Alexander P Reiner

List of Publications by Year
in descending order

233 papers	28,503 citations	9756 73 h-index	7718 150 g-index
247 all docs	247 docs citations	247 times ranked	35318 citing authors

#	Article	IF	Citations
1	An epigenetic biomarker of aging for lifespan and healthspan. Aging, 2018, 10, 573-591.	1.4	1,552
2	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.	9.4	1,307
3	DNA methylation GrimAge strongly predicts lifespan and healthspan. Aging, 2019, 11, 303-327.	1.4	1,128
4	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	9.4	1,124
5	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	13.7	1,069
6	Loss-of-Function Mutations inAPOC3,Triglycerides, and Coronary Disease. New England Journal of Medicine, 2014, 371, 22-31.	13.9	936
7	DNA methylation-based measures of biological age: meta-analysis predicting time to death. Aging, 2016, 8, 1844-1865.	1.4	786
8	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	13.7	679
9	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	13.7	581
10	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	1.0	567
11	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. Lancet, The, 2015, 385, 351-361.	6.3	562
12	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
13	An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. Genome Biology, 2016, 17, 171.	3.8	535
14	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	3.0	528
15	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
16	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, 951-962.	4.9	445
17	Epigenetic clock for skin and blood cells applied to Hutchinson Gilford Progeria Syndrome and ex vivo studies. Aging, 2018, 10, 1758-1775.	1.4	406
18	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388

#	Article	IF	Citations
19	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	13.7	376
20	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
21	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	13.5	353
22	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
23	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	1.5	351
24	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
25	Model-free Estimation of Recent Genetic Relatedness. American Journal of Human Genetics, 2016, 98, 127-148.	2.6	331
26	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	5.5	298
27	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.	1.5	290
28	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.	2.6	287
29	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
30	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	9.4	279
31	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, 165-184.	2.6	266
32	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119.	9.4	260
33	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
34	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	2.6	227
35	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	9.4	223
36	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. Lancet Neurology, The, 2016, 15, 174-184.	4.9	217

#	Article	IF	Citations
37	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	1.2	214
38	Oxidative stress, inflammation, endothelial dysfunction and incidence of type 2 diabetes. Cardiovascular Diabetology, 2016, 15, 51.	2.7	207
39	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.	1.5	203
40	Causal Effects of Body Mass Index on Cardiometabolic Traits and Events: A Mendelian Randomization Analysis. American Journal of Human Genetics, 2014, 94, 198-208.	2.6	199
41	DNA methylation-based estimator of telomere length. Aging, 2019, 11, 5895-5923.	1.4	198
42	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	2.6	193
43	Polymorphisms of the HNF1A Gene Encoding Hepatocyte Nuclear Factor-1Î± are Associated with C-Reactive Protein. American Journal of Human Genetics, 2008, 82, 1193-1201.	2.6	170
44	Association of Sickle Cell Trait With Chronic Kidney Disease and Albuminuria in African Americans. JAMA - Journal of the American Medical Association, 2014, 312, 2115.	3.8	167
45	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	0.6	162
46	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	2.6	158
47	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. Cell, 2019, 179, 984-1002.e36.	13.5	152
48	Genome-wide association analysis of venous thromboembolism identifies new risk loci and genetic overlap with arterial vascular disease. Nature Genetics, 2019, 51, 1574-1579.	9.4	152
49	Population Structure, Admixture, and Aging-Related Phenotypes in African American Adults: The Cardiovascular Health Study. American Journal of Human Genetics, 2005, 76, 463-477.	2.6	146
50	Low-frequency and common genetic variation in ischemic stroke. Neurology, 2016, 86, 1217-1226.	1.5	141
51	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.	1.5	133
52	Genetic Variants of Platelet Glycoprotein Receptors and Risk of Stroke in Young Women. Stroke, 2000, 31, 1628-1633.	1.0	126
53	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.	2.6	123
54	Association of Sickle Cell Trait With Hemoglobin A_{1c} in African Americans. JAMA - Journal of the American Medical Association, 2017, 317, 507.	3.8	122

