

# Eric Boerwinkle

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. Nature Genetics, 2013, 45, 1452-1458.	21.4	3,741
2	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,684
3	A comprehensive 1000 Genomesâ€‘based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	21.4	2,054
4	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
5	Genetic variation in the gene encoding calpain-10 is associated with type 2 diabetes mellitus. Nature Genetics, 2000, 26, 163-175.	21.4	1,403
6	Genome-wide association study of blood pressure and hypertension. Nature Genetics, 2009, 41, 677-687.	21.4	1,224
7	Molecular Findings Among Patients Referred for Clinical Whole-Exome Sequencing. JAMA - Journal of the American Medical Association, 2014, 312, 1870.	7.4	1,171
8	A framework for the interpretation of de novo mutation in human disease. Nature Genetics, 2014, 46, 944-950.	21.4	943
9	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
10	Comparison and integration of deleteriousness prediction methods for nonsynonymous SNVs in whole exome sequencing studies. Human Molecular Genetics, 2015, 24, 2125-2137.	2.9	892
11	dbNSFP v3.0: A One-Stop Database of Functional Predictions and Annotations for Human Nonsynonymous and Splice-Site SNVs. Human Mutation, 2016, 37, 235-241.	2.5	845
12	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	21.4	783
13	Diagnostic Yield and Clinical Utility of Sequencing Familial Hypercholesterolemia Genes in Patients With Severe Hypercholesterolemia. Journal of the American College of Cardiology, 2016, 67, 2578-2589.	2.8	723
14	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	21.4	700
15	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	27.8	679
16	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
17	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	27.8	581
18	The Genetic Basis of Mendelian Phenotypes: Discoveries, Challenges, and Opportunities. American Journal of Human Genetics, 2015, 97, 199-215.	6.2	574

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19	Resolution of Disease Phenotypes Resulting from Multilocus Genomic Variation. <i>New England Journal of Medicine</i> , 2017, 376, 21-31.	27.0	565
20	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018, 50, 1225-1233.	21.4	552
21	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	21.4	549
22	dbNSFP v2.0: A Database of Human Non-synonymous SNVs and Their Functional Predictions and Annotations. <i>Human Mutation</i> , 2013, 34, E2393-E2402.	2.5	546
23	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	27.8	544
24	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. <i>BMJ</i> , The, 2014, 349, g4164-g4164.	6.0	528
25	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , 2018, 9, 2098.	12.8	484
26	DNA sequence diversity in a 9.7-kb region of the human lipoprotein lipase gene. <i>Nature Genetics</i> , 1998, 19, 233-240.	21.4	483
27	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	21.4	470
28	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	21.4	426
29	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	12.8	412
30	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011, 43, 1005-1011.	21.4	403
31	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015, 47, 1415-1425.	21.4	365
32	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016, 48, 1171-1184.	21.4	362
33	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	21.4	357
34	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 559-571.	21.4	356
35	ANGPTL3 Deficiency and Protection Against Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2017, 69, 2054-2063.	2.8	348
36	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	21.4	341

