Hugh Christian Watkins

List of Publications by Year
in descending order

170	48,781	9264 74	5539 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.	27.8	9,051
2	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
3	2014 ESC Guidelines on diagnosis and management of hypertrophic cardiomyopathy. European Heart Journal, 2014, 35, 2733-2779.	2.2	3,469
4	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
5	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	21.4	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.	21.4	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.	21.4	1,818
8	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
9	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	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.	0.7	995
11	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	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.	2.8	723
13	Reassessment of Mendelian gene pathogenicity using 7,855 cardiomyopathy cases and 60,706 reference samples. Genetics in Medicine, 2017, 19, 192-203.	2.4	585
14	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	27.8	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.	21.4	578
16	Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391.	21.4	571
17	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	2.2	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

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19	Genomic Risk Prediction of Coronary Artery Disease in 480,000 Adults. Journal of the American College of Cardiology, 2018, 72, 1883-1893.	2.8	557
20	Mutations in the cardiac myosin binding proteinâ€“C gene on chromosome 11 cause familial hypertrophic cardiomyopathy. Nature Genetics, 1995, 11, 434-437.	21.4	540
21	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	6.0	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.	2.9	472
23	Inherited Cardiomyopathies. New England Journal of Medicine, 2011, 364, 1643-1656.	27.0	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.	21.4	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.	2.8	359
26	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
27	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	3.5	351
28	Distinct genetic architectures for syndromic and nonsyndromic congenital heart defects identified by exome sequencing. Nature Genetics, 2016, 48, 1060-1065.	21.4	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.	8.4	341
30	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
31	Whole-genome sequencing of patients with rare diseases in a national health system. Nature, 2020, 583, 96-102.	27.8	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.	3.5	331
33	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. Nature Genetics, 2015, 47, 717-726.	21.4	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.	6.2	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.	2.4	283
36	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119.	21.4	260

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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.	2.8	216
38	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	2.8	214
39	Evidence From Human Myectomy Samples That MYBPC3 Mutations Cause Hypertrophic Cardiomyopathy Through Haploinsufficiency. Circulation Research, 2009, 105, 219-222.	4.5	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.	4.5	194
41	Phenotypic Characterization of GeneticallyÂLowered Human Lipoprotein(a) Levels. Journal of the American College of Cardiology, 2016, 68, 2761-2772.	2.8	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.	21.4	178
44	Germline selection shapes human mitochondrial DNA diversity. Science, 2019, 364, .	12.6	178
45	Genetic susceptibility to coronary artery disease: from promise to progress. Nature Reviews Genetics, 2006, 7, 163-173.	16.3	176
46	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
47	Common genetic variants and modifiable risk factors underpin hypertrophic cardiomyopathy susceptibility and expressivity. Nature Genetics, 2021, 53, 135-142.	21.4	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.	6.2	158
49	Shared genetic pathways contribute to risk of hypertrophic and dilated cardiomyopathies with opposite directions of effect. Nature Genetics, 2021, 53, 128-134.	21.4	155
50	Distinct Subgroups in Hypertrophic Cardiomyopathy in the NHLBI HCM Registry. Journal of the American College of Cardiology, 2019, 74, 2333-2345.	2.8	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.	7.4	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.	6.2	146
54	Defining the genetic architecture of hypertrophic cardiomyopathy: re-evaluating the role of non-sarcomeric genes. European Heart Journal, 2017, 38, ehw603.	2.2	142

