Eric Boerwinkle

List of Publications by Year
in descending order

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430 papers	52,199 citations	2802 94 h-index	2078 204 g-index
455 all docs	455 docs citations	455 times ranked	63074 citing authors

#	Article	IF	Citations
1	Metabolomics of Dietary Acid Load and Incident Chronic Kidney Disease. , 2022, 32, 292-300.		9
2	Metabolome-wide association study of estimated glomerular filtration rates in Hispanics. Kidney International, 2022, 101, 144-151.	5.2	2
3	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
4	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	6.2	24
5	Type 2 Diabetes Partitioned Polygenic Scores Associate With Disease Outcomes in 454,193 Individuals Across 13 Cohorts. Diabetes Care, 2022, 45, 674-683.	8.6	29
6	Increased prevalence of clonal hematopoiesis of indeterminate potential amongst people living with HIV. Scientific Reports, 2022, 12, 577.	3.3	27
7	American Heart Associationâ€™s Lifeâ€™s Simple 7: Lifestyle Recommendations, Polygenic Risk, and Lifetime Risk of Coronary Heart Disease. Circulation, 2022, 145, 808-818.	1.6	63
8	Blood metabolites predicting mild cognitive impairment in the study of Latinosâ€investigation of neurocognitive aging (HCHS/SOL). Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2022, 14, e12259.	2.4	3
9	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	2.8	2
10	Durability of SARS-CoV-2 Antibodies From Natural Infection in Children and Adolescents. Pediatrics, 2022, 149, .	2.1	11
11	Implementation of preemptive DNA sequenceâ€"based pharmacogenomics testing across a large academic medical center: The Mayo-Baylor RIGHT 10K Study. Genetics in Medicine, 2022, 24, 1062-1072.	2.4	28
12	Serum Metabolomics of Incident Diabetes and Glycemic Changes in a Population With High Diabetes Burden: The Hispanic Community Health Study/Study of Latinos. Diabetes, 2022, 71, 1338-1349.	0.6	4
13	Healthful eating patterns, serum metabolite profile and risk of diabetes in a population-based prospective study of US Hispanics/Latinos. Diabetologia, 2022, 65, 1133-1144.	6.3	14
14	Epidemiology of atrial fibrillation in the All of Us Research Program. PLoS ONE, 2022, 17, e0265498.	2.5	10
15	Predicted gene expression in ancestrally diverse populations leads to discovery of susceptibility loci for lifestyle and cardiometabolic traits. American Journal of Human Genetics, 2022, 109, 669-679.	6.2	5
16	Monogenic and Polygenic Contributions to QTc Prolongation in the Population. Circulation, 2022, 145, 1524-1533.	1.6	14
17	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	21.4	700
18	Apolipoprotein E Polymorphism, Cardiac Remodeling, and Heart Failure in the ARIC Study. Journal of Cardiac Failure, 2022, 28, 1128-1136.	1.7	2

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19	Metabolomic Associations of Asthma in the Hispanic Community Health Study/Study of Latinos. Metabolites, 2022, 12, 359.	2.9	1
20	Genome-Wide Causation Studies of Complex Diseases. Journal of Computational Biology, 2022, 29, 908-931.	1.6	2
21	Genome-wide studies reveal factors associated with circulating uromodulin and its relationships to complex diseases. JCI Insight, 2022, 7, .	5.0	12
22	APOL1 Kidney Risk Variants and Proteomics. Clinical Journal of the American Society of Nephrology: CJASN, 2022, 17, 684-692.	4.5	4
23	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.	2.9	3
24	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases. Nature Communications, 2022, 13, 2408.	12.8	26
25	TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data. American Journal of Human Genetics, 2022, 109, 1175-1181.	6.2	25
26	Plasma proteome analyses in individuals of European and African ancestry identify cis-pQTLs and models for proteome-wide association studies. Nature Genetics, 2022, 54, 593-602.	21.4	98
27	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations. Frontiers in Endocrinology, 2022, 13, 863893.	3.5	7
28	Midlife determinants of healthy cardiovascular aging: The Atherosclerosis Risk in Communities (ARIC) study. Atherosclerosis, 2022, 350, 82-89.	0.8	3
29	A bioinformatics pipeline for estimating mitochondrial DNA copy number and heteroplasmy levels from whole genome sequencing data. NAR Genomics and Bioinformatics, 2022, 4, lqac034.	3.2	12
30	Cardiac Structure and Function Across the Spectrum of Aldosteronism: the Atherosclerosis Risk in Communities Study. Hypertension, 2022, 79, 1984-1993.	2.7	17
31	Assessing the contribution of rare genetic variants to phenotypes of chronic obstructive pulmonary disease using whole-genome sequence data. Human Molecular Genetics, 2022, 31, 3873-3885.	2.9	2
32	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	2.7	12
33	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.	1.7	2
34	Alternative genomic diagnoses for individuals with a clinical diagnosis of Dubowitz syndrome. American Journal of Medical Genetics, Part A, 2021, 185, 119-133.	1.2	17
35	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
36	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.	6.1	14

