

# James G Wilson

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/359796/publications.pdf>

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  | Genome-Wide Association Study of NAFLD Using Electronic Health Records. <i>Hepatology Communications</i> , 2022, 6, 297-308.   | 4.3  | 33        |
| 2  | Genome-wide analysis identifies gallstone-susceptibility loci including genes regulating gastrointestinal motility. <i>Hepatology</i> , 2022, 75, 1081-1094.   | 7.3  | 12        |
| 3  | Whole Genome Sequence Analysis of the Plasma Proteome in Black Adults Provides Novel Insights Into Cardiovascular Disease. <i>Circulation</i> , 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. <i>Human Molecular Genetics</i> , 2022, 31, 1545-1559.                                  | 2.9  | 11        |
| 5  | Mendelian randomization of genetically independent aging phenotypes identifies LPA and VCAM1 as biological targets for human aging. <i>Nature Aging</i> , 2022, 2, 19-30.  | 11.6 | 17        |
| 6  | A multi-omics study of circulating phospholipid markers of blood pressure. <i>Scientific Reports</i> , 2022, 12, 574.  | 3.3  | 10        |
| 7  | 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        |
| 8  | A catalogue of omics biological ageing clocks reveals substantial commonality and associations with disease risk. <i>Aging</i> , 2022, 14, 623-659.  | 3.1  | 22        |
| 9  | Rare coding variants in 35 genes associate with circulating lipid levels—A multi-ancestry analysis of 170,000 exomes. <i>American Journal of Human Genetics</i> , 2022, 109, 81-96.  | 6.2  | 24        |
| 10 | Ancient DNA at the edge of the world: Continental immigration and the persistence of Neolithic male lineages in Bronze Age Orkney. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, . | 7.1  | 12        |
| 11 | Meta-GWAS Reveals Novel Genetic Variants Associated with Urinary Excretion of Uromodulin. <i>Journal of the American Society of Nephrology: JASN</i> , 2022, 33, 511-529.  | 6.1  | 14        |
| 12 | Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus. <i>Nature Communications</i> , 2022, 13, 1222.   | 12.8 | 5         |
| 13 | Genetic regulation of post-translational modification of two distinct proteins. <i>Nature Communications</i> , 2022, 13, 1586.   | 12.8 | 19        |
| 14 | Genetic and phenotypic links between obesity and extracellular vesicles. <i>Human Molecular Genetics</i> , 2022, 31, 3643-3651.  | 2.9  | 2         |
| 15 | Whole-genome sequencing reveals host factors underlying critical COVID-19. <i>Nature</i> , 2022, 607, 97-103.  | 27.8 | 174       |
| 16 | Understanding the complex genetic architecture connecting rheumatoid arthritis, osteoporosis and inflammation: discovering causal pathways. <i>Human Molecular Genetics</i> , 2022, , .  | 2.9  | 3         |
| 17 | Polygenic transcriptome risk scores for COPD and lung function improve cross-ethnic portability of prediction in the NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2022, 109, 857-870.                               | 6.2  | 7         |
| 18 | Genetic Landscape of the ACE2 Coronavirus Receptor. <i>Circulation</i> , 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. <i>Medicine and Science in Sports and Exercise</i> , 2022, 54, 1252-1260.   | 0.4  | 3         |
| 20 | Serum metabolomic profiles associated with subclinical and clinical cardiovascular phenotypes in people with type 2 diabetes. <i>Cardiovascular Diabetology</i> , 2022, 21, 62.   | 6.8  | 6         |
| 21 | 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       |
| 22 | 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       |
| 23 | Gene-based whole genome sequencing meta-analysis of 250 circulating proteins in three isolated European populations. <i>Molecular Metabolism</i> , 2022, 61, 101509.  | 6.5  | 3         |
| 24 | Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits. <i>Nature Communications</i> , 2022, 13, 2743.   | 12.8 | 22        |
| 25 | Using genetic variation to disentangle the complex relationship between food intake and health outcomes. <i>PLoS Genetics</i> , 2022, 18, e1010162.   | 3.5  | 12        |
| 26 | Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022, 5, .  | 4.4  | 17        |
| 27 | Limited Effect of Y Chromosome Variation on Coronary Artery Disease and Mortality in UK Biobank—Brief Report. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2022, 42, 1198-1206.  | 2.4  | 4         |
| 28 | Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. <i>Kidney International</i> , 2021, 99, 926-939.   | 5.2  | 42        |
| 29 | Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, 24.  | 12.8 | 87        |
| 30 | Nontrivial Replication of Loci Detected by Multi-Trait Methods. <i>Frontiers in Genetics</i> , 2021, 12, 627989.  | 2.3  | 4         |
| 31 | Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299.   | 27.8 | 1,069     |
| 32 | Metabolomic Markers of Southern Dietary Patterns in the Jackson Heart Study. <i>Molecular Nutrition and Food Research</i> , 2021, 65, 2000796.  | 3.3  | 4         |
| 33 | Multivariate genome-wide analysis of immunoglobulin G N-glycosylation identifies new loci pleiotropic with immune function. <i>Human Molecular Genetics</i> , 2021, 30, 1259-1270.  | 2.9  | 8         |
| 34 | Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. <i>American Journal of Human Genetics</i> , 2021, 108, 564-582.  | 6.2  | 18        |
| 35 | Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. <i>Nature Communications</i> , 2021, 12, 2182.   | 12.8 | 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. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003191. | 3.6  | 7         |

