Sharon L R Kardia

List of Publications by Year
in descending order

179	19,533	28274	16183
papers	citations	55 h-index	124 g-index

191	191	191	28262
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Gene-expression profiles predict survival of patients with lung adenocarcinoma. Nature Medicine, 2002, 8, 816-824.	30.7	1,788
2	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	21.4	1,331
3	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.	21.4	1,307
4	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
5	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
6	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	21.4	870
7	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
8	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	12.8	533
9	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	12.8	484
10	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
11	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
12	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
13	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356
14	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
15	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
16	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
17	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
18	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	8.8	251

#	Article	IF	Citations
19	GWAS of Longevity in CHARGE Consortium Confirms APOE and FOXO3 Candidacy. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2015, 70, 110-118.	3.6	250
20	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
21	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	21.4	223
22	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	12.8	214
23	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.	3.5	203
24	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
25	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
26	Positional Genomic Analysis Identifies the Î² 2 -Adrenergic Receptor Gene as a Susceptibility Locus for Human Hypertension. Circulation, 2000, 101, 2877-2882.	1.6	170
27	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
28	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	2.9	168
29	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
30	Life course socioeconomic status and DNA methylation in genes related to stress reactivity and inflammation: The multi-ethnic study of atherosclerosis. Epigenetics, 2015, 10, 958-969.	2.7	155
31	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	21.4	146
32	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. Nature Genetics, 2022, 54, 581-592.	21.4	142
33	Characterization of european ancestry nonalcoholic fatty liver disease-associated variants in individuals of african and hispanic descent. Hepatology, 2013, 58, 966-975.	7.3	126
34	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	12.8	118
35	Neighborhood characteristics influence DNA methylation of genes involved in stress response and inflammation: The Multi-Ethnic Study of Atherosclerosis. Epigenetics, 2017, 12, 662-673.	2.7	118
36	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. Nature Genetics, 2017, 49, 125-130.	21.4	116

#	Article	IF	Citations
37	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.	21.4	112
38	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
39	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.	6.2	103
40	Patient-Reported Experiences of Discrimination in the US Health Care System. JAMA Network Open, 2020, 3, e2029650.	5.9	101
41	GENOME-WIDE ASSOCIATION STUDY (GWAS) AND GENOME-WIDE BY ENVIRONMENT INTERACTION STUDY (GWEIS) OF DEPRESSIVE SYMPTOMS IN AFRICAN AMERICAN AND HISPANIC/LATINA WOMEN. Depression and Anxiety, 2016, 33, 265-280.	4.1	99
42	Discovery and fine-mapping of adiposity loci using high density imputation of genome-wide association studies in individuals of African ancestry: African Ancestry Anthropometry Genetics Consortium. PLoS Genetics, 2017, 13, e1006719.	3.5	98
43	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
44	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
45	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	8.8	90
46	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
47	Cerebral small vessel disease genomics and its implications across the lifespan. Nature Communications, 2020, 11, 6285.	12.8	89
48	Education and Lifestyle Factors Are Associated with DNA Methylation Clocks in Older African Americans. International Journal of Environmental Research and Public Health, 2019, 16, 3141.	2.6	88
49	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	3.5	88
50	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
51	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
52	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
53	A Statistical Approach for Testing Cross-Phenotype Effects of Rare Variants. American Journal of Human Genetics, 2016, 98, 525-540.	6.2	75
54	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	12.0	75

