James G Wilson

List of Publications by Year in Descending Order

535 papers	81,755 citations	132 h-index	280 g-index
602 ext. papers	104,523 ext. citations	14.3 avg, IF	6.36 L-index

#	Paper	IF	Citations
535	Mendelian randomization of genetically independent aging phenotypes identifies LPA and VCAM1 as biological targets for human aging. *Nature Aging*, **2022**, 2, 19-30		3
534	A multi-omics study of circulating phospholipid markers of blood pressure.. *Scientific Reports*, **2022**, 12, 574	4.9	0
533	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed.. *Cell Genomics*, **2022**, 2, 100084-100084		1
532	A catalogue of omics biological ageing clocks reveals substantial commonality and associations with disease risk.. *Aging*, **2022**, 14, 623-659	5.6	0
531	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,	11.5	2
530	Meta-GWAS Reveals Novel Genetic Variants Associated with Urinary Excretion of Uromodulin.. *Journal of the American Society of Nephrology: JASN*, **2022**, 33, 511-529	12.7	2
529	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus.. *Nature Communications*, **2022**, 13, 1222	17.4	0
528	Genetic regulation of post-translational modification of two distinct proteins.. *Nature Communications*, **2022**, 13, 1586	17.4	0
527	Whole genome sequencing reveals host factors underlying critical Covid-19.. *Nature*, **2022**,	50.4	8
526	Serum metabolomic profiles associated with subclinical and clinical cardiovascular phenotypes in people with type 2 diabetes.. *Cardiovascular Diabetology*, **2022**, 21, 62	8.7	1
525	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. *Nature Genetics*, **2022**,	36.3	7
524	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects.. *Nature Genetics*, **2022**, 54, 581-592	36.3	6
523	Gene-based whole genome sequencing meta-analysis of 250 circulating proteins in three isolated European populations.. *Molecular Metabolism*, **2022**, 101509	8.8	0
522	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits.. *Nature Communications*, **2022**, 13, 2743	17.4	0
521	Using genetic variation to disentangle the complex relationship between food intake and health outcomes. *PLoS Genetics*, **2022**, 18, e1010162	6	0
520	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. *Communications Biology*, **2022**, 5,	6.7	1
519	Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. *EBioMedicine*, **2021**, 74, 103730	8.8	1

518	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
517	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	10.6	2
516	Whole Genome Sequence Analysis of the Plasma Proteome in Black Adults Provides Novel Insights into Cardiovascular Disease. *Circulation*, **2021**,	16.7	4
515	APOL1 renal risk variants are associated with obesity and body composition in African ancestry adults: An observational genotype-phenotype association study. *Medicine (United States)*, **2021**, 100, e27785	1.8	1
514	Mapping the serum proteome to neurological diseases using whole genome sequencing. *Nature Communications*, **2021**, 12, 7042	17.4	3
513	Association of mitochondrial DNA copy number with cardiometabolic diseases.. *Cell Genomics*, **2021** , 1,		1
512	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	36.3	7
511	Inbreeding, native American ancestry and child mortality: Linking human selection and paediatric medicine. *Human Molecular Genetics*, **2021**,	5.6	1
510	Genetic mechanisms of critical illness in COVID-19. *Nature*, **2021**, 591, 92-98	50.4	451
509	Metabolomic Markers of Southern Dietary Patterns in the Jackson Heart Study. *Molecular Nutrition and Food Research*, **2021**, 65, e2000796	5.9	0
508	Multivariate genome-wide analysis of immunoglobulin G N-glycosylation identifies new loci pleiotropic with immune function. *Human Molecular Genetics*, **2021**, 30, 1259-1270	5.6	0
507	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	11	7
506	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. *Nature Communications*, **2021**, 12, 2182	17.4	5
505	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	5.2	2
504	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. *Aging Cell*, **2021**, 20, e13366	9.9	9
503	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
502	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. *Genome Biology*, **2021**, 22, 194	18.3	14
501	Contribution of common risk variants to multiple sclerosis in Orkney and Shetland. *European Journal of Human Genetics*, **2021**, 29, 1701-1709	5.3	1