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|----|---|------|-----------|
| 37 | Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. <i>Aging Cell</i> , 2021, 20, e13366.  | 6.7  | 72        |
| 38 | The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.  | 21.4 | 341       |
| 39 | Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.   | 8.8  | 90        |
| 40 | Contribution of common risk variants to multiple sclerosis in Orkney and Shetland. <i>European Journal of Human Genetics</i> , 2021, 29, 1701-1709.   | 2.8  | 6         |
| 41 | Retinal arteriolar tortuosity and fractal dimension are associated with long-term cardiovascular outcomes in people with type 2 diabetes. <i>Diabetologia</i> , 2021, 64, 2215-2227.  | 6.3  | 14        |
| 42 | Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. <i>Nature Communications</i> , 2021, 12, 3505.   | 12.8 | 49        |
| 43 | Evaluation of Shared Genetic Susceptibility to High and Low Myopia and Hyperopia. <i>JAMA Ophthalmology</i> , 2021, 139, 601.   | 2.5  | 22        |
| 44 | Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals. <i>American Journal of Human Genetics</i> , 2021, 108, 1350-1355.   | 6.2  | 72        |
| 45 | Associations between everyday discrimination and sleep quality and duration among African-Americans over time in the Jackson Heart Study. <i>Sleep</i> , 2021, 44, .  | 1.1  | 13        |
| 46 | APOL1, Sickle Cell Trait, and CKD in the Jackson Heart Study. <i>Kidney Medicine</i> , 2021, 3, 962-973.e1.   | 2.0  | 2         |
| 47 | Multiethnic Genome-Wide Association Study of Subclinical Atherosclerosis in Individuals With Type 2 Diabetes. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003258.  | 3.6  | 4         |
| 48 | Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.   | 27.8 | 183       |
| 49 | Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. <i>Genome Medicine</i> , 2021, 13, 136.   | 8.2  | 16        |
| 50 | Presence and transmission of mitochondrial heteroplasmic mutations in human populations of European and African ancestry. <i>Mitochondrion</i> , 2021, 60, 33-42.   | 3.4  | 6         |
| 51 | Genome-wide methylation data improves dissection of the effect of smoking on body mass index. <i>PLoS Genetics</i> , 2021, 17, e1009750.  | 3.5  | 7         |
| 52 | Association of Sickle Cell Trait With Incidence of Coronary Heart Disease Among African American Individuals. <i>JAMA Network Open</i> , 2021, 4, e2030435.   | 5.9  | 5         |
| 53 | Metabolomic Profiles and Heart Failure Risk in Black Adults: Insights From the Jackson Heart Study. <i>Circulation: Heart Failure</i> , 2021, 14, e007275.  | 3.9  | 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. <i>Journal of Human Genetics</i> , 2021, 66, 625-636. | 2.3  | 40        |