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37	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	3.5	331
38	COPA mutations impair ER-Golgi transport and cause hereditary autoimmune-mediated lung disease and arthritis. <i>Nature Genetics</i> , 2015, 47, 654-660.	21.4	302
39	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. <i>Nature Communications</i> , 2018, 9, 260.	12.8	295
40	Genome-Wide Association Study of Coronary Heart Disease and Its Risk Factors in 8,090 African Americans: The NHLBI CARE Project. <i>PLoS Genetics</i> , 2011, 7, e1001300.	3.5	290
41	Epigenome-wide association study (EWAS) of BMI, BMI change and waist circumference in African American adults identifies multiple replicated loci. <i>Human Molecular Genetics</i> , 2015, 24, 4464-4479.	2.9	289
42	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. <i>American Journal of Human Genetics</i> , 2014, 94, 223-232.	6.2	287
43	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	21.4	286
44	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , 2017, 49, 946-952.	21.4	279
45	Primary immunodeficiency diseases: Genomic approaches delineate heterogeneous Mendelian disorders. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 232-245.	2.9	261
46	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. <i>Nature Genetics</i> , 2017, 49, 1113-1119.	21.4	260
47	Genes that Affect Brain Structure and Function Identified by Rare Variant Analyses of Mendelian Neurologic Disease. <i>Neuron</i> , 2015, 88, 499-513.	8.1	258
48	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016, 17, 255.	8.8	251
49	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019, 570, 71-76.	27.8	248
50	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. <i>PLoS Medicine</i> , 2017, 14, e1002215.	8.4	246
51	Association of <i>MTOR</i> Mutations With Developmental Brain Disorders, Including Megalencephaly, Focal Cortical Dysplasia, and Pigmentary Mosaicism. <i>JAMA Neurology</i> , 2016, 73, 836.	9.0	234
52	Mutations in the nuclear bile acid receptor FXR cause progressive familial intrahepatic cholestasis. <i>Nature Communications</i> , 2016, 7, 10713.	12.8	227
53	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , 2016, 48, 1162-1170.	21.4	223
54	ACAT: A Fast and Powerful p Value Combination Method for Rare-Variant Analysis in Sequencing Studies. <i>American Journal of Human Genetics</i> , 2019, 104, 410-421.	6.2	219

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55	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. <i>Nature Communications</i> , 2014, 5, 5068.	12.8	216
56	Exome Sequence Analysis Suggests that Genetic Burden Contributes to Phenotypic Variability and Complex Neuropathy. <i>Cell Reports</i> , 2015, 12, 1169-1183.	6.4	211
57	CD163+ macrophages promote angiogenesis and vascular permeability accompanied by inflammation in atherosclerosis. <i>Journal of Clinical Investigation</i> , 2018, 128, 1106-1124.	8.2	209
58	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. <i>PLoS Genetics</i> , 2019, 15, e1008500.	3.5	203
59	Association of Mitochondrial DNA Copy Number With Cardiovascular Disease. <i>JAMA Cardiology</i> , 2017, 2, 1247.	6.1	194
60	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. <i>American Journal of Human Genetics</i> , 2014, 94, 233-245.	6.2	193
61	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. <i>PLoS Genetics</i> , 2014, 10, e1004517.	3.5	191
62	Whole exome sequencing study identifies novel rare and common Alzheimer's-Associated variants involved in immune response and transcriptional regulation. <i>Molecular Psychiatry</i> , 2020, 25, 1859-1875.	7.9	191
63	Human CLP1 Mutations Alter tRNA Biogenesis, Affecting Both Peripheral and Central Nervous System Function. <i>Cell</i> , 2014, 157, 636-650.	28.9	189
64	Molecular diagnostic experience of whole-exome sequencing in adult patients. <i>Genetics in Medicine</i> , 2016, 18, 678-685.	2.4	186
65	Lessons learned from additional research analyses of unsolved clinical exome cases. <i>Genome Medicine</i> , 2017, 9, 26.	8.2	184
66	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	27.8	183
67	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. <i>Nature Communications</i> , 2018, 9, 4455.	12.8	181
68	Association of mitochondrial DNA levels with frailty and all-cause mortality. <i>Journal of Molecular Medicine</i> , 2015, 93, 177-186.	3.9	178
69	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015, 6, 5897.	12.8	173
70	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	27.8	173
71	Convergent genetic and expression data implicate immunity in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2015, 11, 658-671.	0.8	173
72	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	12.8	169