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37	Genome-wide meta-analysis of muscle weakness identifies 15 susceptibility loci in older men and women. Nature Communications, 2021, 12, 654.	12.8	75
38	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
39	Physical Activity-Related Metabolites Are Associated with Mortality: Findings from the Atherosclerosis Risk in Communities (ARIC) Study. Metabolites, 2021, 11, 59.	2.9	2
40	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. Human Molecular Genetics, 2021, 30, 393-409.	2.9	32
41	Genetically determined NLRP3 inflammasome activation associates with systemic inflammation and cardiovascular mortality. European Heart Journal, 2021, 42, 1742-1756.	2.2	63
42	muCNV: genotyping structural variants for population-level sequencing. Bioinformatics, 2021, 37, 2055-2057.	4.1	7
43	Robust, flexible, and scalable tests for Hardyâ€“Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, .	2.9	6
44	The Implementation Science for Genomic Health Translation (INSIGHT) Study in Epilepsy: Protocol for a Learning Health Care System. JMIR Research Protocols, 2021, 10, e25576.	1.0	2
45	Dietary factors, gut microbiota, and serum trimethylamine-N-oxide associated with cardiovascular disease in the Hispanic Community Health Study/Study of Latinos. American Journal of Clinical Nutrition, 2021, 113, 1503-1514.	4.7	32
46	Association Between Midlife Obesity and Kidney Function Trajectories: The Atherosclerosis Risk in Communities (ARIC) Study. American Journal of Kidney Diseases, 2021, 77, 376-385.	1.9	13
47	Multiomics integrative analysis identifies APOE allele-specific blood biomarkers associated to Alzheimerâ€™s disease etiopathogenesis. Aging, 2021, 13, 9277-9329.	3.1	15
48	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
49	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	12.8	17
50	Soluble Angiotensin-Converting Enzyme 2, Cardiac Biomarkers, Structure, and Function, and Cardiovascular Events (from the Atherosclerosis Risk in Communities Study). American Journal of Cardiology, 2021, 146, 15-21.	1.6	8
51	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	6.2	28
52	Plasma amyloid Î² levels are driven by genetic variants near APOE, BACE1, APP, PSEN2: A genomeâ€wide association study in over 12,000 nonâ€demented participants. Alzheimer's and Dementia, 2021, 17, 1663-1674.	0.8	20
53	Large-scale plasma proteomic analysis identifies proteins and pathways associated with dementia risk. Nature Aging, 2021, 1, 473-489.	11.6	69
54	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341

