

# Sharon L R Kardia

## List of Publications by Year in descending order

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Version: 2024-02-01

179  
papers

19,533  
citations

28274  
55  
h-index

16183  
124  
g-index

191  
all docs

191  
docs citations

191  
times ranked

28262  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene-mapping study of extremes of cerebral small vessel disease reveals TRIM47 as a strong candidate. <i>Brain</i> , 2022, 145, 1992-2007.	7.6	6
2	Evaluating and extending the Informed Consent Ontology for representing permissions from the clinical domain. <i>Applied Ontology</i> , 2022, 17, 321-336.	2.0	1
3	Epigenetics of single-site and multi-site atherosclerosis in African Americans from the Genetic Epidemiology Network of Arteriopathy (GENOA). <i>Clinical Epigenetics</i> , 2022, 14, 10.	4.1	6
4	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. <i>Cell Genomics</i> , 2022, 2, 100084.	6.5	29
5	Type 2 Diabetes Partitioned Polygenic Scores Associate With Disease Outcomes in 454,193 Individuals Across 13 Cohorts. <i>Diabetes Care</i> , 2022, 45, 674-683.	8.6	29
6	Multivariate, regional-based genetic analyses of facets of reproductive aging in White and Black women. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2022, 10, e1896.	1.2	1
7	Rare coding variants in RCN3 are associated with blood pressure. <i>BMC Genomics</i> , 2022, 23, 148.	2.8	2
8	Discrimination, trust, and withholding information from providers: Implications for missing data and inequity. <i>SSM - Population Health</i> , 2022, 18, 101092.	2.7	14
9	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. <i>Science Advances</i> , 2022, 8, eabl6579.	10.3	36
10	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	21.4	250
11	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. <i>Nature Genetics</i> , 2022, 54, 581-592.	21.4	142
12	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. <i>Hypertension</i> , 2022, 79, 1656-1667.	2.7	12
13	Epigenome-wide association study identifies DNA methylation sites associated with target organ damage in older African Americans. <i>Epigenetics</i> , 2021, 16, 862-875.	2.7	10
14	A Noncoding Variant Near PPP1R3B Promotes Liver Glycogen Storage and MetS, but Protects Against Myocardial Infarction. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, 372-387.	3.6	12
15	Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. <i>EBioMedicine</i> , 2021, 63, 103157.	6.1	14
16	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, 24.	12.8	87
17	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299.	27.8	1,069
18	Epigenetic age acceleration is associated with cardiometabolic risk factors and clinical cardiovascular disease risk scores in African Americans. <i>Clinical Epigenetics</i> , 2021, 13, 55.	4.1	37

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19	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. <i>Nature Communications</i> , 2021, 12, 2182.	12.8	17
20	Allele-specific variation at <i>APOE</i> increases nonalcoholic fatty liver disease and obesity but decreases risk of Alzheimer's disease and myocardial infarction. <i>Human Molecular Genetics</i> , 2021, 30, 1443-1456.	2.9	20
21	Lessons Learned for Identifying and Annotating Permissions in Clinical Consent Forms. <i>Applied Clinical Informatics</i> , 2021, 12, 429-435.	1.7	1
22	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	21.4	341
23	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	8.8	90
24	Accelerated DNA methylation age and medication use among African Americans. <i>Aging</i> , 2021, 13, 14604-14629.	3.1	14
25	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021, 12, 3987.	12.8	18
26	Regulations and Norms for Reuse of Residual Clinical Biospecimens and Health Data. <i>Western Journal of Nursing Research</i> , 2021, , 019394592110292.	1.4	1
27	Bayesian hierarchical models for high-dimensional mediation analysis with coordinated selection of correlated mediators. <i>Statistics in Medicine</i> , 2021, 40, 6038-6056.	1.6	8
28	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	27.8	183
29	Association of low-frequency and rare coding variants with information processing speed. <i>Translational Psychiatry</i> , 2021, 11, 613.	4.8	2
30	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	27.8	353
31	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , 2021, 12, 7173.	12.8	8
32	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021, 12, 7174.	12.8	30
33	Polygenic risk score for general cognitive function is associated with measures of cognition in South Asians from the LASI-DAD Study.. <i>Alzheimer's and Dementia</i> , 2021, 17 Suppl 3, e053977.	0.8	0
34	Common and rare variants in topologically associated domains for cognitive function in South Asians from the LASI-DAD Study.. <i>Alzheimer's and Dementia</i> , 2021, 17 Suppl 3, e054029.	0.8	0
35	Are we teaching our students visual communication? Evaluation of writing assignments in public health. <i>Journal of Visual Communication in Medicine</i> , 2020, 43, 62-65.	0.6	4
36	Bayesian shrinkage estimation of high dimensional causal mediation effects in omics studies. <i>Biometrics</i> , 2020, 76, 700-710.	1.4	39

