

# Charles Kooperberg

## List of Publications by Year in descending order

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Version: 2024-02-01

221  
papers

44,880  
citations

13854

67  
h-index

2506

196  
g-index

240  
all docs

240  
docs citations

240  
times ranked

47523  
citing authors

#	ARTICLE	IF	CITATIONS
1	Analyses of biomarker traits in diverse UK biobank participants identify associations missed by European-centric analysis strategies. <i>Journal of Human Genetics</i> , 2022, 67, 87-93.	1.1	27
2	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. <i>Stroke</i> , 2022, 53, 788-797.	1.0	88
3	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. <i>Cell Genomics</i> , 2022, 2, 100084.	3.0	29
4	Taking action to advance the study of race and ethnicity: the Women's Health Initiative (WHI). <i>Women's Midlife Health</i> , 2022, 8, 1.	0.5	13
5	Rare coding variants in 35 genes associate with circulating lipid levels—A multi-ancestry analysis of 170,000 exomes. <i>American Journal of Human Genetics</i> , 2022, 109, 81-96.	2.6	24
6	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study. <i>Diabetologia</i> , 2022, 65, 477-489.	2.9	15
7	Rare coding variants in RCN3 are associated with blood pressure. <i>BMC Genomics</i> , 2022, 23, 148.	1.2	2
8	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. <i>Nature Genetics</i> , 2022, 54, 263-273.	9.4	156
9	Genetic Landscape of the ACE2 Coronavirus Receptor. <i>Circulation</i> , 2022, 145, 1398-1411.	1.6	20
10	Predicted gene expression in ancestrally diverse populations leads to discovery of susceptibility loci for lifestyle and cardiometabolic traits. <i>American Journal of Human Genetics</i> , 2022, 109, 669-679.	2.6	5
11	Monogenic and Polygenic Contributions to QTc Prolongation in the Population. <i>Circulation</i> , 2022, 145, 1524-1533.	1.6	14
12	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. <i>Science Advances</i> , 2022, 8, eabl6579.	4.7	36
13	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	9.4	250
14	TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data. <i>American Journal of Human Genetics</i> , 2022, 109, 1175-1181.	2.6	25
15	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations. <i>Frontiers in Endocrinology</i> , 2022, 13, 863893.	1.5	7
16	Integration of rare expression outlier-associated variants improves polygenic risk prediction. <i>American Journal of Human Genetics</i> , 2022, 109, 1055-1064.	2.6	8
17	Longitudinal profiling of clonal hematopoiesis provides insight into clonal dynamics. <i>Immunity and Ageing</i> , 2022, 19, .	1.8	20
18	A multi-ethnic polygenic risk score is associated with hypertension prevalence and progression throughout adulthood. <i>Nature Communications</i> , 2022, 13, .	5.8	27

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19	Contributions of the Women's Health Initiative to Cardiovascular Research. <i>Journal of the American College of Cardiology</i> , 2022, 80, 256-275.	1.2	5
20	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. <i>Hypertension</i> , 2022, 79, 1656-1667.	1.3	12
21	Premature Menopause, Clonal Hematopoiesis, and Coronary Artery Disease in Postmenopausal Women. <i>Circulation</i> , 2021, 143, 410-423.	1.6	87
22	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100013.	1.0	2
23	Non-coding variants in <i>MYH11</i> , <i>FZD3</i> , and <i>SORCS3</i> are associated with dementia in women. <i>Alzheimer's and Dementia</i> , 2021, 17, 215-225.	0.4	18
24	Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. <i>EBioMedicine</i> , 2021, 63, 103157.	2.7	14
25	Genetic architectures of proximal and distal colorectal cancer are partly distinct. <i>Gut</i> , 2021, 70, 1325-1334.	6.1	44
26	A Population-Based Study of Genes Previously Implicated in Breast Cancer. <i>New England Journal of Medicine</i> , 2021, 384, 440-451.	13.9	414
27	Smoking Modifies Pancreatic Cancer Risk Loci on 2q21.3. <i>Cancer Research</i> , 2021, 81, 3134-3143.	0.4	8
28	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299.	13.7	1,069
29	Prediagnostic Inflammation and Pancreatic Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2021, 113, 1186-1193.	3.0	9
30	Healthy Lifestyle and Clonal Hematopoiesis of Indeterminate Potential: Results From the Women's Health Initiative. <i>Journal of the American Heart Association</i> , 2021, 10, e018789.	1.6	43
31	Improving reporting standards for polygenic scores in risk prediction studies. <i>Nature</i> , 2021, 591, 211-219.	13.7	265
32	Multi-ancestry genome-wide gene-sleep interactions identify novel loci for blood pressure. <i>Molecular Psychiatry</i> , 2021, 26, 6293-6304.	4.1	13
33	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. <i>American Journal of Human Genetics</i> , 2021, 108, 564-582.	2.6	18
34	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. <i>Nature Communications</i> , 2021, 12, 2182.	5.8	17
35	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100029.	1.0	23
36	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2021, 108, 874-893.	2.6	28

