

James G Wilson

List of Publications by Year in descending order

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Version: 2024-02-01

514
papers

119,729
citations

246

143
h-index

205

313
g-index

602
all docs

602
docs citations

602
times ranked

105416
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of protein-coding genetic variation in 60,706 humans. <i>Nature</i> , 2016, 536, 285-291.	27.8	9,051
2	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020, 581, 434-443.	27.8	6,140
3	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
4	Biological, clinical and population relevance of 95 loci for blood lipids. <i>Nature</i> , 2010, 466, 707-713.	27.8	3,249
5	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	21.4	2,641
6	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	21.4	2,634
7	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016, 48, 1279-1283.	21.4	2,421
8	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010, 42, 105-116.	21.4	1,982
9	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. <i>Nature Genetics</i> , 2018, 50, 1112-1121.	21.4	1,835
10	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	21.4	1,818
11	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	27.8	1,789
12	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012, 44, 981-990.	21.4	1,748
13	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. <i>Nature Genetics</i> , 2010, 42, 579-589.	21.4	1,631
14	An epigenetic biomarker of aging for lifespan and healthspan. <i>Aging</i> , 2018, 10, 573-591.	3.1	1,552
15	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	27.8	1,328
16	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. <i>Nature Genetics</i> , 2013, 45, 1353-1360.	21.4	1,213
17	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	27.8	1,204
18	DNA methylation GrimAge strongly predicts lifespan and healthspan. <i>Aging</i> , 2019, 11, 303-327.	3.1	1,128

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19	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , 2018, 50, 524-537.	21.4	1,124
20	Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. <i>Nature Genetics</i> , 2012, 44, 491-501.	21.4	1,100
21	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299.	27.8	1,069
22	Genetic mechanisms of critical illness in COVID-19. <i>Nature</i> , 2021, 591, 92-98.	27.8	1,014
23	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014, 46, 234-244.	21.4	959
24	Runs of Homozygosity in European Populations. <i>American Journal of Human Genetics</i> , 2008, 83, 359-372.	6.2	958
25	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	27.8	952
26	Loss-of-Function Mutations in <i>APOC3</i> , Triglycerides, and Coronary Disease. <i>New England Journal of Medicine</i> , 2014, 371, 22-31.	27.0	936
27	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	21.4	924
28	The interleukin-6 receptor as a target for prevention of coronary heart disease: a mendelian randomisation analysis. <i>Lancet</i> , The, 2012, 379, 1214-1224.	13.7	886
29	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	21.4	836
30	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. <i>Nature Genetics</i> , 2009, 41, 47-55.	21.4	776
31	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. <i>Nature Genetics</i> , 2012, 44, 659-669.	21.4	762
32	Common variants associated with plasma triglycerides and risk for coronary artery disease. <i>Nature Genetics</i> , 2013, 45, 1345-1352.	21.4	754
33	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. <i>Science</i> , 2013, 340, 1467-1471.	12.6	750
34	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012, 44, 991-1005.	21.4	746
35	Genomic insights into the origin of farming in the ancient Near East. <i>Nature</i> , 2016, 536, 419-424.	27.8	733
36	Diagnostic Yield and Clinical Utility of Sequencing Familial Hypercholesterolemia Genes in Patients With Severe Hypercholesterolemia. <i>Journal of the American College of Cardiology</i> , 2016, 67, 2578-2589.	2.8	723

