Patrick T Ellinor

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

390 39,391 90 193 h-index g-index citations papers 6.89 464 52,037 11.9 L-index avg, IF ext. papers ext. citations

#	Paper	IF	Citations
390	Bacon: a comprehensive computational benchmarking framework for evaluating targeted chromatin conformation capture-specific methodologies <i>Genome Biology</i> , 2022 , 23, 30	18.3	1
389	Vascular smooth muscle cell phenotype switching in carotid atherosclerosis <i>JVS Vascular Science</i> , 2022 , 3, 41-47	1.3	0
388	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed <i>Cell Genomics</i> , 2022 , 2, 100084-100084		1
387	Genome-wide association study reveals novel genetic loci: a new polygenic risk score for mitral valve prolapse <i>European Heart Journal</i> , 2022 ,	9.5	2
386	Increased atrial effectiveness of flecainide conferred by altered biophysical properties of sodium channels <i>Journal of Molecular and Cellular Cardiology</i> , 2022 , 166, 23-35	5.8	O
385	Analysis of rare genetic variation underlying cardiometabolic diseases and traits among 200,000 individuals in the UK Biobank <i>Nature Genetics</i> , 2022 ,	36.3	4
384	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data <i>Nature Genetics</i> , 2022 ,	36.3	6
383	Association of Habitual Alcohol Intake With Risk of Cardiovascular Disease <i>JAMA Network Open</i> , 2022 , 5, e223849	10.4	10
382	Association of the Interaction Between Familial Hypercholesterolemia Variants and Adherence to a Healthy Lifestyle With Risk of Coronary Artery Disease <i>JAMA Network Open</i> , 2022 , 5, e222687	10.4	O
381	TAILS identifies candidate substrates and biomarkers of ADAMTS7, a therapeutic protease target in coronary artery disease <i>Molecular and Cellular Proteomics</i> , 2022 , 100223	7.6	0
380	Screening for Atrial Fibrillation in Older Adults at Primary Care Visits: the VITAL-AF Randomized Controlled Trial <i>Circulation</i> , 2022 ,	16.7	4
379	Genetic Association of Body Mass Index With Pathologic Left Ventricular Remodeling <i>Journal of the American Heart Association</i> , 2022 , e024408	6	
378	Cohort design and natural language processing to reduce bias in electronic health records research <i>Npj Digital Medicine</i> , 2022 , 5, 47	15.7	2
377	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential <i>Science Advances</i> , 2022 , 8, eabl6579	14.3	3
376	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations <i>Frontiers in Endocrinology</i> , 2022 , 13, 863893	5.7	
375	Transethnic Transferability of a Genome-Wide Polygenic Score for Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2021 , 14, e003092	5.2	5
374	Electrocardiogram-based Deep Learning and Clinical Risk Factors to Predict Atrial Fibrillation. <i>Circulation</i> , 2021 ,	16.7	11

(2021-2021)

373	Deep Learning of the Retina Enables Phenome- and Genome-wide Analyses of the Microvasculature. <i>Circulation</i> , 2021 ,	16.7	7
372	Supraventricular Arrhythmias 2021 , 307-322		
371	Deep learning enables genetic analysis of the human thoracic aorta. <i>Nature Genetics</i> , 2021 ,	36.3	6
370	Selection of 51 predictors from 13,782 candidate multimodal features using machine learning improves coronary artery disease prediction <i>Patterns</i> , 2021 , 2, 100364	5.1	3
369	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	36.3	7
368	SnRNA sequencing defines signaling by RBC-derived extracellular vesicles in the murine heart. <i>Life Science Alliance</i> , 2021 , 4,	5.8	4
367	Re-CHARGE-AF: Recalibration of the CHARGE-AF Model for Atrial Fibrillation Risk Prediction in Patients With Acute Stroke. <i>Journal of the American Heart Association</i> , 2021 , 10, e022363	6	2
