James G Wilson

List of Publications by Year
in descending order

514	119,729	246	205
papers	citations	143 h-index	313 g-index

602	602	602	105416
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genomeâ€Wide Association Study of NAFLD Using Electronic Health Records. Hepatology Communications, 2022, 6, 297-308.	2.0	33
2	Genomeâ€wide analysis identifies gallstoneâ€susceptibility loci including genes regulating gastrointestinal motility. Hepatology, 2022, 75, 1081-1094.	3.6	12
3	Whole Genome Sequence Analysis of the Plasma Proteome in Black Adults Provides Novel Insights Into Cardiovascular Disease. Circulation, 2022, 145, 357-370.	1.6	39
4	Investigation of the causal relationships between human IgG N-glycosylation and 12 common diseases associated with changes in the IgG N-glycome. Human Molecular Genetics, 2022, 31, 1545-1559.	1.4	11
5	Mendelian randomization of genetically independent aging phenotypes identifies LPA and VCAM1 as biological targets for human aging. Nature Aging, 2022, 2, 19-30.	5.3	17
6	A multi-omics study of circulating phospholipid markers of blood pressure. Scientific Reports, 2022, 12, 574.	1.6	10
7	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	3.0	29
8	A catalogue of omics biological ageing clocks reveals substantial commonality and associations with disease risk. Aging, 2022, 14, 623-659.	1.4	22
9	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
10	Ancient DNA at the edge of the world: Continental immigration and the persistence of Neolithic male lineages in Bronze Age Orkney. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	12
11	Meta-GWAS Reveals Novel Genetic Variants Associated with Urinary Excretion of Uromodulin. Journal of the American Society of Nephrology: JASN, 2022, 33, 511-529.	3.0	14
12	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus. Nature Communications, 2022, 13, 1222.	5.8	5
13	Genetic regulation of post-translational modification of two distinct proteins. Nature Communications, 2022, 13, 1586.	5.8	19
14	Genetic and phenotypic links between obesity and extracellular vesicles. Human Molecular Genetics, 2022, 31, 3643-3651.	1.4	2
15	Whole-genome sequencing reveals host factors underlying critical COVID-19. Nature, 2022, 607, 97-103.	13.7	174
16	Understanding the complex genetic architecture connecting rheumatoid arthritis, osteoporosis and inflammation: discovering causal pathways. Human Molecular Genetics, 2022, , .	1.4	3
17	Polygenic transcriptome risk scores for COPD and lung function improve cross-ethnic portability of prediction in the NHLBI TOPMed program. American Journal of Human Genetics, 2022, 109, 857-870.	2.6	7
18	Genetic Landscape of the ACE2 Coronavirus Receptor. Circulation, 2022, 145, 1398-1411.	1.6	20

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19	Genome-wide Association Study of Liking for Several Types of Physical Activity in the UK Biobank and Two Replication Cohorts. Medicine and Science in Sports and Exercise, 2022, 54, 1252-1260.	0.2	3
20	Serum metabolomic profiles associated with subclinical and clinical cardiovascular phenotypes in people with type 2 diabetes. Cardiovascular Diabetology, 2022, 21, 62.	2.7	6
21	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
22	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. Nature Genetics, 2022, 54, 581-592.	9.4	142
23	Gene-based whole genome sequencing meta-analysis of 250 circulating proteins in three isolated European populations. Molecular Metabolism, 2022, 61, 101509.	3.0	3
24	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits. Nature Communications, 2022, 13, 2743.	5.8	22
25	Using genetic variation to disentangle the complex relationship between food intake and health outcomes. PLoS Genetics, 2022, 18, e1010162.	1.5	12
26	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
27	Limited Effect of Y Chromosome Variation on Coronary Artery Disease and Mortality in UK Biobankâ€"Brief Report. Arteriosclerosis, Thrombosis, and Vascular Biology, 2022, 42, 1198-1206.	1.1	4
28	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	2.6	42
29	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	5.8	87
30	Nontrivial Replication of Loci Detected by Multi-Trait Methods. Frontiers in Genetics, 2021, 12, 627989.	1.1	4
31	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	13.7	1,069
32	Metabolomic Markers of Southern Dietary Patterns in the Jackson Heart Study. Molecular Nutrition and Food Research, 2021, 65, 2000796.	1.5	4
33	Multivariate genome-wide analysis of immunoglobulin G N-glycosylation identifies new loci pleiotropic with immune function. Human Molecular Genetics, 2021, 30, 1259-1270.	1.4	8
34	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
35	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	5.8	17
36	Multiomic Profiling in Black and White Populations Reveals Novel Candidate Pathways in Left Ventricular Hypertrophy and Incident Heart Failure Specific to Black Adults. Circulation Genomic and Precision Medicine, 2021, 14, e003191.	1.6	7

