Charles Kooperberg

List of Publications by Citations

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	Risks and benefits of estrogen plus progestin in healthy postmenopausal women: principal results From the Women's Health Initiative randomized controlled trial. *JAMA - Journal of the American Medical Association*, **2002**, 288, 321-33	27.4	12115
208	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
207	A reference panel of 64,976 haplotypes for genotype imputation. *Nature Genetics*, **2016**, 48, 1279-83	36.3	1447
206	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
205	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
204	Loss-of-function mutations in APOC3, triglycerides, and coronary disease. *New England Journal of Medicine*, **2014**, 371, 22-31	59.2	721
203	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
202	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
201	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. *Nature*, **2015**, 518, 102-6	50.4	463
200	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
199	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. *BMJ, The*, **2014**, 349, g4164	5.9	406
198	Improved recognition of native-like protein structures using a combination of sequence-dependent and sequence-independent features of proteins. *Proteins: Structure, Function and Bioinformatics*, **1999**, 34, 82-95	4.2	337
197	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
196	Genetic analyses of diverse populations improves discovery for complex traits. *Nature*, **2019**, 570, 514-518	50.4	291
195	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. *Nature*, **2021**, 590, 290-299	50.4	268
194	Logic Regression. *Journal of Computational and Graphical Statistics*, **2003**, 12, 475-511	1.4	238
193	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

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192	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
191	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. *Nature Genetics*, **2014**, 46, 994-1000	36.3	226
190	Large-scale gene-centric meta-analysis across 32 studies identifies multiple lipid loci. *American Journal of Human Genetics*, **2012**, 91, 823-38	11	189
189	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
188	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. *Nature Genetics*, **2017**, 49, 1113-1119	36.3	184
187	Discovery of common and rare genetic risk variants for colorectal cancer. *Nature Genetics*, **2019**, 51, 76-87	36.3	177
186	Identifying interacting SNPs using Monte Carlo logic regression. *Genetic Epidemiology*, **2005**, 28, 157-70	2.6	174
185	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
184	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
183	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
182	Increasing the power of identifying gene x gene interactions in genome-wide association studies. *Genetic Epidemiology*, **2008**, 32, 255-63	2.6	146
181	Meta-analysis of gene-level tests for rare variant association. *Nature Genetics*, **2014**, 46, 200-4	36.3	142
180	The Next PAGE in understanding complex traits: design for the analysis of Population Architecture Using Genetics and Epidemiology (PAGE) Study. *American Journal of Epidemiology*, **2011**, 174, 849-59	3.8	141
179	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. *Nature*, **2020**, 586, 763-768	50.4	127
178	A Population-Based Study of Genes Previously Implicated in Breast Cancer. *New England Journal of Medicine*, **2021**, 384, 440-451	59.2	115
177	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. *Nature Communications*, **2015**, 6, 7138	17.4	106
176	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
175	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. *Nature Communications*, **2018**, 9, 556	17.4	103

174	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. *PLoS Genetics*, **2017**, 13, e1006528	6	103
173	Risk prediction using genome-wide association studies. *Genetic Epidemiology*, **2010**, 34, 643-52	2.6	98
172	Sequence analysis using logic regression. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S626-31	2.6	98
171	Improved background correction for spotted DNA microarrays. *Journal of Computational Biology*, **2002**, 9, 55-66	1.7	97
170	Two-stage testing procedures with independent filtering for genome-wide gene-environment interaction. *Biometrika*, **2012**, 99, 929-944	2	94
169	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
168	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
167	Genome-wide association study of breast cancer in Latinas identifies novel protective variants on 6q25. *Nature Communications*, **2014**, 5, 5260	17.4	89
166	A meta-analysis and genome-wide association study of platelet count and mean platelet volume in african americans. *PLoS Genetics*, **2012**, 8, e1002491	6	84
165	A phenomics-based strategy identifies loci on APOC1, BRAP, and PLCG1 associated with metabolic syndrome phenotype domains. *PLoS Genetics*, **2011**, 7, e1002322	6	78
164	Characterization of large structural genetic mosaicism in human autosomes. *American Journal of Human Genetics*, **2015**, 96, 487-97	11	77
163	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
162	Improving reporting standards for polygenic scores in risk prediction studies. *Nature*, **2021**, 591, 211-219	50.4	70
161	DNA methylation-based estimator of telomere length. *Aging*, **2019**, 11, 5895-5923	5.6	69
160	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. *Oncotarget*, **2016**, 7, 66328-66343	3.3	66
159	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
158	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. *Blood*, **2019**, 134, 1645-1657	2.2	63
157	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

