# Hugh Christian Watkins

List of Publications by Year
in descending order



| 170 | 48,781 | 9234 74 | 5519 163 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 179 | 179 | 179 | 65122 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Analysis of protein-coding genetic variation in 60,706 humans. Nature, 2016, 536, 285-291. | 13.7 | 9,051 |
| 2 | Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206. | 13.7 | 3,823 |
| 3 | 2014 ESC Guidelines on diagnosis and management of hypertrophic cardiomyopathy. European Heart Journal, 2014, 35, 2733-2779. | 1.0 | 3,469 |
| 4 | Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948. | 9.4 | 2,634 |
| 5 | A comprehensive 1000 Genomesâ€"based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130. | 9.4 | 2,054 |
| 6 | New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116. | 9.4 | 1,982 |
| 7 | Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186. | 9.4 | 1,818 |
| 8 | Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838. | 13.7 | 1,789 |
| 9 | New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196. | 13.7 | 1,328 |
| 10 | HRS/EHRA Expert Consensus Statement on the State of Genetic Testing for the Channelopathies and Cardiomyopathies. Heart Rhythm, 2011, 8, 1308-1339. | 0.3 | 995 |
| 11 | 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 |
| 12 | Diagnostic Yield and Clinical Utility of Sequencing Familial Hypercholesterolemia Genes in Patients With Severe Hypercholesterolemia. Journal of the American College of Cardiology, 2016, 67, 2578-2589. | 1.2 | 723 |
| 13 | Reassessment of Mendelian gene pathogenicity using 7,855 cardiomyopathy cases and 60,706 reference samples. Genetics in Medicine, 2017, 19, 192-203. | 1.1 | 585 |
| 14 | Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106. | 13.7 | 581 |
| 15 | Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512. | 9.4 | 578 |
| 16 | Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391. | 9.4 | 571 |
| 17 | Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550. | 1.0 | 567 |
| 18 | Functional Polymorphism in the Regulatory Region of Gelatinase B Gene in Relation to Severity of Coronary Atherosclerosis. Circulation, 1999, 99, 1788-1794. | 1.6 | 564 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Genomic Risk Prediction of Coronary Artery Disease in 480,000 Adults. Journal of the American College of Cardiology, 2018, 72, 1883-1893. | 1.2 | 557 |
| 20 | Mutations in the cardiac myosin binding proteinâ€“C gene on chromosome 11 cause familial hypertrophic cardiomyopathy. Nature Genetics, 1995, 11, 434-437. | 9.4 | 540 |
| 21 | Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164. | 3.0 | 528 |
| 22 | Susceptibility to coronary artery disease and diabetes is encoded by distinct, tightly linked SNPs in the ANRIL locus on chromosome 9p. Human Molecular Genetics, 2008, 17, 806-814. | 1.4 | 472 |
| 23 | Inherited Cardiomyopathies. New England Journal of Medicine, 2011, 364, 1643-1656. | 13.9 | 430 |
| 24 | The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184. | 9.4 | 362 |
| 25 | Hypertrophic cardiomyopathy due to sarcomeric gene mutations is characterized by impaired energy metabolism irrespective of the degree of hypertrophy. Journal of the American College of Cardiology, 2003, 41, 1776-1782. | 1.2 | 359 |
| 26 | The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679. | 13.7 | 353 |
| 27 | Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494. | 1.5 | 351 |
| 28 | Distinct genetic architectures for syndromic and nonsyndromic congenital heart defects identified by exome sequencing. Nature Genetics, 2016, 48, 1060-1065. | 9.4 | 351 |
| 29 | 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. PLoS Medicine, 2017, 14, e1002383. | 3.9 | 341 |
| 30 | The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860. | 9.4 | 341 |