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37	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. <i>Aging Cell</i> , 2021, 20, e13366.	3.0	72
38	Multi-ethnic genome-wide association analyses of white blood cell and platelet traits in the Population Architecture using Genomics and Epidemiology (PAGE) study. <i>BMC Genomics</i> , 2021, 22, 432.	1.2	6
39	Hepcidin-regulating iron metabolism genes and pancreatic ductal adenocarcinoma: a pathway analysis of genome-wide association studies. <i>American Journal of Clinical Nutrition</i> , 2021, 114, 1408-1417.	2.2	9
40	Association of Clonal Hematopoiesis With Incident Heart Failure. <i>Journal of the American College of Cardiology</i> , 2021, 78, 42-52.	1.2	101
41	Transcriptome-Wide Association Study of Blood Cell Traits in African Ancestry and Hispanic/Latino Populations. <i>Genes</i> , 2021, 12, 1049.	1.0	11
42	BinomiRare: A robust test for association of a rare genetic variant with a binary outcome for mixed models and any case-control proportion. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100040.	1.0	2
43	Rare Coding Variants Associated With Electrocardiographic Intervals Identify Monogenic Arrhythmia Susceptibility Genes: A Multi-Ancestry Analysis. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003300.	1.6	7
44	Identification of novel and rare variants associated with handgrip strength using whole genome sequence data from the NHLBI Trans-Omics in Precision Medicine (TOPMed) Program. <i>PLoS ONE</i> , 2021, 16, e0253611.	1.1	4
45	Epigenome-wide association study of mitochondrial genome copy number. <i>Human Molecular Genetics</i> , 2021, 31, 309-319.	1.4	6
46	Associations between ambient air pollutants and clonal hematopoiesis of indeterminate potential (CHIP). <i>ISEE Conference Abstracts</i> , 2021, 2021, .	0.0	0
47	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	13.7	183
48	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2021, 108, 1836-1851.	2.6	14
49	Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. <i>Stroke</i> , 2021, , STROKEAHA120031792.	1.0	16
50	Full title: A large-scale transcriptome-wide association study (TWAS) of 10 blood cell phenotypes reveals complexities of TWAS fine-mapping. <i>Genetic Epidemiology</i> , 2021, , .	0.6	2
51	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	13.7	353
52	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , 2020, 25, 2392-2409.	4.1	83
53	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. <i>Journal of the National Cancer Institute</i> , 2020, 112, 1003-1012.	3.0	59
54	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020, 586, 763-768.	13.7	376

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55	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.	9.4	91
56	Genome-Wide Association Study Meta-Analysis of Stroke in 22 000 Individuals of African Descent Identifies Novel Associations With Stroke. <i>Stroke</i> , 2020, 51, 2454-2463.	1.0	26
57	Mendelian Randomization Analysis of n-6 Polyunsaturated Fatty Acid Levels and Pancreatic Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 2735-2739.	1.1	6
58	A general framework for functionally informed set-based analysis: Application to a large-scale colorectal cancer study. <i>PLoS Genetics</i> , 2020, 16, e1008947.	1.5	6
59	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, 387-395.	1.6	16
60	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. <i>Nature Communications</i> , 2020, 11, 6417.	5.8	39
61	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. <i>PLoS ONE</i> , 2020, 15, e0230815.	1.1	10
62	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.	5.8	59
63	Genome-Wide Gene-Gene Interaction Scan in 8,255 Cases and 11,900 Controls from PanScan and PanC4 Consortia. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1784-1791.	1.1	5
64	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002772.	1.6	11
65	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study. <i>PLoS Genetics</i> , 2020, 16, e1008684.	1.5	17
66	Genome-Wide Association Study Data Reveal Genetic Susceptibility to Chronic Inflammatory Intestinal Diseases and Pancreatic Ductal Adenocarcinoma Risk. <i>Cancer Research</i> , 2020, 80, 4004-4013.	0.4	5
67	Multi-Ethnic Genome-Wide Association Study of Decomposed Cardioelectric Phenotypes Illustrates Strategies to Identify and Characterize Evidence of Shared Genetic Effects for Complex Traits. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002680.	1.6	4
68	Association of Leukocyte Telomere Length With Mortality Among Adult Participants in 3 Longitudinal Studies. <i>JAMA Network Open</i> , 2020, 3, e200023.	2.8	62
69	Associations between Genetically Predicted Blood Protein Biomarkers and Pancreatic Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1501-1508.	1.1	18
70	Title is missing!. , 2020, 16, e1008684.		0
71	Title is missing!. , 2020, 16, e1008684.		0
72	Title is missing!. , 2020, 16, e1008684.		0

