Connie R Bezzina

List of Publications by Citations

189 papers	11,784 citations	59 h-index	105 g-index
215 ext. papers	14,202 ext. citations	9.7 avg, IF	5.81 L-index

#	Paper	IF	Citations
189	A single Na(+) channel mutation causing both long-QT and Brugada syndromes. *Circulation Research*, **1999**, 85, 1206-13	15.7	526
188	Mutation in the KCNQ1 gene leading to the short QT-interval syndrome. *Circulation*, **2004**, 109, 2394-7	16.7	514
187	Common variants at SCN5A-SCN10A and HEY2 are associated with Brugada syndrome, a rare disease with high risk of sudden cardiac death. *Nature Genetics*, **2013**, 45, 1044-9	36.3	345
186	A sodium-channel mutation causes isolated cardiac conduction disease. *Nature*, **2001**, 409, 1043-7	50.4	341
185	Right ventricular fibrosis and conduction delay in a patient with clinical signs of Brugada syndrome: a combined electrophysiological, genetic, histopathologic, and computational study. *Circulation*, **2005**, 112, 2769-77	16.7	338
184	Sodium channel 1 subunit mutations associated with Brugada syndrome and cardiac conduction disease in humans. *Journal of Clinical Investigation*, **2008**, 118, 2260-8	15.9	337
183	Genotype-phenotype relationship in Brugada syndrome: electrocardiographic features differentiate SCN5A-related patients from non-SCN5A-related patients. *Journal of the American College of Cardiology*, **2002**, 40, 350-6	15.1	315
182	Two distinct congenital arrhythmias evoked by a multidysfunctional Na(+) channel. *Circulation Research*, **2000**, 86, E91-7	15.7	236
181	A cardiac sodium channel mutation cosegregates with a rare connexin40 genotype in familial atrial standstill. *Circulation Research*, **2003**, 92, 14-22	15.7	229
180	Familial sudden death is an important risk factor for primary ventricular fibrillation: a case-control study in acute myocardial infarction patients. *Circulation*, **2006**, 114, 1140-5	16.7	214
179	Genetic variation in SCN10A influences cardiac conduction. *Nature Genetics*, **2010**, 42, 149-52	36.3	209
178	Cardiomyocytes derived from pluripotent stem cells recapitulate electrophysiological characteristics of an overlap syndrome of cardiac sodium channel disease. *Circulation*, **2012**, 125, 3079-91	16.7	200
177	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. *Nature Genetics*, **2014**, 46, 826-36	36.3	199
176	Compound heterozygosity for mutations (W156X and R225W) in SCN5A associated with severe cardiac conduction disturbances and degenerative changes in the conduction system. *Circulation Research*, **2003**, 92, 159-68	15.7	190
175	Large-scale gene-centric meta-analysis across 32 studies identifies multiple lipid loci. *American Journal of Human Genetics*, **2012**, 91, 823-38	11	189
174	Common sodium channel promoter haplotype in asian subjects underlies variability in cardiac conduction. *Circulation*, **2006**, 113, 338-44	16.7	186
173	Type of SCN5A mutation determines clinical severity and degree of conduction slowing in loss-of-function sodium channelopathies. *Heart Rhythm*, **2009**, 6, 341-8	6.7	182

