Charles Kooperberg

List of Publications by Year in Descending Order

209 papers	30,131 citations	57 h-index	173 g-index
240 ext. papers	38,690 ext. citations	12.1 avg, IF	5.71 L-index

#	Paper	IF	Citations
209	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed.. *Cell Genomics*, **2022**, 2, 100084-100084		1
208	Taking action to advance the study of race and ethnicity: the Women's Health Initiative (WHI).. *Women's Midlife Health*, **2022**, 8, 1	2.3	1
207	Rare coding variants in RCN3 are associated with blood pressure.. *BMC Genomics*, **2022**, 23, 148	4.5	
206	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data.. *Nature Genetics*, **2022**,	36.3	6
205	Predicted gene expression in ancestrally diverse populations leads to discovery of susceptibility loci for lifestyle and cardiometabolic traits.. *American Journal of Human Genetics*, **2022**,	11	1
204	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential.. *Science Advances*, **2022**, 8, eabl6579	14.3	3
203	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. *Nature Genetics*, **2022**,	36.3	7
202	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations.. *Frontiers in Endocrinology*, **2022**, 13, 863893	5.7	
201	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study.. *Diabetologia*, **2021**, 65, 477	10.3	1
200	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
199	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. *Stroke*, **2021**, STROKEAHA121037388	6.7	7
198	Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. *Stroke*, **2021**, STROKEAHA120031792	6.7	2
197	Prediagnostic Inflammation and Pancreatic Cancer Survival. *Journal of the National Cancer Institute*, **2021**, 113, 1186-1193	9.7	1
196	Healthy Lifestyle and Clonal Hematopoiesis of Indeterminate Potential: Results From the Women's Health Initiative. *Journal of the American Heart Association*, **2021**, 10, e018789	6	9
195	Improving reporting standards for polygenic scores in risk prediction studies. *Nature*, **2021**, 591, 211-219	50.4	70
194	Multi-ancestry genome-wide gene-sleep interactions identify novel loci for blood pressure. *Molecular Psychiatry*, **2021**,	15.1	3
193	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	11	7

192	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. *Nature Communications*, **2021**, 12, 2182	17.4	5
191	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. *Human Genetics and Genomics Advances*, **2021**, 2, 100029-100029	0.8	7
190	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. *American Journal of Human Genetics*, **2021**, 108, 874-893	11	5
189	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. *Aging Cell*, **2021**, 20, e13366	9.9	9
188	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	4.5	0
187	Hepcidin-regulating iron metabolism genes and pancreatic ductal adenocarcinoma: a pathway analysis of genome-wide association studies. *American Journal of Clinical Nutrition*, **2021**, 114, 1408-1417	7	2
186	Premature Menopause, Clonal Hematopoiesis, and Coronary Artery Disease in Postmenopausal Women. *Circulation*, **2021**, 143, 410-423	16.7	31
185	Non-coding variants in MYH11, FZD3, and SORCS3 are associated with dementia in women. *Alzheimer's and Dementia*, **2021**, 17, 215-225	1.2	3
184	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	8.8	3
183	Genetic architectures of proximal and distal colorectal cancer are partly distinct. *Gut*, **2021**, 70, 1325-1334	19.2	7
182	A Population-Based Study of Genes Previously Implicated in Breast Cancer. *New England Journal of Medicine*, **2021**, 384, 440-451	59.2	115
181	Smoking Modifies Pancreatic Cancer Risk Loci on 2q21.3. *Cancer Research*, **2021**, 81, 3134-3143	10.1	2
180	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. *Nature*, **2021**, 590, 290-299	50.4	268
179	Supplemental Association of Clonal Hematopoiesis With Incident Heart Failure. *Journal of the American College of Cardiology*, **2021**, 78, 42-52	15.1	16
178	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,	0.8	1
177	Rare Coding Variants Associated With Electrocardiographic Intervals Identify Monogenic Arrhythmia Susceptibility Genes: A Multi-Ancestry Analysis. *Circulation Genomic and Precision Medicine*, **2021**, 14, e003300	5.2	0
176	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. *PLoS ONE*, **2021**, 16, e0253611	3.7	1
175	Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397	50.4	28