366	Lp(a) (Lipoprotein[a]) Concentrations and Incident Atherosclerotic Cardiovascular Disease: New Insights From a Large National Biobank. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021 , 41, 465	5-4 7 4	32
365	Deep learning to estimate cardiac magnetic resonance-derived left ventricular mass <i>Cardiovascular Digital Health Journal</i> , 2021 , 2, 109-117	2	2
364	Role of genetics in atrial fibrillation management. <i>Europace</i> , 2021 , 23, ii4-ii8	3.9	O
363	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. <i>Nature Communications</i> , 2021 , 12, 2182	17.4	5
362	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. <i>Nature</i> , 2021 , 595, 107-113	50.4	124
361	Identification of two preclinical canine models of atrial fibrillation to facilitate drug discovery. <i>Heart Rhythm</i> , 2021 , 18, 632-640	6.7	
360	A System for Phenotype Harmonization in the National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Program. <i>American Journal of Epidemiology</i> , 2021 , 190, 1977-1992	3.8	3
359	Accelerometer-derived physical activity and risk of atrial fibrillation. <i>European Heart Journal</i> , 2021 , 42, 2472-2483	9.5	9
358	Usefulness of Rhythm Monitoring Following Acute Ischemic Stroke. <i>American Journal of Cardiology</i> , 2021 , 147, 44-51	3	1
357	Deep Learning to Predict Cardiac Magnetic Resonance-Derived Left Ventricular Mass and Hypertrophy From 12-Lead ECGs. <i>Circulation: Cardiovascular Imaging</i> , 2021 , 14, e012281	3.9	5
356	Plasma Proteomics of COVID-19 Associated Cardiovascular Complications: Implications for Pathophysiology and Therapeutics 2021 ,		1

355	Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. <i>Nature Medicine</i> , 2021 , 27, 1012-1024	50.5	16
354	Association of Rare Genetic Variants and Early-Onset Atrial Fibrillation in Ethnic Minority Individuals. <i>JAMA Cardiology</i> , 2021 , 6, 811-819	16.2	11
353	Assessing absolute stroke risk in patients with atrial fibrillation using a risk factor-based approach. <i>European Heart Journal - Cardiovascular Pharmacotherapy</i> , 2021 , 7, f3-f10	6.4	7
352	Clinical Application of a Novel Genetic Risk Score for Ischemic Stroke in Patients With Cardiometabolic Disease. <i>Circulation</i> , 2021 , 143, 470-478	16.7	13
351	Performance of Atrial Fibrillation Risk Prediction Models in Over 4 Million Individuals. <i>Circulation: Arrhythmia and Electrophysiology</i> , 2021 , 14, e008997	6.4	13
350	Enhancing rare variant interpretation in inherited arrhythmias through quantitative analysis of consortium disease cohorts and population controls. <i>Genetics in Medicine</i> , 2021 , 23, 47-58	8.1	13
349	Non-Vitamin K Antagonist Oral Anticoagulant vs Warfarin for Post Cardiac Surgery Atrial Fibrillation. <i>Annals of Thoracic Surgery</i> , 2021 , 112, 1392-1401	2.7	3
348	Genetic Risk Score to Identify Risk of Venous Thromboembolism in Patients With Cardiometabolic Disease. <i>Circulation Genomic and Precision Medicine</i> , 2021 , 14, e003006	5.2	1
347	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021 , 590, 290-299	50.4	268
346	Rare Coding Variants Associated With Electrocardiographic Intervals Identify Monogenic Arrhythmia Susceptibility Genes: A Multi-Ancestry Analysis. <i>Circulation Genomic and Precision Medicine</i> , 2021 , 14, e003300	5.2	0
345	Coronary Disease Association With ADAMTS7 Is Due to Protease Activity. <i>Circulation Research</i> , 2021 , 129, 458-470	15.7	6
344	Population sequencing data reveal a compendium of mutational processes in the human germ line. <i>Science</i> , 2021 , 373, 1030-1035	33.3	7
343	Predictive Accuracy of a Clinical and Genetic Risk Model for Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2021 , 14, e003355	5.2	2