172	A mutation in the human cardiac sodium channel (E161K) contributes to sick sinus syndrome, conduction disease and Brugada syndrome in two families. *Journal of Molecular and Cellular Cardiology*, **2005**, 38, 969-81	5.8	168
171	Genetics of sudden cardiac death. *Circulation Research*, **2015**, 116, 1919-36	15.7	161
170	Overlap syndrome of cardiac sodium channel disease in mice carrying the equivalent mutation of human SCN5A-1795insD. *Circulation*, **2006**, 114, 2584-94	16.7	153
169	Cardiac sodium channel overlap syndromes: different faces of SCN5A mutations. *Trends in Cardiovascular Medicine*, **2008**, 18, 78-87	6.9	151
168	Intercalated disc abnormalities, reduced Na(+) current density, and conduction slowing in desmoglein-2 mutant mice prior to cardiomyopathic changes. *Cardiovascular Research*, **2012**, 95, 409-18	9.9	145
167	Genetic variation in T-box binding element functionally affects SCN5A/SCN10A enhancer. *Journal of Clinical Investigation*, **2012**, 122, 2519-30	15.9	143
166	Myocyte necrosis underlies progressive myocardial dystrophy in mouse dsg2-related arrhythmogenic right ventricular cardiomyopathy. *Journal of Experimental Medicine*, **2009**, 206, 1787-802	16.6	140
165	Induced pluripotent stem cell derived cardiomyocytes as models for cardiac arrhythmias. *Frontiers in Physiology*, **2012**, 3, 346	4.6	134
164	HCN4 mutations in multiple families with bradycardia and left ventricular noncompaction cardiomyopathy. *Journal of the American College of Cardiology*, **2014**, 64, 745-56	15.1	133
163	A common polymorphism in KCNH2 (HERG) hastens cardiac repolarization. *Cardiovascular Research*, **2003**, 59, 27-36	9.9	133
162	Genome-wide association study identifies a susceptibility locus at 21q21 for ventricular fibrillation in acute myocardial infarction. *Nature Genetics*, **2010**, 42, 688-691	36.3	132
161	A common genetic variant within SCN10A modulates cardiac SCN5A expression. *Journal of Clinical Investigation*, **2014**, 124, 1844-52	15.9	132
160	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. *American Journal of Human Genetics*, **2014**, 94, 349-60	11	131
159	A large candidate gene survey identifies the KCNE1 D85N polymorphism as a possible modulator of drug-induced torsades de pointes. *Circulation: Cardiovascular Genetics*, **2012**, 5, 91-9		127
158	Utility of Post-Mortem Genetic Testing in Cases of Sudden Arrhythmic Death Syndrome. *Journal of the American College of Cardiology*, **2017**, 69, 2134-2145	15.1	126
157	Genetic control of sodium channel function. *Cardiovascular Research*, **2003**, 57, 961-73	9.9	125
156	A mutation in CALM1 encoding calmodulin in familial idiopathic ventricular fibrillation in childhood and adolescence. *Journal of the American College of Cardiology*, **2014**, 63, 259-66	15.1	124
155	Haplotype-sharing analysis implicates chromosome 7q36 harboring DPP6 in familial idiopathic ventricular fibrillation. *American Journal of Human Genetics*, **2009**, 84, 468-76	11	121