156	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
155	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
154	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. *Nature Communications*, **2016**, 7, 11843	17.4	59
153	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
152	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
151	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. *Human Molecular Genetics*, **2016**, 25, 358-70	5.6	54
150	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
149	Simultaneously testing for marginal genetic association and gene-environment interaction. *American Journal of Epidemiology*, **2012**, 176, 164-73	3.8	53
148	Significance testing for small microarray experiments. *Statistics in Medicine*, **2005**, 24, 2281-98	2.3	51
147	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. *Nature Genetics*, **2016**, 48, 1303-1312	36.3	51
146	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
145	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. *Nature Communications*, **2017**, 8, 15805	17.4	50
144	TERT gene harbors multiple variants associated with pancreatic cancer susceptibility. *International Journal of Cancer*, **2015**, 137, 2175-83	7.5	46
143	Leveraging population admixture to characterize the heritability of complex traits. *Nature Genetics*, **2014**, 46, 1356-62	36.3	45
142	Trans-ethnic meta-analysis of white blood cell phenotypes. *Human Molecular Genetics*, **2014**, 23, 6944-60	5.6	45
141	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
140	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
139	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

138	Meta-Analysis of Genome-Wide Association Studies Identifies Genetic Risk Factors for Stroke in African Americans. *Stroke*, **2015**, 46, 2063-8	6.7	44
137	Meta-analysis of loci associated with age at natural menopause in African-American women. *Human Molecular Genetics*, **2014**, 23, 3327-42	5.6	44
136	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. *American Journal of Human Genetics*, **2016**, 99, 636-646	11	44
135	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
134	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. *American Journal of Epidemiology*, **2019**, 188, 1033-1054	3.8	39
133	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
132	Gene-centric meta-analysis of lipid traits in African, East Asian and Hispanic populations. *PLoS ONE*, **2012**, 7, e50198	3.7	37
131	SNPs and breast cancer risk prediction for African American and Hispanic women. *Breast Cancer Research and Treatment*, **2015**, 154, 583-9	4.4	35
130	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
129	Genome-wide interaction study of smoking and bladder cancer risk. *Carcinogenesis*, **2014**, 35, 1737-44	4.6	33
128	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
127	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
126	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. *Human Molecular Genetics*, **2015**, 24, 559-71	5.6	31
125	Premature Menopause, Clonal Hematopoiesis, and Coronary Artery Disease in Postmenopausal Women. *Circulation*, **2021**, 143, 410-423	16.7	31
124	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
123	Postmenopausal estrogen and progestin effects on the serum proteome. *Genome Medicine*, **2009**, 1, 121	14.4	29
122	Can biomarkers identify women at increased stroke risk? The Women's Health Initiative Hormone Trials. *PLOS Clinical Trials*, **2007**, 2, e28		29
121	Leukocyte telomere length, T cell composition and DNA methylation age. *Aging*, **2017**, 9, 1983-1995	5.6	29

120	Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397	50.4	28
119	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
118	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. *Genome Biology*, **2018**, 19, 87	18.3	25
117	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
116	Association of Leukocyte Telomere Length With Mortality Among Adult Participants in 3 Longitudinal Studies. *JAMA Network Open*, **2020**, 3, e200023	10.4	24
115	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
114	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
113	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
112	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
111	Logic regression for analysis of the association between genetic variation in the renin-angiotensin system and myocardial infarction or stroke. *American Journal of Epidemiology*, **2007**, 165, 334-43	3.8	22
110	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
109	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
108	The 19q12 bladder cancer GWAS signal: association with cyclin E function and aggressive disease. *Cancer Research*, **2014**, 74, 5808-18	10.1	19
107	Triogram Models. *Journal of the American Statistical Association*, **1998**, 93, 101-119	2.8	19
106	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
105	Discovery of novel heart rate-associated loci using the Exome Chip. *Human Molecular Genetics*, **2017**, 26, 2346-2363	5.6	17
104	Leisure-time physical activity and leukocyte telomere length among older women. *Experimental Gerontology*, **2017**, 95, 141-147	4.5	17
103	Cross-cancer pleiotropic analysis of endometrial cancer: PAGE and E2C2 consortia. *Carcinogenesis*, **2014**, 35, 2068-73	4.6	17

102	Semiparametric estimation exploiting covariate independence in two-phase randomized trials. *Biometrics*, **2009**, 65, 178-87	1.8	17
101	Prospective associations of coronary heart disease loci in African Americans using the MetaboChip: the PAGE study. *PLoS ONE*, **2014**, 9, e113203	3.7	17
100	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. *Nature Communications*, **2020**, 11, 6417	17.4	17
99	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. *Nature Communications*, **2020**, 11, 2542	17.4	16
98	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
97	Copy number alterations detected by whole-exome and whole-genome sequencing of esophageal adenocarcinoma. *Human Genomics*, **2015**, 9, 22	6.8	16
96	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
95	Evaluating test statistics to select interesting genes in microarray experiments. *Human Molecular Genetics*, **2002**, 11, 2223-32	5.6	16
94	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
93	Supplemental Association of Clonal Hematopoiesis With Incident Heart Failure. *Journal of the American College of Cardiology*, **2021**, 78, 42-52	15.1	16
92	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
91	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
90	Genetics of Chronic Kidney Disease Stages Across Ancestries: The PAGE Study. *Frontiers in Genetics*, **2019**, 10, 494	4.5	14
89	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
88	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
87	Pleiotropy of cancer susceptibility variants on the risk of non-Hodgkin lymphoma: the PAGE consortium. *PLoS ONE*, **2014**, 9, e89791	3.7	14
86	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
85	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