342	Comparative Clinical Effectiveness of Population-Based Atrial Fibrillation Screening Using Contemporary Modalities: A Decision-Analytic Model. <i>Journal of the American Heart Association</i> , 2021 , 10, e020330	6	1
341	The genomics of heart failure: design and rationale of the HERMES consortium. <i>ESC Heart Failure</i> , 2021 ,	3.7	1
340	Epigenetic Age and the Risk of Incident Atrial Fibrillation. Circulation, 2021,	16.7	2
339	Early-Onset Atrial Fibrillation and the Prevalence of Rare Variants in Cardiomyopathy and Arrhythmia Genes. <i>JAMA Cardiology</i> , 2021 ,	16.2	9
338	Machine learning enables new insights into genetic contributions to liver fat accumulation <i>Cell Genomics</i> , 2021 , 1,		3

(2020-2020)

Epigenetic Analyses of Human Left Atrial Tissue Identifies Gene Networks Underlying Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e003085	5.2	7
Associations Between Alcohol Intake and Genetic Predisposition With Atrial Fibrillation Risk in a National Biobank. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e003111	5.2	1
Genetically Determined Birthweight Associates With Atrial Fibrillation: A Mendelian Randomization Study. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e002553	5.2	3
Transethnic Genome-Wide Association Study Provides Insights in the Genetic Architecture and Heritability of Long QT Syndrome. <i>Circulation</i> , 2020 , 142, 324-338	16.7	27
Analysis of cardiac magnetic resonance imaging in 36,000 individuals yields genetic insights into dilated cardiomyopathy. <i>Nature Communications</i> , 2020 , 11, 2254	17.4	40
Limitations of Contemporary Guidelines for Managing Patients at High Genetic Risk of Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2020 , 75, 2769-2780	15.1	33
Transcriptional and Cellular Diversity of the Human Heart. Circulation, 2020, 142, 466-482	16.7	124
Association of Rare Pathogenic DNA Variants for Familial Hypercholesterolemia, Hereditary Breast and Ovarian Cancer Syndrome, and Lynch Syndrome With Disease Risk in Adults According to Family History. <i>JAMA Network Open</i> , 2020 , 3, e203959	10.4	31
The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020 , 581, 434-443	50.4	2278
Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020 , 11, 2542	17.4	16
Epigenomes of Human Hearts Reveal New Genetic Variants Relevant for Cardiac Disease and Phenotype. <i>Circulation Research</i> , 2020 , 127, 761-777	15.7	8
Loss of Asb2 Impairs Cardiomyocyte Differentiation and Leads to Congenital Double Outlet Right Ventricle. <i>IScience</i> , 2020 , 23, 100959	6.1	5
Titin Truncating Variants in Adults Without Known Congestive Heart[Failure. <i>Journal of the American College of Cardiology</i> , 2020 , 75, 1239-1241	15.1	10
The Effect of PCSK9 (Proprotein Convertase Subtilisin/Kexin Type 9) Inhibition on the Risk of Venous Thromboembolism. <i>Circulation</i> , 2020 , 141, 1600-1607	16.7	32
Myocyte-Specific Upregulation of in Cardiovascular Disease: Implications for SARS-CoV-2-Mediated Myocarditis. <i>Circulation</i> , 2020 , 142, 708-710	16.7	47
Epigenetic and Transcriptional Networks Underlying Atrial Fibrillation. <i>Circulation Research</i> , 2020 , 127, 34-50	15.7	22
Genetics of Atrial Fibrillation in 2020: GWAS, Genome Sequencing, Polygenic Risk, and Beyond. <i>Circulation Research</i> , 2020 , 127, 21-33	15.7	37
Genetic Susceptibility for Atrial Fibrillation in Patients Undergoing Atrial Fibrillation Ablation. <i>Circulation: Arrhythmia and Electrophysiology</i> , 2020 , 13, e007676	6.4	12