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37	New loci associated with kidney function and chronic kidney disease. <i>Nature Genetics</i> , 2010, 42, 376-384.	21.4	710
38	A Genetic Atlas of Human Admixture History. <i>Science</i> , 2014, 343, 747-751.	12.6	691
39	SLC2A9 is a newly identified urate transporter influencing serum urate concentration, urate excretion and gout. <i>Nature Genetics</i> , 2008, 40, 437-442.	21.4	678
40	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013, 45, 145-154.	21.4	675
41	Interleukin-6 receptor pathways in coronary heart disease: a collaborative meta-analysis of 82 studies. <i>Lancet, The</i> , 2012, 379, 1205-1213.	13.7	668
42	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. <i>Nature Genetics</i> , 2010, 42, 142-148.	21.4	591
43	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. <i>Nature Genetics</i> , 2010, 42, 436-440.	21.4	581
44	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. <i>Nature</i> , 2015, 518, 102-106.	27.8	581
45	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512.	21.4	578
46	Meta-Analysis of 28,141 Individuals Identifies Common Variants within Five New Loci That Influence Uric Acid Concentrations. <i>PLoS Genetics</i> , 2009, 5, e1000504.	3.5	572
47	Mendelian randomization of blood lipids for coronary heart disease. <i>European Heart Journal</i> , 2015, 36, 539-550.	2.2	567
48	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. <i>Lancet, The</i> , 2015, 385, 351-361.	13.7	562
49	A General Approach for Haplotype Phasing across the Full Spectrum of Relatedness. <i>PLoS Genetics</i> , 2014, 10, e1004234.	3.5	553
50	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	21.4	549
51	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	27.8	544
52	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. <i>Nature Genetics</i> , 2019, 51, 245-257.	21.4	536
53	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. <i>BMJ, The</i> , 2014, 349, g4164-g4164.	6.0	528
54	Genome-wide association study identifies five loci associated with lung function. <i>Nature Genetics</i> , 2010, 42, 36-44.	21.4	518

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55	Runs of homozygosity: windows into population history and trait architecture. <i>Nature Reviews Genetics</i> , 2018, 19, 220-234.	16.3	497
56	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , 2018, 9, 2098.	12.8	484
57	Abundant Pleiotropy in Human Complex Diseases and Traits. <i>American Journal of Human Genetics</i> , 2011, 89, 607-618.	6.2	478
58	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	21.4	470
59	Meta-Analysis of Genome-Wide Association Studies in >80 000 Subjects Identifies Multiple Loci for C-Reactive Protein Levels. <i>Circulation</i> , 2011, 123, 731-738.	1.6	461
60	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 1077-1085.	21.4	445
61	High Throughput Isolation and Glycosylation Analysis of IgG Variability and Heritability of the IgG Glycome in Three Isolated Human Populations. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.010090.	3.8	443
62	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. <i>Science</i> , 2016, 351, 1166-1171.	12.6	438
63	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. <i>Nature Genetics</i> , 2014, 46, 357-363.	21.4	428
64	Genomic Runs of Homozygosity Record Population History and Consanguinity. <i>PLoS ONE</i> , 2010, 5, e13996.	2.5	427
65	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	21.4	426
66	Population genetic structure of variable drug response. <i>Nature Genetics</i> , 2001, 29, 265-269.	21.4	425
67	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. <i>PLoS Genetics</i> , 2012, 8, e1002607.	3.5	419
68	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
69	Genome-wide associations for birth weight and correlations with adult disease. <i>Nature</i> , 2016, 538, 248-252.	27.8	406
70	Epigenetic clock for skin and blood cells applied to Hutchinson Gilford Progeria Syndrome and ex vivo studies. <i>Aging</i> , 2018, 10, 1758-1775.	3.1	406
71	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011, 43, 1005-1011.	21.4	403
72	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. <i>Nature Genetics</i> , 2019, 51, 804-814.	21.4	402

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73	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. <i>Nature Genetics</i> , 2013, 45, 314-318.	21.4	398
74	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. <i>Diabetes</i> , 2010, 59, 3229-3239.	0.6	387
75	Inactivating Mutations in <i>NPC1L1</i> and Protection from Coronary Heart Disease. <i>New England Journal of Medicine</i> , 2014, 371, 2072-2082.	27.0	386
76	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	27.8	383
77	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020, 586, 763-768.	27.8	376
78	Integrated allelic, transcriptional, and phenomic dissection of the cardiac effects of titin truncations in health and disease. <i>Science Translational Medicine</i> , 2015, 7, 270ra6.	12.4	375
79	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. <i>PLoS Genetics</i> , 2013, 9, e1003500.	3.5	371
80	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. <i>Nature Genetics</i> , 2011, 43, 1082-1090.	21.4	367
81	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016, 48, 1171-1184.	21.4	362
82	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
83	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
84	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	27.8	353
85	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. <i>Nature Genetics</i> , 2019, 51, 481-493.	21.4	350
86	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. <i>PLoS Medicine</i> , 2017, 14, e1002383.	8.4	341
87	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	21.4	341
88	Concept, Design and Implementation of a Cardiovascular Gene-Centric 50 K SNP Array for Large-Scale Genomic Association Studies. <i>PLoS ONE</i> , 2008, 3, e3583.	2.5	339
89	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	3.5	331
90	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020, 2, 1135-1148.	11.9	327

