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	From GWAS variant to function: A study of â¼148,000 variants for blood cell traits. Human Genetics and Genomics Advances, 2022, 3, 100063.	1.0	9
2	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. Stroke, 2022, 53, 788-797.	1.0	88
3	Clonal hematopoiesis in sickle cell disease. Journal of Clinical Investigation, 2022, 132, .	3.9	26
4	Super interactive promoters provide insight into cell type-specific regulatory networks in blood lineage cell types. PLoS Genetics, 2022, 18, e1009984.	1.5	4
5	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	3.0	29
6	Upregulated heme biosynthesis increases obstructive sleep apnea severity: a pathway-based Mendelian randomization study. Scientific Reports, 2022, 12, 1472.	1.6	2
7	Transcriptome-wide association study in UK Biobank Europeans identifies associations with blood cell traits. Human Molecular Genetics, 2022, 31, 2333-2347.	1.4	6
8	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	1.2	2
9	Intake and Sources of Dietary Fiber, Inflammation, and Cardiovascular Disease in Older US Adults. JAMA Network Open, 2022, 5, e225012.	2.8	15
10	Genetic Landscape of the ACE2 Coronavirus Receptor. Circulation, 2022, 145, 1398-1411.	1.6	20
11	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
12	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
13	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
14	Integration of rare expression outlier-associated variants improves polygenic risk prediction. American Journal of Human Genetics, 2022, 109, 1055-1064.	2.6	8
15	Contributions of the Womenâ€™s Health Initiative to Cardiovascular Research. Journal of the American College of Cardiology, 2022, 80, 256-275.	1.2	5
16	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
17	Premature Menopause, Clonal Hematopoiesis, and Coronary Artery Disease in Postmenopausal Women. Circulation, 2021, 143, 410-423.	1.6	87
18	Mendelian randomization analysis with survival outcomes. Genetic Epidemiology, 2021, 45, 16-23.	0.6	6

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19	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
20	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
21	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
22	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	13.7	1,069
23	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
24	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	5.8	17
25	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
26	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
27	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. Aging Cell, 2021, 20, e13366.	3.0	72
28	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
29	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	3.8	90
30	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
31	DNAm-based signatures of accelerated aging and mortality in blood are associated with low renal function. Clinical Epigenetics, 2021, 13, 121.	1.8	13
32	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
33	Association of Clonal Hematopoiesis With Incident HeartÂFailure. Journal of the American College of Cardiology, 2021, 78, 42-52.	1.2	101
34	Transcriptome-Wide Association Study of Blood Cell Traits in African Ancestry and Hispanic/Latino Populations. Genes, 2021, 12, 1049.	1.0	11
35	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
36	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

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37	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
38	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
39	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
40	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
41	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
42	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
43	Meta-analyses identify DNA methylation associated with kidney function and damage. Nature Communications, 2021, 12, 7174.	5.8	30
44	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
45	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388
46	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	13.7	376
47	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
48	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
49	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.3	26
50	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	5.8	39
51	Comparison of Proteomic Assessment Methods in Multiple Cohort Studies. Proteomics, 2020, 20, e1900278.	1.3	103
52	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	5.8	59
53	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
54	Cellular Adhesion Molecules in YoungÂAdulthood and Cardiac Function in LaterÂLife. Journal of the American College of Cardiology, 2020, 75, 2156-2165.	1.2	33

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55	Soluble CD14 and Risk of Heart Failure and Its Subtypes in Older Adults. Journal of Cardiac Failure, 2020, 26, 410-419.	0.7	12
56	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
57	Association of Leukocyte Telomere Length With Mortality Among Adult Participants in 3 Longitudinal Studies. JAMA Network Open, 2020, 3, e200023.	2.8	62
58	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
59	Interferon gamma-induced protein 10 (IP-10) and cardiovascular disease in African Americans. PLoS ONE, 2020, 15, e0231013.	1.1	12
60	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
61	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	0.6	162
62	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
63	Statistical inference of genetic pathway analysis in high dimensions. Biometrika, 2019, 106, 651-651.	1.3	2
64	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. Cell, 2019, 179, 984-1002.e36.	13.5	152
65	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
66	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
67	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
68	A largeâ€scale exome array analysis of venous thromboembolism. Genetic Epidemiology, 2019, 43, 449-457.	0.6	22
69	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	1.6	85
70	A fully adjusted twoâ€stage procedure for rankâ€normalization in genetic association studies. Genetic Epidemiology, 2019, 43, 263-275.	0.6	60
71	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
72	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	13.7	679