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55	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	8.8	90
56	Common variants in Alzheimerâ€™s disease and risk stratification by polygenic risk scores. Nature Communications, 2021, 12, 3417.	12.8	140
57	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. Nature Communications, 2021, 12, 3987.	12.8	18
58	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	12.8	49
59	Leveraging a health information exchange for analyses of COVID-19 outcomes including an example application using smoking history and mortality. PLoS ONE, 2021, 16, e0247235.	2.5	4
60	Exome sequence association study of levels and longitudinal change of cardiovascular risk factor phenotypes in European Americans and African Americans from the Atherosclerosis Risk in Communities Study. Genetic Epidemiology, 2021, 45, 651-663.	1.3	2
61	Predictive Analytics for Glaucoma Using Data From the All of Us Research Program. American Journal of Ophthalmology, 2021, 227, 74-86.	3.3	25
62	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.	1.7	2
63	Rare Coding Variants Associated With Electrocardiographic Intervals Identify Monogenic Arrhythmia Susceptibility Genes: A Multi-Ancestry Analysis. Circulation Genomic and Precision Medicine, 2021, 14, e003300.	3.6	7
64	Genetic susceptibility, obesity and lifetime risk of type 2 diabetes: The ARIC study and Rotterdam Study. Diabetic Medicine, 2021, 38, e14639.	2.3	9
65	Epigenome-wide association study of mitochondrial genome copy number. Human Molecular Genetics, 2021, 31, 309-319.	2.9	6
66	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
67	Genetic testing in ambulatory cardiology clinics reveals high rate of findings with clinical management implications. Genetics in Medicine, 2021, 23, 2404-2414.	2.4	14
68	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 1836-1851.	6.2	14
69	Epidemiologic and Genetic Associations of Erythropoietin With Blood Pressure, Hypertension, and Coronary Artery Disease. Hypertension, 2021, 78, 1555-1566.	2.7	1
70	Germline Cancer Predisposition Variants inâ€, Pediatric Rhabdomyosarcoma: A Report From the Childrenâ€™s Oncology Group. Journal of the National Cancer Institute, 2021, 113, 875-883.	6.3	55
71	Association of mitochondrial DNA copy number with cardiometabolic diseases. Cell Genomics, 2021, 1, 100006.	6.5	26
72	Identification of Functional Genetic Determinants of Cardiac Troponin T and I in a Multiethnic Population and Causal Associations With Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2021, 14, CIRCGEN121003460.	3.6	5

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73	Analysis of COVID-19 Infection and Mortality Among Patients With Psychiatric Disorders, 2020. JAMA Network Open, 2021, 4, e2134969.	5.9	27
74	Proteomics and Risk of Atrial Fibrillation in Older Adults (From the Atherosclerosis Risk in) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 Td (	1.6	7
75	Pediatric data from the All of Us research program: demonstration of pediatric obesity over time. JAMIA Open, 2021, 4, ooab112.	2.0	1
76	Strategies to Estimate Prevalence of SARS-CoV-2 Antibodies in a Texas Vulnerable Population: Results From Phase I of the Texas Coronavirus Antibody Response Survey. Frontiers in Public Health, 2021, 9, 753487.	2.7	4
77	Examining Social Vulnerability and the Association With COVID-19 Incidence in Harris County, Texas. Frontiers in Public Health, 2021, 9, 798085.	2.7	4
78	Association of low-frequency and rare coding variants with information processing speed. Translational Psychiatry, 2021, 11, 613.	4.8	2
79	Geographic Variation in Obesity at the State Level in the All of Us Research Program. Preventing Chronic Disease, 2021, 18, E104.	3.4	6
80	Whole exome sequencing study identifies novel rare and common Alzheimerâ€™s-Associated variants involved in immune response and transcriptional regulation. Molecular Psychiatry, 2020, 25, 1859-1875.	7.9	191
81	Epigenetic Age Acceleration and Cognitive Function in African American Adults in Midlife: The Atherosclerosis Risk in Communities Study. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2020, 75, 473-480.	3.6	15
82	Cohort Profile: The Right Drug, Right Dose, Right Time: Using Genomic Data to Individualize Treatment Protocol (RIGHT Protocol). International Journal of Epidemiology, 2020, 49, 23-24k.	1.9	34
83	A diagnostic ceiling for exome sequencing in cerebellar ataxia and related neurological disorders. Human Mutation, 2020, 41, 487-501.	2.5	58
84	Mitochondrial DNA copy number can influence mortality and cardiovascular disease via methylation of nuclear DNA CpGs. Genome Medicine, 2020, 12, 84.	8.2	63
85	Urine 6-Bromotryptophan: Associations with Genetic Variants and Incident End-Stage Kidney Disease. Scientific Reports, 2020, 10, 10018.	3.3	6
86	A Genome-wide Association Study Discovers 46 Loci of the Human Metabolome in the Hispanic Community Health Study/Study of Latinos. American Journal of Human Genetics, 2020, 107, 849-863.	6.2	48
87	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
88	A Mendelian randomization of Î³â€² and total fibrinogen levels in relation to venous thromboembolism and ischemic stroke. Blood, 2020, 136, 3062-3069.	1.4	25
89	HEARTCARE: ADVANCING PRECISION MEDICINE THROUGH COMPREHENSIVE CARDIOVASCULAR GENETIC TESTING. Journal of the American College of Cardiology, 2020, 75, 3643.	2.8	4
90	Efficient geneâ€“environment interaction tests for large biobankâ€scale sequencing studies. Genetic Epidemiology, 2020, 44, 908-923.	1.3	15

