Charles Kooperberg

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6217468/publications.pdf

Version: 2024-02-01

221 papers	44,880 citations	13827 67 h-index	2558 195 g-index
240 all docs	240 docs citations	240 times ranked	47523 citing authors

#	Article	IF	Citations
1	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, 321-333.	3.8	14,536
2	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
3	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
4	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
5	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
6	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.	9.4	1,307
7	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	9.4	1,124
8	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	13.7	1,069
9	Loss-of-Function Mutations inAPOC3,Triglycerides, and Coronary Disease. New England Journal of Medicine, 2014, 371, 22-31.	13.9	936
10	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	13.7	679
11	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	13.7	581
12	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
13	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	3.0	528
14	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
15	A Population-Based Study of Genes Previously Implicated in Breast Cancer. New England Journal of Medicine, 2021, 384, 440-451.	13.9	414
16	Improved recognition of native-like protein structures using a combination of sequence-dependent and sequence-independent features of proteins. , 1999, 34, 82-95.		389
17	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	9.4	377
18	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	13.7	376

#	Article	IF	Citations
19	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
20	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
21	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.	2.6	326
22	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. Nature Genetics, 2014, 46, 994-1000.	9.4	294
23	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, 223-232.	2.6	287
24	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
25	Logic Regression. Journal of Computational and Graphical Statistics, 2003, 12, 475-511.	0.9	274
26	Improving reporting standards for polygenic scores in risk prediction studies. Nature, 2021, 591, 211-219.	13.7	265
27	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119.	9.4	260
28	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
29	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	2.6	227
30	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	9.4	223
31	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.	1.5	203
32	DNA methylation-based estimator of telomere length. Aging, 2019, 11, 5895-5923.	1.4	198
33	Identifying interacting SNPs using Monte Carlo logic regression. Genetic Epidemiology, 2005, 28, 157-170.	0.6	195
34	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	2.6	193
35	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. Nature Communications, 2018, 9, 556.	5.8	188
36	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183

#	Article	IF	Citations
37	Meta-analysis of gene-level tests for rare variant association. Nature Genetics, 2014, 46, 200-204.	9.4	178
38	Increasing the power of identifying gene Ã— gene interactions in genomeâ€wide association studies. Genetic Epidemiology, 2008, 32, 255-263.	0.6	175
39	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	5.8	169
40	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	0.6	162
41	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, 849-859.	1.6	161
42	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158
43	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	9.4	156
44	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
45	Two-stage testing procedures with independent filtering for genome-wide gene-environment interaction. Biometrika, 2012, 99, 929-944.	1.3	148
46	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. Nature Communications, 2015, 6, 7138.	5.8	138
47	Genome-wide association study of breast cancer in Latinas identifies novel protective variants on 6q25. Nature Communications, 2014, 5, 5260.	5.8	123
48	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.	2.6	123
49	Risk prediction using genomeâ€wide association studies. Genetic Epidemiology, 2010, 34, 643-652.	0.6	116
50	Sequence Analysis Using Logic Regression. Genetic Epidemiology, 2001, 21, S626-31.	0.6	114
51	Improved Background Correction for Spotted DNA Microarrays. Journal of Computational Biology, 2002, 9, 55-66.	0.8	114
52	Rare and low-frequency coding variants in CXCR2 and other genes are associated with hematological traits. Nature Genetics, 2014, 46, 629-634.	9.4	113
53	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. Nature Communications, 2019, 10, 29.	5.8	113
54	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	9.4	112