#	Article	IF	Citations
55	Public preferences regarding informed consent models for participation in population-based genomic research. Genetics in Medicine, 2014, 16, 11-18.	2.4	74
56	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	2.9	73
57	Current Applications of Genetic Risk Scores to Cardiovascular Outcomes and Subclinical Phenotypes. Current Epidemiology Reports, 2015, 2, 180-190.	2.4	70
58	Disproportionate Sterilization of Latinos Under Californiaâ€™s Eugenic Sterilization Program, 1920â€“1945. American Journal of Public Health, 2018, 108, 611-613.	2.7	68
59	Meta-analysis of epigenome-wide association studies of cognitive abilities. Molecular Psychiatry, 2018, 23, 2133-2144.	7.9	68
60	Public Trust in Health Information Sharing: Implications for Biobanking and Electronic Health Record Systems. Journal of Personalized Medicine, 2015, 5, 3-21.	2.5	65
61	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. Epigenomics, 2019, 11, 1487-1500.	2.1	64
62	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
63	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62
64	Application of machine learning algorithms to predict coronary artery calcification with a sibshipâ€based design. Genetic Epidemiology, 2008, 32, 350-360.	1.3	59
65	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. Human Molecular Genetics, 2014, 23, 2490-2497.	2.9	56
66	Trans-ethnic Meta-analysis and Functional Annotation Illuminates theÂGenetic Architecture of Fasting Glucose and Insulin. American Journal of Human Genetics, 2016, 99, 56-75.	6.2	55
67	Meta-analysis of loci associated with age at natural menopause in African-American women. Human Molecular Genetics, 2014, 23, 3327-3342.	2.9	54
68	Californiaâ€™s Sterilization Survivors: An Estimate and Call for Redress. American Journal of Public Health, 2017, 107, 50-54.	2.7	53
69	Facebook Advertising Across an Engagement Spectrum: A Case Example for Public Health Communication. JMIR Public Health and Surveillance, 2016, 2, e27.	2.6	53
70	Public Trust in Health Information Sharing: A Measure of System Trust. Health Services Research, 2018, 53, 824-845.	2.0	52
71	<scp>GWAS</scp> analysis of handgrip and lower body strength in older adults in the <scp>CHARGE</scp> consortium. Aging Cell, 2016, 15, 792-800.	6.7	51
72	An Empirical Comparison of Metaâ€analysis and Megaâ€analysis of Individual Participant Data for Identifying Geneâ€Environment Interactions. Genetic Epidemiology, 2014, 38, 369-378.	1.3	48

#	Article	IF	Citations
73	Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. Molecular Psychiatry, 2019, 24, 1920-1932.	7.9	44
74	Religion as a Health Promoter During the 2019/2020 COVID Outbreak: View from Detroit. Journal of Religion and Health, 2020, 59, 2243-2255.	1.7	42
75	Context-dependent genetic effects in hypertension. Current Hypertension Reports, 2000, 2, 32-38.	3.5	41
76	Testing an Online, Dynamic Consent Portal for Large Population Biobank Research. Public Health Genomics, 2015, 18, 26-39.	1.0	41
77	Insulin Resistance Exacerbates Genetic Predisposition to Nonalcoholic Fatty Liver Disease in Individuals Without Diabetes. Hepatology Communications, 2019, 3, 894-907.	4.3	41
78	A Peripheral Blood DNA Methylation Signature of Hepatic Fat Reveals a Potential Causal Pathway for Nonalcoholic Fatty Liver Disease. Diabetes, 2019, 68, 1073-1083.	0.6	41
79	Bayesian shrinkage estimation of high dimensional causal mediation effects in omics studies. Biometrics, 2020, 76, 700-710.	1.4	39
80	Novel DNA methylation sites associated with cigarette smoking among African Americans. Epigenetics, 2019, 14, 383-391.	2.7	38
81	Epigenetic age acceleration is associated with cardiometabolic risk factors and clinical cardiovascular disease risk scores in African Americans. Clinical Epigenetics, 2021, 13, 55.	4.1	37
82	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
83	Hypertrophyâ€Associated Polymorphisms Ascertained in a Founder Cohort Applied to Heart Failure Risk and Mortality. Clinical and Translational Science, 2011, 4, 17-23.	3.1	35
84	A scan statistic for identifying chromosomal patterns of SNP association. Genetic Epidemiology, 2006, 30, 627-635.	1.3	34
85	A Genome-wide study of blood pressure in African Americans accounting for gene-smoking interaction. Scientific Reports, 2016, 6, 18812.	3.3	34
86	Multivariate linkage analysis of blood pressure and body mass index. Genetic Epidemiology, 2004, 27, 64-73.	1.3	32
87	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
88	The publicâ€™s comfort with sharing health data with third-party commercial companies. Humanities and Social Sciences Communications, 2020, 7, .	2.9	30
89	Meta-analyses identify DNA methylation associated with kidney function and damage. Nature Communications, 2021, 12, 7174.	12.8	30
90	Laying Anchor: Inserting Precision Health into a Public Health Genetics Policy Course. Healthcare (Switzerland), 2018, 6, 93.	2.0	29