#	Article	IF	Citations
55	Soluble CD14. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 158-164.	1.1	114
56	Rare and low-frequency coding variants in CXCR2 and other genes are associated with hematological traits. Nature Genetics, 2014, 46, 629-634.	9.4	113
57	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.	9.4	112
58	Cystatin C and Cardiovascular Disease. Journal of the American College of Cardiology, 2016, 68, 934-945.	1.2	109
59	Kidney Stones and Subclinical Atherosclerosis in Young Adults: The CARDIA Study. Journal of Urology, 2011, 185, 920-925.	0.2	108
60	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, 502-512.	2.6	107
61	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	0.5	107
62	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.	2.6	103
63	Comparison of Proteomic Assessment Methods in Multiple Cohort Studies. Proteomics, 2020, 20, e1900278.	1.3	103
64	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
65	Association of Clonal Hematopoiesis With Incident HeartÂFailure. Journal of the American College of Cardiology, 2021, 78, 42-52.	1.2	101
66	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	5.8	95
67	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. International Journal of Epidemiology, 2016, 45, 1927-1937.	0.9	94
68	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	3.8	90
69	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
70	Generalizing polygenic risk scores from Europeans to Hispanics/Latinos. Genetic Epidemiology, 2019, 43, 50-62.	0.6	89
71	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	1.5	88
72	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. Stroke, 2022, 53, 788-797.	1.0	88

#	Article	IF	Citations
73	Premature Menopause, Clonal Hematopoiesis, and Coronary Artery Disease in Postmenopausal Women. Circulation, 2021, 143, 410-423.	1.6	87
74	Shorter telomere length in Europeans than in Africans due to polygenetic adaptation. Human Molecular Genetics, 2016, 25, 2324-2330.	1.4	86
75	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	1.6	85
76	Inflammation and Thrombosis Biomarkers and Incident Frailty in Postmenopausal Women. American Journal of Medicine, 2009, 122, 947-954.	0.6	83
77	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	4.1	83
78	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	2.6	82
79	Genetic association analysis highlights new loci that modulate hematological trait variation in Caucasians and African Americans. Human Genetics, 2011, 129, 307-317.	1.8	81
80	Genetic ancestry, population sub-structure, and cardiovascular disease-related traits among African-American participants in the CARDIA Study. Human Genetics, 2007, 121, 565-575.	1.8	79
81	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.	2.6	79
82	Sickle Cell Trait and the Risk of ESRD in Blacks. Journal of the American Society of Nephrology: JASN, 2017, 28, 2180-2187.	3.0	79
83	Four Susceptibility Loci for Gallstone Disease Identified in a Meta-analysis of Genome-Wide Association Studies. Gastroenterology, 2016, 151, 351-363.e28.	0.6	74
84	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. Aging Cell, 2021, 20, e13366.	3.0	72
85	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. American Journal of Human Genetics, 2016, 98, 229-242.	2.6	71
86	Leveraging population admixture to characterize the heritability of complex traits. Nature Genetics, 2014, 46, 1356-1362.	9.4	69
87	HUGIn: Hi-C Unifying Genomic Interrogator. Bioinformatics, 2017, 33, 3793-3795.	1.8	69
88	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	0.7	69
89	Polymorphisms of the IL1-Receptor Antagonist Gene (IL1RN) Are Associated With Multiple Markers of Systemic Inflammation. Arteriosclerosis, Thrombosis, and Vascular Biology, 2008, 28, 1407-1412.	1.1	68
90	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. American Journal of Human Genetics, 2016, 99, 636-646.	2.6	67