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|----|--|------|-----------|
| 55 | Genetic mechanisms of critical illness in COVID-19. <i>Nature</i> , 2021, 591, 92-98.  | 27.8 | 1,014     |
| 56 | Association of mitochondrial DNA copy number with cardiometabolic diseases. <i>Cell Genomics</i> , 2021, 1, 100006.  | 6.5  | 26        |
| 57 | A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. <i>Nature Genetics</i> , 2021, 53, 1504-1516.                                  | 21.4 | 69        |
| 58 | Inbreeding, native American ancestry and child mortality: Linking human selection and paediatric medicine. <i>Human Molecular Genetics</i> , 2021, , .   | 2.9  | 1         |
| 59 | SARS-CoV-2 susceptibility and COVID-19 disease severity are associated with genetic variants affecting gene expression in a variety of tissues. <i>Cell Reports</i> , 2021, 37, 110020.                              | 6.4  | 25        |
| 60 | APOL1 renal risk variants are associated with obesity and body composition in African ancestry adults. <i>Medicine (United States)</i> , 2021, 100, e27785.  | 1.0  | 6         |
| 61 | Mapping the serum proteome to neurological diseases using whole genome sequencing. <i>Nature Communications</i> , 2021, 12, 7042.  | 12.8 | 29        |
| 62 | Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. <i>EBioMedicine</i> , 2021, 74, 103730.  | 6.1  | 5         |
| 63 | The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.   | 27.8 | 353       |
| 64 | Coffee Consumption and Kidney Function: A Mendelian Randomization Study. <i>American Journal of Kidney Diseases</i> , 2020, 75, 753-761.   | 1.9  | 56        |
| 65 | Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. <i>Nature Communications</i> , 2020, 11, 5182.  | 12.8 | 32        |
| 66 | Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020, 2, 1135-1148.   | 11.9 | 327       |
| 67 | Glycosylation Alterations in Multiple Sclerosis Show Increased Proinflammatory Potential. <i>Biomedicines</i> , 2020, 8, 410.  | 3.2  | 26        |
| 68 | Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020, 586, 763-768.   | 27.8 | 376       |
| 69 | Coagulation factor VIII: Relationship to cardiovascular disease risk and whole genome sequence and epigenome-wide analysis in African Americans. <i>Journal of Thrombosis and Haemostasis</i> , 2020, 18, 1335-1347. | 3.8  | 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. <i>BMJ Open</i> , 2020, 10, e034299.         | 1.9  | 4         |
| 71 | Multivariate genomic scan implicates novel loci and haem metabolism in human ageing. <i>Nature Communications</i> , 2020, 11, 3570.  | 12.8 | 84        |
| 72 | Autozygosity influences cardiometabolic disease-associated traits in the AWI-Gen sub-Saharan African study. <i>Nature Communications</i> , 2020, 11, 5754.   | 12.8 | 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. <i>Stroke</i> , 2020, 51, 2454-2463.   | 2.0  | 26        |
| 74 | Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. <i>Lancet Respiratory Medicine</i> , 2020, 8, 696-708.   | 10.7 | 69        |
| 75 | Circulating testican-2 is a podocyte-derived marker of kidney health. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25026-25035.   | 7.1  | 19        |
| 76 | Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. <i>Diabetes</i> , 2020, 69, 2806-2818.   | 0.6  | 26        |
| 77 | 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       |
| 78 | Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. <i>Nature Communications</i> , 2020, 11, 6417.   | 12.8 | 39        |
| 79 | Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. <i>PLoS ONE</i> , 2020, 15, e0230815.   | 2.5  | 10        |
| 80 | The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020, 581, 434-443.  | 27.8 | 6,140     |
| 81 | Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.  | 12.8 | 59        |
| 82 | Prioritization of causal genes for coronary artery disease based on cumulative evidence from experimental and in silico studies. <i>Scientific Reports</i> , 2020, 10, 10486.  | 3.3  | 22        |
| 83 | Linking protein to phenotype with Mendelian Randomization detects 38 proteins with causal roles in human diseases and traits. <i>PLoS Genetics</i> , 2020, 16, e1008785.   | 3.5  | 29        |
| 84 | Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. <i>Science Advances</i> , 2020, 6, eaax0301.  | 10.3 | 90        |
| 85 | De novo mutations across 1,465 diverse genomes reveal mutational insights and reductions in the Amish founder population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 2560-2569. | 7.1  | 71        |
| 86 | Association of HLA-DRB1*09:01 with tlgE levels among African-ancestry individuals with asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 146, 147-155.   | 2.9  | 14        |
| 87 | Interferon gamma-induced protein 10 (IP-10) and cardiovascular disease in African Americans. <i>PLoS ONE</i> , 2020, 15, e0231013.   | 2.5  | 12        |
| 88 | A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. <i>PLoS Genetics</i> , 2020, 16, e1008629.   | 3.5  | 101       |
| 89 | Variants associated with HHIP expression have sex-differential effects on lung function. <i>Wellcome Open Research</i> , 2020, 5, 111.   | 1.8  | 3         |
| 90 | The Association of <i>ARMC5</i> with the Renin-Angiotensin-Aldosterone System, Blood Pressure, and Glycemia in African Americans. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, 2625-2633.                        | 3.6  | 9         |