#	Article	IF	Citations
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.	3.8	29
92	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
93	Type 2 Diabetes Partitioned Polygenic Scores Associate With Disease Outcomes in 454,193 Individuals Across 13 Cohorts. Diabetes Care, 2022, 45, 674-683.	8.6	29
94	Intrinsic and extrinsic epigenetic age acceleration are associated with hypertensive target organ damage in older African Americans. BMC Medical Genomics, 2019, 12, 141.	1.5	28
95	Classification of rheumatoid arthritis status with candidate gene and genome-wide single-nucleotide polymorphisms using random forests. BMC Proceedings, 2007, 1, S62.	1.6	27
96	Associations between self-referral and health behavior responses to genetic risk information. Genome Medicine, 2015, 7, 10.	8.2	27
97	Matrix Gla Protein Gene Polymorphism Is Associated With Increased Coronary Artery Calcification Progression. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 645-651.	2.4	22
98	A Statistical Approach for Rare-Variant Association Testing in Affected Sibships. American Journal of Human Genetics, 2015, 96, 543-554.	6.2	21
99	The complex genetics of gait speed: genome-wide meta-analysis approach. Aging, 2017, 9, 209-246.	3.1	21
100	Investigating the complex genetic architecture of ankle-brachial index, a measure of peripheral arterial disease, in non-Hispanic whites. BMC Medical Genomics, 2008, 1, 16.	1.5	20
101	Allele-specific variation atAPOEincreases nonalcoholic fatty liver disease and obesity but decreases risk of Alzheimerâ€™s disease and myocardial infarction. Human Molecular Genetics, 2021, 30, 1443-1456.	2.9	20
102	Key influence of sex on urine volume and osmolality. Biology of Sex Differences, 2016, 7, 12.	4.1	19
103	An Empirical Comparison of Joint and Stratified Frameworks for Studying G Ã— E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Geneâ€Lifestyle Interactions Working Group. Genetic Epidemiology, 2016, 40, 404-415.	1.3	18
104	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. Nature Communications, 2021, 12, 3987.	12.8	18
105	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. PLoS Genetics, 2017, 13, e1006678.	3.5	18
106	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
107	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	12.8	17
108	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. Blood, 2018, 132, 1842-1850.	1.4	16

#	Article	IF	Citations
109	SLC2A9 Genotype Is Associated with SLC2A9 Gene Expression and Urinary Uric Acid Concentration. PLoS ONE, 2015, 10, e0128593.	2.5	16
110	The Role of Health Education and Behavior in Public Health Genetics. Health Education and Behavior, 2005, 32, 583-588.	2.5	15
111	Copy Number Variations Associated With Obesityâ€Related Traits in African Americans: A Joint Analysis Between GENOA and HyperGEN. Obesity, 2012, 20, 2431-2437.	3.0	15
112	Set-Based Tests for the Geneâ€“Environment Interaction in Longitudinal Studies. Journal of the American Statistical Association, 2017, 112, 966-978.	3.1	14
113	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.	6.1	14
114	Accelerated DNA methylation age and medication use among African Americans. Aging, 2021, 13, 14604-14629.	3.1	14
115	Discrimination, trust, and withholding information from providers: Implications for missing data and inequity. SSM - Population Health, 2022, 18, 101092.	2.7	14
116	Setâ€based tests for genetic association in longitudinal studies. Biometrics, 2015, 71, 606-615.	1.4	13
117	Heritability of dietary traits that contribute to nephrolithiasis in a cohort of adult sibships. Journal of Nephrology, 2016, 29, 45-51.	2.0	13
118	Genetic diversity is a predictor of mortality in humans. BMC Genetics, 2014, 15, 159.	2.7	12
119	Epigenetic loci for blood pressure are associated with hypertensive target organ damage in older African Americans from the genetic epidemiology network of Arteriopathy (GENOA) study. BMC Medical Genomics, 2020, 13, 131.	1.5	12
120	A Noncoding Variant Near PPP1R3B Promotes Liver Glycogen Storage and MetS, but Protects Against Myocardial Infarction. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 372-387.	3.6	12
121	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	2.7	12
122	Interaction between Social/Psychosocial Factors and Genetic Variants on Body Mass Index: A Gene-Environment Interaction Analysis in a Longitudinal Setting. International Journal of Environmental Research and Public Health, 2017, 14, 1153.	2.6	11
123	Social regulation of inflammation related gene expression in the multi-ethnic study of atherosclerosis. Psychoneuroendocrinology, 2020, 117, 104654.	2.7	11
124	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. Circulation Genomic and Precision Medicine, 2020, 13, e002772.	3.6	11
125	Willingness to Participate in Health Information Networks with Diverse Data Use: Evaluating Public Perspectives. EGEMS (Washington, DC), 2019, 7, 33.	2.0	11
126	Identification of correlated genetic variants jointly associated with rheumatoid arthritis using ridge regression. BMC Proceedings, 2009, 3, S67.	1.6	10