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37	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. Aging Cell, 2021, 20, e13366.	3.0	72
38	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
39	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	3.8	90
40	Contribution of common risk variants to multiple sclerosis in Orkney and Shetland. European Journal of Human Genetics, 2021, 29, 1701-1709.	1.4	6
41	Retinal arteriolar tortuosity and fractal dimension are associated with long-term cardiovascular outcomes in people with type 2 diabetes. Diabetologia, 2021, 64, 2215-2227.	2.9	14
42	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	5.8	49
43	Evaluation of Shared Genetic Susceptibility to High and Low Myopia and Hyperopia. JAMA Ophthalmology, 2021, 139, 601.	1.4	22
44	Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals. American Journal of Human Genetics, 2021, 108, 1350-1355.	2.6	72
45	Associations between everyday discrimination and sleep quality and duration among African-Americans over time in the Jackson Heart Study. Sleep, 2021, 44, .	0.6	13
46	APOL1, Sickle Cell Trait, and CKD in the Jackson Heart Study. Kidney Medicine, 2021, 3, 962-973.e1.	1.0	2
47	Multiethnic Genome-Wide Association Study of Subclinical Atherosclerosis in Individuals With Type 2 Diabetes. Circulation Genomic and Precision Medicine, 2021, 14, e003258.	1.6	4
48	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
49	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. Genome Medicine, 2021, 13, 136.	3.6	16
50	Presence and transmission of mitochondrial heteroplasmic mutations in human populations of European and African ancestry. Mitochondrion, 2021, 60, 33-42.	1.6	6
51	Genome-wide methylation data improves dissection of the effect of smoking on body mass index. PLoS Genetics, 2021, 17, e1009750.	1.5	7
52	Association of Sickle Cell Trait With Incidence of Coronary Heart Disease Among African American Individuals. JAMA Network Open, 2021, 4, e2030435.	2.8	5
53	Metabolomic Profiles and Heart Failure Risk in Black Adults: Insights From the Jackson Heart Study. Circulation: Heart Failure, 2021, 14, e007275.	1.6	29
54	Variation in the SERPINA6/SERPINA1 locus alters morning plasma cortisol, hepatic corticosteroid binding globulin expression, gene expression in peripheral tissues, and risk of cardiovascular disease. Journal of Human Genetics, 2021, 66, 625-636.	1.1	40

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55	Genetic mechanisms of critical illness in COVID-19. Nature, 2021, 591, 92-98.	13.7	1,014
56	Association of mitochondrial DNA copy number with cardiometabolic diseases. Cell Genomics, 2021, 1, 100006.	3.0	26
57	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. Nature Genetics, 2021, 53, 1504-1516.	9.4	69
58	Inbreeding, native American ancestry and child mortality: Linking human selection and paediatric medicine. Human Molecular Genetics, 2021, , .	1.4	1
59	SARS-CoV-2 susceptibility and COVID-19 disease severity are associated with genetic variants affecting gene expression in a variety of tissues. Cell Reports, 2021, 37, 110020.	2.9	25
60	APOL1 renal risk variants are associated with obesity and body composition in African ancestry adults. Medicine (United States), 2021, 100, e27785.	0.4	6
61	Mapping the serum proteome to neurological diseases using whole genome sequencing. Nature Communications, 2021, 12, 7042.	5.8	29
62	Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. EBioMedicine, 2021, 74, 103730.	2.7	5
63	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
64	Coffee Consumption and Kidney Function: A Mendelian Randomization Study. American Journal of Kidney Diseases, 2020, 75, 753-761.	2.1	56
65	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	5.8	32
66	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. Nature Metabolism, 2020, 2, 1135-1148.	5.1	327
67	Glycosylation Alterations in Multiple Sclerosis Show Increased Proinflammatory Potential. Biomedicines, 2020, 8, 410.	1.4	26
68	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	13.7	376
69	Coagulation factor VIII: Relationship to cardiovascular disease risk and whole genome sequence and epigenomeâ€wide analysis in African Americans. Journal of Thrombosis and Haemostasis, 2020, 18, 1335-1347.	1.9	17
70	Trends in disease incidence and survival and their effect on mortality in Scotland: nationwide cohort study of linked hospital admission and death records 2001â€“2016. BMJ Open, 2020, 10, e034299.	0.8	4
71	Multivariate genomic scan implicates novel loci and haem metabolism in human ageing. Nature Communications, 2020, 11, 3570.	5.8	84
72	Autozygosity influences cardiometabolic disease-associated traits in the AWI-Gen sub-Saharan African study. Nature Communications, 2020, 11, 5754.	5.8	23