#	Article	IF	Citations
55	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.	2.6	103
56	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	2.6	101
57	Association of Clonal Hematopoiesis With Incident HeartÂFailure. Journal of the American College of Cardiology, 2021, 78, 42-52.	1.2	101
58	A Meta-Analysis and Genome-Wide Association Study of Platelet Count and Mean Platelet Volume in African Americans. PLoS Genetics, 2012, 8, e1002491.	1.5	97
59	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	5.8	95
60	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. International Journal of Epidemiology, 2016, 45, 1927-1937.	0.9	94
61	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94
62	A Phenomics-Based Strategy Identifies Loci on APOC1, BRAP, and PLCG1 Associated with Metabolic Syndrome Phenotype Domains. PLoS Genetics, 2011, 7, e1002322.	1.5	92
63	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91
64	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, 6616-6633.	1.4	90
65	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. Oncotarget, 2016, 7, 66328-66343.	0.8	88
66	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	1.5	88
67	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. Stroke, 2022, 53, 788-797.	1.0	88
68	Premature Menopause, Clonal Hematopoiesis, and Coronary Artery Disease in Postmenopausal Women. Circulation, 2021, 143, 410-423.	1.6	87
69	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	5.8	86
70	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	1.6	85
71	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	4.1	83
72	Four Susceptibility Loci for Gallstone Disease Identified in a Meta-analysis of Genome-Wide Association Studies. Gastroenterology, 2016, 151, 351-363.e28.	0.6	74

#	Article	IF	Citations
73	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	1.4	73
74	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. Aging Cell, 2021, 20, e13366.	3.0	72
75	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, 590-597.	0.6	70
76	Leveraging population admixture to characterize the heritability of complex traits. Nature Genetics, 2014, 46, 1356-1362.	9.4	69
77	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	0.7	69
78	Simultaneously Testing for Marginal Genetic Association and Gene-Environment Interaction. American Journal of Epidemiology, 2012, 176, 164-173.	1.6	67
79	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. American Journal of Human Genetics, 2016, 99, 636-646.	2.6	67
80	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	9.4	66
81	Meta-Analysis of Genome-Wide Association Studies Identifies Genetic Risk Factors for Stroke in African Americans. Stroke, 2015, 46, 2063-2068.	1.0	63
82	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
83	Association of Leukocyte Telomere Length With Mortality Among Adult Participants in 3 Longitudinal Studies. JAMA Network Open, 2020, 3, e200023.	2.8	62
84	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	1.4	60
85	Significance testing for small microarray experiments. Statistics in Medicine, 2005, 24, 2281-2298.	0.8	59
86	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. Journal of the National Cancer Institute, 2020, 112, 1003-1012.	3.0	59
87	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	5.8	59
88	<scp>TERT</scp> gene harbors multiple variants associated with pancreatic cancer susceptibility. International Journal of Cancer, 2015, 137, 2175-2183.	2.3	57
89	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	0.6	55
90	Meta-analysis of loci associated with age at natural menopause in African-American women. Human Molecular Genetics, 2014, 23, 3327-3342.	1.4	54

#	Article	IF	Citations
91	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, 2225-2231.	1.1	53
92	Genome-wide interaction study of smoking and bladder cancer risk. Carcinogenesis, 2014, 35, 1737-1744.	1.3	50
93	Rare and Coding Region Genetic Variants Associated With Risk of Ischemic Stroke. JAMA Neurology, 2015, 72, 781.	4.5	49
94	SNPs and breast cancer risk prediction for African American and Hispanic women. Breast Cancer Research and Treatment, 2015, 154, 583-589.	1.1	49
95	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. Genome Biology, 2018, 19, 87.	3.8	47
96	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
97	Genetic architectures of proximal and distal colorectal cancer are partly distinct. Gut, 2021, 70, 1325-1334.	6.1	44
98	Healthy Lifestyle and Clonal Hematopoiesis of Indeterminate Potential: Results From the Women's Health Initiative. Journal of the American Heart Association, 2021, 10, e018789.	1.6	43
99	Leukocyte telomere length, T cell composition and DNA methylation age. Aging, 2017, 9, 1983-1995.	1.4	42
100	Gene-Centric Meta-Analysis of Lipid Traits in African, East Asian and Hispanic Populations. PLoS ONE, 2012, 7, e50198.	1.1	40
101	SOS2 and ACP1 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.	3.0	39
102	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	5.8	39
103	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, 1203-1214.	1.4	38
104	Postmenopausal estrogen and progestin effects on the serum proteome. Genome Medicine, 2009, 1, 121.	3.6	36
105	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. Human Molecular Genetics, 2015, 24, 559-571.	1.4	36
106	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	4.7	36
107	Can Biomarkers Identify Women at Increased Stroke Risk? The Women's Health Initiative Hormone Trials. PLOS Clinical Trials, 2007, 2, e28.	3.5	31
108	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.	1.8	31