500	Retinal arteriolar tortuosity and fractal dimension are associated with long-term cardiovascular outcomes in people with type 2 diabetes. *Diabetologia*, **2021**, 64, 2215-2227	10.3	3
499	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. *Nature Communications*, **2021**, 12, 3505	17.4	5
498	Evaluation of Shared Genetic Susceptibility to High and Low Myopia and Hyperopia. *JAMA Ophthalmology*, **2021**, 139, 601-609	3.9	4
497	Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals. *American Journal of Human Genetics*, **2021**, 108, 1350-1355	11	25
496	Associations between everyday discrimination and sleep quality and duration among African-Americans over time in the Jackson Heart Study. *Sleep*, **2021**, 44,	1.1	2
495	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. *Kidney International*, **2021**, 99, 926-939	9.9	6
494	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. *Nature Communications*, **2021**, 12, 24	17.4	30
493	Nontrivial Replication of Loci Detected by Multi-Trait Methods. *Frontiers in Genetics*, **2021**, 12, 627989	4.5	0
492	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. *Nature*, **2021**, 590, 290-299	50.4	268
491	, Sickle Cell Trait, and CKD in the Jackson Heart Study.. *Kidney Medicine*, **2021**, 3, 962-973.e1	2.8	
490	Multiethnic Genome-Wide Association Study of Subclinical Atherosclerosis in Individuals With Type 2 Diabetes. *Circulation Genomic and Precision Medicine*, **2021**, 14, e003258	5.2	0
489	Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397	50.4	28
488	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. *Genome Medicine*, **2021**, 13, 136	14.4	3
487	Presence and transmission of mitochondrial heteroplasmic mutations in human populations of European and African ancestry. *Mitochondrion*, **2021**, 60, 33-42	4.9	0
486	Genome-Wide Association Study of NAFLD Using Electronic Health Records. *Hepatology Communications*, **2021**,	6	3
485	Genome-wide methylation data improves dissection of the effect of smoking on body mass index. *PLoS Genetics*, **2021**, 17, e1009750	6	1
484	Association of Sickle Cell Trait With Incidence of Coronary Heart Disease Among African American Individuals. *JAMA Network Open*, **2021**, 4, e2030435	10.4	3
483	Metabolomic Profiles and Heart Failure Risk in Black Adults: Insights From the Jackson Heart Study. *Circulation: Heart Failure*, **2021**, 14, e007275	7.6	6

482	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	4.3	12
481	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. *PLoS ONE*, **2020**, 15, e0230815	3.7	4
480	The mutational constraint spectrum quantified from variation in 141,456 humans. *Nature*, **2020**, 581, 434-443	50.4	2278
479	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. *Nature Communications*, **2020**, 11, 2542	17.4	16
478	Prioritization of causal genes for coronary artery disease based on cumulative evidence from experimental and in silico studies. *Scientific Reports*, **2020**, 10, 10486	4.9	8
477	Linking protein to phenotype with Mendelian Randomization detects 38 proteins with causal roles in human diseases and traits. *PLoS Genetics*, **2020**, 16, e1008785	6	12
476	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. *Science Advances*, **2020**, 6, eaax0301	14.3	38
475	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	11.5	29
474	Association of HLA-DRB1*09:01 with tIgE levels among African-ancestry individuals with asthma. *Journal of Allergy and Clinical Immunology*, **2020**, 146, 147-155	11.5	6
473	Interferon gamma-induced protein 10 (IP-10) and cardiovascular disease in African Americans. *PLoS ONE*, **2020**, 15, e0231013	3.7	4
472	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. *PLoS Genetics*, **2020**, 16, e1008629	6	49
471	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,	5.6	5
470	Global variability of the human IgG glycome. *Aging*, **2020**, 12, 15222-15259	5.6	15
469	Variants associated with HHIP expression have sex-differential effects on lung function. *Wellcome Open Research*, **2020**, 5, 111	4.8	0
468	Coffee Consumption and Kidney Function: A Mendelian Randomization Study. *American Journal of Kidney Diseases*, **2020**, 75, 753-761	7.4	18
467	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. *Nature Communications*, **2020**, 11, 5182	17.4	6
466	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. *Nature Metabolism*, **2020**, 2, 1135-1148	14.6	61
465	Glycosylation Alterations in Multiple Sclerosis Show Increased Proinflammatory Potential. *Biomedicines*, **2020**, 8,	4.8	8