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91	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706.	6.2	326
92	Loci Associated with N-Glycosylation of Human Immunoglobulin G Show Pleiotropy with Autoimmune Diseases and Haematological Cancers. <i>PLoS Genetics</i> , 2013, 9, e1003225.	3.5	323
93	The landscape of recombination in African Americans. <i>Nature</i> , 2011, 476, 170-175.	27.8	319
94	Association of vitamin D status with arterial blood pressure and hypertension risk: a mendelian randomisation study. <i>Lancet Diabetes and Endocrinology</i> , 2014, 2, 719-729.	11.4	319
95	Novel Associations of Multiple Genetic Loci With Plasma Levels of Factor VII, Factor VIII, and von Willebrand Factor. <i>Circulation</i> , 2010, 121, 1382-1392.	1.6	311
96	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. <i>Nature Genetics</i> , 2010, 42, 1068-1076.	21.4	308
97	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. <i>PLoS Genetics</i> , 2016, 12, e1006125.	3.5	308
98	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. <i>Nature Genetics</i> , 2012, 44, 260-268.	21.4	303
99	Glycans Are a Novel Biomarker of Chronological and Biological Ages. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2014, 69, 779-789.	3.6	297
100	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. <i>Nature Communications</i> , 2018, 9, 260.	12.8	295
101	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. <i>Nature Genetics</i> , 2013, 45, 76-82.	21.4	293
102	Genome-Wide Association Study of Coronary Heart Disease and Its Risk Factors in 8,090 African Americans: The NHLBI CARE Project. <i>PLoS Genetics</i> , 2011, 7, e1001300.	3.5	290
103	Genetic variation near <i>IRS1</i> associates with reduced adiposity and an impaired metabolic profile. <i>Nature Genetics</i> , 2011, 43, 753-760.	21.4	289
104	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. <i>JAMA Psychiatry</i> , 2015, 72, 642.	11.0	289
105	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. <i>American Journal of Human Genetics</i> , 2014, 94, 223-232.	6.2	287
106	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
107	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	21.4	284
108	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013, 45, 621-631.	21.4	282

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109	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014, 46, 826-836.	21.4	281
110	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. <i>Nature Genetics</i> , 2019, 51, 30-35.	21.4	276
111	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. <i>Nature Genetics</i> , 2013, 45, 155-163.	21.4	269
112	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. <i>Nature Genetics</i> , 2017, 49, 416-425.	21.4	257
113	Life-Course Genome-wide Association Study Meta-analysis of Total Body BMD and Assessment of Age-Specific Effects. <i>American Journal of Human Genetics</i> , 2018, 102, 88-102.	6.2	252
114	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	21.4	251
115	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
116	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019, 570, 71-76.	27.8	248
117	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495.	12.8	245
118	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. <i>American Journal of Human Genetics</i> , 2012, 90, 410-425.	6.2	239
119	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. <i>Nature Genetics</i> , 2018, 50, 834-848.	21.4	239
120	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. <i>American Journal of Human Genetics</i> , 2012, 91, 823-838.	6.2	227
121	Positive Selection on a High-Sensitivity Allele of the Human Bitter-Taste Receptor TAS2R16. <i>Current Biology</i> , 2005, 15, 1257-1265.	3.9	224
122	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. <i>Nature Genetics</i> , 2010, 42, 430-435.	21.4	223
123	Best Practices and Joint Calling of the Human Exome BeadChip: The CHARGE Consortium. <i>PLoS ONE</i> , 2013, 8, e68095.	2.5	219
124	Genomics Meets Glycomics—The First GWAS Study of Human N-Glycome Identifies HNF1 α as a Master Regulator of Plasma Protein Fucosylation. <i>PLoS Genetics</i> , 2010, 6, e1001256.	3.5	213
125	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. <i>Nature Genetics</i> , 2014, 46, 1126-1130.	21.4	212
126	Genetic Adaptation of Fatty-Acid Metabolism: A Human-Specific Haplotype Increasing the Biosynthesis of Long-Chain Omega-3 and Omega-6 Fatty Acids. <i>American Journal of Human Genetics</i> , 2012, 90, 809-820.	6.2	205