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|-----|--|------|-----------|
| 91  | Global variability of the human IgG glycome. Aging, 2020, 12, 15222-15259.   | 3.1  | 37        |
| 92  | Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.   | 1.8  | 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-by-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. | 2.0  | 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.  | 2.4  | 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, .   | 1.1  | 34        |
| 100 | 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         |
| 101 | An actionable KCNH2 Long QT Syndrome variant detected by sequence and haplotype analysis in a population research cohort. Scientific Reports, 2019, 9, 10964.                                    | 3.3  | 17        |
| 102 | Lipidomics, Atrial Conduction, and Body Mass Index. Circulation Genomic and Precision Medicine, 2019, 12, e002384.   | 3.6  | 9         |
| 103 | New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.   | 12.0 | 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.         | 2.8  | 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.     | 2.4  | 23        |
| 106 | The genetic underpinnings of obesity. Current Opinion in Physiology, 2019, 12, 57-64.  | 1.8  | 0         |
| 107 | Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.   | 4.7  | 38        |
| 108 | Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.  | 12.8 | 84        |

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|-----|--|------|-----------|
| 109 | Sequencing Analysis at 8p23 Identifies Multiple Rare Variants in DLC1 Associated with Sleep-Related Oxyhemoglobin Saturation Level. <i>American Journal of Human Genetics</i> , 2019, 105, 1057-1068.              | 6.2  | 10        |
| 110 | 0336 Associations of Psychosocial Factors, Short Sleep and Insomnia, and Hypertension Control among African-Americans: the Jackson Heart Sleep Study (JHSS). <i>Sleep</i> , 2019, 42, A137-A138.                   | 1.1  | 2         |
| 111 | The genetic landscape of Scotland and the Isles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19064-19070.  | 7.1  | 24        |
| 112 | Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.   | 21.4 | 251       |
| 113 | Maternal relationships within an Iron Age burial at the High Pasture Cave, Isle of Skye, Scotland. <i>Journal of Archaeological Science</i> , 2019, 110, 104978.   | 2.4  | 6         |
| 114 | Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. <i>Nature Communications</i> , 2019, 10, 357.   | 12.8 | 30        |
| 115 | Genome-wide association meta-analysis of 30,000 samples identifies seven novel loci for quantitative ECG traits. <i>European Journal of Human Genetics</i> , 2019, 27, 952-962.                                    | 2.8  | 29        |
| 116 | Association Between Sleep Apnea and Blood Pressure Control Among Blacks. <i>Circulation</i> , 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. <i>Human Genetics</i> , 2019, 138, 199-210.             | 3.8  | 29        |
| 118 | Genetic Correlations Between Diabetes and Glaucoma: An Analysis of Continuous and Dichotomous Phenotypes. <i>American Journal of Ophthalmology</i> , 2019, 206, 245-255.   | 3.3  | 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. <i>Journal of Neurology</i> , 2019, 266, 2376-2386.  | 3.6  | 22        |
| 120 | Genomics-First Evaluation of Heart Disease Associated With Titin-Truncating Variants. <i>Circulation</i> , 2019, 140, 42-54.   | 1.6  | 97        |