464	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. *Nature*, **2020**, 586, 763-768	50.4	127
463	Coagulation factor VIII: Relationship to cardiovascular disease risk and whole genome sequence and epigenome-wide analysis in African Americans. *Journal of Thrombosis and Haemostasis*, **2020**, 18, 1335-1347	15.4	9
462	Trends in disease incidence and survival and their effect on mortality in Scotland: nationwide cohort study of linked hospital admission and death records 2001-2016. *BMJ Open*, **2020**, 10, e034299	3	2
461	Multivariate genomic scan implicates novel loci and haem metabolism in human ageing. *Nature Communications*, **2020**, 11, 3570	17.4	33
460	Autozygosity influences cardiometabolic disease-associated traits in the AWI-Gen sub-Saharan African study. *Nature Communications*, **2020**, 11, 5754	17.4	1
459	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	6.7	7
458	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	35.1	29
457	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	11.5	7
456	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. *Diabetes*, **2020**, 69, 2806-2818	0.9	10
455	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	36.3	33
454	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. *Nature Communications*, **2020**, 11, 6417	17.4	17
453	Variants associated with expression have sex-differential effects on lung function. *Wellcome Open Research*, **2020**, 5, 111	4.8	0
452	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
451	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
450	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
449	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
448	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	1.1	2
447	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	11.5	10

446	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. *Nature Genetics*, **2019**, 51, 1459-1474	36.3	122
445	Maternal relationships within an Iron Age burial at the High Pasture Cave, Isle of Skye, Scotland. *Journal of Archaeological Science*, **2019**, 110, 104978	2.9	5
444	Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. *Nature Communications*, **2019**, 10, 357	17.4	12
443	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	5.3	18
442	Association Between Sleep Apnea and Blood Pressure Control Among Blacks. *Circulation*, **2019**, 139, 1275-1284	16.7	30
441	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	6.3	14
440	Genetic Correlations Between Diabetes and Glaucoma: An Analysis of Continuous and Dichotomous Phenotypes. *American Journal of Ophthalmology*, **2019**, 206, 245-255	4.9	6
439	Regional variation in the incidence rate and sex ratio of multiple sclerosis in Scotland 2010-2017: findings from the Scottish Multiple Sclerosis Register. *Journal of Neurology*, **2019**, 266, 2376-2386	5.5	11
438	Genomics-First Evaluation of Heart Disease Associated With Titin-Truncating Variants. *Circulation*, **2019**, 140, 42-54	16.7	46
437	Association of Dimethylguanidino Valeric Acid With Partial Resistance to Metabolic Health Benefits of Regular Exercise. *JAMA Cardiology*, **2019**, 4, 636-643	16.2	19
436	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. *American Journal of Human Genetics*, **2019**, 105, 15-28	11	12
435	A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nature Genetics*, **2019**, 51, 957-972	36.3	217
434	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. *Nature*, **2019**, 570, 71-76	50.4	129
433	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	5.2	30
432	Genome-wide association study identifies novel loci for type 2 diabetes-attributed end-stage kidney disease in African Americans. *Human Genomics*, **2019**, 13, 21	6.8	18
431	DNA methylation GrimAge strongly predicts lifespan and healthspan. *Aging*, **2019**, 11, 303-327	5.6	424
430	Associations of variants In the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. *PLoS Genetics*, **2019**, 15, e1007739	6	14
429	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. *Nature Genetics*, **2019**, 51, 804-814	36.3	181