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37	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020, 586, 763-768.	27.8	376
38	Detecting fitness epistasis in recently admixed populations with genome-wide data. <i>BMC Genomics</i> , 2020, 21, 476.	2.8	4
39	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020, 52, 1314-1332.	21.4	91
40	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€“DAD). <i>Journal of the American Geriatrics Society</i> , 2020, 68, S45-S53.	2.6	10
41	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. <i>Journal of Nutrition</i> , 2020, 150, 2635-2645.	2.9	4
42	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. <i>BMC Medical Genomics</i> , 2020, 13, 131.	1.5	12
43	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. <i>Nature Genetics</i> , 2020, 52, 969-983.	21.4	146
44	Common and rare variants in Alzheimerâ€™s disease genes are associated with episodic memory in South Asians from the LASIâ€“DAD study. <i>Alzheimer's and Dementia</i> , 2020, 16, e045189.	0.8	0
45	Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020, 11, 6285.	12.8	89
46	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , 2020, 26, 2111-2125.	7.9	17
47	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. <i>PLoS ONE</i> , 2020, 15, e0230815.	2.5	10
48	Social regulation of inflammation related gene expression in the multi-ethnic study of atherosclerosis. <i>Psychoneuroendocrinology</i> , 2020, 117, 104654.	2.7	11
49	Religion as a Health Promoter During the 2019/2020 COVID Outbreak: View from Detroit. <i>Journal of Religion and Health</i> , 2020, 59, 2243-2255.	1.7	42
50	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002772.	3.6	11
51	Patient-Reported Experiences of Discrimination in the US Health Care System. <i>JAMA Network Open</i> , 2020, 3, e2029650.	5.9	101
52	The publicâ€™s comfort with sharing health data with third-party commercial companies. <i>Humanities and Social Sciences Communications</i> , 2020, 7, .	2.9	30
53	Do people have an ethical obligation to share their health information? Comparing narratives of altruism and health information sharing in a nationally representative sample. <i>PLoS ONE</i> , 2020, 15, e0244767.	2.5	9
54	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0

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55	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
56	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
57	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
58	Title is missing!. , 2020, 15, e0244767.		0
59	Title is missing!. , 2020, 15, e0244767.		0
60	Title is missing!. , 2020, 15, e0244767.		0
61	Title is missing!. , 2020, 15, e0244767.		0
62	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
63	Genome-wide meta-analysis of SNP and antihypertensive medication interactions on left ventricular traits in African Americans. Molecular Genetics & Genomic Medicine, 2019, 7, e00788.	1.2	4
64	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	12.8	214
65	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	12.0	75
66	Insulin Resistance Exacerbates Genetic Predisposition to Nonalcoholic Fatty Liver Disease in Individuals Without Diabetes. Hepatology Communications, 2019, 3, 894-907.	4.3	41
67	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
68	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
69	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
70	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
71	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. Epigenomics, 2019, 11, 1487-1500.	2.1	64
72	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85

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73	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
74	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
75	Novel DNA methylation sites associated with cigarette smoking among African Americans. Epigenetics, 2019, 14, 383-391.	2.7	38
76	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
77	Expression of socially sensitive genes: The multi-ethnic study of atherosclerosis. PLoS ONE, 2019, 14, e0214061.	2.5	9
78	A multi-ancestry genome-wide study incorporating gene×smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
79	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.	21.4	112
80	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
81	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
82	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
83	When Genetics Meets Religion: What Scientists and Religious Leaders Can Learn from Each Other. Public Health Genomics, 2019, 22, 174-188.	1.0	5
84	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
85	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
86	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
87	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
88	Willingness to Participate in Health Information Networks with Diverse Data Use: Evaluating Public Perspectives. EGEMS (Washington, DC), 2019, 7, 33.	2.0	11
89	Disproportionate Sterilization of Latinos Under California's Eugenic Sterilization Program, 1920-1945. American Journal of Public Health, 2018, 108, 611-613.	2.7	68
90	Testing cross-phenotype effects of rare variants in longitudinal studies of complex traits. Genetic Epidemiology, 2018, 42, 320-332.	1.3	5