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73	Title is missing!. , 2020, 16, e1008684.		0
74	Title is missing!. , 2020, 16, e1008684.		0
75	Title is missing!. , 2020, 16, e1008684.		0
76	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
77	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
78	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
79	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
80	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	0.6	162
81	Statistical inference of genetic pathway analysis in high dimensions. Biometrika, 2019, 106, 651-651.	1.3	2
82	GWAS of QRS duration identifies new loci specific to Hispanic/Latino populations. PLoS ONE, 2019, 14, e0217796.	1.1	8
83	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
84	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
85	Effects of Colorectal Cancer Risk Factors on the Association Between Aspirin and Colorectal Cancer. Anticancer Research, 2019, 39, 4877-4884.	0.5	4
86	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
87	A large-scale exome array analysis of venous thromboembolism. Genetic Epidemiology, 2019, 43, 449-457.	0.6	22
88	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	1.6	85
89	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
90	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	13.7	679

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91	Genetics of Chronic Kidney Disease Stages Across Ancestries: The PAGE Study. <i>Frontiers in Genetics</i> , 2019, 10, 494.	1.1	29
92	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.	9.4	112
93	A phenome-wide association study (PheWAS) in the Population Architecture using Genomics and Epidemiology (PAGE) study reveals potential pleiotropy in African Americans. <i>PLoS ONE</i> , 2019, 14, e0226771.	1.1	15
94	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.	1.5	203
95	Agnostic Pathway/Gene Set Analysis of Genome-Wide Association Data Identifies Associations for Pancreatic Cancer. <i>Journal of the National Cancer Institute</i> , 2019, 111, 557-567.	3.0	21
96	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. <i>Nature Communications</i> , 2019, 10, 29.	5.8	113
97	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.	2.6	103
98	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. <i>Nature Genetics</i> , 2019, 51, 237-244.	9.4	1,307
99	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. <i>Biological Psychiatry</i> , 2019, 85, 946-955.	0.7	69
100	Discovery of common and rare genetic risk variants for colorectal cancer. <i>Nature Genetics</i> , 2019, 51, 76-87.	9.4	377
101	DNA methylation-based estimator of telomere length. <i>Aging</i> , 2019, 11, 5895-5923.	1.4	198
102	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.	2.6	123
103	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. <i>Nature Communications</i> , 2018, 9, 556.	5.8	188
104	Genome-wide association study of PR interval in Hispanics/Latinos identifies novel locus at <i>ID2</i> . <i>Heart</i> , 2018, 104, 904-911.	1.2	12
105	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e001758.	1.6	27
106	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706.	2.6	326
107	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002037.	1.6	19
108	The genetic underpinnings of variation in ages at menarche and natural menopause among women from the multi-ethnic Population Architecture using Genomics and Epidemiology (PAGE) Study: A trans-ethnic meta-analysis. <i>PLoS ONE</i> , 2018, 13, e0200486.	1.1	25

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109	Generalization and fine mapping of red blood cell trait genetic associations to multiethnic populations: The PAGE study. <i>American Journal of Hematology</i> , 2018, 93, 1061-1073.	2.0	5
110	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. <i>Genome Biology</i> , 2018, 19, 87.	3.8	47
111	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. <i>Human Molecular Genetics</i> , 2018, 27, 2940-2953.	1.4	16
112	Identifying Disease-Associated Copy Number Variations by a Doubly Penalized Regression Model. <i>Biometrics</i> , 2018, 74, 1341-1350.	0.8	5
113	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166.	1.1	94
114	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.	9.4	286
115	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , 2018, 50, 524-537.	9.4	1,124
116	Fine mapping of QT interval regions in global populations refines previously identified QT interval loci and identifies signals unique to African and Hispanic descent populations. <i>Heart Rhythm</i> , 2017, 14, 572-580.	0.3	19
117	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	13.7	544
118	Trans-ethnic fine-mapping of genetic loci for body mass index in the diverse ancestral populations of the Population Architecture using Genomics and Epidemiology (PAGE) Study reveals evidence for multiple signals at established loci. <i>Human Genetics</i> , 2017, 136, 771-800.	1.8	31
119	Discovery of novel heart rate-associated loci using the Exome Chip. <i>Human Molecular Genetics</i> , 2017, 26, 2346-2363.	1.4	29
120	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.	5.8	169
121	Leisure-time physical activity and leukocyte telomere length among older women. <i>Experimental Gerontology</i> , 2017, 95, 141-147.	1.2	28
122	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. <i>Nature Communications</i> , 2017, 8, 15805.	5.8	95
123	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. <i>Heart Rhythm</i> , 2017, 14, 1675-1684.	0.3	18
124	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. <i>Nature Genetics</i> , 2017, 49, 1113-1119.	9.4	260
125	Association of Accelerometer-Measured Physical Activity With Leukocyte Telomere Length Among Older Women. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2017, 72, 1532-1537.	1.7	19
126	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 981-994.	3.0	39