174	Analyses of biomarker traits in diverse UK biobank participants identify associations missed by European-centric analysis strategies. *Journal of Human Genetics*, **2021**,	4.3	6
173	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	11	1
172	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. *PLoS ONE*, **2020**, 15, e0230815	3.7	4
171	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. *Nature Communications*, **2020**, 11, 2542	17.4	16
170	Genome-Wide Gene-Diabetes and Gene-Obesity Interaction Scan in 8,255 Cases and 11,900 Controls from PanScan and PanC4 Consortia. *Cancer Epidemiology Biomarkers and Prevention*, **2020**, 29, 1784-1791	4	4
169	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002772	5.2	8
168	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study. *PLoS Genetics*, **2020**, 16, e1008684	6	5
167	Genome-Wide Association Study Data Reveal Genetic Susceptibility to Chronic Inflammatory Intestinal Diseases and Pancreatic Ductal Adenocarcinoma Risk. *Cancer Research*, **2020**, 80, 4004-4013	10.1	1
166	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	5.2	3
165	Association of Leukocyte Telomere Length With Mortality Among Adult Participants in 3 Longitudinal Studies. *JAMA Network Open*, **2020**, 3, e200023	10.4	24
164	Associations between Genetically Predicted Blood Protein Biomarkers and Pancreatic Cancer Risk. *Cancer Epidemiology Biomarkers and Prevention*, **2020**, 29, 1501-1508	4	9
163	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. *Journal of the National Cancer Institute*, **2020**, 112, 1003-1012	9.7	25
162	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. *Nature*, **2020**, 586, 763-768	50.4	127
161	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. *Nature Genetics*, **2020**, 52, 1314-1332	36.3	26
160	Genome-Wide Association Study Meta-Analysis of Stroke in 22 000 Individuals of African Descent Identifies Novel Associations With Stroke. *Stroke*, **2020**, 51, 2454-2463	6.7	7
159	Mendelian Randomization Analysis of n-6 Polyunsaturated Fatty Acid Levels and Pancreatic Cancer Risk. *Cancer Epidemiology Biomarkers and Prevention*, **2020**, 29, 2735-2739	4	2
158	A general framework for functionally informed set-based analysis: Application to a large-scale colorectal cancer study. *PLoS Genetics*, **2020**, 16, e1008947	6	1
157	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. *Circulation Genomic and Precision Medicine*, **2020**, 13, 387-395	5.2	4

156	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. *Nature Communications*, **2020**, 11, 6417	17.4	17
155	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. *Molecular Psychiatry*, **2020**, 25, 2392-2409	15.1	45
154	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study **2020**, 16, e1008684		
153	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study **2020**, 16, e1008684		
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148	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
147	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
146	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
145	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
144	Effects of Colorectal Cancer Risk Factors on the Association Between Aspirin and Colorectal Cancer. *Anticancer Research*, **2019**, 39, 4877-4884	2.3	4
143	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	11	22
142	A large-scale exome array analysis of venous thromboembolism. *Genetic Epidemiology*, **2019**, 43, 449-457	2.6	11
141	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. *American Journal of Epidemiology*, **2019**, 188, 1033-1054	3.8	39
140	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	6.3	14
139	Genetic analyses of diverse populations improves discovery for complex traits. *Nature*, **2019**, 570, 514-518	50.4	291