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91	Methylome-wide association study of central adiposity implicates genes involved in immune and endocrine systems. Epigenomics, 2020, 12, 1483-1499.	2.1	6
92	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	21.4	146
93	Largeâ€scale plasma proteomic analysis identifies proteins and biological pathways associated with incident dementia. Alzheimer's and Dementia, 2020, 16, e038307.	0.8	1
94	Assessing whole genome sequencing variation for Alzheimerâ€™s disease in 4707 individuals from the Alzheimerâ€™s Disease Sequencing Project (ADSP). Alzheimer's and Dementia, 2020, 16, e045548.	0.8	0
95	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
96	GSTM1 Deletion Exaggerates Kidney Injury in Experimental Mouse Models and Confers the Protective Effect of Cruciferous Vegetables in Mice and Humans. Journal of the American Society of Nephrology: JASN, 2020, 31, 102-116.	6.1	28
97	Mitochondrial DNA Copy Number and Incident Heart Failure. Circulation, 2020, 141, 1823-1825.	1.6	17
98	A bidirectional Mendelian randomization study supports causal effects of kidney function onÂbloodÂpressure. Kidney International, 2020, 98, 708-716.	5.2	70
99	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
100	Analysis of putative cis-regulatory elements regulating blood pressure variation. Human Molecular Genetics, 2020, 29, 1922-1932.	2.9	7
101	Serum sphingolipids and incident diabetes in a US population with high diabetes burden: the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). American Journal of Clinical Nutrition, 2020, 112, 57-65.	4.7	29
102	Serum metabolites reflecting gut microbiome alpha diversity predict type 2 diabetes. Gut Microbes, 2020, 11, 1632-1642.	9.8	65
103	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. Circulation Genomic and Precision Medicine, 2020, 13, e002772.	3.6	11
104	Forecasting and Evaluating Multiple Interventions for COVID-19 Worldwide. Frontiers in Artificial Intelligence, 2020, 3, 41.	3.4	41
105	<scp>Wolffâ€“Parkinsonâ€“White</scp> syndrome: De novo variants and evidence for mutational burden in genes associated with atrial fibrillation. American Journal of Medical Genetics, Part A, 2020, 182, 1387-1399.	1.2	14
106	Sorting nexin 1 loss results in increased oxidative stress and hypertension. FASEB Journal, 2020, 34, 7941-7957.	0.5	8
107	Biallelic GRM7 variants cause epilepsy, microcephaly, and cerebral atrophy. Annals of Clinical and Translational Neurology, 2020, 7, 610-627.	3.7	15
108	Parliament2: Accurate structural variant calling at scale. GigaScience, 2020, 9, .	6.4	51