	Fibrillation. Circulation Genomic and Precision Medicine, 2020, 13, e003085 Associations Between Alcohol Intake and Genetic Predisposition With Atrial Fibrillation Risk in a National Biobank. Circulation Genomic and Precision Medicine, 2020, 13, e003111 Genetically Determined Birthweight Associates With Atrial Fibrillation: A Mendelian Randomization Study. Circulation Genomic and Precision Medicine, 2020, 13, e002553 Transethnic Genome-Wide Association Study Provides Insights in the Genetic Architecture and Heritability of Long QT Syndrome. Circulation, 2020, 142, 324-338 Analysis of cardiac magnetic resonance imaging in 36,000 individuals yields genetic insights into dilated cardiomyopathy. Nature Communications, 2020, 11, 2254 Limitations of Contemporary Guidelines for Managing Patients at High Genetic Risk of Coronary Artery Disease. Journal of the American College of Cardiology, 2020, 75, 2769-2780 Transcriptional and Cellular Diversity of the Human Heart. Circulation, 2020, 142, 466-482 Association of Rare Pathogenic DNA Variants for Familial Hypercholesterolemia, Hereditary Breast and Ovarian Cancer Syndrome, and Lynch Syndrome With Disease Risk in Adults According to Family History. JAMA Network Open, 2020, 3, e203959 The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443 Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542 Epigenomes of Human Hearts Reveal New Genetic Variants Relevant for Cardiac Disease and Phenotype. Circulation Research, 2020, 127, 761-777 Loss of Ab5 Impairs Cardiomyocyte Differentiation and Leads to Congenital Double Outlet Right Ventricle. Iscience, 2020, 23, 100959 Titin Truncating Variants in Adults Without Known Congestive HeartiFailure. Journal of the American College of Cardiology, 2020, 75, 1239-1241 The Effect of PCSK9 (Proprotein Convertase Subtilisin/Kexin Type 9) Inhibition on the Risk of Venous Thromboembolism.	Associations Between Alcohol Intake and Genetic Predisposition With Atrial Fibrillation Risk in a National Biobank. Circulation Genomic and Precision Medicine, 2020, 13, e003111 Genetically Determined Birthweight Associates With Atrial Fibrillation: A Mendelian Randomization Study. Circulation Genomic and Precision Medicine, 2020, 13, e002553 Transethnic Genome-Wide Association Study Provides Insights in the Genetic Architecture and Heritability of Long QT Syndrome. Circulation, 2020, 142, 324-338 Analysis of cardiac magnetic resonance imaging in 36,000 individuals yields genetic insights into dilated cardiomyopathy. Nature Communications, 2020, 11, 2254 Limitations of Contemporary Guidelines for Managing Patients at High Genetic Risk of Coronary Artery Disease. Journal of the American College of Cardiology, 2020, 75, 2769-2780 Transcriptional and Cellular Diversity of the Human Heart. Circulation, 2020, 142, 466-482 Association of Rare Pathogenic DNA Variants for Familial Hypercholesterolemia, Hereditary Breast and Ovarian Cancer Syndrome, and Lynch Syndrome With Disease Risk in Adults According to Family History. JAMA Network Open, 2020, 3, e203959 The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443 Multi-ancestry GWAS of the electrocardiographic PR Interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542 Epigenomes of Human Hearts Reveal New Genetic Variants Relevant for Cardiac Disease and Phenotype. Circulation Research, 2020, 127, 761-777 Loss of Asb2 Impairs Cardiomyocyte Differentiation and Leads to Congenital Double Outlet Right Ventricle. Iscience, 2020, 23, 100959 Titin Truncating Variants in Adults Without Known Congestive Heart/Failure. Journal of the American College of Cardiology, 2020, 75, 1239-1241 The Effect of PCSK9 (Proprotein Convertase Subtilisin/Kexin Type 9) Inhibition on the Risk of Venous Thromboembolism. Circulation, 2020, 141, 1600-1607 Myocyte-Specific Upregulation of in Card