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73	Insights into genetics, human biology and disease gleaned from family based genomic studies. <i>Genetics in Medicine</i> , 2019, 21, 798-812.	2.4	161
74	Identifying Genes Whose Mutant Transcripts Cause Dominant Disease Traits by Potential Gain-of-Function Alleles. <i>American Journal of Human Genetics</i> , 2018, 103, 171-187.	6.2	160
75	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. <i>American Journal of Human Genetics</i> , 2014, 94, 349-360.	6.2	158
76	Genome-wide physical activity interactions in adiposity • A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	3.5	158
77	Essential Hypertension vs. Secondary Hypertension Among Children. <i>American Journal of Hypertension</i> , 2015, 28, 73-80.	2.0	157
78	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. <i>PLoS ONE</i> , 2014, 9, e94661.	2.5	155
79	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017, 101, 888-902.	6.2	154
80	Assessing structural variation in a personal genome—towards a human reference diploid genome. <i>BMC Genomics</i> , 2015, 16, 286.	2.8	153
81	Epigenome-wide study identifies novel methylation loci associated with body mass index and waist circumference. <i>Obesity</i> , 2015, 23, 1493-1501.	3.0	152
82	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. <i>Circulation</i> , 2019, 140, 645-657.	1.6	151
83	Recurrent De Novo and Biallelic Variation of ATAD3A , Encoding a Mitochondrial Membrane Protein, Results in Distinct Neurological Syndromes. <i>American Journal of Human Genetics</i> , 2016, 99, 831-845.	6.2	146
84	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. <i>Nature Genetics</i> , 2020, 52, 969-983.	21.4	146
85	Epigenome-wide association studies identify DNA methylation associated with kidney function. <i>Nature Communications</i> , 2017, 8, 1286.	12.8	145
86	Association Between Titin Loss-of-Function Variants and Early-Onset Atrial Fibrillation. <i>JAMA - Journal of the American Medical Association</i> , 2018, 320, 2354.	7.4	144
87	Loci influencing blood pressure identified using a cardiovascular gene-centric array. <i>Human Molecular Genetics</i> , 2013, 22, 1663-1678.	2.9	141
88	Common variants in Alzheimer's disease and risk stratification by polygenic risk scores. <i>Nature Communications</i> , 2021, 12, 3417.	12.8	140
89	High-throughput multiplex SNP genotyping with MALDI-TOF mass spectrometry: Practice, problems and promise. <i>Human Mutation</i> , 2001, 17, 296-304.	2.5	137
90	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. <i>Diabetes</i> , 2016, 65, 803-817.	0.6	131

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91	In silico tools for splicing defect prediction: a survey from the viewpoint of end users. <i>Genetics in Medicine</i> , 2014, 16, 497-503.	2.4	124
92	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018, 102, 375-400.	6.2	123
93	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. <i>Nature Communications</i> , 2018, 9, 5141.	12.8	119
94	Association between Mitochondrial DNA Copy Number in Peripheral Blood and Incident CKD in the Atherosclerosis Risk in Communities Study. <i>Journal of the American Society of Nephrology: JASN</i> , 2016, 27, 2467-2473.	6.1	112
95	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648.	21.4	112
96	Gene-Age Interactions in Blood Pressure Regulation: A Large-Scale Investigation with the CHARGE, Global BPgen, and ICBP Consortia. <i>American Journal of Human Genetics</i> , 2014, 95, 24-38.	6.2	109
97	Pleiotropic genes for metabolic syndrome and inflammation. <i>Molecular Genetics and Metabolism</i> , 2014, 112, 317-338.	1.1	107
98	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. <i>American Journal of Human Genetics</i> , 2019, 104, 260-274.	6.2	103
99	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. <i>Circulation</i> , 2019, 139, 620-635.	1.6	102
100	A genomic approach to therapeutic target validation identifies a glucose-lowering <i>GLP1R</i> variant protective for coronary heart disease. <i>Science Translational Medicine</i> , 2016, 8, 341ra76.	12.4	100
101	A Genome-Wide Association Study for Venous Thromboembolism: The Extended Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. <i>Genetic Epidemiology</i> , 2013, 37, 512-521.	1.3	99
102	Homozygous and hemizygous CNV detection from exome sequencing data in a Mendelian disease cohort. <i>Nucleic Acids Research</i> , 2017, 45, gkw1237.	14.5	98
103	Recurrent Muscle Weakness with Rhabdomyolysis, Metabolic Crises, and Cardiac Arrhythmia Due to Bi-allelic <i>TANGO2</i> Mutations. <i>American Journal of Human Genetics</i> , 2016, 98, 347-357.	6.2	98
104	Plasma proteome analyses in individuals of European and African ancestry identify cis-pQTLs and models for proteome-wide association studies. <i>Nature Genetics</i> , 2022, 54, 593-602.	21.4	98
105	Prospective Study of Epigenetic Age Acceleration and Incidence of Cardiovascular Disease Outcomes in the ARIC Study (Atherosclerosis Risk in Communities). <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e001937.	3.6	97
106	Evaluation of mitochondrial DNA copy number estimation techniques. <i>PLoS ONE</i> , 2020, 15, e0228166.	2.5	97
107	WGSA: an annotation pipeline for human genome sequencing studies. <i>Journal of Medical Genetics</i> , 2016, 53, 111-112.	3.2	96
108	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. <i>Nature Genetics</i> , 2017, 49, 1560-1563.	21.4	93