428	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. *Nature Communications*, **2019**, 10, 1383	17.4	21
427	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	12.7	21
426	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. *Nature Genetics*, **2019**, 51, 481-493	36.3	156
425	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	3.5	3
424	Genomic characterization of the RH locus detects complex and novel structural variation in multi-ethnic cohorts. *Genetics in Medicine*, **2019**, 21, 477-486	8.1	17
423	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,	1.1	16
422	Genome-wide meta-analysis of SNP and antihypertensive medication interactions on left ventricular traits in African Americans. *Molecular Genetics & Genomic Medicine*, **2019**, 7, e00788	2.3	3
421	An actionable KCNH2 Long QT Syndrome variant detected by sequence and haplotype analysis in a population research cohort. *Scientific Reports*, **2019**, 9, 10964	4.9	6
420	Lipidomics, Atrial Conduction, and Body Mass Index. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002384	5.2	3
419	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. *Nature Human Behaviour*, **2019**, 3, 950-961	12.8	32
418	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. *Journal of the American College of Cardiology*, **2019**, 73, 3118-3131	15.1	12
417	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	9.4	11
416	The genetic underpinnings of obesity. *Current Opinion in Physiology*, **2019**, 12, 57-64	2.6	
415	Disentangling the genetics of lean mass. *American Journal of Clinical Nutrition*, **2019**, 109, 276-287	7	24
414	Associations of autozygosity with a broad range of human phenotypes. *Nature Communications*, **2019**, 10, 4957	17.4	40
413	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	11	4
412	DNA methylation-based estimator of telomere length. *Aging*, **2019**, 11, 5895-5923	5.6	69
411	Epigenome-wide association study of leukocyte telomere length. *Aging*, **2019**, 11, 5876-5894	5.6	4

410	Genomics of 1 million parent lifespans implicates novel pathways and common diseases and distinguishes survival chances. *ELife*, **2019**, 8,	8.9	82
409	Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. *Nature Communications*, **2019**, 10, 880	17.4	36
408	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
407	Kidney Risk Variants and Cardiovascular Disease: An Individual Participant Data Meta-Analysis. *Journal of the American Society of Nephrology: JASN*, **2019**, 30, 2027-2036	12.7	16
406	Increased ultra-rare variant load in an isolated Scottish population impacts exonic and regulatory regions. *PLoS Genetics*, **2019**, 15, e1008480	6	5
405	Multi-trait genome-wide association study identifies new loci associated with optic disc parameters. *Communications Biology*, **2019**, 2, 435	6.7	10
404	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	6	90
403	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. *American Journal of Human Genetics*, **2019**, 104, 112-138	11	54
402	DNA Sequence Variation in Encoding the Activin Receptor-Like Kinase 7 Influences Body Fat Distribution and Protects Against Type 2 Diabetes. *Diabetes*, **2019**, 68, 226-234	0.9	12
401	Association of psychosocial factors with leukocyte telomere length among African Americans in the Jackson Heart Study. *Stress and Health*, **2019**, 35, 138-145	3.7	4
400	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. *Nature Genetics*, **2019**, 51, 30-35	36.3	153
399	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. *Circulation*, **2019**, 139, 620-635	16.7	51
398	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	11	43
397	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	36.3	259
396	Association of Sickle Cell Trait With Ischemic Stroke Among African Americans: A Meta-analysis. *JAMA Neurology*, **2018**, 75, 802-807	17.2	22
395	Genome-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	2.6	11
394	Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. *Nature Communications*, **2018**, 9, 1613	17.4	55
393	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221

392	Transethnic Evaluation Identifies Low-Frequency Loci Associated With 25-Hydroxyvitamin D Concentrations. *Journal of Clinical Endocrinology and Metabolism*, **2018**, 103, 1380-1392	5.6	18
391	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	4.4	8
390	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. *Nature Communications*, **2018**, 9, 260	17.4	174
389	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	11.5	21
388	Whole genome sequence analyses of brain imaging measures in the Framingham Study. *Neurology*, **2018**, 90, e188-e196	6.5	19
387	Runs of homozygosity: windows into population history and trait architecture. *Nature Reviews Genetics*, **2018**, 19, 220-234	30.1	231
386	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	4.3	5
385	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	11	119
384	Negative effect of vitamin D on kidney function: a Mendelian randomization study. *Nephrology Dialysis Transplantation*, **2018**, 33, 2139-2145	4.3	4
383	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	15.7	48
382	modifies -induced kidney disease risk. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 3446-3451	11.5	31
381	West African Ancestry and Nocturnal Blood Pressure in African Americans: The Jackson Heart Study. *American Journal of Hypertension*, **2018**, 31, 706-714	2.3	2
380	Phenotypic Consequences of a Genetic Predisposition to Enhanced Nitric Oxide Signaling. *Circulation*, **2018**, 137, 222-232	16.7	53
379	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	36.3	950
378	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. *Nature Communications*, **2018**, 9, 2904	17.4	39
377	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. *Nature Communications*, **2018**, 9, 2606	17.4	53
376	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. *Genome Biology*, **2018**, 19, 87	18.3	25
375	An Exome-wide Association Study for Type 2 Diabetes-Attributed End-Stage Kidney Disease in African Americans. *Kidney International Reports*, **2018**, 3, 867-878	4.1	9