#	Article	IF	Citations
109	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.	1.4	29
110	Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363.	1.4	29
111	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
112	Genetics of Chronic Kidney Disease Stages Across Ancestries: The PAGE Study. Frontiers in Genetics, 2019, 10, 494.	1.1	29
113	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	3.0	29
114	Leisure-time physical activity and leukocyte telomere length among older women. Experimental Gerontology, 2017, 95, 141-147.	1.2	28
115	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	2.6	28
116	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.	1.6	27
117	Analyses of biomarker traits in diverse UK biobank participants identify associations missed by European-centric analysis strategies. Journal of Human Genetics, 2022, 67, 87-93.	1.1	27
118	Prospective Associations of Coronary Heart Disease Loci in African Americans Using the MetaboChip: The PAGE Study. PLoS ONE, 2014, 9, e113203.	1.1	27
119	A multi-ethnic polygenic risk score is associated with hypertension prevalence and progression throughout adulthood. Nature Communications, 2022, 13, .	5.8	27
120	Logic Regression for Analysis of the Association between Genetic Variation in the Renin-Angiotensin System and Myocardial Infarction or Stroke. American Journal of Epidemiology, 2006, 165, 334-343.	1.6	26
121	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.	1.0	26
122	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.	1.1	25
123	TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data. American Journal of Human Genetics, 2022, 109, 1175-1181.	2.6	25
124	Triogram Models. Journal of the American Statistical Association, 1998, 93, 101-119.	1.8	24
125	The 19q12 Bladder Cancer GWAS Signal: Association with Cyclin E Function and Aggressive Disease. Cancer Research, 2014, 74, 5808-5818.	0.4	24
126	Variant Discovery and Fine Mapping of Genetic Loci Associated with Blood Pressure Traits in Hispanics and African Americans. PLoS ONE, 2016, 11, e0164132.	1.1	24

#	Article	IF	Citations
127	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	2.6	24
128	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, 2568-2578.	1.1	23
129	GWAS of the electrocardiographic QT interval in Hispanics/Latinos generalizes previously identified loci and identifies population-specific signals. Scientific Reports, 2017, 7, 17075.	1.6	23
130	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. Human Genetics and Genomics Advances, 2021, 2, 100029.	1.0	23
131	Evaluating test statistics to select interesting genes in microarray experiments. Human Molecular Genetics, 2002, 11, 2223-2232.	1.4	22
132	Leveraging Multi-ethnic Evidence for Mapping Complex Traits in Minority Populations: An Empirical Bayes Approach. American Journal of Human Genetics, 2015, 96, 740-752.	2.6	22
133	A largeâ€scale exome array analysis of venous thromboembolism. Genetic Epidemiology, 2019, 43, 449-457.	0.6	22
134	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.	0.3	21
135	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.	3.0	21
136	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.	2.9	20
137	Genetic Landscape of the ACE2 Coronavirus Receptor. Circulation, 2022, 145, 1398-1411.	1.6	20
138	Longitudinal profiling of clonal hematopoiesis provides insight into clonal dynamics. Immunity and Ageing, 2022, 19, .	1.8	20
139	Semiparametric Estimation Exploiting Covariate Independence in Twoâ€Phase Randomized Trials. Biometrics, 2009, 65, 178-187.	0.8	19
140	Copy number alterations detected by whole-exome and whole-genome sequencing of esophageal adenocarcinoma. Human Genomics, 2015, 9, 22.	1.4	19
141	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.	1.1	19
142	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.	0.3	19
143	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.	1.7	19
144	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	1.6	19