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55	Altered Regulatory Properties of Human Cardiac Troponin I Mutants That Cause Hypertrophic Cardiomyopathy. Journal of Biological Chemistry, 2000, 275, 22069-22074.	3.4	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.	3.4	133
57	Hypertrophic cardiomyopathy mutations in MYBPC3 dysregulate myosin. Science Translational Medicine, 2019, 11, .	12.4	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.	3.4	125
59	Hypertrophic Cardiomyopathy Registry: The rationale and design of an international, observational study of hypertrophic cardiomyopathy. American Heart Journal, 2015, 170, 223-230.	2.7	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.	2.4	119
62	Secretory Phospholipase A2-IIA and Cardiovascular Disease. Journal of the American College of Cardiology, 2013, 62, 1966-1976.	2.8	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.	21.4	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.	6.2	109
65	Familial Dilated Cardiomyopathy Caused by an Alpha-Tropomyosin Mutation. Journal of the American College of Cardiology, 2010, 55, 320-329.	2.8	104
66	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. PLoS Genetics, 2020, 16, e1008629.	3.5	101
67	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. International Journal of Epidemiology, 2016, 45, 1927-1937.	1.9	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.	2.5	94
69	Progression of myocardial fibrosis in hypertrophic cardiomyopathy: mechanisms and clinical implications. European Heart Journal Cardiovascular Imaging, 2019, 20, 157-167.	1.2	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.	8.2	90
71	Identification of Myocardial Disarray inÂPatients With HypertrophicÂCardiomyopathy and Ventricular Arrhythmias. Journal of the American College of Cardiology, 2019, 73, 2493-2502.	2.8	88
72	Chronic Activation of Î³2 AMPK Induces Obesity and Reduces Î² Cell Function. Cell Metabolism, 2016, 23, 821-836.	16.2	87

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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.	12.8	87
75	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	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.	4.5	81
77	Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. Nature Communications, 2018, 9, 1613.	12.8	78
78	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
79	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	2.9	73
80	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	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.	3.4	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.	2.8	65
83	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	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.	3.4	58
85	Genetic Risk Score for CoronaryÂDiseaseÂIdentifies Predispositions to Cardiovascular andÂNoncardiovascular Diseases. Journal of the American College of Cardiology, 2019, 73, 2932-2942.	2.8	58
86	Distinct ECG Phenotypes Identified in Hypertrophic Cardiomyopathy Using Machine Learning Associate With Arrhythmic Risk Markers. Frontiers in Physiology, 2018, 9, 213.	2.8	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.	3.6	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.	2.4	56
89	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	1.4	55
90	A De Novo Mutation in Î±-Tropomyosin That Causes Hypertrophic Cardiomyopathy. Circulation, 1995, 91, 2302-2305.	1.6	53

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91	HspB1 phosphorylation regulates its intramolecular dynamics and mechanosensitive molecular chaperone interaction with filamin C. Science Advances, 2019, 5, eaav8421.	10.3	52
92	Human stromelysin gene promoter activity is modulated by transcription factor ZBP-89. FEBS Letters, 1999, 450, 268-272.	2.8	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.	2.4	45
95	Genetic variation in CADM2 as a link between psychological traits and obesity. Scientific Reports, 2019, 9, 7339.	3.3	45
96	HeterozygousABCG5Gene Deficiency and Risk of Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2020, 13, 417-423.	3.6	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.	2.7	44
98	Measurement of Myofilament-Localized Calcium Dynamics in Adult Cardiomyocytes and the Effect of Hypertrophic Cardiomyopathy Mutations. Circulation Research, 2019, 124, 1228-1239.	4.5	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.	2.4	44
100	Mammalian Î³2 AMPK regulates intrinsic heart rate. Nature Communications, 2017, 8, 1258.	12.8	43
101	Network analysis of coronary artery disease risk genes elucidates disease mechanisms and druggable targets. Scientific Reports, 2018, 8, 3434.	3.3	43
102	Mavacamten rescues increased myofilament calcium sensitivity and dysregulation of Ca²⁺ flux caused by thin filament hypertrophic cardiomyopathy mutations. American Journal of Physiology - Heart and Circulatory Physiology, 2020, 318, H715-H722.	3.2	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.	7.1	39
104	Exome sequencing identifies rare variants in multiple genes in atrioventricular septal defect. Genetics in Medicine, 2016, 18, 189-198.	2.4	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.	7.1	37
106	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. Human Molecular Genetics, 2015, 24, 559-571.	2.9	36
107	Common Genetic Determinants of Lung Function, Subclinical Atherosclerosis and Risk of Coronary Artery Disease. PLoS ONE, 2014, 9, e104082.	2.5	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.	3.3	35