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109	Evaluation of mitochondrial DNA copy number estimation techniques. PLoS ONE, 2020, 15, e0228166.	2.5	97
110	Genetic loci associated with prevalent and incident myocardial infarction and coronary heart disease in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. PLoS ONE, 2020, 15, e0230035.	2.5	5
111	Evaluation of mitochondrial DNA copy number estimation techniques. , 2020, 15, e0228166.		0
112	Evaluation of mitochondrial DNA copy number estimation techniques. , 2020, 15, e0228166.		0
113	Evaluation of mitochondrial DNA copy number estimation techniques. , 2020, 15, e0228166.		0
114	Evaluation of mitochondrial DNA copy number estimation techniques. , 2020, 15, e0228166.		0
115	Quality control and integration of genotypes from two calling pipelines for whole genome sequence data in the Alzheimer's disease sequencing project. Genomics, 2019, 111, 808-818.	2.9	26
116	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. Circulation, 2019, 140, 645-657.	1.6	151
117	Association of sickle cell trait with measures of cognitive function and dementia in African Americans. ENeurologicalSci, 2019, 16, 100201.	1.3	3
118	Pharmacogenomics of statin-related myopathy: Meta-analysis of rare variants from whole-exome sequencing. PLoS ONE, 2019, 14, e0218115.	2.5	18
119	The Genomics of Arthrogryposis, a Complex Trait: Candidate Genes and Further Evidence for Oligogenic Inheritance. American Journal of Human Genetics, 2019, 105, 132-150.	6.2	74
120	A Genocentric Approach to Discovery of Mendelian Disorders. American Journal of Human Genetics, 2019, 105, 974-986.	6.2	30
121	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62
122	Sequencing Analysis at 8p23 Identifies Multiple Rare Variants in DLC1 Associated with Sleep-Related Oxyhemoglobin Saturation Level. American Journal of Human Genetics, 2019, 105, 1057-1068.	6.2	10
123	Hypertensive APOL1 risk allele carriers demonstrate greater blood pressure reduction with angiotensin receptor blockade compared to low risk carriers. PLoS ONE, 2019, 14, e0221957.	2.5	7
124	Unraveling the functional role of the orphan solute carrier, SLC22A24 in the transport of steroid conjugates through metabolomic and genome-wide association studies. PLoS Genetics, 2019, 15, e1008208.	3.5	23
125	Impact of Rare and Common Genetic Variants on Diabetes Diagnosis by Hemoglobin A1c in Multi-Ancestry Cohorts: The Trans-Omics for Precision Medicine Program. American Journal of Human Genetics, 2019, 105, 706-718.	6.2	44
126	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64

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127	Leveraging linkage evidence to identify low-frequency and rare variants on 16p13 associated with blood pressure using TOPMed whole genome sequencing data. Human Genetics, 2019, 138, 199-210.	3.8	29
128	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	27.8	679
129	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
130	Innovation in Genomic Data Sharing at the NIH. New England Journal of Medicine, 2019, 380, 2192-2195.	27.0	4
131	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	27.8	248
132	Multiple SCN5A variant enhancers modulate its cardiac gene expression and the QT interval. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10636-10645.	7.1	22
133	Î²₂â€Adrenergic Receptor Gene Affects the Heart Rate Response of Î²â€Blockers: Evidence From 3 Clinical Studies. Journal of Clinical Pharmacology, 2019, 59, 1462-1470.	2.0	9
134	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. PLoS ONE, 2019, 14, e0216222.	2.5	17
135	Metabolomic Pattern Predicts Incident Coronary Heart Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 1475-1482.	2.4	65
136	Genomic Association Analysis Reveals Variants Associated With Blood Pressure Response to Betaâ€Blockers in European Americans. Clinical and Translational Science, 2019, 12, 497-504.	3.1	13
137	Atlas-CNV: a validated approach to call single-exon CNVs in the eMERGESeq gene panel. Genetics in Medicine, 2019, 21, 2135-2144.	2.4	19
138	Association of FMO3 Variants with Blood Pressure in the Atherosclerosis Risk in Communities Study. International Journal of Hypertension, 2019, 2019, 1-8.	1.3	3
139	Reproducibility and Variability of Protein Analytes Measured Using a Multiplexed Modified Aptamer Assay. journal of applied laboratory medicine, The, 2019, 4, 30-39.	1.3	61
140	A prospective study of serum metabolites and risk of ischemic stroke. Neurology, 2019, 92, e1890-e1898.	1.1	48
141	ACAT: A Fast and Powerful p Value Combination Method for Rare-Variant Analysis in Sequencing Studies. American Journal of Human Genetics, 2019, 104, 410-421.	6.2	219
142	Serum Metabolomics and Incidence of Atrial Fibrillation (from the Atherosclerosis Risk in) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142 Td (	1.6	32
143	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
144	Dynamic Scan Procedure for Detecting Rare-Variant Association Regions in Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 802-814.	6.2	43