| 31 | Whole-genome sequencing of patients with rare diseases in a national health system. Nature, 2020, 583, 96-102. | 13.7 | 338 |
| 32 | The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378. | 1.5 | 331 |
| 33 | Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. Nature Genetics, 2015, 47, 717-726. | 9.4 | 310 |
| 34 | Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. American Journal of Human Genetics, 2014, 94, 223-232. | 2.6 | 287 |
| 35 | Adaptation and validation of the ACMG/AMP variant classification framework for MYH7-associated inherited cardiomyopathies: recommendations by ClinGenâ€™s Inherited Cardiomyopathy Expert Panel. Genetics in Medicine, 2018, 20, 351-359. | 1.1 | 283 |
| 36 | Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119. | 9.4 | 260 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | Severe disease expression of cardiac troponin C and T mutations in patients with idiopathic dilated cardiomyopathy. Journal of the American College of Cardiology, 2004, 44, 2033-2040. | 1.2 | 216 |
| 38 | Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836. | 1.2 | 214 |
| 39 | Evidence From Human Myectomy Samples That MYBPC3 Mutations Cause Hypertrophic Cardiomyopathy Through Haploinsufficiency. Circulation Research, 2009, 105, 219-222. | 2.0 | 210 |
| 40 | Dilated and Hypertrophic Cardiomyopathy Mutations in Troponin and Î±-Tropomyosin Have Opposing Effects on the Calcium Affinity of Cardiac Thin Filaments. Circulation Research, 2007, 101, 1266-1273. | 2.0 | 194 |
| 41 | Phenotypic Characterization of GeneticallyÂLowered Human Lipoprotein(a) Levels. Journal of the American College of Cardiology, 2016, 68, 2761-2772. | 1.2 | 186 |
| 42 | Myosin Sequestration Regulates Sarcomere Function, Cardiomyocyte Energetics, and Metabolism, Informing the Pathogenesis of Hypertrophic Cardiomyopathy. Circulation, 2020, 141, 828-842. | 1.6 | 181 |
| 43 | Meta-analysis of gene-level tests for rare variant association. Nature Genetics, 2014, 46, 200-204. | 9.4 | 178 |
| 44 | Germline selection shapes human mitochondrial DNA diversity. Science, 2019, 364, . | 6.0 | 178 |
| 45 | Genetic susceptibility to coronary artery disease: from promise to progress. Nature Reviews Genetics, 2006, 7, 163-173. | 7.7 | 176 |
| 46 | Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897. | 5.8 | 173 |
| 47 | Common genetic variants and modifiable risk factors underpin hypertrophic cardiomyopathy susceptibility and expressivity. Nature Genetics, 2021, 53, 135-142. | 9.4 | 165 |
| 48 | Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360. | 2.6 | 158 |
| 49 | Shared genetic pathways contribute to risk of hypertrophic and dilated cardiomyopathies with opposite directions of effect. Nature Genetics, 2021, 53, 128-134. | 9.4 | 155 |
| 50 | Distinct Subgroups in Hypertrophic Cardiomyopathy in the NHLBI HCM Registry. Journal of the American College of Cardiology, 2019, 74, 2333-2345. | 1.2 | 152 |
| 51 | Association of Rare and Common Variation in the Lipoprotein Lipase Gene With Coronary Artery Disease. JAMA - Journal of the American Medical Association, 2017, 317, 937. | 3.8 | 148 |
| 52 | Reevaluating the Genetic Contribution of Monogenic Dilated Cardiomyopathy. Circulation, 2020, 141, 387-398. | 1.6 | 148 |
| 53 | Rare Variants in NR2F2 Cause Congenital Heart Defects in Humans. American Journal of Human Genetics, 2014, 94, 574-585. | 2.6 | 146 |
| 54 | Defining the genetic architecture of hypertrophic cardiomyopathy: re-evaluating the role of non-sarcomeric genes. European Heart Journal, 2017, 38, ehw603. | 1.0 | 142 |

| # | Article | IF | Citations |
|---|---|---|---|
| 55 | Altered Regulatory Properties of Human Cardiac Troponin I Mutants That Cause Hypertrophic Cardiomyopathy. Journal of Biological Chemistry, 2000, 275, 22069-22074. | 1.6 | 136 |