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73	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
74	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. Lancet Respiratory Medicine,the, 2020, 8, 696-708.	5.2	69
75	Circulating testican-2 is a podocyte-derived marker of kidney health. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25026-25035.	3.3	19
76	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.3	26
77	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.	9.4	146
78	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	5.8	39
79	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. PLoS ONE, 2020, 15, e0230815.	1.1	10
80	The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443.	13.7	6,140
81	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	5.8	59
82	Prioritization of causal genes for coronary artery disease based on cumulative evidence from experimental and in silico studies. Scientific Reports, 2020, 10, 10486.	1.6	22
83	Linking protein to phenotype with Mendelian Randomization detects 38 proteins with causal roles in human diseases and traits. PLoS Genetics, 2020, 16, e1008785.	1.5	29
84	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. Science Advances, 2020, 6, eaax0301.	4.7	90
85	De novo mutations across 1,465 diverse genomes reveal mutational insights and reductions in the Amish founder population. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2560-2569.	3.3	71
86	Association of HLA-DRB1âˆ—09:01 with tIgE levels among African-ancestry individuals with asthma. Journal of Allergy and Clinical Immunology, 2020, 146, 147-155.	1.5	14
87	Interferon gamma-induced protein 10 (IP-10) and cardiovascular disease in African Americans. PLoS ONE, 2020, 15, e0231013.	1.1	12
88	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. PLoS Genetics, 2020, 16, e1008629.	1.5	101
89	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	0.9	3
90	The Association of ARMC5 with the Renin-Angiotensin-Aldosterone System, Blood Pressure, and Glycemia in African Americans. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 2625-2633.	1.8	9

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91	Global variability of the human IgG glycome. Aging, 2020, 12, 15222-15259.	1.4	37
92	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	0.9	4
93	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
94	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
95	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
96	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
97	Genome-wide meta-analysis of SNP-by9-ACEI/ARB and SNP-by-thiazide diuretic and effect on serum potassium in cohorts of European and African ancestry. Pharmacogenomics Journal, 2019, 19, 97-108.	0.9	3
98	Genomic characterization of the RH locus detects complex and novel structural variation in multi-ethnic cohorts. Genetics in Medicine, 2019, 21, 477-486.	1.1	24
99	Evening intake of alcohol, caffeine, and nicotine: night-to-night associations with sleep duration and continuity among African Americans in the Jackson Heart Sleep Study. Sleep, 2019, 42, .	0.6	34
100	Genomeâ€wide metaâ€analysis of SNP and antihypertensive medication interactions on left ventricular traits in African Americans. Molecular Genetics & Genomic Medicine, 2019, 7, e00788.	0.6	4
101	An actionable KCNH2 Long QT Syndrome variant detected by sequence and haplotype analysis in a population research cohort. Scientific Reports, 2019, 9, 10964.	1.6	17
102	Lipidomics, Atrial Conduction, and Body Mass Index. Circulation Genomic and Precision Medicine, 2019, 12, e002384.	1.6	9
103	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	6.2	75
104	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. Journal of the American College of Cardiology, 2019, 73, 3118-3131.	1.2	27
105	Novel Genetic Locus Influencing Retinal Venular Tortuosity Is Also Associated With Risk of Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 2542-2552.	1.1	23
106	The genetic underpinnings of obesity. Current Opinion in Physiology, 2019, 12, 57-64.	0.9	0
107	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	2.2	38
108	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84