#	Article	IF	Citations
91	DCAF4, a novel gene associated with leucocyte telomere length. Journal of Medical Genetics, 2015, 52, 157-162.	1.5	66
92	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	9.4	66
93	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	5.8	62
94	Association of Leukocyte Telomere Length With Mortality Among Adult Participants in 3 Longitudinal Studies. JAMA Network Open, 2020, 3, e200023.	2.8	62
95	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	1.4	60
96	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	2.6	60
97	A fully adjusted twoâ€stage procedure for rankâ€normalization in genetic association studies. Genetic Epidemiology, 2019, 43, 263-275.	0.6	60
98	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	5.8	59
99	Genome-wide association analysis of red blood cell traits in African Americans: the COGENT Network. Human Molecular Genetics, 2013, 22, 2529-2538.	1.4	57
100	African Ancestryâ€“Specific Alleles and Kidney Disease Risk in Hispanics/Latinos. Journal of the American Society of Nephrology: JASN, 2017, 28, 915-922.	3.0	57
101	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	0.6	55
102	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, 2225-2231.	1.1	53
103	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.	1.5	53
104	Soluble P-Selectin,SELPPolymorphisms, and Atherosclerotic Risk in European-American and African-African Young Adults. Arteriosclerosis, Thrombosis, and Vascular Biology, 2008, 28, 1549-1555.	1.1	50
105	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.	2.6	50
106	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.	4.7	47
107	Coagulation factor XIII polymorphisms and the risk of myocardial infarction and ischaemic stroke in young women. British Journal of Haematology, 2002, 116, 376-382.	1.2	46
108	Genetic variants of coagulation factor XIII, postmenopausal estrogen therapy, and risk of nonfatal myocardial infarction. Blood, 2003, 102, 25-30.	0.6	46

#	Article	IF	Citations
109	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, 481-488.	2.6	45
110	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.	2.6	45
111	Common Î±-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. PLoS Genetics, 2018, 14, e1007293.	1.5	45
112	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.	2.6	44
113	Common Coding Variants of theHNF1AGene Are Associated With Multiple Cardiovascular Risk Phenotypes in Community-Based Samples of Younger and Older European-American Adults. Circulation: Cardiovascular Genetics, 2009, 2, 244-254.	5.1	43
114	Plasma Levels of Soluble Interleukin-2 Receptor Î±. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 2246-2253.	1.1	43
115	Leukocyte telomere length, T cell composition and DNA methylation age. Aging, 2017, 9, 1983-1995.	1.4	42
116	A powerful statistical framework for generalization testing in GWAS, with application to the HCHS/SOL. Genetic Epidemiology, 2017, 41, 251-258.	0.6	41
117	D-Dimer in African Americans. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 2220-2227.	1.1	40
118	Gene-Centric Meta-Analysis of Lipid Traits in African, East Asian and Hispanic Populations. PLoS ONE, 2012, 7, e50198.	1.1	40
119	The effect of phenotypic outliers and non-normality on rare-variant association testing. European Journal of Human Genetics, 2016, 24, 1188-1194.	1.4	39
120	Coronary Artery Calcium Score and Association with Recurrent Nephrolithiasis: The Multi-Ethnic Study of Atherosclerosis. Journal of Urology, 2016, 195, 971-976.	0.2	39
121	Rare coding variants pinpoint genes that control human hematological traits. PLoS Genetics, 2017, 13, e1006925.	1.5	39
122	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	5.8	39
123	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.	0.3	38
124	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.	1.4	38
125	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.	1.4	37
126	Imputation of coding variants in African Americans: better performance using data from the exome sequencing project. Bioinformatics, 2013, 29, 2744-2749.	1.8	36

#	Article	IF	Citations
127	Cellular Adhesion Molecules in YoungÂAdulthood and Cardiac Function in LaterÂLife. Journal of the American College of Cardiology, 2020, 75, 2156-2165.	1.2	33
128	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, 7756.	5.8	32
129	Large multiethnic Candidate Gene Study for C-reactive protein levels: identification of a novel association at CD36 in African Americans. Human Genetics, 2014, 133, 985-995.	1.8	31
130	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.	1.4	31
131	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.	1.4	31
132	Leukocyte telomere length and cardiovascular disease in African Americans: The Jackson Heart Study. Atherosclerosis, 2017, 266, 41-47.	0.4	30
133	Meta-analyses identify DNA methylation associated with kidney function and damage. Nature Communications, 2021, 12, 7174.	5.8	30
134	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.	1.4	29
135	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.	1.8	29
136	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.	1.6	29
137	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.	1.1	29
138	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	3.0	29
139	Leisure-time physical activity and leukocyte telomere length among older women. Experimental Gerontology, 2017, 95, 141-147.	1.2	28
140	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	2.6	28
141	Prospective Associations of Coronary Heart Disease Loci in African Americans Using the MetaboChip: The PAGE Study. PLoS ONE, 2014, 9, e113203.	1.1	27
142	APOL1Nephropathy Risk Variants and Incident Cardiovascular Disease Events in Community-Dwelling Black Adults. Circulation Genomic and Precision Medicine, 2018, 11, e002098.	1.6	26
143	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.3	26
144	Clonal hematopoiesis in sickle cell disease. Journal of Clinical Investigation, 2022, 132, .	3.9	26