#	Article	IF	Citations
127	Epigenomic Indicators of Age in African Americans. Hereditary Genetics: Current Research, 2014, 03, .	0.1	10
128	Epigenome-wide association study identifies DNA methylation sites associated with target organ damage in older African Americans. Epigenetics, 2021, 16, 862-875.	2.7	10
129	Association Between Episodic Memory and Genetic Risk Factors for Alzheimer's Disease in South Asians from the Longitudinal Aging Study in Indiaâ€"Diagnostic Assessment of Dementia (LASIâ€ĐAD). Journal of the American Geriatrics Society, 2020, 68, S45-S53.	2.6	10
130	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. PLoS ONE, 2020, 15, e0230815.	2.5	10
131	Low-density lipoprotein particle size and coronary atherosclerosis in subjects belonging to hypertensive sibships. American Journal of Hypertension, 2004, 17, 845-851.	2.0	9
132	Epigenetic Markers of Renal Function in African Americans. Nursing Research and Practice, 2013, 2013, 1-9.	1.0	9
133	Genomeâ€wide survey in African Americans demonstrates potential epistasis of fitness in the human genome. Genetic Epidemiology, 2017, 41, 122-135.	1.3	9
134	Expression of socially sensitive genes: The multi-ethnic study of atherosclerosis. PLoS ONE, 2019, 14, e0214061.	2.5	9
135	Do people have an ethical obligation to share their health information? Comparing narratives of altruism and health information sharing in a nationally representative sample. PLoS ONE, 2020, 15, e0244767.	2.5	9
136	A Common Copy Number Variation on Chromosome 6 Association With the Gene Expression Level of Endothelin 1 in Transformed B Lymphocytes From Three Racial Groups. Circulation: Cardiovascular Genetics, 2009, 2, 483-488.	5.1	8
137	Applying Novel Methods for Assessing Individual- and Neighborhood-Level Social and Psychosocial Environment Interactions with Genetic Factors in the Prediction of Depressive Symptoms in the Multi-Ethnic Study of Atherosclerosis. Behavior Genetics, 2016, 46, 89-99.	2.1	8
138	Bayesian hierarchical models for highâ€dimensional mediation analysis with coordinated selection of correlated mediators. Statistics in Medicine, 2021, 40, 6038-6056.	1.6	8
139	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. Nature Communications, 2021, 12, 7173.	12.8	8
140	Association of urinary citrate excretion, pH, and net gastrointestinal alkali absorption with diet, diuretic use, and blood glucose concentration. Physiological Reports, 2017, 5, e13411.	1.7	7
141	Epistatic effects between two genes in the renin-angiotensin system and systolic blood pressure and coronary artery calcification. Medical Science Monitor, 2006, 12, CR150-8.	1.1	7
142	Association between Stress Response Genes and Features of Diurnal Cortisol Curves in the Multi-Ethnic Study of Atherosclerosis: A New Multi-Phenotype Approach for Gene-Based Association Tests. PLoS ONE, 2015, 10, e0126637.	2.5	6
143	Engaging a state: Facebook comments on a large population biobank. Journal of Community Genetics, 2017, 8, 183-197.	1.2	6
144	Joint Influence of SNPs and DNA Methylation on Lipids in African Americans From Hypertensive Sibships. Biological Research for Nursing, 2018, 20, 161-167.	1.9	6