84	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. *Heart Rhythm*, **2017**, 14, 1675-1684	6.7	11
83	A large-scale exome array analysis of venous thromboembolism. *Genetic Epidemiology*, **2019**, 43, 449-457	2.6	11
82	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
81	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
80	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
79	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. *PLoS Genetics*, **2017**, 13, e1006678	6	11
78	Inherited Causes of Clonal Hematopoiesis of Indeterminate Potential in TOPMed Whole Genomes		11
77	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. *Circulation Genomic and Precision Medicine*, **2018**, 11, e002037	5.2	11
76	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
75	Bivariate Density Estimation with an Application to Survival Analysis. *Journal of Computational and Graphical Statistics*, **1998**, 7, 322-341	1.4	9
74	Linear regression for bivariate censored data via multiple imputation. *Statistics in Medicine*, **1999**, 18, 3111-21	2.3	9
73	Associations between Genetically Predicted Blood Protein Biomarkers and Pancreatic Cancer Risk. *Cancer Epidemiology Biomarkers and Prevention*, **2020**, 29, 1501-1508	4	9
72	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
71	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. *Aging Cell*, **2021**, 20, e13366	9.9	9
70	Improved recognition of native-like protein structures using a combination of sequence-dependent and sequence-independent features of proteins **1999**, 34, 82		9
69	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
68	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
67	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

66	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
65	Testing the role of predicted gene knockouts in human anthropometric trait variation. *Human Molecular Genetics*, **2016**, 25, 2082-2092	5.6	7
64	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. *Stroke*, **2021**, STROKEAHA121037388	6.7	7
63	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
62	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
61	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. *Human Genetics and Genomics Advances*, **2021**, 2, 100029-100029	0.8	7
60	Genetic architectures of proximal and distal colorectal cancer are partly distinct. *Gut*, **2021**, 70, 1325-1334	19.2	7
59	Genome-wide association study of PR interval in Hispanics/Latinos identifies novel locus at. *Heart*, **2018**, 104, 904-911	5.1	7
58	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. *Nature Genetics*, **2022**,	36.3	7
57	Quantification of Multiple Tumor Clones Using Gene Array and Sequencing Data. *Annals of Applied Statistics*, **2017**, 11, 967-991	2.1	6
56	Triogram Models		6
55	Augmented case-only designs for randomized clinical trials with failure time endpoints. *Biometrics*, **2016**, 72, 30-8	1.8	6
54	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
53	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data.. *Nature Genetics*, **2022**,	36.3	6
52	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
51	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. *Nature Communications*, **2021**, 12, 2182	17.4	5
50	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
49	Effects of Colorectal Cancer Risk Factors on the Association Between Aspirin and Colorectal Cancer. *Anticancer Research*, **2019**, 39, 4877-4884	2.3	4

48   Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. *PLoS ONE*, **2020**, 15, e0230815   3.7   4

47   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

46   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

45   Comparison of Parametric and Bootstrap Approaches to Obtaining Confidence Intervals for Logspline Density Estimation. *Journal of Computational and Graphical Statistics*, **2004**, 13, 106-122   1.4   4

44   Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. *Circulation Genomic and Precision Medicine*, **2020**, 13, 387-395   5.2   4

43   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

42   GWAS of QRS duration identifies new loci specific to Hispanic/Latino populations. *PLoS ONE*, **2019**, 14, e0217796   3.7   3

41   Multi-ancestry genome-wide gene-sleep interactions identify novel loci for blood pressure. *Molecular Psychiatry*, **2021**,   15.1   3

40   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

39   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

38   Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential.. *Science Advances*, **2022**, 8, eabl6579   14.3   3

37   Identifying disease-associated copy number variations by a doubly penalized regression model. *Biometrics*, **2018**, 74, 1341-1350   1.8   2

36   Structured detection of interactions with the directed lasso. *Statistics in Biosciences*, **2017**, 9, 676-691   1.5   2

35   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

34   Efficient variant set mixed model association tests for continuous and binary traits in large-scale whole genome sequencing studies   2

33   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

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31   Smoking Modifies Pancreatic Cancer Risk Loci on 2q21.3. *Cancer Research*, **2021**, 81, 3134-3143   10.1   2

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