| 56 | Dilated Cardiomyopathy Mutations in Three Thin Filament Regulatory Proteins Result in a Common Functional Phenotype. Journal of Biological Chemistry, 2005, 280, 28498-28506. | 1.6 | 133 |
| 57 | Hypertrophic cardiomyopathy mutations in MYBPC3 dysregulate myosin. Science Translational Medicine, 2019, 11, . | 5.8 | 133 |
| 58 | Alterations in Thin Filament Regulation Induced by a Human Cardiac Troponin T Mutant That Causes Dilated Cardiomyopathy Are Distinct from Those Induced by Troponin T Mutants That Cause Hypertrophic Cardiomyopathy. Journal of Biological Chemistry, 2002, 277, 40710-40716. | 1.6 | 125 |
| 59 | Hypertrophic Cardiomyopathy Registry: The rationale and design of an international, observational study of hypertrophic cardiomyopathy. American Heart Journal, 2015, 170, 223-230. | 1.2 | 123 |
| 60 | Effect of Selective Heart Rate Slowing in Heart Failure With Preserved Ejection Fraction. Circulation, 2015, 132, 1719-1725. | 1.6 | 119 |
| 61 | Stakeholder views on secondary findings in whole-genome and whole-exome sequencing: a systematic review of quantitative and qualitative studies. Genetics in Medicine, 2017, 19, 283-293. | 1.1 | 119 |
| 62 | Secretory Phospholipase A2-IIA and Cardiovascular Disease. Journal of the American College of Cardiology, 2013, 62, 1966-1976. | 1.2 | 115 |
| 63 | Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648. | 9.4 | 112 |
| 64 | Gene-Age Interactions in Blood Pressure Regulation: A Large-Scale Investigation with the CHARGE, Global BPgen, and ICBP Consortia. American Journal of Human Genetics, 2014, 95, 24-38. | 2.6 | 109 |
| 65 | Familial Dilated Cardiomyopathy Caused by an Alpha-Tropomyosin Mutation. Journal of the American College of Cardiology, 2010, 55, 320-329. | 1.2 | 104 |
| 66 | A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. PLoS Genetics, 2020, 16, e1008629. | 1.5 | 101 |
| 67 | Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. International Journal of Epidemiology, 2016, 45, 1927-1937. | 0.9 | 94 |
| 68 | Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166. | 1.1 | 94 |
| 69 | Progression of myocardial fibrosis in hypertrophic cardiomyopathy: mechanisms and clinical implications. European Heart Journal Cardiovascular Imaging, 2019, 20, 157-167. | 0.5 | 92 |
| 70 | Quantitative approaches to variant classification increase the yield and precision of genetic testing in Mendelian diseases: the case of hypertrophic cardiomyopathy. Genome Medicine, 2019, 11, 5. | 3.6 | 90 |
| 71 | Identification of Myocardial Disarray inÂPatients With HypertrophicÂCardiomyopathy and Ventricular Arrhythmias. Journal of the American College of Cardiology, 2019, 73, 2493-2502. | 1.2 | 88 |
| 72 | Chronic Activation of Î³2 AMPK Induces Obesity and Reduces Î² Cell Function. Cell Metabolism, 2016, 23, 821-836. | 7.2 | 87 |

| # | Article | IF | Citations |
|---|---|---|---|
| 73 | Phenotypic Consequences of a Genetic Predisposition to Enhanced Nitric Oxide Signaling. Circulation, 2018, 137, 222-232. | 1.6 | 87 |
| 74 | Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24. | 5.8 | 87 |
| 75 | Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054. | 1.6 | 85 |
| 76 | Identification and Functional Characterization of Cardiac Troponin I As a Novel Disease Gene in Autosomal Dominant Dilated Cardiomyopathy. Circulation Research, 2009, 105, 375-382. | 2.0 | 81 |
| 77 | Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. Nature Communications, 2018, 9, 1613. | 5.8 | 78 |
| 78 | A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357. | 5.8 | 74 |
| 79 | A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370. | 1.4 | 73 |
| 80 | Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312. | 9.4 | 66 |
| 81 | The Effect of Mutations in Î±-Tropomyosin (E40K and E54K) That Cause Familial Dilated Cardiomyopathy on the Regulatory Mechanism of Cardiac Muscle Thin Filaments. Journal of Biological Chemistry, 2007, 282, 13487-13497. | 1.6 | 65 |