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73	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	2.6	21
74	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
75	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
76	DNA methylation GrimAge strongly predicts lifespan and healthspan. Aging, 2019, 11, 303-327.	1.4	1,128
77	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
78	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
79	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
80	Genome-wide Significance Thresholds for Admixture Mapping Studies. American Journal of Human Genetics, 2019, 104, 454-465.	2.6	25
81	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
82	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
83	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
84	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
85	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
86	Generalizing polygenic risk scores from Europeans to Hispanics/Latinos. Genetic Epidemiology, 2019, 43, 50-62.	0.6	89
87	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
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	DNA methylation-based estimator of telomere length. Aging, 2019, 11, 5895-5923.	1.4	198
90	Epigenome-wide association study of leukocyte telomere length. Aging, 2019, 11, 5876-5894.	1.4	19

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91	Genome-wide association study and meta-analysis identify loci associated with ventricular and supraventricular ectopy. Scientific Reports, 2018, 8, 5675.	1.6	4
92	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
93	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
94	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
95	An epigenetic biomarker of aging for lifespan and healthspan. Aging, 2018, 10, 573-591.	1.4	1,552
96	APOL1Nephropathy Risk Variants and Incident Cardiovascular Disease Events in Community-Dwelling Black Adults. Circulation Genomic and Precision Medicine, 2018, 11, e002098.	1.6	26
97	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
98	Association of APOL1 With Heart Failure With Preserved Ejection Fraction in Postmenopausal African American Women. JAMA Cardiology, 2018, 3, 712.	3.0	17
99	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
100	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
101	Common Î±-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. PLoS Genetics, 2018, 14, e1007293.	1.5	45
102	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
103	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
104	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
105	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
106	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
107	A powerful statistical framework for generalization testing in GWAS, with application to the HCHS/SOL. Genetic Epidemiology, 2017, 41, 251-258.	0.6	41
108	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

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109	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
110	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
111	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
112	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
113	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
114	Leisure-time physical activity and leukocyte telomere length among older women. Experimental Gerontology, 2017, 95, 141-147.	1.2	28
115	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	5.8	95
116	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
117	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
118	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. Heart Rhythm, 2017, 14, 1675-1684.	0.3	18
119	HUGIn: Hi-C Unifying Genomic Interrogator. Bioinformatics, 2017, 33, 3793-3795.	1.8	69
120	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119.	9.4	260
121	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
122	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
123	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
124	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
125	Leukocyte telomere length and cardiovascular disease in African Americans: The Jackson Heart Study. Atherosclerosis, 2017, 266, 41-47.	0.4	30
126	D-Dimer in African Americans. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 2220-2227.	1.1	40

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127	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
128	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
129	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
130	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
131	Rare coding variants pinpoint genes that control human hematological traits. PLoS Genetics, 2017, 13, e1006925.	1.5	39
132	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. BioData Mining, 2017, 10, 25.	2.2	7
133	Genome-wide Association Study of Susceptibility to Particulate Matterâ€“Associated QT Prolongation. Environmental Health Perspectives, 2017, 125, 067002.	2.8	7
134	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
135	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
136	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
137	Leukocyte telomere length, T cell composition and DNA methylation age. Aging, 2017, 9, 1983-1995.	1.4	42
138	Association Between Absolute Neutrophil Count and Variation at TCIRG1: The NHLBI Exome Sequencing Project. Genetic Epidemiology, 2016, 40, 470-474.	0.6	11
139	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	2.6	60
140	Low-frequency and common genetic variation in ischemic stroke. Neurology, 2016, 86, 1217-1226.	1.5	141
141	Oxidative stress, inflammation, endothelial dysfunction and incidence of type 2 diabetes. Cardiovascular Diabetology, 2016, 15, 51.	2.7	207
142	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
143	Elevated D-dimer levels in African Americans with sickle cell trait. Blood, 2016, 127, 2261-2263.	0.6	24
144	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. American Journal of Human Genetics, 2016, 99, 636-646.	2.6	67

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145	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
146	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
147	Cystatin C and Cardiovascular Disease. Journal of the American College of Cardiology, 2016, 68, 934-945.	1.2	109
148	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	9.4	66
149	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
150	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
151	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
152	An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. Genome Biology, 2016, 17, 171.	3.8	535
153	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
154	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
155	Association of Exome Sequences With Cardiovascular Traits Among Blacks in the Jackson Heart Study. Circulation: Cardiovascular Genetics, 2016, 9, 368-374.	5.1	8
156	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
157	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	2.6	82
158	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
159	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
160	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
161	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
162	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

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163	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. Lancet Neurology, The, 2016, 15, 174-184.	4.9	217
164	Testing the role of predicted gene knockouts in human anthropometric trait variation. Human Molecular Genetics, 2016, 25, 2082-2092.	1.4	10
165	APOL1 Variants. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, 219-220.	1.1	6
166	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
167	Shorter telomere length in Europeans than in Africans due to polygenetic adaptation. Human Molecular Genetics, 2016, 25, 2324-2330.	1.4	86
168	Model-free Estimation of Recent Genetic Relatedness. American Journal of Human Genetics, 2016, 98, 127-148.	2.6	331
169	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
170	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
171	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
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