#	Article	IF	Citations
145	Screening for nonsense mutations in patients with severe hemophilia A can provide rapid, direct carrier detection. Human Genetics, 1992, 89, 88-94.	1.8	25
146	USF1 Gene Variants, Cardiovascular Risk, and Mortality in European Americans. Arteriosclerosis, Thrombosis, and Vascular Biology, 2007, 27, 2736-2742.	1.1	25
147	Genome-wide Significance Thresholds for Admixture Mapping Studies. American Journal of Human Genetics, 2019, 104, 454-465.	2.6	25
148	TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data. American Journal of Human Genetics, 2022, 109, 1175-1181.	2.6	25
149	Adiposity Patterns and the Risk for ESRD in Postmenopausal Women. Clinical Journal of the American Society of Nephrology: CJASN, 2015, 10, 241-250.	2.2	24
150	Elevated D-dimer levels in African Americans with sickle cell trait. Blood, 2016, 127, 2261-2263.	0.6	24
151	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.	1.6	24
152	Genomic characterization of the RH locus detects complex and novel structural variation in multi-ethnic cohorts. Genetics in Medicine, 2019, 21, 477-486.	1.1	24
153	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, 106-112.	1.4	23
154	Genome-wide and gene-centric analyses of circulating myeloperoxidase levels in the charge and care consortia. Human Molecular Genetics, 2013, 22, 3381-3393.	1.4	22
155	Leveraging Multi-ethnic Evidence for Mapping Complex Traits in Minority Populations: An Empirical Bayes Approach. American Journal of Human Genetics, 2015, 96, 740-752.	2.6	22
156	A largeâ€scale exome array analysis of venous thromboembolism. Genetic Epidemiology, 2019, 43, 449-457.	0.6	22
157	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	2.6	21
158	Geneâ€centric approach identifies new and known loci for <scp>F</scp>VIII activity and <scp>VWF</scp> antigen levels in <scp>E</scp>uropean <scp>A</scp>mericans and <scp>A</scp>frican <scp>A</scp>mericans. American Journal of Hematology, 2015, 90, 534-540.	2.0	20
159	Genetic Landscape of the ACE2 Coronavirus Receptor. Circulation, 2022, 145, 1398-1411.	1.6	20
160	A novel isoform of platelet glycoprotein Ib? is prevalent in African Americans. , 1999, 60, 77-79.		19
161	Common promoter polymorphisms of inflammation and thrombosis genes and longevity in older adults: The cardiovascular health study. Atherosclerosis, 2005, 181, 175-183.	0.4	19
162	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.	1.7	19