#	Article	IF	Citations
145	Cross-cancer pleiotropic analysis of endometrial cancer: PAGE and E2C2 consortia. Carcinogenesis, 2014, 35, 2068-2073.	1.3	18
146	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. Heart Rhythm, 2017, 14, 1675-1684.	0.3	18
147	Genetic architecture of lipid traits in the Hispanic community health study/study of Latinos. Lipids in Health and Disease, 2017, 16, 200.	1.2	18
148	Nonâ€coding variants in MYH11, FZD3, and SORCS3 are associated with dementia in women. Alzheimer's and Dementia, 2021, 17, 215-225.	0.4	18
149	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.	2.6	18
150	Associations between Genetically Predicted Blood Protein Biomarkers and Pancreatic Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1501-1508.	1.1	18
151	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. PLoS Genetics, 2017, 13, e1006678.	1.5	18
152	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.	1.5	17
153	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	5.8	17
154	Pleiotropy of Cancer Susceptibility Variants on the Risk of Non-Hodgkin Lymphoma: The PAGE Consortium. PLoS ONE, 2014, 9, e89791.	1.1	16
155	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.	1.4	16
156	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2020, 13, 387-395.	1.6	16
157	Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. Stroke, 2021, , STROKEAHA120031792.	1.0	16
158	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.	1.1	15
159	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study. Diabetologia, 2022, 65, 477-489.	2.9	15
160	Whole-exome imputation of sequence variants identified two novel alleles associated with adult body height in African Americans. Human Molecular Genetics, 2014, 23, 6607-6615.	1.4	14
161	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.	2.7	14
162	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.	2.6	14

#	Article	IF	Citations
163	Monogenic and Polygenic Contributions to QTc Prolongation in the Population. Circulation, 2022, 145, 1524-1533.	1.6	14
164	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	4.1	13
165	Taking action to advance the study of race and ethnicity: the Womenâ€™s Health Initiative (WHI). Women's Midlife Health, 2022, 8, 1.	0.5	13
166	Bivariate Density Estimation with an Application to Survival Analysis. Journal of Computational and Graphical Statistics, 1998, 7, 322-341.	0.9	12
167	Replication of Genome-Wide Association Study Findings of Longevity in White, African American, and Hispanic Women: The Womenâ€™s Health Initiative. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2016, 72, glw198.	1.7	12
168	Genome-wide association study of PR interval in Hispanics/Latinos identifies novel locus at ID2. Heart, 2018, 104, 904-911.	1.2	12
169	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	1.3	12
170	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. Circulation Genomic and Precision Medicine, 2020, 13, e002772.	1.6	11
171	Transcriptome-Wide Association Study of Blood Cell Traits in African Ancestry and Hispanic/Latino Populations. Genes, 2021, 12, 1049.	1.0	11
172	Linear regression for bivariate censored data via multiple imputation. , 1999, 18, 3111-3121.		10
173	Testing the role of predicted gene knockouts in human anthropometric trait variation. Human Molecular Genetics, 2016, 25, 2082-2092.	1.4	10
174	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. PLoS ONE, 2020, 15, e0230815.	1.1	10
175	Augmented Case-Only Designs for Randomized Clinical Trials with Failure Time Endpoints. Biometrics, 2016, 72, 30-38.	0.8	9
176	Prediagnostic Inflammation and Pancreatic Cancer Survival. Journal of the National Cancer Institute, 2021, 113, 1186-1193.	3.0	9
177	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.	2.2	9
178	Improved recognition of native-like protein structures using a combination of sequence-dependent and sequence-independent features of proteins. , 1999, 34, 82.		9
179	GWAS of QRS duration identifies new loci specific to Hispanic/Latino populations. PLoS ONE, 2019, 14, e0217796.	1.1	8
180	Smoking Modifies Pancreatic Cancer Risk Loci on 2q21.3. Cancer Research, 2021, 81, 3134-3143.	0.4	8