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145	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
146	The Consortium of Metabolomics Studies (COMETS): Metabolomics in 47 Prospective Cohort Studies. American Journal of Epidemiology, 2019, 188, 991-1012.	3.4	81
147	Metabolomics Identifies Novel Blood Biomarkers of Pulmonary Function and COPD in the General Population. Metabolites, 2019, 9, 61.	2.9	30
148	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates AÎ², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	21.4	1,962
149	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
150	Effect of plasma MicroRNA on antihypertensive response to beta blockers in the Pharmacogenomic Evaluation of Antihypertensive Responses (PEAR) studies. European Journal of Pharmaceutical Sciences, 2019, 131, 93-98.	4.0	13
151	APOL1 Kidney Risk Variants and Cardiovascular Disease: An Individual Participant Data Meta-Analysis. Journal of the American Society of Nephrology: JASN, 2019, 30, 2027-2036.	6.1	26
152	Genome Wide Analysis Approach Suggests Chromosome 2 Locus to be Associated with Thiazide and Thiazide Like-Diuretics Blood Pressure Response. Scientific Reports, 2019, 9, 17323.	3.3	5
153	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations. PLoS Genetics, 2019, 15, e1008500.	3.5	203
154	HFE H63D Polymorphism and the Risk for Systemic Hypertension, Myocardial Remodeling, and Adverse Cardiovascular Events in the ARIC Study. Hypertension, 2019, 73, 68-74.	2.7	7
155	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
156	Insights into genetics, human biology and disease gleaned from family based genomic studies. Genetics in Medicine, 2019, 21, 798-812.	2.4	161
157	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 260-274.	6.2	103
158	Genetic architecture of laterality defects revealed by whole exome sequencing. European Journal of Human Genetics, 2019, 27, 563-573.	2.8	44
159	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. Human Molecular Genetics, 2019, 28, 1212-1224.	2.9	12
160	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. Blood, 2019, 133, 967-977.	1.4	34
161	A biallelic ANTXR1 variant expands the anthrax toxin receptor associated phenotype to tooth agenesis. American Journal of Medical Genetics, Part A, 2018, 176, 1015-1022.	1.2	11
162	Genomeâ€Wide Association Approach Identified Novel Genetic Predictors of Heart Rate Response to Î²â€Blockers. Journal of the American Heart Association, 2018, 7, .	3.7	18

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163	Genetic Variation in Genes Underlying Diverse Dementias May Explain a Small Proportion of Cases in the Alzheimerâ€™s Disease Sequencing Project. Dementia and Geriatric Cognitive Disorders, 2018, 45, 1-17.	1.5	22
164	Effects of Gender-Specific Differences, Inflammatory Response, and Genetic Variation on the Associations Among Depressive Symptoms and the Risk of Major Adverse Coronary Events in Patients With Acute Coronary Syndrome. Biological Research for Nursing, 2018, 20, 168-176.	1.9	3
165	Prospective Study of Epigenetic Age Acceleration and Incidence of Cardiovascular Disease Outcomes in the ARIC Study (Atherosclerosis Risk in Communities). Circulation Genomic and Precision Medicine, 2018, 11, e001937.	3.6	97
166	The role of FREM2 and FRAS1 in the development of congenital diaphragmatic hernia. Human Molecular Genetics, 2018, 27, 2064-2075.	2.9	16
167	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356
168	Sequence-Based Analysis of Lipid-Related Metabolites in a Multiethnic Study. Genetics, 2018, 209, 607-616.	2.9	8
169	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
170	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. Nature Communications, 2018, 9, 260.	12.8	295
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