319	Initial Precipitants and Recurrence of Atrial Fibrillation. <i>Circulation: Arrhythmia and Electrophysiology</i> , 2020 , 13, e007716	6.4	18
318	Protein Biomarkers and Risk of Atrial Fibrillation: The FHS. <i>Circulation: Arrhythmia and Electrophysiology</i> , 2020 , 13, e007607	6.4	12
317	Hematopoietic mosaic chromosomal alterations and risk for infection among 767,891 individuals without blood cancer 2020 ,		2
316	Myocyte Specific Upregulation of ACE2 in Cardiovascular Disease: Implications for SARS-CoV-2 mediated myocarditis 2020 ,		8
315	Hematopoietic mosaic chromosomal alterations and risk for infection among 767,891 individuals without blood cancer 2020 ,		5
314	Monogenic and Polygenic Contributions to Atrial Fibrillation Risk: Results From a National Biobank. <i>Circulation Research</i> , 2020 , 126, 200-209	15.7	26
313	Predicting Benefit From Evolocumab Therapy in Patients With Atherosclerotic Disease Using a Genetic Risk Score: Results From the FOURIER Trial. <i>Circulation</i> , 2020 , 141, 616-623	16.7	61
312	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <i>Nature Communications</i> , 2020 , 11, 163	17.4	140
311	Integrative Omics Approach to Identifying Genes Associated With Atrial Fibrillation. <i>Circulation Research</i> , 2020 , 126, 350-360	15.7	21
310	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020 , 586, 763-768	50.4	127
309	Ibrutinib-Mediated Atrial Fibrillation Attributable to Inhibition of C-Terminal Src Kinase. <i>Circulation</i> , 2020 , 142, 2443-2455	16.7	43
308	Polygenic background modifies penetrance of monogenic variants for tier 1 genomic conditions. <i>Nature Communications</i> , 2020 , 11, 3635	17.4	88
307	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, 387-395	5.2	4
306	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. <i>Nature Communications</i> , 2020 , 11, 6417	17.4	17
305	Novel Risk Modeling Approach of Atrial Fibrillation With Restricted Mean Survival Times: Application in the Framingham Heart Study Community-Based Cohort. <i>Circulation: Cardiovascular Quality and Outcomes</i> , 2020 , 13, e005918	5.8	9
304	Identification of Functional Variant Enhancers Associated With Atrial Fibrillation. <i>Circulation Research</i> , 2020 , 127, 229-243	15.7	12
303	Atrial Fibrillation Risk and Discrimination of Cardioembolic From Noncardioembolic Stroke. <i>Stroke</i> , 2020 , 51, 1396-1403	6.7	5
302	Leveraging Human Genetics to Estimate Clinical Risk Reductions Achievable by Inhibiting Factor XI. <i>Stroke</i> , 2019 , 50, 3004-3012	6.7	11

301	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. <i>Chest</i> , 2019 , 156, 1068-1079	5.3	3
300	2019 AHA/ACC/HRS Focused Update of the 2014 AHA/ACC/HRS Guideline for the Management of Patients With Atrial Fibrillation: A Report of the American College of Cardiology/American Heart Association Task Force on Clinical Practice Guidelines and the Heart Rhythm Society in	16.7	1020
299	2019 AHA/ACC/HRS focused update of the 2014 AHA/ACC/HRS guideline for the management of patients with atrial fibrillation: A Report of the American College of Cardiology/American Heart Association Task Force on Clinical Practice Guidelines and the Heart Rhythm Society. <i>Heart Rhythm</i> ,	6.7	176
298	2019 AHA/ACC/HRS Focused Update of the 2014 AHA/ACC/HRS Guideline for the Management of Patients With Atrial Fibrillation: A Report of the American College of Cardiology/American Heart Association Task Force on Clinical Practice Guidelines and the Heart Rhythm Society. <i>Journal of the</i>	15.1	807
297	Assessment of the Relationship Between Genetic Determinants of Thyroid Function and Atrial Fibrillation: A Mendelian Randomization Study. <i>JAMA Cardiology</i> , 2019 , 4, 144-152	16.2	36
