54	2.4	69
17	Polymorphisms of the HNF1A gene encoding hepatocyte nuclear factor-1 alpha are associated with C-reactive protein. *American Journal of Human Genetics*, **2008**, 82, 1193-201	11	155
16	Soluble P-selectin, SELP polymorphisms, and atherosclerotic risk in European-American and African-African young adults: the Coronary Artery Risk Development in Young Adults (CARDIA) Study. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2008**, 28, 1549-55	9.4	47
15	Polymorphisms of the IL1-receptor antagonist gene (IL1RN) are associated with multiple markers of systemic inflammation. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2008**, 28, 1407-12	9.4	64
14	Genetic ancestry, population sub-structure, and cardiovascular disease-related traits among African-American participants in the CARDIA Study. *Human Genetics*, **2007**, 121, 565-75	6.3	68
13	USF1 gene variants, cardiovascular risk, and mortality in European Americans: analysis of two US cohort studies. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2007**, 27, 2736-42	9.4	19
12	Common promoter polymorphisms of inflammation and thrombosis genes and longevity in older adults: the cardiovascular health study. *Atherosclerosis*, **2005**, 181, 175-83	3.1	18
11	Population structure, admixture, and aging-related phenotypes in African American adults: the Cardiovascular Health Study. *American Journal of Human Genetics*, **2005**, 76, 463-77	11	127
10	Genetic variants of coagulation factor XIII, postmenopausal estrogen therapy, and risk of nonfatal myocardial infarction. *Blood*, **2003**, 102, 25-30	2.2	41

9	Diabetes duration may modify the association between genetic variation in the glycoprotein Ia subunit of the platelet collagen receptor and risk of severe diabetic retinopathy: a working hypothesis. *Thrombosis and Haemostasis*, **2003**, 89, 142-8	7	2
8	Factor V Leiden, prothrombin G20210A, and risk of sudden coronary death in apparently healthy persons. *American Journal of Cardiology*, **2002**, 90, 66-8	3	13
7	Coagulation factor XIII polymorphisms and the risk of myocardial infarction and ischaemic stroke in young women. *British Journal of Haematology*, **2002**, 116, 376-82	4.5	41
6	Genetic variants of platelet glycoprotein receptors and risk of stroke in young women. *Stroke*, **2000** , 31, 1628-33	6.7	117
5	A novel isoform of platelet glycoprotein Ib alpha is prevalent in African Americans. *American Journal of Hematology*, **1999**, 60, 77-9	7.1	17
4	Screening for nonsense mutations in patients with severe hemophilia A can provide rapid, direct carrier detection. *Human Genetics*, **1992**, 89, 88-94	6.3	22
3	The PAGE Study: How Genetic Diversity Improves Our Understanding of the Architecture of Complex Traits		14
2	Whole genome sequencing association analysis of quantitative red blood cell phenotypes: the NHLBI TOPMed program		1
1	From GWAS Variant to Function: a Study of ~148,000 Variants for Blood Cell Traits		1