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91	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 559-571.	21.4	356
92	Joint Influence of SNPs and DNA Methylation on Lipids in African Americans From Hypertensive Sibships. <i>Biological Research for Nursing</i> , 2018, 20, 161-167.	1.9	6
93	Meta-analysis of epigenome-wide association studies of cognitive abilities. <i>Molecular Psychiatry</i> , 2018, 23, 2133-2144.	7.9	68
94	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. <i>European Journal of Contraception and Reproductive Health Care</i> , 2018, 23, 105-115.	1.5	1
95	Public Trust in Health Information Sharing: A Measure of System Trust. <i>Health Services Research</i> , 2018, 53, 824-845.	2.0	52
96	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <i>Nature Genetics</i> , 2018, 50, 1505-1513.	21.4	1,331
97	Laying Anchor: Inserting Precision Health into a Public Health Genetics Policy Course. <i>Healthcare (Switzerland)</i> , 2018, 6, 93.	2.0	29
98	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , 2018, 9, 2098.	12.8	484
99	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. <i>Blood</i> , 2018, 132, 1842-1850.	1.4	16
100	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166.	2.5	94
101	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	21.4	286
102	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	27.8	544
103	Long-term risk of reproductive cancer among Vietnamese women using the quinacrine hydrochloride pellet system vs. intrauterine devices or tubal ligation for contraception. <i>European Journal of Contraception and Reproductive Health Care</i> , 2017, 22, 123-130.	1.5	2
104	Set-Based Tests for the Gene-Environment Interaction in Longitudinal Studies. <i>Journal of the American Statistical Association</i> , 2017, 112, 966-978.	3.1	14
105	Engaging a state: Facebook comments on a large population biobank. <i>Journal of Community Genetics</i> , 2017, 8, 183-197.	1.2	6
106	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	12.8	169
107	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. <i>Nature Genetics</i> , 2017, 49, 125-130.	21.4	116
108	Genome-wide survey in African Americans demonstrates potential epistasis of fitness in the human genome. <i>Genetic Epidemiology</i> , 2017, 41, 122-135.	1.3	9



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109	Rare-variant association tests in longitudinal studies, with an application to the Multi-Ethnic Study of Atherosclerosis (MESA). <i>Genetic Epidemiology</i> , 2017, 41, 801-810.	1.3	3
110	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. <i>Nature Communications</i> , 2017, 8, 910.	12.8	118
111	Association of urinary citrate excretion, pH, and net gastrointestinal alkali absorption with diet, diuretic use, and blood glucose concentration. <i>Physiological Reports</i> , 2017, 5, e13411.	1.7	7
112	Neighborhood characteristics influence DNA methylation of genes involved in stress response and inflammation: The Multi-Ethnic Study of Atherosclerosis. <i>Epigenetics</i> , 2017, 12, 662-673.	2.7	118
113	California's Sterilization Survivors: An Estimate and Call for Redress. <i>American Journal of Public Health</i> , 2017, 107, 50-54.	2.7	53
114	Interaction between Social/Psychosocial Factors and Genetic Variants on Body Mass Index: A Gene-Environment Interaction Analysis in a Longitudinal Setting. <i>International Journal of Environmental Research and Public Health</i> , 2017, 14, 1153.	2.6	11
115	Gene-by-Psychosocial Factor Interactions Influence Diastolic Blood Pressure in European and African Ancestry Populations: Meta-Analysis of Four Cohort Studies. <i>International Journal of Environmental Research and Public Health</i> , 2017, 14, 1596.	2.6	5
116	Genome-wide physical activity interactions in adiposity • A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	3.5	158
117	Rare variants in fox-1 homolog A (RFX1) are associated with lower blood pressure. <i>PLoS Genetics</i> , 2017, 13, e1006678.	3.5	18
118	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. <i>PLoS Genetics</i> , 2017, 13, e1006719.	3.5	98
119	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. <i>PLoS Genetics</i> , 2017, 13, e1006728.	3.5	88
120	The complex genetics of gait speed: genome-wide meta-analysis approach. <i>Aging</i> , 2017, 9, 209-246.	3.1	21
121	Whole Exome Analyses to Examine the Impact of Rare Variants on Left Ventricular Traits in African American Participants from the HyperGEN and GENOA Studies. <i>Journal of Hypertension and Management</i> , 2017, 3, .	0.2	0
122	An Empirical Comparison of Joint and Stratified Frameworks for Studying G × E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Gene-Lifestyle Interactions Working Group. <i>Genetic Epidemiology</i> , 2016, 40, 404-415.	1.3	18
123	GENOME-WIDE ASSOCIATION STUDY (GWAS) AND GENOME-WIDE BY ENVIRONMENT INTERACTION STUDY (GWEIS) OF DEPRESSIVE SYMPTOMS IN AFRICAN AMERICAN AND HISPANIC/LATINA WOMEN. <i>Depression and Anxiety</i> , 2016, 33, 265-280.	4.1	99
124	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016, 17, 255.	8.8	251
125	P14118: Association of Low-Frequency and Rare Coding Variants with Information Processing Speed. <i>Alzheimer's and Dementia</i> , 2016, 12, P448.	0.8	0
126	A Genome-wide study of blood pressure in African Americans accounting for gene-smoking interaction. <i>Scientific Reports</i> , 2016, 6, 18812.	3.3	34