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109	Serum Metabolomic Profiling and Incident CKD among African Americans. <i>Clinical Journal of the American Society of Nephrology: CJASN</i> , 2014, 9, 1410-1417.	4.5	92
110	Mutations in PURA Cause Profound Neonatal Hypotonia, Seizures, and Encephalopathy in 5q31.3 Microdeletion Syndrome. <i>American Journal of Human Genetics</i> , 2014, 95, 579-583.	6.2	92
111	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020, 52, 1314-1332.	21.4	91
112	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	8.8	90
113	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	21.4	89
114	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. <i>PLoS Genetics</i> , 2017, 13, e1006728.	3.5	88
115	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, 24.	12.8	87
116	Genetic Determinants Influencing Human Serum Metabolome among African Americans. <i>PLoS Genetics</i> , 2014, 10, e1004212.	3.5	84
117	Cladistic Structure Within the Human Lipoprotein Lipase Gene and Its Implications for Phenotypic Association Studies. <i>Genetics</i> , 2000, 156, 1259-1275.	2.9	84
118	Variation at the M235T locus of the angiotensinogen gene and essential hypertension: a population-based case-control study from Rochester, Minnesota. <i>Human Genetics</i> , 1995, 96, 295-300.	3.8	82
119	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. <i>American Journal of Human Genetics</i> , 2016, 99, 40-55.	6.2	82
120	The Consortium of Metabolomics Studies (COMETS): Metabolomics in 47 Prospective Cohort Studies. <i>American Journal of Epidemiology</i> , 2019, 188, 991-1012.	3.4	81
121	Exome sequencing in mostly consanguineous Arab families with neurologic disease provides a high potential molecular diagnosis rate. <i>BMC Medical Genomics</i> , 2016, 9, 42.	1.5	80
122	POGZ truncating alleles cause syndromic intellectual disability. <i>Genome Medicine</i> , 2016, 8, 3.	8.2	78
123	Genome-wide meta-analysis of muscle weakness identifies 15 susceptibility loci in older men and women. <i>Nature Communications</i> , 2021, 12, 654.	12.8	75
124	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	12.8	74
125	The Genomics of Arthrogyrosis, a Complex Trait: Candidate Genes and Further Evidence for Oligogenic Inheritance. <i>American Journal of Human Genetics</i> , 2019, 105, 132-150.	6.2	74
126	Genetic Variants in LRP1 and ULK4 Are Associated with Acute Aortic Dissections. <i>American Journal of Human Genetics</i> , 2016, 99, 762-769.	6.2	73