296	Association of Thyroid Function Genetic Predictors With Atrial Fibrillation: A Phenome-Wide Association Study and Inverse-Variance Weighted Average Meta-analysis. <i>JAMA Cardiology</i> , 2019 , 4, 136	16,2 5-143	20
295	Genetic Link Between Arterial Stiffness and Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2019 , 12, e002453	5.2	6
294	Single-Cell Analysis of the Normal Mouse Aorta Reveals Functionally Distinct Endothelial Cell Populations. <i>Circulation</i> , 2019 , 140, 147-163	16.7	104
293	Primary cilia defects causing mitral valve prolapse. Science Translational Medicine, 2019, 11,	17.5	39
292	Cardioprotective Effects of MTSS1 Enhancer Variants. <i>Circulation</i> , 2019 , 139, 2073-2076	16.7	2
291	Genome-Wide Association Study-Driven Gene-Set Analyses, Genetic, and Functional Follow-Up Suggest GLIS1 as a Susceptibility Gene for Mitral Valve Prolapse. <i>Circulation Genomic and Precision Medicine</i> , 2019 , 12, e002497	5.2	18
290	A Genetic Risk Score for Atrial Fibrillation Predicts the Response to Catheter Ablation. <i>Korean Circulation Journal</i> , 2019 , 49, 338-349	2.2	12
289	Proteomics Profiling and Risk of New-Onset Atrial Fibrillation: Framingham Heart Study. <i>Journal of the American Heart Association</i> , 2019 , 8, e010976	6	24
288	Refining the Association Between Body Mass Index and Atrial Fibrillation: G-Formula and Restricted Mean Survival Times. <i>Journal of the American Heart Association</i> , 2019 , 8, e013011	6	6
287	Design and rationale of a pragmatic trial integrating routine screening for atrial fibrillation at primary care visits: The VITAL-AF trial. <i>American Heart Journal</i> , 2019 , 215, 147-156	4.9	13
286	Long-range enhancer-promoter interactions prevent predisposition to atrial fibrillation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 22692-22698	3 ^{11.5}	25
285	Development and Validation of a Prediction Model for Atrial Fibrillation Using Electronic Health Records. <i>JACC: Clinical Electrophysiology</i> , 2019 , 5, 1331-1341	4.6	24
284			9

283	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	6	90
282	Identification of atrial fibrillation associated genes and functional non-coding variants. <i>Nature Communications</i> , 2019 , 10, 4755	17.4	36
281	Response by Aragam et al to Letter Regarding Article, "Phenotypic Refinement of Heart Failure in a National Biobank Facilitates Genetic Discovery". <i>Circulation</i> , 2019 , 140, e7-e8	16.7	6
280	ROBO4 variants predispose individuals to bicuspid aortic valve and thoracic aortic aneurysm. <i>Nature Genetics</i> , 2019 , 51, 42-50	36.3	56
279	An HDAC9-MALAT1-BRG1 complex mediates smooth muscle dysfunction in thoracic aortic aneurysm. <i>Nature Communications</i> , 2018 , 9, 1009	17.4	72
278	2017 HRS/EHRA/ECAS/APHRS/SOLAECE expert consensus statement on catheter and surgical ablation of atrial fibrillation. <i>Europace</i> , 2018 , 20, e1-e160	3.9	461
277	2017 HRS/EHRA/ECAS/APHRS/SOLAECE expert consensus statement on catheter and surgical ablation of atrial fibrillation: Executive summary. <i>Europace</i> , 2018 , 20, 157-208	3.9	227
276	Lifetime risk of atrial fibrillation according to optimal, borderline, or elevated levels of risk factors: cohort study based on longitudinal data from the Framingham Heart Study. <i>BMJ, The</i> , 2018 , 361, k1453	5.9	110
275	Genetics of Atrial Fibrillation 2018 , 465-472		
274	Genomic basis of atrial fibrillation. <i>Heart</i> , 2018 , 104, 201-206	5.1	27
²⁷⁴ ²⁷³	Genomic basis of atrial fibrillation. <i>Heart</i> , 2018 , 104, 201-206 PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018 , 9, 2904	5.1 17.4	27 39
	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and		