| 82 | Pre-symptomatic genetic testing for inherited cardiac conditions: a qualitative exploration of psychosocial and ethical implications. European Journal of Human Genetics, 2014, 22, 88-93. | 1.4 | 65 |
| 83 | Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752. | 1.1 | 64 |
| 84 | Hypertrophic cardiomyopathy mutations increase myofilament Ca2+ buffering, alter intracellular Ca2+ handling, and stimulate Ca2+-dependent signaling. Journal of Biological Chemistry, 2018, 293, 10487-10499. | 1.6 | 58 |
| 85 | Genetic Risk Score for CoronaryÂDiseaseÂIdentifies Predispositions to Cardiovascular andÂNoncardiovascular Diseases. Journal of the American College of Cardiology, 2019, 73, 2932-2942. | 1.2 | 58 |
| 86 | Distinct ECG Phenotypes Identified in Hypertrophic Cardiomyopathy Using Machine Learning Associate With Arrhythmic Risk Markers. Frontiers in Physiology, 2018, 9, 213. | 1.3 | 57 |
| 87 | 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 |
| 88 | â€œNot pathogenic until proven otherwiseâ€• perspectives of UK clinical genomics professionals toward secondary findings in context of a Genomic Medicine Multidisciplinary Team and the 100,000 Genomes Project. Genetics in Medicine, 2018, 20, 320-328. | 1.1 | 56 |
| 89 | Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29. | 0.6 | 55 |
| 90 | A De Novo Mutation in Î±-Tropomyosin That Causes Hypertrophic Cardiomyopathy. Circulation, 1995, 91, 2302-2305. | 1.6 | 53 |

| # | Article | IF | Citations |
|---|---|---|---|
| 91 | HspB1 phosphorylation regulates its intramolecular dynamics and mechanosensitive molecular chaperone interaction with filamin C. Science Advances, 2019, 5, eaav8421. | 4.7 | 52 |
| 92 | Human stromelysin gene promoter activity is modulated by transcription factor ZBP-89. FEBS Letters, 1999, 450, 268-272. | 1.3 | 51 |
| 93 | Toward Replacing Late Gadolinium Enhancement With Artificial Intelligence Virtual Native Enhancement for Gadolinium-Free Cardiovascular Magnetic Resonance Tissue Characterization in Hypertrophic Cardiomyopathy. Circulation, 2021, 144, 589-599. | 1.6 | 48 |
| 94 | A Common LPA Null Allele Associates With Lower Lipoprotein(a) Levels and Coronary Artery Disease Risk. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 2095-2099. | 1.1 | 45 |
| 95 | Genetic variation in CADM2 as a link between psychological traits and obesity. Scientific Reports, 2019, 9, 7339. | 1.6 | 45 |
| 96 | HeterozygousABCG5Gene Deficiency and Risk of Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2020, 13, 417-423. | 1.6 | 45 |
| 97 | Design and rationale of a prospective, collaborative meta-analysis of all randomized controlled trials of angiotensin receptor antagonists in Marfan syndrome, based on individual patient data: A report from the Marfan Treatment Trialists' Collaboration. American Heart Journal, 2015, 169, 605-612. | 1.2 | 44 |
| 98 | Measurement of Myofilament-Localized Calcium Dynamics in Adult Cardiomyocytes and the Effect of Hypertrophic Cardiomyopathy Mutations. Circulation Research, 2019, 124, 1228-1239. | 2.0 | 44 |
| 99 | Analysis of 51 proposed hypertrophic cardiomyopathy genes from genome sequencing data in sarcomere negative cases has negligible diagnostic yield. Genetics in Medicine, 2019, 21, 1576-1584. | 1.1 | 44 |
| 100 | Mammalian Î³2 AMPK regulates intrinsic heart rate. Nature Communications, 2017, 8, 1258. | 5.8 | 43 |
| 101 | Network analysis of coronary artery disease risk genes elucidates disease mechanisms and druggable targets. Scientific Reports, 2018, 8, 3434. | 1.6 | 43 |
| 102 | Mavacamten rescues increased myofilament calcium sensitivity and dysregulation of Ca<sup>2+</sup> flux caused by thin filament hypertrophic cardiomyopathy mutations. American Journal of Physiology - Heart and Circulatory Physiology, 2020, 318, H715-H722. | 1.5 | 42 |