#	Article	IF	Citations
181	Integration of rare expression outlier-associated variants improves polygenic risk prediction. American Journal of Human Genetics, 2022, 109, 1055-1064.	2.6	8
182	Comparison of Parametric and Bootstrap Approaches to Obtaining Confidence Intervals for Logspline Density Estimation. Journal of Computational and Graphical Statistics, 2004, 13, 106-122.	0.9	7
183	Quantification of multiple tumor clones using gene array and sequencing data. Annals of Applied Statistics, 2017, 11, 967-991.	0.5	7
184	Rare Coding Variants Associated With Electrocardiographic Intervals Identify Monogenic Arrhythmia Susceptibility Genes: A Multi-Ancestry Analysis. Circulation Genomic and Precision Medicine, 2021, 14, e003300.	1.6	7
185	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations. Frontiers in Endocrinology, 2022, 13, 863893.	1.5	7
186	Mendelian Randomization Analysis of n-6 Polyunsaturated Fatty Acid Levels and Pancreatic Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2735-2739.	1.1	6
187	A general framework for functionally informed set-based analysis: Application to a large-scale colorectal cancer study. PLoS Genetics, 2020, 16, e1008947.	1.5	6
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.	1.2	6
189	Epigenome-wide association study of mitochondrial genome copy number. Human Molecular Genetics, 2021, 31, 309-319.	1.4	6
190	Triogram Models. , 0, .		6
191	Generalization and fine mapping of red blood cell trait genetic associations to multiâ€ethnic populations: The PAGE study. American Journal of Hematology, 2018, 93, 1061-1073.	2.0	5
192	Identifying Disease-Associated Copy Number Variations by a Doubly Penalized Regression Model. Biometrics, 2018, 74, 1341-1350.	0.8	5
193	Genome-Wide Geneâ€“Diabetes and Geneâ€“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.	1.1	5
194	Genome-Wide Association Study Data Reveal Genetic Susceptibility to Chronic Inflammatory Intestinal Diseases and Pancreatic Ductal Adenocarcinoma Risk. Cancer Research, 2020, 80, 4004-4013.	0.4	5
195	Predicted gene expression in ancestrally diverse populations leads to discovery of susceptibility loci for lifestyle and cardiometabolic traits. American Journal of Human Genetics, 2022, 109, 669-679.	2.6	5
196	Contributions of the Womenâ€™s Health Initiative to Cardiovascular Research. Journal of the American College of Cardiology, 2022, 80, 256-275.	1.2	5
197	Effects of Colorectal Cancer Risk Factors on the Association Between Aspirin and Colorectal Cancer. Anticancer Research, 2019, 39, 4877-4884.	0.5	4
198	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.	1.6	4

#	Article	IF	Citations
199	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.	1.1	4
200	Group association test using a hidden Markov model. Biostatistics, 2016, 17, 221-234.	0.9	2
201	Structured Detection of Interactions with the Directed Lasso. Statistics in Biosciences, 2017, 9, 676-691.	0.6	2
202	Statistical inference of genetic pathway analysis in high dimensions. Biometrika, 2019, 106, 651-651.	1.3	2
203	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.0	2
204	BinomiRare: A robust test for association of a rare genetic variant with a binary outcome for mixed models and any case-control proportion. Human Genetics and Genomics Advances, 2021, 2, 100040.	1.0	2
205	Full title: A largeâ€scale transcriptomeâ€wide association study (TWAS) of 10 blood cell phenotypes reveals complexities of TWAS fineâ€mapping. Genetic Epidemiology, 2021, , .	0.6	2
206	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	1.2	2
207	Stochastic Optimization Methods for Fitting Polyclass and Feed-Forward Neural Network Models. Journal of Computational and Graphical Statistics, 1999, 8, 169-189.	0.9	1
208	Response to Letter Regarding Articles â€œElectrocardiographic Abnormalities That Predict Coronary Heart Disease Events and Mortality in Postmenopausal Women: The Womenâ€™s Health Initiativeâ€•and â€œElectrocardiographic Predictors of Incident Congestive Heart Failure and All-Cause Mortality in Postmenopausal Women: the Womenâ€™s Health Initiativeâ€• Circulation, 2006, 113, .	1.6	0
209	Preface to the Issue of Statistics in Biosciences in Honor of Ross Prentice. Statistics in Biosciences, 2013, 5, 221-223.	0.6	0
210	Associations between ambient air pollutants and clonal hematopoiesis of indeterminate potential (CHIP). ISEE Conference Abstracts, 2021, 2021, .	0.0	0
211	Microarray Analyses in a Case-Control Cohort of T-ALL Samples Identifies Gene Signature of Potential Prognostic Significance.. Blood, 2005, 106, 1448-1448.	0.6	0
212	Title is missing!. , 2020, 16, e1008684.		0
213	Title is missing!. , 2020, 16, e1008684.		0
214	Title is missing!. , 2020, 16, e1008684.		0
215	Title is missing!. , 2020, 16, e1008684.		0
216	Title is missing!. , 2020, 16, e1008684.		0

#	Article	IF	Citations
217	Title is missing!. , 2020, 16, e1008684.		0
218	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
219	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
220	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
221	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0