273	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018 , 9, 2904 Electronic physician notifications to improve guideline-based anticoagulation in atrial fibrillation: a	17.4	39
²⁷³	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018 , 9, 2904 Electronic physician notifications to improve guideline-based anticoagulation in atrial fibrillation: a randomized controlled trial. <i>Journal of General Internal Medicine</i> , 2018 , 33, 2070-2077 Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including	17.4 4	39 15
273 272 271	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018 , 9, 2904 Electronic physician notifications to improve guideline-based anticoagulation in atrial fibrillation: a randomized controlled trial. <i>Journal of General Internal Medicine</i> , 2018 , 33, 2070-2077 Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. <i>Genome Biology</i> , 2018 , 19, 87 Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to	17.4 4 18.3 36.3	39 15 25
273272271270	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018 , 9, 2904 Electronic physician notifications to improve guideline-based anticoagulation in atrial fibrillation: a randomized controlled trial. <i>Journal of General Internal Medicine</i> , 2018 , 33, 2070-2077 Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. <i>Genome Biology</i> , 2018 , 19, 87 Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations. <i>Nature Genetics</i> , 2018 , 50, 1219-1224	17.4 4 18.3 36.3	39 15 25 1073
273272271270269	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018 , 9, 2904 Electronic physician notifications to improve guideline-based anticoagulation in atrial fibrillation: a randomized controlled trial. <i>Journal of General Internal Medicine</i> , 2018 , 33, 2070-2077 Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. <i>Genome Biology</i> , 2018 , 19, 87 Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations. <i>Nature Genetics</i> , 2018 , 50, 1219-1224 Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018 , 50, 1225-1233 Genetic Reduction in Left Ventricular Protein Kinase C-Band Adverse Ventricular Remodeling in	17.4 4 18.3 36.3	39 15 25 1073

(2017-2018)

265	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , 2018 , 50, 524-537	36.3	536
264	Phenotypic Refinement of Heart Failure in a National Biobank Facilitates Genetic Discovery. <i>Circulation</i> , 2018 ,	16.7	51
263	Genetic Predisposition, Clinical Risk Factor Burden, and Lifetime Risk of Atrial Fibrillation. <i>Circulation</i> , 2018 , 137, 1027-1038	16.7	133
262	Response by Ma et al to Letter Regarding Article, "Novel Mutation in (Filamin C) Causes Familial Restrictive Cardiomyopathy". <i>Circulation Genomic and Precision Medicine</i> , 2018 , 11, e002140	5.2	
261	Atrial fibrillation genetic risk differentiates cardioembolic stroke from other stroke subtypes. <i>Neurology: Genetics</i> , 2018 , 4, e293	3.8	19
260	Association Between Titin Loss-of-Function Variants and Early-Onset Atrial Fibrillation. <i>JAMA - Journal of the American Medical Association</i> , 2018 , 320, 2354-2364	27.4	75
259	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. <i>Circulation Genomic and Precision Medicine</i> , 2018 , 11, e001758	5.2	14
258	Rare truncating variants in the sarcomeric protein titin associate with familial and early-onset atrial fibrillation. <i>Nature Communications</i> , 2018 , 9, 4316	17.4	58
257	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. <i>Circulation Genomic and Precision Medicine</i> , 2018 , 11, e002037	5.2	11
256	Common Coding Variants in Are Associated With the Nav1.8 Late Current and Cardiac Conduction. <i>Circulation Genomic and Precision Medicine</i> , 2018 , 11, e001663	5.2	14