| 103 | Mutation of Fnip1 is associated with B-cell deficiency, cardiomyopathy, and elevated AMPK activity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3706-15. | 3.3 | 39 |
| 104 | Exome sequencing identifies rare variants in multiple genes in atrioventricular septal defect. Genetics in Medicine, 2016, 18, 189-198. | 1.1 | 39 |
| 105 | iASPP, a previously unidentified regulator of desmosomes, prevents arrhythmogenic right ventricular cardiomyopathy (ARVC)-induced sudden death. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E973-E981. | 3.3 | 37 |
| 106 | Association of exome sequences with plasma C-reactive protein levels in >9000 participants. Human Molecular Genetics, 2015, 24, 559-571. | 1.4 | 36 |
| 107 | Common Genetic Determinants of Lung Function, Subclinical Atherosclerosis and Risk of Coronary Artery Disease. PLoS ONE, 2014, 9, e104082. | 1.1 | 36 |
| 108 | Measuring inorganic phosphate and intracellular pH in the healthy and hypertrophic cardiomyopathy hearts by in vivo 7T 31P-cardiovascular magnetic resonance spectroscopy. Journal of Cardiovascular Magnetic Resonance, 2019, 21, 19. | 1.6 | 35 |

| # | Article | IF | Citations |
|---|---|---|---|
| 109 | Genetically modulated educational attainment and coronary disease risk. European Heart Journal, 2019, 40, 2413-2420. | 1.0 | 32 |
| 110 | Time to Think Differently About Sarcomere-Negative Hypertrophic Cardiomyopathy. Circulation, 2021, 143, 2415-2417. | 1.6 | 32 |
| 111 | A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633. | 1.4 | 31 |
| 112 | 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 |
| 113 | Reevaluation of the South Asian MYBPC3 <sup>Î”25bp</sup> Intronic Deletion in Hypertrophic Cardiomyopathy. Circulation Genomic and Precision Medicine, 2020, 13, e002783. | 1.6 | 31 |
| 114 | CalTrack: High-Throughput Automated Calcium Transient Analysis in Cardiomyocytes. Circulation Research, 2021, 129, 326-341. | 2.0 | 31 |
| 115 | Two mutations in troponin I that cause hypertrophic cardiomyopathy have contrasting effects on cardiac muscle contractility. Biochemical Journal, 2002, 362, 443-451. | 1.7 | 30 |
| 116 | Views of rare disease participants in aÂUK whole-genome sequencing study towards secondary findings: a qualitative study. European Journal of Human Genetics, 2018, 26, 652-659. | 1.4 | 30 |
| 117 | Electrocardiogram phenotypes in hypertrophic cardiomyopathy caused by distinct mechanisms: apico-basal repolarization gradients vs. Purkinje-myocardial coupling abnormalities. Europace, 2018, 20, iii102-iii112. | 0.7 | 29 |
| 118 | Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. PLoS ONE, 2017, 12, e0167742. | 1.1 | 29 |
| 119 | Two mutations in troponin I that cause hypertrophic cardiomyopathy have contrasting effects on cardiac muscle contractility. Biochemical Journal, 2002, 362, 443. | 1.7 | 27 |
| 120 | Improvements in ECG accuracy for diagnosis of left ventricular hypertrophy in obesity. Heart, 2016, 102, 1566-1572. | 1.2 | 27 |
| 121 | Neonatal MicroRNA Profile Determines Endothelial Function in Offspring of Hypertensive Pregnancies. Hypertension, 2018, 72, 937-945. | 1.3 | 26 |
| 122 | No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. Scientific Reports, 2016, 6, 35278. | 1.6 | 25 |
| 123 | ImplementationÂof a genomic medicine multi-disciplinary team approach for rare diseaseÂin the clinical setting: a prospective exome sequencingÂcase series. Genome Medicine, 2019, 11, 46. | 3.6 | 25 |
| 124 | Insights from early experience of a Rare Disease Genomic Medicine Multidisciplinary Team: a qualitative study. European Journal of Human Genetics, 2017, 25, 680-686. | 1.4 | 24 |
| 125 | Plasma cytokines and risk of coronary heart disease in the PROCARDIS study. Open Heart, 2018, 5, e000807. | 0.9 | 24 |
| 126 | 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 |

| # | Article | IF | Citations |