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127	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016, 48, 624-633.	21.4	870
128	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	27.8	1,204
129	<scp>GWAS</scp> analysis of handgrip and lower body strength in older adults in the <scp>CHARGE</scp> consortium. <i>Aging Cell</i> , 2016, 15, 792-800.	6.7	51
130	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , 2016, 48, 1162-1170.	21.4	223
131	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	21.4	284
132	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13366-13371.	7.1	110
133	Key influence of sex on urine volume and osmolality. <i>Biology of Sex Differences</i> , 2016, 7, 12.	4.1	19
134	Trans-ethnic Meta-analysis and Functional Annotation Illuminates the Genetic Architecture of Fasting Glucose and Insulin. <i>American Journal of Human Genetics</i> , 2016, 99, 56-75.	6.2	55
135	Heritability of dietary traits that contribute to nephrolithiasis in a cohort of adult sibships. <i>Journal of Nephrology</i> , 2016, 29, 45-51.	2.0	13
136	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	12.8	412
137	A Statistical Approach for Testing Cross-Phenotype Effects of Rare Variants. <i>American Journal of Human Genetics</i> , 2016, 98, 525-540.	6.2	75
138	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. <i>Human Molecular Genetics</i> , 2016, 25, 358-370.	2.9	73
139	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. <i>Behavior Genetics</i> , 2016, 46, 89-99.	2.1	8
140	Facebook Advertising Across an Engagement Spectrum: A Case Example for Public Health Communication. <i>JMIR Public Health and Surveillance</i> , 2016, 2, e27.	2.6	53
141	Set-based tests for genetic association in longitudinal studies. <i>Biometrics</i> , 2015, 71, 606-615.	1.4	13
142	Public Trust in Health Information Sharing: Implications for Biobanking and Electronic Health Record Systems. <i>Journal of Personalized Medicine</i> , 2015, 5, 3-21.	2.5	65
143	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. <i>PLoS ONE</i> , 2015, 10, e0126637.	2.5	6
144	Associations between self-referral and health behavior responses to genetic risk information. <i>Genome Medicine</i> , 2015, 7, 10.	8.2	27

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145	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	27.8	173
146	A Statistical Approach for Rare-Variant Association Testing in Affected Sibships. <i>American Journal of Human Genetics</i> , 2015, 96, 543-554.	6.2	21
147	GWAS of Longevity in CHARGE Consortium Confirms APOE and FOXO3 Candidacy. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2015, 70, 110-118.	3.6	250
148	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	21.4	357
149	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015, 6, 8570.	12.8	533
150	Testing an Online, Dynamic Consent Portal for Large Population Biobank Research. <i>Public Health Genomics</i> , 2015, 18, 26-39.	1.0	41
151	Current Applications of Genetic Risk Scores to Cardiovascular Outcomes and Subclinical Phenotypes. <i>Current Epidemiology Reports</i> , 2015, 2, 180-190.	2.4	70
152	Life course socioeconomic status and DNA methylation in genes related to stress reactivity and inflammation: The multi-ethnic study of atherosclerosis. <i>Epigenetics</i> , 2015, 10, 958-969.	2.7	155
153	SLC2A9 Genotype Is Associated with SLC2A9 Gene Expression and Urinary Uric Acid Concentration. <i>PLoS ONE</i> , 2015, 10, e0128593.	2.5	16
154	Epigenomic Indicators of Age in African Americans. <i>Hereditary Genetics: Current Research</i> , 2014, 03, .	0.1	10
155	Public preferences regarding informed consent models for participation in population-based genomic research. <i>Genetics in Medicine</i> , 2014, 16, 11-18.	2.4	74
156	An Empirical Comparison of Meta-analysis and Mega-analysis of Individual Participant Data for Identifying Gene-Environment Interactions. <i>Genetic Epidemiology</i> , 2014, 38, 369-378.	1.3	48
157	Genetic diversity is a predictor of mortality in humans. <i>BMC Genetics</i> , 2014, 15, 159.	2.7	12
158	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. <i>Human Molecular Genetics</i> , 2014, 23, 2490-2497.	2.9	56
159	Meta-analysis of loci associated with age at natural menopause in African-American women. <i>Human Molecular Genetics</i> , 2014, 23, 3327-3342.	2.9	54
160	Characterization of european ancestry nonalcoholic fatty liver disease-associated variants in individuals of african and hispanic descent. <i>Hepatology</i> , 2013, 58, 966-975.	7.3	126
161	Epigenetic Markers of Renal Function in African Americans. <i>Nursing Research and Practice</i> , 2013, 2013, 1-9.	1.0	9
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