#	Article	IF	Citations
163	Epigenome-wide association study of leukocyte telomere length. Aging, 2019, 11, 5876-5894.	1.4	19
164	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. Heart Rhythm, 2017, 14, 1675-1684.	0.3	18
165	Genetic architecture of lipid traits in the Hispanic community health study/study of Latinos. Lipids in Health and Disease, 2017, 16, 200.	1.2	18
166	Nonâ€coding variants in MYH11, FZD3, and SORCS3 are associated with dementia in women. Alzheimer's and Dementia, 2021, 17, 215-225.	0.4	18
167	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.	2.6	18
168	Genetic Determinants of Pelvic Organ Prolapse among African American and Hispanic Women in the Womenâ€™s Health Initiative. PLoS ONE, 2015, 10, e0141647.	1.1	17
169	Association of APOL1 With Heart Failure With Preserved Ejection Fraction in Postmenopausal African American Women. JAMA Cardiology, 2018, 3, 712.	3.0	17
170	Coagulation factor VIII: Relationship to cardiovascular disease risk and whole genome sequence and epigenomeâ€wide analysis in African Americans. Journal of Thrombosis and Haemostasis, 2020, 18, 1335-1347.	1.9	17
171	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	5.8	17
172	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.	1.4	16
173	A Cross-Sectional Analysis of Telomere Length and Sleep in the Womenâ€™s Health Initiative. American Journal of Epidemiology, 2019, 188, 1616-1626.	1.6	16
174	Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. Stroke, 2021, , STROKEAHA120031792.	1.0	16
175	Factor V leiden, prothrombin g20210a, and risk of sudden coronary death in apparently healthy persons. American Journal of Cardiology, 2002, 90, 66-68.	0.7	15
176	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.	1.1	15
177	Whole genome sequence association with E-selectin levels reveals loss-of-function variant in African Americans. Human Molecular Genetics, 2019, 28, 515-523.	1.4	15
178	Intake and Sources of Dietary Fiber, Inflammation, and Cardiovascular Disease in Older US Adults. JAMA Network Open, 2022, 5, e225012.	2.8	15
179	Whole-exome imputation of sequence variants identified two novel alleles associated with adult body height in African Americans. Human Molecular Genetics, 2014, 23, 6607-6615.	1.4	14
180	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.	2.7	14

#	Article	IF	Citations
181	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.	2.6	14
182	DNAm-based signatures of accelerated aging and mortality in blood are associated with low renal function. Clinical Epigenetics, 2021, 13, 121.	1.8	13
183	Replication of Genome-Wide Association Study Findings of Longevity in White, African American, and Hispanic Women: The Womenâ€™s Health Initiative. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2016, 72, glw198.	1.7	12
184	Soluble CD14 and Risk of Heart Failure and Its Subtypes in Older Adults. Journal of Cardiac Failure, 2020, 26, 410-419.	0.7	12
185	Interferon gamma-induced protein 10 (IP-10) and cardiovascular disease in African Americans. PLoS ONE, 2020, 15, e0231013.	1.1	12
186	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	1.3	12
187	A genetic risk score comprising known venous thromboembolism loci is associated with chronic venous disease in a multi-ethnic cohort. Thrombosis Research, 2015, 136, 966-973.	0.8	11
188	Genetic meta-analysis of 15,901 African Americans identifies variation in EXOC3L1 is associated with HDL concentration. Journal of Lipid Research, 2015, 56, 1781-1786.	2.0	11
189	Association Between Absolute Neutrophil Count and Variation at TCIRG1: The NHLBI Exome Sequencing Project. Genetic Epidemiology, 2016, 40, 470-474.	0.6	11
190	Identifying geneâ€“gene interactions that are highly associated with four quantitative lipid traits across multiple cohorts. Human Genetics, 2017, 136, 165-178.	1.8	11
191	Pre-pregnancy endothelial dysfunction and birth outcomes: The Coronary Artery Risk Development in Young Adults (CARDIA) Study. Hypertension Research, 2018, 41, 282-289.	1.5	11
192	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. Circulation Genomic and Precision Medicine, 2020, 13, e002772.	1.6	11
193	Transcriptome-Wide Association Study of Blood Cell Traits in African Ancestry and Hispanic/Latino Populations. Genes, 2021, 12, 1049.	1.0	11
194	Testing the role of predicted gene knockouts in human anthropometric trait variation. Human Molecular Genetics, 2016, 25, 2082-2092.	1.4	10
195	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.	1.5	9
196	Thirtyâ€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.	2.0	9
197	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. American Journal of Human Genetics, 2020, 106, 112-120.	2.6	9
198	From GWAS variant to function: A study of â^¼148,000 variants for blood cell traits. Human Genetics and Genomics Advances, 2022, 3, 100063.	1.0	9