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127	Polygenic Scores for Major Depressive Disorder and Risk of Alcohol Dependence. <i>JAMA Psychiatry</i> , 2017, 74, 1153.	11.0	73
128	An Enhancer Polymorphism at the Cardiomyocyte Intercalated Disc Protein NOS1AP Locus Is a Major Regulator of the QT Interval. <i>American Journal of Human Genetics</i> , 2014, 94, 854-869.	6.2	72
129	Whole-Exome Sequencing in Familial Parkinson Disease. <i>JAMA Neurology</i> , 2016, 73, 68.	9.0	71
130	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018, 9, 2904.	12.8	71
131	Risk of Type 2 Diabetes and Obesity Is Differentially Associated with Variation in FTO in Whites and African-Americans in the ARIC Study. <i>PLoS ONE</i> , 2010, 5, e10521.	2.5	70
132	A bidirectional Mendelian randomization study supports causal effects of kidney function on blood pressure. <i>Kidney International</i> , 2020, 98, 708-716.	5.2	70
133	Genome-Wide Association Study for Incident Myocardial Infarction and Coronary Heart Disease in Prospective Cohort Studies: The CHARGE Consortium. <i>PLoS ONE</i> , 2016, 11, e0144997.	2.5	69
134	An exome array study of the plasma metabolome. <i>Nature Communications</i> , 2016, 7, 12360.	12.8	69
135	Large-scale plasma proteomic analysis identifies proteins and pathways associated with dementia risk. <i>Nature Aging</i> , 2021, 1, 473-489.	11.6	69
136	Association between mitochondrial DNA copy number and sudden cardiac death: findings from the Atherosclerosis Risk in Communities study (ARIC). <i>European Heart Journal</i> , 2017, 38, 3443-3448.	2.2	68
137	Genome-wide Studies of Verbal Declarative Memory in Nondemented Older People: The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. <i>Biological Psychiatry</i> , 2015, 77, 749-763.	1.3	67
138	Gender- and age-dependent relationships between the E-selectin S128R polymorphism and coronary artery calcification. <i>Journal of Molecular Medicine</i> , 2001, 79, 390-398.	3.9	66
139	Monoallelic and Biallelic Variants in EMC1 Identified in Individuals with Global Developmental Delay, Hypotonia, Scoliosis, and Cerebellar Atrophy. <i>American Journal of Human Genetics</i> , 2016, 98, 562-570.	6.2	66
140	Metabolomic Pattern Predicts Incident Coronary Heart Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2019, 39, 1475-1482.	2.4	65
141	Serum metabolites reflecting gut microbiome alpha diversity predict type 2 diabetes. <i>Gut Microbes</i> , 2020, 11, 1632-1642.	9.8	65
142	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	12.8	64
143	PacBio-LITS: a large-insert targeted sequencing method for characterization of human disease-associated chromosomal structural variations. <i>BMC Genomics</i> , 2015, 16, 214.	2.8	63
144	Mitochondrial DNA copy number can influence mortality and cardiovascular disease via methylation of nuclear DNA CpGs. <i>Genome Medicine</i> , 2020, 12, 84.	8.2	63

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145	Genetically determined NLRP3 inflammasome activation associates with systemic inflammation and cardiovascular mortality. <i>European Heart Journal</i> , 2021, 42, 1742-1756.	2.2	63
146	American Heart Association's Life's Simple 7: Lifestyle Recommendations, Polygenic Risk, and Lifetime Risk of Coronary Heart Disease. <i>Circulation</i> , 2022, 145, 808-818.	1.6	63
147	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. <i>Nature Communications</i> , 2019, 10, 5121.	12.8	62
148	Genetic Variants in SGLT1, Glucose Tolerance, and Cardiometabolic Risk. <i>Journal of the American College of Cardiology</i> , 2018, 72, 1763-1773.	2.8	61
149	Reproducibility and Variability of Protein Analytes Measured Using a Multiplexed Modified Aptamer Assay. <i>Journal of Applied Laboratory Medicine</i> , 2019, 4, 30-39.	1.3	61
150	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. <i>American Journal of Human Genetics</i> , 2016, 99, 8-21.	6.2	60
151	Seafood Consumption and Blood Mercury Concentrations in Jamaican Children With and Without Autism Spectrum Disorders. <i>Neurotoxicity Research</i> , 2013, 23, 22-38.	2.7	59
152	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.	12.8	59
153	A diagnostic ceiling for exome sequencing in cerebellar ataxia and related neurological disorders. <i>Human Mutation</i> , 2020, 41, 487-501.	2.5	58
154	Plasma phospholipids and prevalence of mild cognitive impairment and/or dementia in the ARIC Neurocognitive Study (ARIC-NCNS). <i>Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring</i> , 2016, 3, 73-82.	2.4	57
155	Causal Role of Alcohol Consumption in an Improved Lipid Profile: The Atherosclerosis Risk in Communities (ARIC) Study. <i>PLoS ONE</i> , 2016, 11, e0148765.	2.5	57
156	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. <i>Blood</i> , 2015, 126, e19-e29.	1.4	55
157	Trans-ethnic Meta-analysis and Functional Annotation Illuminates the Genetic Architecture of Fasting Glucose and Insulin. <i>American Journal of Human Genetics</i> , 2016, 99, 56-75.	6.2	55
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