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109	Genetically modulated educational attainment and coronary disease risk. European Heart Journal, 2019, 40, 2413-2420.	2.2	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.	2.9	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.	0.6	31
113	Reevaluation of the South Asian MYBPC3 ^{Î”25bp} Intronic Deletion in Hypertrophic Cardiomyopathy. Circulation Genomic and Precision Medicine, 2020, 13, e002783.	3.6	31
114	CalTrack: High-Throughput Automated Calcium Transient Analysis in Cardiomyocytes. Circulation Research, 2021, 129, 326-341.	4.5	31
115	Two mutations in troponin I that cause hypertrophic cardiomyopathy have contrasting effects on cardiac muscle contractility. Biochemical Journal, 2002, 362, 443-451.	3.7	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.	2.8	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.	1.7	29
118	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. PLoS ONE, 2017, 12, e0167742.	2.5	29
119	Two mutations in troponin I that cause hypertrophic cardiomyopathy have contrasting effects on cardiac muscle contractility. Biochemical Journal, 2002, 362, 443.	3.7	27
120	Improvements in ECG accuracy for diagnosis of left ventricular hypertrophy in obesity. Heart, 2016, 102, 1566-1572.	2.9	27
121	Neonatal MicroRNA Profile Determines Endothelial Function in Offspring of Hypertensive Pregnancies. Hypertension, 2018, 72, 937-945.	2.7	26
122	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. Scientific Reports, 2016, 6, 35278.	3.3	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.	8.2	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.	2.8	24
125	Plasma cytokines and risk of coronary heart disease in the PROCARDIS study. Open Heart, 2018, 5, e000807.	2.3	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.	6.2	24

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127	A key role for the novel coronary artery disease gene JCAD in atherosclerosis via shear stress mechanotransduction. Cardiovascular Research, 2020, 116, 1863-1874.	3.8	23
128	Bi-allelic MCM10 variants associated with immune dysfunction and cardiomyopathy cause telomere shortening. Nature Communications, 2021, 12, 1626.	12.8	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.	2.5	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.	2.4	20
131	Mutant Muscle LIM Protein C58G causes cardiomyopathy through protein depletion. Journal of Molecular and Cellular Cardiology, 2018, 121, 287-296.	1.9	19
132	Maximal Wall Thickness Measurement in Hypertrophic Cardiomyopathy. JACC: Cardiovascular Imaging, 2021, 14, 2123-2134.	5.3	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.	5.9	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.	3.6	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.	3.3	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.	2.8	13
137	Heritability and family-based GWAS analyses of the N-acyl ethanolamine and ceramide plasma lipidome. Human Molecular Genetics, 2021, 30, 500-513.	2.9	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.	3.7	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.	3.3	9
141	Obesity-related ventricular remodelling is exacerbated in dilated and hypertrophic cardiomyopathy. Cardiovascular Diagnosis and Therapy, 2020, 10, 559-567.	1.7	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.	3.2	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.	2.5	8
144	Human Genetic Evidence for Involvement of CD137 in Atherosclerosis. Molecular Medicine, 2014, 20, 456-465.	4.4	8

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145	From Genotype to Phenotype. Circulation Genomic and Precision Medicine, 2018, 11, e002316.	3.6	8
146	Manhattan++: displaying genome-wide association summary statistics with multiple annotation layers. BMC Bioinformatics, 2019, 20, 610.	2.6	6
147	Heritability of haemodynamics in the ascending aorta. Scientific Reports, 2020, 10, 14356.	3.3	5
148	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. Circulation Genomic and Precision Medicine, 2020, 13, e002769.	3.6	5
149	Rationale and design of the African Cardiomyopathy and Myocarditis Registry Program: The IMHOTEP study. International Journal of Cardiology, 2021, 333, 119-126.	1.7	5
150	Robust estimates of heritable coronary disease risk in individuals with type 2 diabetes. Genetic Epidemiology, 2022, 46, 51-62.	1.3	5
151	Tackling the Achillesâ€™ Heel of Genetic Testing. Science Translational Medicine, 2015, 7, 270fs1.	12.4	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.	3.8	4
154	Marked variation in heritability estimates of left ventricular mass depending on modality of measurement. Scientific Reports, 2019, 9, 13556.	3.3	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.	0.8	3
156	Data-driven modelling of mutational hotspots and in silico predictors in hypertrophic cardiomyopathy. Journal of Medical Genetics, 2021, 58, 556-564.	3.2	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.	2.6	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.	0.7	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.	3.8	1
161	Lp(a) (Lipoprotein[a]), an Exemplar for Precision Medicine: Insights From UK Biobank. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 475-477.	2.4	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.	2.9	0

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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.	2.8	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.	3.8	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, .	2.4	0