#	Article	IF	Citations
145	The metabolic network coherence of human transcriptomes is associated with genetic variation at the cadherin 18 locus. Human Genetics, 2019, 138, 375-388.	3.8	6
146	Gene-mapping study of extremes of cerebral small vessel disease reveals TRIM47 as a strong candidate. Brain, 2022, 145, 1992-2007.	7.6	6
147	Epigenetics of single-site and multi-site atherosclerosis in African Americans from the Genetic Epidemiology Network of Arteriopathy (GENOA). Clinical Epigenetics, 2022, 14, 10.	4.1	6
148	Gene-by-Psychosocial Factor Interactions Influence Diastolic Blood Pressure in European and African Ancestry Populations: Meta-Analysis of Four Cohort Studies. International Journal of Environmental Research and Public Health, 2017, 14, 1596.	2.6	5
149	Testing crossâ€phenotype effects of rare variants in longitudinal studies of complex traits. Genetic Epidemiology, 2018, 42, 320-332.	1.3	5
150	When Genetics Meets Religion: What Scientists and Religious Leaders Can Learn from Each Other. Public Health Genomics, 2019, 22, 174-188.	1.0	5
151	Combined linkage and association analysis identifies rare and low frequency variants for blood pressure at 1q31. European Journal of Human Genetics, 2019, 27, 269-277.	2.8	5
152	Genomeâ€wide metaâ€analysis of SNP and antihypertensive medication interactions on left ventricular traits in African Americans. Molecular Genetics & Genomic Medicine, 2019, 7, e00788.	1.2	4
153	Are we teaching our students visual communication? Evaluation of writing assignments in public health. Journal of Visual Communication in Medicine, 2020, 43, 62-65.	0.6	4
154	Detecting fitness epistasis in recently admixed populations with genome-wide data. BMC Genomics, 2020, 21, 476.	2.8	4
155	Genome-Wide Association Meta-Analysis of Individuals of European Ancestry Identifies Suggestive Loci for Sodium Intake, Potassium Intake, and Their Ratio Measured from 24-Hour or Half-Day Urine Samples. Journal of Nutrition, 2020, 150, 2635-2645.	2.9	4
156	Rareâ€variant association tests in longitudinal studies, with an application to the Multiâ€Ethnic Study of Atherosclerosis (MESA). Genetic Epidemiology, 2017, 41, 801-810.	1.3	3
157	Hidden Markov Model for Defining Genomic Changes in Lung Cancer Using Gene Expression Data. OMICS A Journal of Integrative Biology, 2006, 10, 276-288.	2.0	2
158	Long-term risk of reproductive cancer among Vietnamese women using the quinacrine hydrochloride pellet system vs. intrauterine devices or tubal ligation for contraception. European Journal of Contraception and Reproductive Health Care, 2017, 22, 123-130.	1.5	2
159	Using Genetic Burden Scores for Gene-by-Methylation Interaction Analysis on Metabolic Syndrome in African Americans. Biological Research for Nursing, 2019, 21, 279-285.	1.9	2
160	Association of low-frequency and rare coding variants with information processing speed. Translational Psychiatry, 2021, 11, 613.	4.8	2
161	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	2.8	2
162	Long-term risk of hysterectomy and ectopic pregnancy among Vietnamese women using the quinacrine hydrochloride pellet system vs. intrauterine devices or tubal ligation for contraception. European Journal of Contraception and Reproductive Health Care, 2018, 23, 105-115.	1.5	1

#	Article	IF	Citations
163	Lessons Learned for Identifying and Annotating Permissions in Clinical Consent Forms. Applied Clinical Informatics, 2021, 12, 429-435.	1.7	1
164	Regulations and Norms for Reuse of Residual Clinical Biospecimens and Health Data. Western Journal of Nursing Research, 2021, , 019394592110292.	1.4	1
165	Evaluating and extending the Informed Consent Ontology for representing permissions from the clinical domain. Applied Ontology, 2022, 17, 321-336.	2.0	1
166	Multivariate, regionâ€based genetic analyses of facets of reproductive aging in White and Black women. Molecular Genetics & Genomic Medicine, 2022, 10, e1896.	1.2	1
167	P1â€118: Association of Lowâ€Frequency and Rare Coding Variants with Information Processing Speed. Alzheimer's and Dementia, 2016, 12, P448.	0.8	0
168	Common and rare variants in Alzheimerâ€™s disease genes are associated with episodic memory in South Asians from the LASIâ€DAD study. Alzheimer's and Dementia, 2020, 16, e045189.	0.8	0
169	Whole Exome Analyses to Examine the Impact of Rare Variants on Left Ventricular Traits in African American Participants from the HyperGEN and GENOA Studies. Journal of Hypertension and Management, 2017, 3, .	0.2	0
170	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
171	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
172	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
173	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
174	Title is missing!. , 2020, 15, e0244767.		0
175	Title is missing!. , 2020, 15, e0244767.		0
176	Title is missing!. , 2020, 15, e0244767.		0
177	Title is missing!. , 2020, 15, e0244767.		0
178	Polygenic risk score for general cognitive function is associated with measures of cognition in South Asians from the LASI-DAD Study.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e053977.	0.8	0
179	Common and rare variants in topologically associated domains for cognitive function in South Asians from the LASI-DAD Study.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e054029.	0.8	0