374	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. *Nature Communications*, **2018**, 9, 3391	17.4	90
373	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. *Nature Communications*, **2018**, 9, 2976	17.4	45
372	Common β-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. *PLoS Genetics*, **2018**, 14, e1007293	6	25
371	Weighted functional linear regression models for gene-based association analysis. *PLoS ONE*, **2018**, 13, e0190486	3.7	4
370	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*, **2018**, 3, 4	4.8	16
369	Epigenetic clock for skin and blood cells applied to Hutchinson Gilford Progeria Syndrome and studies. *Aging*, **2018**, 10, 1758-1775	5.6	187
368	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
367	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. *Nature Genetics*, **2018**, 50, 524-537	36.3	536
366	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	2.4	15
365	An epigenetic biomarker of aging for lifespan and healthspan. *Aging*, **2018**, 10, 573-591	5.6	658
364	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. *Nature Communications*, **2018**, 9, 5141	17.4	64
363	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	5.2	14
362	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	11	151
361	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
360	Prevalence and correlates of obstructive sleep apnea among African Americans: the Jackson Heart Sleep Study. *Sleep*, **2018**, 41,	1.1	40
359	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	3.7	2
358	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. *Nature Genetics*, **2018**, 50, 834-848	36.3	135
357	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. *Circulation Genomic and Precision Medicine*, **2018**, 11, e002037	5.2	11

356	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. *Nature Communications*, **2018**, 9, 2098	17.4	254
355	Cross-ancestry genome-wide association analysis of corneal thickness strengthens link between complex and Mendelian eye diseases. *Nature Communications*, **2018**, 9, 1864	17.4	37
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33	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*,3, 4	4.8	6

32	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*,3, 4	4.8	1
31	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals		4
30	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries		1
29	Discovering patterns of pleiotropy in genome-wide association studies		1
28	Novel genetic determinants of telomere length from a trans-ethnic analysis of 109,122 whole genome sequences in TOPMed		1
27	Genome-wide association study of susceptibility to hospitalised respiratory infections. *Wellcome Open Research*,6, 290	4.8	0
26	Beyond power: Multivariate discovery, replication, and interpretation of pleiotropic loci using summary association statistics		8
25	Novel blood pressure locus and gene discovery using GWAS and expression datasets from blood and the kidney		1
24	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes		4
23	Ninety-nine independent genetic loci influencing general cognitive function include genes associated with brain health and structure (N = 280,360)		6
22	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
21	Association of mitochondrial DNA copy number with cardiometabolic diseases in a large cross-sectional study of multiple ancestries		2
20	Genome-wide association studies identify 137 loci for DNA methylation biomarkers of ageing		8
19	Genetic mechanisms of critical illness in Covid-19		51
18	Rare Non-coding Variation Identified by Large Scale Whole Genome Sequencing Reveals Unexplained Heritability of Type 2 Diabetes		2
17	Rare coding variants in 35 genes associate with circulating lipid levels a multi-ancestry analysis of 170,000 exomes		2
16	New genetic signals for lung function highlight pathways and pleiotropy, and chronic obstructive pulmonary disease associations across multiple ancestries		5
15	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution		1

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13	Genetic discovery and translational decision support from exome sequencing of 20,791 type 2 diabetes cases and 24,440 controls from five ancestries	2
12	Global variability of the human IgG glycome	2
11	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program	68
10	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease	4
9	Associations of "relative corticosterone deficiency" with genetic variation in CYP17A1 and metabolic syndrome features	1
8	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	2
7	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation	4
6	Using genetic variation to disentangle the complex relationship between food intake and health outcomes	6
5	Genomic analyses for age at menarche identify 389 independent signals and indicate BMI-independent effects of puberty timing on cancer susceptibility	1
4	Within-sibship GWAS improve estimates of direct genetic effects	14
3	Large-scale genome-wide association study of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits	2
2	Whole genome sequencing identifies multiple loci for critical illness caused by COVID-19	2
1	Genetics and the Origins of the British Population	1