|---|---|---|---|
| 127 | A key role for the novel coronary artery disease gene JCAD in atherosclerosis via shear stress mechanotransduction. Cardiovascular Research, 2020, 116, 1863-1874. | 1.8 | 23 |
| 128 | Bi-allelic MCM10 variants associated with immune dysfunction and cardiomyopathy cause telomere shortening. Nature Communications, 2021, 12, 1626. | 5.8 | 22 |
| 129 | Analysis of the Role of Interleukin 6 Receptor Haplotypes in the Regulation of Circulating Levels of Inflammatory Biomarkers and Risk of Coronary Heart Disease. PLoS ONE, 2015, 10, e0119980. | 1.1 | 21 |
| 130 | Differential Gene Expression in Macrophages From Human Atherosclerotic Plaques Shows Convergence on Pathways Implicated by Genome-Wide Association Study Risk Variants. Arteriosclerosis, Thrombosis, and Vascular Biology, 2018, 38, 2718-2730. | 1.1 | 20 |
| 131 | Mutant Muscle LIM Protein C58G causes cardiomyopathy through protein depletion. Journal of Molecular and Cellular Cardiology, 2018, 121, 287-296. | 0.9 | 19 |
| 132 | Maximal Wall Thickness Measurement in Hypertrophic Cardiomyopathy. JACC: Cardiovascular Imaging, 2021, 14, 2123-2134. | 2.3 | 18 |
| 133 | Functional analysis of a gene-edited mouse model to gain insights into the disease mechanisms of a titin missense variant. Basic Research in Cardiology, 2021, 116, 14. | 2.5 | 16 |
| 134 | Provocation Testing and Therapeutic Response in a Newly Described Channelopathy: RyR2 Calcium Release Deficiency Syndrome. Circulation Genomic and Precision Medicine, 2022, 15, CIRCGEN121003589. | 1.6 | 15 |
| 135 | Incremental value of left atrial booster and reservoir strain in predicting atrial fibrillation in patients with hypertrophic cardiomyopathy: a cardiovascular magnetic resonance study. Journal of Cardiovascular Magnetic Resonance, 2021, 23, 109. | 1.6 | 14 |
| 136 | Secondary findings in inherited heart conditions: a genotype-first feasibility study to assess phenotype, behavioural and psychosocial outcomes. European Journal of Human Genetics, 2020, 28, 1486-1496. | 1.4 | 13 |
| 137 | Heritability and family-based GWAS analyses of the N-acyl ethanolamine and ceramide plasma lipidome. Human Molecular Genetics, 2021, 30, 500-513. | 1.4 | 13 |
| 138 | Why does Russia have such high cardiovascular mortality rates? Comparisons of blood-based biomarkers with Norway implicate non-ischaemic cardiac damage. Journal of Epidemiology and Community Health, 2020, 74, jech-2020-213885. | 2.0 | 10 |
| 139 | Dilated Cardiomyopathy and the Desmin Gene. Circulation, 2000, 102, E100-1. | 1.6 | 9 |
| 140 | Lack of genetic support for shared aetiology of Coronary Artery Disease and Late-onset Alzheimerâ€™s disease. Scientific Reports, 2018, 8, 7102. | 1.6 | 9 |
| 141 | Obesity-related ventricular remodelling is exacerbated in dilated and hypertrophic cardiomyopathy. Cardiovascular Diagnosis and Therapy, 2020, 10, 559-567. | 0.7 | 9 |
| 142 | Dilated cardiomyopathy mutations in thin-filament regulatory proteins reduce contractility, suppress systolic Ca2+, and activate NFAT and Akt signaling. American Journal of Physiology - Heart and Circulatory Physiology, 2020, 319, H306-H319. | 1.5 | 9 |
| 143 | No Evidence for Genome-Wide Interactions on Plasma Fibrinogen by Smoking, Alcohol Consumption and Body Mass Index: Results from Meta-Analyses of 80,607 Subjects. PLoS ONE, 2014, 9, e111156. | 1.1 | 8 |
| 144 | Human Genetic Evidence for Involvement of CD137 in Atherosclerosis. Molecular Medicine, 2014, 20, 456-465. | 1.9 | 8 |

| # | Article | IF | Citations |
|---|---|---|---|
| 145 | From Genotype to Phenotype. Circulation Genomic and Precision Medicine, 2018, 11, e002316. | 1.6 | 8 |
| 146 | Manhattan++: displaying genome-wide association summary statistics with multiple annotation layers. BMC Bioinformatics, 2019, 20, 610. | 1.2 | 6 |