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109	Sequencing Analysis at 8p23 Identifies Multiple Rare Variants in DLC1 Associated with Sleep-Related Oxyhemoglobin Saturation Level. American Journal of Human Genetics, 2019, 105, 1057-1068.	2.6	10
110	0336 Associations of Psychosocial Factors, Short Sleep and Insomnia, and Hypertension Control among African-Americans: the Jackson Heart Sleep Study (JHSS). Sleep, 2019, 42, A137-A138.	0.6	2
111	The genetic landscape of Scotland and the Isles. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19064-19070.	3.3	24
112	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
113	Maternal relationships within an Iron Age burial at the High Pasture Cave, Isle of Skye, Scotland. Journal of Archaeological Science, 2019, 110, 104978.	1.2	6
114	Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. Nature Communications, 2019, 10, 357.	5.8	30
115	Genome-wide association meta-analysis of 30,000 samples identifies seven novel loci for quantitative ECG traits. European Journal of Human Genetics, 2019, 27, 952-962.	1.4	29
116	Association Between Sleep Apnea and Blood Pressure Control Among Blacks. Circulation, 2019, 139, 1275-1284.	1.6	53
117	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
118	Genetic Correlations Between Diabetes and Glaucoma: An Analysis of Continuous and Dichotomous Phenotypes. American Journal of Ophthalmology, 2019, 206, 245-255.	1.7	12
119	Regional variation in the incidence rate and sex ratio of multiple sclerosis in Scotland 2010â€“2017: findings from the Scottish Multiple Sclerosis Register. Journal of Neurology, 2019, 266, 2376-2386.	1.8	22
120	Genomics-First Evaluation of Heart Disease Associated With Titin-Truncating Variants. Circulation, 2019, 140, 42-54.	1.6	97
121	Association of Dimethylguanidino Valeric Acid With Partial Resistance to Metabolic Health Benefits of Regular Exercise. JAMA Cardiology, 2019, 4, 636.	3.0	37
122	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	2.6	21
123	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
124	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
125	Rare Protein-Truncating Variants in APOB , Lower Low-Density Lipoprotein Cholesterol, and Protection Against Coronary Heart Disease. Circulation Genomic and Precision Medicine, 2019, 12, e002376.	1.6	57
126	Genome-wide association study identifies novel loci for type 2 diabetes-attributed end-stage kidney disease in African Americans. Human Genomics, 2019, 13, 21.	1.4	32

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127	DNA methylation GrimAge strongly predicts lifespan and healthspan. Aging, 2019, 11, 303-327.	1.4	1,128
128	Associations of variants In the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. PLoS Genetics, 2019, 15, e1007739.	1.5	28
129	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	9.4	402
130	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. Nature Communications, 2019, 10, 1383.	5.8	37
131	You Are Just Now Telling Us About This? African American Perspectives of Testing for Genetic Susceptibility to Kidney Disease. Journal of the American Society of Nephrology: JASN, 2019, 30, 526-530.	3.0	31
132	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. Nature Genetics, 2019, 51, 481-493.	9.4	350
133	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. Nature Communications, 2019, 10, 880.	5.8	71
134	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
135	APOL1 Kidney Risk Variants and Cardiovascular Disease: An Individual Participant Data Meta-Analysis. Journal of the American Society of Nephrology: JASN, 2019, 30, 2027-2036.	3.0	26
136	Increased ultra-rare variant load in an isolated Scottish population impacts exonic and regulatory regions. PLoS Genetics, 2019, 15, e1008480.	1.5	17
137	Multi-trait genome-wide association study identifies new loci associated with optic disc parameters. Communications Biology, 2019, 2, 435.	2.0	22
138	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
139	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	2.6	106
140	DNA Sequence Variation in ACVR1C Encoding the Activin Receptor-Like Kinase 7 Influences Body Fat Distribution and Protects Against Type 2 Diabetes. Diabetes, 2019, 68, 226-234.	0.3	31
141	Association of psychosocial factors with leukocyte telomere length among African Americans in the Jackson Heart Study. Stress and Health, 2019, 35, 138-145.	1.4	5
142	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. Nature Genetics, 2019, 51, 30-35.	9.4	276
143	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. Circulation, 2019, 139, 620-635.	1.6	102
144	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