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127	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	9.4	470
128	Transethnic insight into the genetics of glycaemic traits: fine-mapping results from the Population Architecture using Genomics and Epidemiology (PAGE) consortium. <i>Diabetologia</i> , 2017, 60, 2384-2398.	2.9	20
129	Quantification of multiple tumor clones using gene array and sequencing data. <i>Annals of Applied Statistics</i> , 2017, 11, 967-991.	0.5	7
130	Structured Detection of Interactions with the Directed Lasso. <i>Statistics in Biosciences</i> , 2017, 9, 676-691.	0.6	2
131	GWAS of the electrocardiographic QT interval in Hispanics/Latinos generalizes previously identified loci and identifies population-specific signals. <i>Scientific Reports</i> , 2017, 7, 17075.	1.6	23
132	Genetic architecture of lipid traits in the Hispanic community health study/study of Latinos. <i>Lipids in Health and Disease</i> , 2017, 16, 200.	1.2	18
133	Genome-wide physical activity interactions in adiposity – A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	1.5	158
134	Rare variants in fox-1 homolog A (RFX1) are associated with lower blood pressure. <i>PLoS Genetics</i> , 2017, 13, e1006678.	1.5	18
135	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.	1.5	88
136	Leukocyte telomere length, T cell composition and DNA methylation age. <i>Aging</i> , 2017, 9, 1983-1995.	1.4	42
137	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. <i>Oncotarget</i> , 2016, 7, 66328-66343.	0.8	88
138	Variant Discovery and Fine Mapping of Genetic Loci Associated with Blood Pressure Traits in Hispanics and African Americans. <i>PLoS ONE</i> , 2016, 11, e0164132.	1.1	24
139	Four Susceptibility Loci for Gallstone Disease Identified in a Meta-analysis of Genome-Wide Association Studies. <i>Gastroenterology</i> , 2016, 151, 351-363.e28.	0.6	74
140	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. <i>American Journal of Human Genetics</i> , 2016, 99, 636-646.	2.6	67
141	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. <i>Nature Genetics</i> , 2016, 48, 1303-1312.	9.4	66
142	Replication of Genome-Wide Association Study Findings of Longevity in White, African American, and Hispanic Women: The Women's Health Initiative. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2016, 72, glw198.	1.7	12
143	Augmented Case-Only Designs for Randomized Clinical Trials with Failure Time Endpoints. <i>Biometrics</i> , 2016, 72, 30-38.	0.8	9
144	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016, 48, 1279-1283.	9.4	2,421

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145	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , 2016, 48, 1162-1170.	9.4	223
146	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , 2016, 7, 11843.	5.8	86
147	Fine-mapping of lipid regions in global populations discovers ethnic-specific signals and refines previously identified lipid loci. <i>Human Molecular Genetics</i> , 2016, 25, 5500-5512.	1.4	29
148	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. <i>International Journal of Epidemiology</i> , 2016, 45, 1927-1937.	0.9	94
149	Testing the role of predicted gene knockouts in human anthropometric trait variation. <i>Human Molecular Genetics</i> , 2016, 25, 2082-2092.	1.4	10
150	Identification of a novel susceptibility locus at 13q34 and refinement of the 20p12.2 region as a multi-signal locus associated with bladder cancer risk in individuals of European ancestry. <i>Human Molecular Genetics</i> , 2016, 25, 1203-1214.	1.4	38
151	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. <i>Human Molecular Genetics</i> , 2016, 25, 358-370.	1.4	73
152	Group association test using a hidden Markov model. <i>Biostatistics</i> , 2016, 17, 221-234.	0.9	2
153	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. <i>Blood</i> , 2015, 126, e19-e29.	0.6	55
154	Copy number alterations detected by whole-exome and whole-genome sequencing of esophageal adenocarcinoma. <i>Human Genomics</i> , 2015, 9, 22.	1.4	19
155	<i>TERT</i> gene harbors multiple variants associated with pancreatic cancer susceptibility. <i>International Journal of Cancer</i> , 2015, 137, 2175-2183.	2.3	57
156	Pleiotropic and Sex-Specific Effects of Cancer GWAS SNPs on Melanoma Risk in the Population Architecture Using Genomics and Epidemiology (PAGE) Study. <i>PLoS ONE</i> , 2015, 10, e0120491.	1.1	19
157	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. <i>Human Molecular Genetics</i> , 2015, 24, 559-571.	1.4	36
158	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. <i>American Journal of Human Genetics</i> , 2015, 96, 487-497.	2.6	101
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