#	Article	IF	Citations
199	A genetic association study of D-dimer levels with 50K SNPs from a candidate gene chip in four ethnic groups. Thrombosis Research, 2014, 134, 462-467.	0.8	8
200	Association of Exome Sequences With Cardiovascular Traits Among Blacks in the Jackson Heart Study. Circulation: Cardiovascular Genetics, 2016, 9, 368-374.	5.1	8
201	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. Nature Communications, 2021, 12, 7173.	5.8	8
202	Integration of rare expression outlier-associated variants improves polygenic risk prediction. American Journal of Human Genetics, 2022, 109, 1055-1064.	2.6	8
203	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. BioData Mining, 2017, 10, 25.	2.2	7
204	Genome-wide Association Study of Susceptibility to Particulate Matterâ€“Associated QT Prolongation. Environmental Health Perspectives, 2017, 125, 067002.	2.8	7
205	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.	1.1	7
206	A common TCN1 loss-of-function variant is associated with lower vitamin B12 concentration in African Americans. Blood, 2018, 131, 2859-2863.	0.6	7
207	Soluble Urokinase Plasminogen Activator Receptor: Genetic Variation and Cardiovascular Disease Risk in Black Adults. Circulation Genomic and Precision Medicine, 2021, 14, CIRCGEN121003421.	1.6	7
208	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations. Frontiers in Endocrinology, 2022, 13, 863893.	1.5	7
209	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, 1695-1704.	0.8	6
210	APOL1 Variants. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, 219-220.	1.1	6
211	Mendelian randomization analysis with survival outcomes. Genetic Epidemiology, 2021, 45, 16-23.	0.6	6
212	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.	1.2	6
213	Transcriptome-wide association study in UK Biobank Europeans identifies associations with blood cell traits. Human Molecular Genetics, 2022, 31, 2333-2347.	1.4	6
214	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.	0.8	5
215	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, 1181-1187.	1.4	5
216	Generalization and fine mapping of red blood cell trait genetic associations to multiâ€ethnic populations: The PAGE study. American Journal of Hematology, 2018, 93, 1061-1073.	2.0	5

#	Article	IF	Citations
217	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.	1.1	5
218	Contributions of the Womenâ€™s Health Initiative to Cardiovascular Research. Journal of the American College of Cardiology, 2022, 80, 256-275.	1.2	5
219	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, 418-424.	1.1	4
220	Genome-wide association study and meta-analysis identify loci associated with ventricular and supraventricular ectopy. Scientific Reports, 2018, 8, 5675.	1.6	4
221	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.	1.6	4
222	Super interactive promoters provide insight into cell type-specific regulatory networks in blood lineage cell types. PLoS Genetics, 2022, 18, e1009984.	1.5	4
223	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.	0.8	3
224	Effect of Sickle Cell Trait and APOL1 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.	2.2	3
225	Whole-exome sequencing of 14â€‰389 individuals from the ESP and CHARGE consortia identifies novel rare variation associated with hemostatic factors. Human Molecular Genetics, 2022, 31, 3120-3132.	1.4	3
226	Statistical inference of genetic pathway analysis in high dimensions. Biometrika, 2019, 106, 651-651.	1.3	2
227	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.0	2
228	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, 100040.	1.0	2
229	Full title: A largeâ€scale transcriptomeâ€wide association study (TWAS) of 10 blood cell phenotypes reveals complexities of TWAS fineâ€mapping. Genetic Epidemiology, 2021, , .	0.6	2
230	Upregulated heme biosynthesis increases obstructive sleep apnea severity: a pathway-based Mendelian randomization study. Scientific Reports, 2022, 12, 1472.	1.6	2
231	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.	1.8	2
232	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	1.2	2
233	Association Between Hemoglobin A1c and Glycemia in African Americans with and without Sickle Cell trait and Whites, Results from CARDIA and the Jackson Heart Study.. Journal of Diabetes and Treatment, 2018, 3, .	0.5	0