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127	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. <i>PLoS Genetics</i> , 2019, 15, e1008500.	3.5	203
128	Causal Effects of Body Mass Index on Cardiometabolic Traits and Events: A Mendelian Randomization Analysis. <i>American Journal of Human Genetics</i> , 2014, 94, 198-208.	6.2	199
129	DNA methylation-based estimator of telomere length. <i>Aging</i> , 2019, 11, 5895-5923.	3.1	198
130	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. <i>PLoS ONE</i> , 2012, 7, e29202.	2.5	197
131	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. <i>American Journal of Human Genetics</i> , 2014, 94, 233-245.	6.2	193
132	Meta-analysis of genome-wide association studies from the CHARGE consortium identifies common variants associated with carotid intima media thickness and plaque. <i>Nature Genetics</i> , 2011, 43, 940-947.	21.4	191
133	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. <i>PLoS Genetics</i> , 2014, 10, e1004517.	3.5	191
134	Stratifying Type 2 Diabetes Cases by BMI Identifies Genetic Risk Variants in LAMA1 and Enrichment for Risk Variants in Lean Compared to Obese Cases. <i>PLoS Genetics</i> , 2012, 8, e1002741.	3.5	190
135	Phenotypic Characterization of Genetically Lowered Human Lipoprotein(a) Levels. <i>Journal of the American College of Cardiology</i> , 2016, 68, 2761-2772.	2.8	186
136	A Y Chromosome Census of the British Isles. <i>Current Biology</i> , 2003, 13, 979-984.	3.9	185
137	Genetic Determinants of Circulating Sphingolipid Concentrations in European Populations. <i>PLoS Genetics</i> , 2009, 5, e1000672.	3.5	184
138	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	27.8	183
139	Genetic evidence for different male and female roles during cultural transitions in the British Isles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 5078-5083.	7.1	182
140	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. <i>PLoS Genetics</i> , 2012, 8, e1002490.	3.5	181
141	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. <i>Behavior Genetics</i> , 2016, 46, 170-182.	2.1	178
142	Y Chromosomes Traveling South: The Cohen Modal Haplotype and the Origins of the Lemba—the “Black Jews of Southern Africa”. <i>American Journal of Human Genetics</i> , 2000, 66, 674-686.	6.2	174
143	Whole-genome sequencing reveals host factors underlying critical COVID-19. <i>Nature</i> , 2022, 607, 97-103.	27.8	174
144	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015, 6, 5897.	12.8	173

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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	Admixture Mapping of White Cell Count: Genetic Locus Responsible for Lower White Blood Cell Count in the Health ABC and Jackson Heart Studies. <i>American Journal of Human Genetics</i> , 2008, 82, 81-87.	6.2	172
147	Genomics of 1 million parent lifespans implicates novel pathways and common diseases and distinguishes survival chances. <i>ELife</i> , 2019, 8, .	6.0	170
148	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
149	Association of Sickle Cell Trait With Chronic Kidney Disease and Albuminuria in African Americans. <i>JAMA - Journal of the American Medical Association</i> , 2014, 312, 2115.	7.4	167
150	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. <i>PLoS Genetics</i> , 2012, 8, e1002584.	3.5	166
151	Genome-wide physical activity interactions in adiposity • A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	3.5	158
152	Association of Rare and Common Variation in the Lipoprotein Lipase Gene With Coronary Artery Disease. <i>JAMA - Journal of the American Medical Association</i> , 2017, 317, 937.	7.4	148
153	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017, 8, 80.	12.8	147
154	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
155	A Predominantly Indigenous Paternal Heritage for the Austronesian-Speaking Peoples of Insular Southeast Asia and Oceania. <i>American Journal of Human Genetics</i> , 2001, 68, 432-443.	6.2	145
156	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. <i>PLoS Genetics</i> , 2013, 9, e1003796.	3.5	142
157	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
158	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. <i>Nature Communications</i> , 2018, 9, 3391.	12.8	140
159	Candidate Gene Association Resource (CARE). <i>Circulation: Cardiovascular Genetics</i> , 2010, 3, 267-275.	5.1	139
160	Nine Loci for Ocular Axial Length Identified through Genome-wide Association Studies, Including Shared Loci with Refractive Error. <i>American Journal of Human Genetics</i> , 2013, 93, 264-277.	6.2	139
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