| 147 | Heritability of haemodynamics in the ascending aorta. Scientific Reports, 2020, 10, 14356. | 1.6 | 5 |
| 148 | Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. Circulation Genomic and Precision Medicine, 2020, 13, e002769. | 1.6 | 5 |
| 149 | Rationale and design of the African Cardiomyopathy and Myocarditis Registry Program: The IMHOTEP study. International Journal of Cardiology, 2021, 333, 119-126. | 0.8 | 5 |
| 150 | Robust estimates of heritable coronary disease risk in individuals with type 2 diabetes. Genetic Epidemiology, 2022, 46, 51-62. | 0.6 | 5 |
| 151 | Tackling the Achillesâ€™ Heel of Genetic Testing. Science Translational Medicine, 2015, 7, 270fs1. | 5.8 | 4 |
| 152 | Association Between Sarcomeric Variants in Hypertrophic Cardiomyopathy and Myocardial Oxygenation: Insights From a Novel Oxygen-Sensitive Cardiovascular Magnetic Resonance Approach. Circulation, 2021, 144, 1656-1658. | 1.6 | 4 |
| 153 | PHACTR1modulates vascular compliance but not endothelial function: a translational study. Cardiovascular Research, 2023, 119, 599-610. | 1.8 | 4 |
| 154 | Marked variation in heritability estimates of left ventricular mass depending on modality of measurement. Scientific Reports, 2019, 9, 13556. | 1.6 | 3 |
| 155 | Identification of a novel proinsulin-associated SNP and demonstration that proinsulin is unlikely to be a causal factor in subclinical vascular remodelling using Mendelian randomisation. Atherosclerosis, 2017, 266, 196-204. | 0.4 | 3 |
| 156 | Data-driven modelling of mutational hotspots and in silico predictors in hypertrophic cardiomyopathy. Journal of Medical Genetics, 2021, 58, 556-564. | 1.5 | 2 |
| 157 | Response to Letter Regarding Article, â€œThe Effect of Selective Heart Rate Slowing in Heart Failure With Preserved Ejection Fractionâ€. Circulation, 2016, 133, e604. | 1.6 | 1 |
| 158 | Discrepancy Between Pathological Progression and Clinical Stability in a Young Patient With Hypertrophic Cardiomyopathy. Circulation: Cardiovascular Imaging, 2018, 11, e008154. | 1.3 | 1 |
| 159 | Massively Parallel Sequencing of 43 Arrhythmia Genes in a Selected SUDI Cohort from Cape Town. Journal of Pediatric Genetics, 2022, 11, 292-297. | 0.3 | 1 |
| 160 | FGL1 as a modulator of plasma Dâ€dimer levels: Exomeâ€wide marker analysis of plasma tPA, PAIâ€1, and Dâ€dimer. Journal of Thrombosis and Haemostasis, 2021, 19, 2019-2028. | 1.9 | 1 |
| 161 | Lp(a) (Lipoprotein[a]), an Exemplar for Precision Medicine: Insights From UK Biobank. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 475-477. | 1.1 | 1 |
| 162 | 011â€…Adenosine stress T1 mapping: a novel contrast free method to assess myocardial perfusion and ischaemia in hypertrophic cardiomyopathy. Heart, 2017, 103, A8.2-A9. | 1.2 | 0 |

| # | Article | IF | Citations |
|---|---|---|---|
| 163 | 6â€…Diffusion tensor magnetic resonance imaging of myocardial disarray in hypertrophic cardiomyopathy. , 2018, , . | | 0 |
| 164 | In Memoriam. Circulation, 2018, 138, 1079-1081. | 1.6 | 0 |
| 165 | Reply. Journal of the American College of Cardiology, 2019, 74, 1848. | 1.2 | 0 |
| 166 | Dâ€…Stress myocardial oxygenation and not perfusion reserve determines arrhythmic risk in hypertrophic cardiomyopathy: insights from a novel oxygen-sensitive CMR approach. , 2019, , . | | 0 |
| 167 | 22â€…Impaired stress-induced oxygenation in hypertrophic cardiomyopathy is associated with an increased risk of ventricular arrhythmia. , 2019, , . | | 0 |
| 168 | 6â€…RV function deteriorates earlier than LV function and predicts adverse cardiovascular outcomes. , 2019, , . | | 0 |
| 169 | A titan of Cardiovascular Research: Professor Peter Sleight (1929â€“2020). Cardiovascular Research, 2021, 117, e64-e66. | 1.8 | 0 |
| 170 | Abstract 534: A Common Null Allele of LPA is Associated With Lp(a) Levels and Coronary Artery Disease Risk. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, . | 1.1 | 0 |