| 121 | Association of Dimethylguanidino Valeric Acid With Partial Resistance to Metabolic Health Benefits of Regular Exercise. <i>JAMA Cardiology</i> , 2019, 4, 636.   | 6.1  | 37        |
| 122 | Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. <i>American Journal of Human Genetics</i> , 2019, 105, 15-28.   | 6.2  | 21        |
| 123 | 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       |
| 124 | Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019, 570, 71-76.   | 27.8 | 248       |
| 125 | Rare Protein-Truncating Variants in <i>APOB</i> , Lower Low-Density Lipoprotein Cholesterol, and Protection Against Coronary Heart Disease. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, e002376. | 3.6  | 57        |
| 126 | Genome-wide association study identifies novel loci for type 2 diabetes-attributed end-stage kidney disease in African Americans. <i>Human Genomics</i> , 2019, 13, 21.  | 2.9  | 32        |



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|-----|---|------|-----------|
| 127 | DNA methylation GrimAge strongly predicts lifespan and healthspan. <i>Aging</i> , 2019, 11, 303-327.  | 3.1  | 1,128     |
| 128 | Associations of variants in the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. <i>PLoS Genetics</i> , 2019, 15, e1007739.   | 3.5  | 28        |
| 129 | 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       |
| 130 | Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. <i>Nature Communications</i> , 2019, 10, 1383.  | 12.8 | 37        |
| 131 | You Are Just Now Telling Us About This? African American Perspectives of Testing for Genetic Susceptibility to Kidney Disease. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 526-530.  | 6.1  | 31        |
| 132 | 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       |
| 133 | Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. <i>Nature Communications</i> , 2019, 10, 880.   | 12.8 | 71        |
| 134 | Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.   | 21.4 | 89        |
| 135 | APOL1 Kidney Risk Variants and Cardiovascular Disease: An Individual Participant Data Meta-Analysis. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 2027-2036.  | 6.1  | 26        |
| 136 | Increased ultra-rare variant load in an isolated Scottish population impacts exonic and regulatory regions. <i>PLoS Genetics</i> , 2019, 15, e1008480.  | 3.5  | 17        |
| 137 | Multi-trait genome-wide association study identifies new loci associated with optic disc parameters. <i>Communications Biology</i> , 2019, 2, 435.  | 4.4  | 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. <i>PLoS Genetics</i> , 2019, 15, e1008500. | 3.5  | 203       |
| 139 | Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. <i>American Journal of Human Genetics</i> , 2019, 104, 112-138.   | 6.2  | 106       |
| 140 | DNA Sequence Variation in <i>ACVR1C</i> Encoding the Activin Receptor-Like Kinase 7 Influences Body Fat Distribution and Protects Against Type 2 Diabetes. <i>Diabetes</i> , 2019, 68, 226-234.   | 0.6  | 31        |
| 141 | Association of psychosocial factors with leukocyte telomere length among African Americans in the Jackson Heart Study. <i>Stress and Health</i> , 2019, 35, 138-145.  | 2.6  | 5         |
| 142 | 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       |
| 143 | Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. <i>Circulation</i> , 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. <i>American Journal of Human Genetics</i> , 2019, 104, 260-274.  | 6.2  | 103       |

| #   | ARTICLE   | IF   | CITATIONS |
|-----|---|------|-----------|
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