138	Genetics of Chronic Kidney Disease Stages Across Ancestries: The PAGE Study. *Frontiers in Genetics*, **2019**, 10, 494	4.5	14
137	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. *Nature Genetics*, **2019**, 51, 636-648	36.3	59
136	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. *Blood*, **2019**, 134, 1645-1657	2.2	63
135	Statistical inference of genetic pathway analysis in high dimensions. *Biometrika*, **2019**, 106, 651	2	0
134	GWAS of QRS duration identifies new loci specific to Hispanic/Latino populations. *PLoS ONE*, **2019**, 14, e0217796	3.7	3
133	Genome-wide association analysis of venous thromboembolism identifies new risk loci and genetic overlap with arterial vascular disease. *Nature Genetics*, **2019**, 51, 1574-1579	36.3	56
132	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. *Nature Communications*, **2019**, 10, 5121	17.4	31
131	DNA methylation-based estimator of telomere length. *Aging*, **2019**, 11, 5895-5923	5.6	69
130	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	3.7	8
129	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	6	90
128	Agnostic Pathway/Gene Set Analysis of Genome-Wide Association Data Identifies Associations for Pancreatic Cancer. *Journal of the National Cancer Institute*, **2019**, 111, 557-567	9.7	16
127	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. *Nature Communications*, **2019**, 10, 29	17.4	51
126	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	11	43
125	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	36.3	516
124	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. *Biological Psychiatry*, **2019**, 85, 946-955	7.9	35
123	Discovery of common and rare genetic risk variants for colorectal cancer. *Nature Genetics*, **2019**, 51, 76-87	36.3	177
122	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	11	59
121	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. *Nature Communications*, **2018**, 9, 556	17.4	103

120	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. *PLoS ONE*, **2018**, 13, e0200486	3.7	14
119	Generalization and fine mapping of red blood cell trait genetic associations to multi-ethnic populations: The PAGE Study. *American Journal of Hematology*, **2018**, 93, 1061	7.1	4
118	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. *Genome Biology*, **2018**, 19, 87	18.3	25
117	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	5.6	8
116	Identifying disease-associated copy number variations by a doubly penalized regression model. *Biometrics*, **2018**, 74, 1341-1350	1.8	2
115	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. *PLoS ONE*, **2018**, 13, e0198166	3.7	31
114	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
113	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. *Nature Genetics*, **2018**, 50, 524-537	36.3	536
112	Genome-wide association study of PR interval in Hispanics/Latinos identifies novel locus at. *Heart*, **2018**, 104, 904-911	5.1	7
111	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. *Circulation Genomic and Precision Medicine*, **2018**, 11, e001758	5.2	14
110	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. *American Journal of Human Genetics*, **2018**, 103, 691-706	11	151
109	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. *Circulation Genomic and Precision Medicine*, **2018**, 11, e002037	5.2	11
108	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. *Heart Rhythm*, **2017**, 14, 572-580	6.7	15
107	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
106	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. *Human Genetics*, **2017**, 136, 771-800	6.3	23
105	Discovery of novel heart rate-associated loci using the Exome Chip. *Human Molecular Genetics*, **2017**, 26, 2346-2363	5.6	17
104	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. *Nature Communications*, **2017**, 8, 14977	17.4	105
103	Leisure-time physical activity and leukocyte telomere length among older women. *Experimental Gerontology*, **2017**, 95, 141-147	4.5	17

102	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. *Nature Communications*, **2017**, 8, 15805	17.4	50
101	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. *Heart Rhythm*, **2017**, 14, 1675-1684	6.7	11
100	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. *Nature Genetics*, **2017**, 49, 1113-1119	36.3	184
99	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	6.4	13
98	and Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. *Journal of the American Society of Nephrology: JASN*, **2017**, 28, 981-994	12.7	30
97	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
96	Transethnic insight into the genetics of glycaemic traits: fine-mapping results from the Population Architecture using Genomics and Epidemiology (PAGE) consortium. *Diabetologia*, **2017**, 60, 2384-2398	10.3	16
95	Quantification of Multiple Tumor Clones Using Gene Array and Sequencing Data. *Annals of Applied Statistics*, **2017**, 11, 967-991	2.1	6
94	Structured detection of interactions with the directed lasso. *Statistics in Biosciences*, **2017**, 9, 676-691	1.5	2
93	GWAS of the electrocardiographic QT interval in Hispanics/Latinos generalizes previously identified loci and identifies population-specific signals. *Scientific Reports*, **2017**, 7, 17075	4.9	8
92	Genetic architecture of lipid traits in the Hispanic community health study/study of Latinos. *Lipids in Health and Disease*, **2017**, 16, 200	4.4	11
91	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. *PLoS Genetics*, **2017**, 13, e1006528	6	103
90	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. *PLoS Genetics* , **2017**, 13, e1006678	6	11
89	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. *PLoS Genetics*, **2017**, 13, e1006728	6	58
88	Leukocyte telomere length, T cell composition and DNA methylation age. *Aging*, **2017**, 9, 1983-1995	5.6	29
87	Replication of Genome-Wide Association Study Findings of Longevity in White, African American, and Hispanic Women: The Women's Health Initiative. *Journals of Gerontology - Series A Biological Sciences and Medical Sciences*, **2017**, 72, 1401-1406	6.4	10
86	A reference panel of 64,976 haplotypes for genotype imputation. *Nature Genetics*, **2016**, 48, 1279-83	36.3	1447
85	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. *Nature Genetics*, **2016**, 48, 1162-70	36.3	152