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145	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. Nature Genetics, 2019, 51, 245-257.	9.4	536
146	DNA methylation-based estimator of telomere length. Aging, 2019, 11, 5895-5923.	1.4	198
147	Epigenome-wide association study of leukocyte telomere length. Aging, 2019, 11, 5876-5894.	1.4	19
148	Genomics of 1 million parent lifespans implicates novel pathways and common diseases and distinguishes survival chances. ELife, 2019, 8, .	2.8	170
149	Association of Sickle Cell Trait With Ischemic Stroke Among African Americans. JAMA Neurology, 2018, 75, 802.	4.5	25
150	Genomeâ€wide interaction with the insulin secretion locus MTNR1B reveals CMIP as a novel type 2 diabetes susceptibility gene in African Americans. Genetic Epidemiology, 2018, 42, 559-570.	0.6	17
151	Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. Nature Communications, 2018, 9, 1613.	5.8	78
152	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
153	Transethnic Evaluation Identifies Low-Frequency Loci Associated With 25-Hydroxyvitamin D Concentrations. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 1380-1392.	1.8	33
154	Deletion of the Duffy antigen receptor for chemokines (DARC) promotes insulin resistance and adipose tissue inflammation during high fat feeding. Molecular and Cellular Endocrinology, 2018, 473, 79-88.	1.6	12
155	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. Nature Communications, 2018, 9, 260.	5.8	295
156	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 379-384.	3.3	28
157	Whole genome sequence analyses of brain imaging measures in the Framingham Study. Neurology, 2018, 90, e188-e196.	1.5	34
158	Runs of homozygosity: windows into population history and trait architecture. Nature Reviews Genetics, 2018, 19, 220-234.	7.7	497
159	Genome-wide association study of homocysteine in African Americans from the Jackson Heart Study, the Multi-Ethnic Study of Atherosclerosis, and the Coronary Artery Risk in Young Adults study. Journal of Human Genetics, 2018, 63, 327-337.	1.1	7
160	Life-Course Genome-wide Association Study Meta-analysis of Total Body BMD and Assessment of Age-Specific Effects. American Journal of Human Genetics, 2018, 102, 88-102.	2.6	252
161	Negative effect of vitamin D on kidney function: a Mendelian randomization study. Nephrology Dialysis Transplantation, 2018, 33, 2139-2145.	0.4	18
162	Glycosylation Profile of Immunoglobulin G Is Cross-Sectionally Associated With Cardiovascular Disease Risk Score and Subclinical Atherosclerosis in Two Independent Cohorts. Circulation Research, 2018, 122, 1555-1564.	2.0	87

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163	UBD modifies APOL1 -induced kidney disease risk. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3446-3451.	3.3	52
164	West African Ancestry and Nocturnal Blood Pressure in African Americans: The Jackson Heart Study. American Journal of Hypertension, 2018, 31, 706-714.	1.0	4
165	Phenotypic Consequences of a Genetic Predisposition to Enhanced Nitric Oxide Signaling. Circulation, 2018, 137, 222-232.	1.6	87
166	Identification of a novel locus on chromosome 2q13, which predisposes to clinical vertebral fractures independently of bone density. Annals of the Rheumatic Diseases, 2018, 77, 378-385.	0.5	21
167	An epigenetic biomarker of aging for lifespan and healthspan. Aging, 2018, 10, 573-591.	1.4	1,552
168	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	5.8	119
169	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
170	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
171	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
172	Prevalence and correlates of obstructive sleep apnea among African Americans: the Jackson Heart Sleep Study. Sleep, 2018, 41, .	0.6	76
173	KCNJ11 variants and their effect on the association between serum potassium and diabetes risk in the Atherosclerosis Risk in Communities (ARIC) Study and Jackson Heart Study (JHS) cohorts. PLoS ONE, 2018, 13, e0203213.	1.1	4
174	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. Nature Genetics, 2018, 50, 834-848.	9.4	239
175	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	1.6	19
176	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	5.8	484
177	Cross-ancestry genome-wide association analysis of corneal thickness strengthens link between complex and Mendelian eye diseases. Nature Communications, 2018, 9, 1864.	5.8	63
178	Reply to â€˜Misestimation of heritability and prediction accuracy of male-pattern baldnessâ€™. Nature Communications, 2018, 9, 2538.	5.8	0
179	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. Nature Genetics, 2018, 50, 1112-1121.	9.4	1,835
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