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84	Genome-wide association studies in cardiac electrophysiology: recent discoveries and implications for clinical practice. <i>Heart Rhythm</i> , 2010 , 7, 1141-8	6.7	24
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77	Identification of a Kir3.4 mutation in congenital long QT syndrome. <i>American Journal of Human Genetics</i> , 2010 , 86, 872-80	11	156
76	P wave indices: current status and future directions in epidemiology, clinical, and research applications. <i>Circulation: Arrhythmia and Electrophysiology</i> , 2009 , 2, 72-9	6.4	91
75	Prevention of atrial fibrillation: report from a national heart, lung, and blood institute workshop. <i>Circulation</i> , 2009 , 119, 606-18	16.7	378
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70	Development of a risk score for atrial fibrillation (Framingham Heart Study): a community-based cohort study. <i>Lancet, The</i> , 2009 , 373, 739-45	40	715
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42	In vivo recording of adult zebrafish electrocardiogram and assessment of drug-induced QT prolongation. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2006 , 291, H269-73	5.2	165
41	Potassium channel gene mutations rarely cause atrial fibrillation. <i>BMC Medical Genetics</i> , 2006 , 7, 70	2.1	51
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20	Characterization of cDNA clones encoding two putative isoforms of the alpha 1 subunit of the dihydropyridine-sensitive voltage-dependent calcium channel isolated from rat brain and rat aorta. <i>FEBS Letters</i> , 1989 , 250, 386-8	3.8	45
19	Analysis of cardiac magnetic resonance imaging traits in 29,000 individuals reveals shared genetic basis with dilated cardiomyopathy		1
18	Genetics of Myocardial Interstitial Fibrosis in the Human Heart and Association with Disease		2
17	Discovering patterns of pleiotropy in genome-wide association studies		1
16	Genome-wide association study provides new insights into the genetic architecture and pathogenesis of heart failure		2
15	Deep Learning to Estimate Cardiac Magnetic Resonance-Derived Left Ventricular Mass		1
14	Polygenic background modifies penetrance of monogenic variants conferring risk for coronary artery disease, breast cancer, or colorectal cancer		5

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13	Transcriptional and Cellular Diversity of the Human Heart	4
12	Deep learning enables genetic analysis of the human thoracic aorta	6
11	Machine learning enables new insights into clinical significance of and genetic contributions to liver fat accumulation	5
10	Rare Genetic Variation Underlying Human Diseases and Traits: Results from 200,000 Individuals in the UK Biobank	3
9	Rare coding variants in 35 genes associate with circulating lipid levels 🗈 multi-ancestry analysis of 170,000 exomes	2
8	Cohort Design and Natural Language Processing to Reduce Bias in Electronic Health Records Research: The Community Care Cohort Project	1
7	Association of machine learning-derived measures of body fat distribution in >40,000 individuals with cardiometabolic diseases	5
6	Discovery and systematic characterization of risk variants and genes for coronary artery disease in over a million participants	5
5	Genetic Analysis of Right Heart Structure and Function in 40,000 People	1
4	Deep Learning of Left Atrial Structure and Function Provides Link to Atrial Fibrillation Risk	1
3	Inherited basis of visceral, abdominal subcutaneous and gluteofemoral fat depots	2
2	Transcriptome variation in human tissues revealed by long-read sequencing	6
1	Single-nucleus profiling of human dilated and hypertrophic cardiomyopathy. <i>Nature</i> ,	50.4 6