84	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. *Nature Communications*, **2016**, 7, 11843	17.4	59
83	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	5.6	22
82	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. *International Journal of Epidemiology*, **2016**, 45, 1927-1937	7.8	65
81	Testing the role of predicted gene knockouts in human anthropometric trait variation. *Human Molecular Genetics*, **2016**, 25, 2082-2092	5.6	7
80	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. *Human Molecular Genetics*, **2016**, 25, 1203-14	5.6	20
79	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. *Human Molecular Genetics*, **2016**, 25, 358-70	5.6	54
78	Group association test using a hidden Markov model. *Biostatistics*, **2016**, 17, 221-34	3.7	1
77	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. *Oncotarget*, **2016**, 7, 66328-66343	3.3	66
76	Variant Discovery and Fine Mapping of Genetic Loci Associated with Blood Pressure Traits in Hispanics and African Americans. *PLoS ONE*, **2016**, 11, e0164132	3.7	19
75	Four Susceptibility Loci for Gallstone Disease Identified in a Meta-analysis of Genome-Wide Association Studies. *Gastroenterology*, **2016**, 151, 351-363.e28	13.3	54
74	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. *American Journal of Human Genetics*, **2016**, 99, 636-646	11	44
73	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. *Nature Genetics*, **2016**, 48, 1303-1312	36.3	51
72	Augmented case-only designs for randomized clinical trials with failure time endpoints. *Biometrics*, **2016**, 72, 30-8	1.8	6
71	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. *Nature Communications*, **2015**, 6, 7138	17.4	106
70	Meta-Analysis of Genome-Wide Association Studies Identifies Genetic Risk Factors for Stroke in African Americans. *Stroke*, **2015**, 46, 2063-8	6.7	44
69	Rare and Coding Region Genetic Variants Associated With Risk of Ischemic Stroke: The NHLBI Exome Sequence Project. *JAMA Neurology*, **2015**, 72, 781-8	17.2	37
68	Leveraging Multi-ethnic Evidence for Mapping Complex Traits in Minority Populations: An Empirical Bayes Approach. *American Journal of Human Genetics*, **2015**, 96, 740-52	11	11
67	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. *Nature Genetics*, **2015**, 47, 1294-1303	36.3	226

66	SNPs and breast cancer risk prediction for African American and Hispanic women. *Breast Cancer Research and Treatment*, **2015**, 154, 583-9	4.4	35
65	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. *Nature*, **2015**, 518, 102-6	50.4	463
64	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. *Blood*, **2015**, 126, e19-29	2.2	45
63	Copy number alterations detected by whole-exome and whole-genome sequencing of esophageal adenocarcinoma. *Human Genomics*, **2015**, 9, 22	6.8	16
62	TERT gene harbors multiple variants associated with pancreatic cancer susceptibility. *International Journal of Cancer*, **2015**, 137, 2175-83	7.5	46
61	Pleiotropic and sex-specific effects of cancer GWAS SNPs on melanoma risk in the population architecture using genomics and epidemiology (PAGE) study. *PLoS ONE*, **2015**, 10, e0120491	3.7	14
60	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. *Human Molecular Genetics*, **2015**, 24, 559-71	5.6	31
59	Characterization of large structural genetic mosaicism in human autosomes. *American Journal of Human Genetics*, **2015**, 96, 487-97	11	77
58	Leukocyte Telomere Length and Risks of Incident Coronary Heart Disease and Mortality in a Racially Diverse Population of Postmenopausal Women. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2015**, 35, 2225-31	9.4	45
57	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
56	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
55	Genome-wide interaction study of smoking and bladder cancer risk. *Carcinogenesis*, **2014**, 35, 1737-44	4.6	33
54	Association of low-frequency and rare coding-sequence variants with blood lipids and coronary heart disease in 56,000 whites and blacks. *American Journal of Human Genetics*, **2014**, 94, 223-32	11	233
53	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal of Human Genetics*, **2014**, 94, 233-45	11	170
52	Cross-cancer pleiotropic analysis of endometrial cancer: PAGE and E2C2 consortia. *Carcinogenesis*, **2014**, 35, 2068-73	4.6	17
51	Leveraging population admixture to characterize the heritability of complex traits. *Nature Genetics*, **2014**, 46, 1356-62	36.3	45
50	The 19q12 bladder cancer GWAS signal: association with cyclin E function and aggressive disease. *Cancer Research*, **2014**, 74, 5808-18	10.1	19
49	Genome-wide association study of breast cancer in Latinas identifies novel protective variants on 6q25. *Nature Communications*, **2014**, 5, 5260	17.4	89

48	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. *Nature Genetics*, **2014**, 46, 994-1000	36.3	226
47	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
46	Rare and low-frequency coding variants in CXCR2 and other genes are associated with hematological traits. *Nature Genetics*, **2014**, 46, 629-34	36.3	92
45	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. *BMJ, The*, **2014**, 349, g4164	5.9	406
44	Trans-ethnic meta-analysis of white blood cell phenotypes. *Human Molecular Genetics*, **2014**, 23, 6944-60	5.6	45
43	Meta-analysis of gene-level tests for rare variant association. *Nature Genetics*, **2014**, 46, 200-4	36.3	142
42	Meta-analysis of loci associated with age at natural menopause in African-American women. *Human Molecular Genetics*, **2014**, 23, 3327-42	5.6	44
41	Loss-of-function mutations in APOC3, triglycerides, and coronary disease. *New England Journal of Medicine*, **2014**, 371, 22-31	59.2	721
40	Pleiotropy of cancer susceptibility variants on the risk of non-Hodgkin lymphoma: the PAGE consortium. *PLoS ONE*, **2014**, 9, e89791	3.7	14
39	Replication of associations between GWAS SNPs and melanoma risk in the Population Architecture Using Genomics and Epidemiology (PAGE) Study. *Journal of Investigative Dermatology*, **2014**, 134, 2049-2052	4.3	16
38	Whole-exome imputation of sequence variants identified two novel alleles associated with adult body height in African Americans. *Human Molecular Genetics*, **2014**, 23, 6607-15	5.6	11
37	Association of cancer susceptibility variants with risk of multiple primary cancers: The population architecture using genomics and epidemiology study. *Cancer Epidemiology Biomarkers and Prevention*, **2014**, 23, 2568-78	4	21
36	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. *Human Molecular Genetics*, **2014**, 23, 6616-33	5.6	77
35	Prospective associations of coronary heart disease loci in African Americans using the MetaboChip: the PAGE study. *PLoS ONE*, **2014**, 9, e113203	3.7	17
34	Preface to the Issue of Statistics in Biosciences in Honor of Ross Prentice. *Statistics in Biosciences*, **2013**, 5, 221-223	1.5	
33	Common and rare von Willebrand factor (VWF) coding variants, VWF levels, and factor VIII levels in African Americans: the NHLBI Exome Sequencing Project. *Blood*, **2013**, 122, 590-7	2.2	60
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