154	Clinical Aspects of Type 3 Long-QT Syndrome: An International Multicenter Study. *Circulation*, **2016**, 134, 872-82	16.7	118
153	Contribution of sodium channel mutations to bradycardia and sinus node dysfunction in LQT3 families. *Circulation Research*, **2003**, 92, 976-83	15.7	118
152	Possible bradycardic mode of death and successful pacemaker treatment in a large family with features of long QT syndrome type 3 and Brugada syndrome. *Journal of Cardiovascular Electrophysiology*, **2001**, 12, 630-6	2.7	117
151	SARS-CoV-2, COVID-19, and inherited arrhythmia syndromes. *Heart Rhythm*, **2020**, 17, 1456-1462	6.7	115
150	Variants in the 3Runtranslated region of the KCNQ1-encoded Kv7.1 potassium channel modify disease severity in patients with type 1 long QT syndrome in an allele-specific manner. *European Heart Journal*, **2012**, 33, 714-23	9.5	113
149	Multilevel analyses of SCN5A mutations in arrhythmogenic right ventricular dysplasia/cardiomyopathy suggest non-canonical mechanisms for disease pathogenesis. *Cardiovascular Research*, **2017**, 113, 102-111	9.9	111
148	Functional Nav1.8 channels in intracardiac neurons: the link between SCN10A and cardiac electrophysiology. *Circulation Research*, **2012**, 111, 333-43	15.7	107
147	Identification of FOXP1 deletions in three unrelated patients with mental retardation and significant speech and language deficits. *Human Mutation*, **2010**, 31, E1851-60	4.7	105
146	Genetics of cardiac arrhythmias. *Heart*, **2005**, 91, 1352-8	5.1	102
145	Diagnostic value of flecainide testing in unmasking SCN5A-related Brugada syndrome. *Journal of Cardiovascular Electrophysiology*, **2006**, 17, 857-64	2.7	101
144	Sodium channel (dys)function and cardiac arrhythmias. *Cardiovascular Therapeutics*, **2010**, 28, 287-94	3.3	98
143	Identification of a sudden cardiac death susceptibility locus at 2q24.2 through genome-wide association in European ancestry individuals. *PLoS Genetics*, **2011**, 7, e1002158	6	95
142	Genome-wide association study of multiple congenital heart disease phenotypes identifies a susceptibility locus for atrial septal defect at chromosome 4p16. *Nature Genetics*, **2013**, 45, 822-4	36.3	91
141	Mechanism of right precordial ST-segment elevation in structural heart disease: excitation failure by current-to-load mismatch. *Heart Rhythm*, **2010**, 7, 238-48	6.7	88
140	Role of common and rare variants in SCN10A: results from the Brugada syndrome QRS locus gene discovery collaborative study. *Cardiovascular Research*, **2015**, 106, 520-9	9.9	86
139	Genome-wide association of multiple complex traits in outbred mice by ultra-low-coverage sequencing. *Nature Genetics*, **2016**, 48, 912-8	36.3	81
138	PDZ domain-binding motif regulates cardiomyocyte compartment-specific NaV1.5 channel expression and function. *Circulation*, **2014**, 130, 147-60	16.7	77
137	52 Genetic Loci Influencing Myocardial Mass. *Journal of the American College of Cardiology*, **2016**, 68, 1435-1448	15.1	76

136	Gating-dependent mechanisms for flecainide action in SCN5A-linked arrhythmia syndromes. *Circulation*, **2001**, 104, 1200-5	16.7	75
135	Fever-induced QTc prolongation and ventricular arrhythmias in individuals with type 2 congenital long QT syndrome. *Journal of Clinical Investigation*, **2008**, 118, 2552-61	15.9	64
134	Genetically determined differences in sodium current characteristics modulate conduction disease severity in mice with cardiac sodium channelopathy. *Circulation Research*, **2009**, 104, 1283-92	15.7	63
133	Whole Exome Sequencing Reveals the Major Genetic Contributors to Nonsyndromic Tetralogy of Fallot. *Circulation Research*, **2019**, 124, 553-563	15.7	62
132	Calmodulin mutations and life-threatening cardiac arrhythmias: insights from the International Calmodulinopathy Registry. *European Heart Journal*, **2019**, 40, 2964-2975	9.5	61
131	Reduced sodium channel function unmasks residual embryonic slow conduction in the adult right ventricular outflow tract. *Circulation Research*, **2013**, 113, 137-41	15.7	59
130	Arrhythmogenic cardiomyopathy: pathology, genetics, and concepts in pathogenesis. *Cardiovascular Research*, **2017**, 113, 1521-1531	9.9	58
129	Beyond the One Gene-One Disease Paradigm: Complex Genetics and Pleiotropy in Inheritable Cardiac Disorders. *Circulation*, **2019**, 140, 595-610	16.7	56
128	Long QT syndrome caused by a large duplication in the KCNH2 (HERG) gene undetectable by current polymerase chain reaction-based exon-scanning methodologies. *Heart Rhythm*, **2006**, 3, 52-5	6.7	55
127	Tubulin polymerization modifies cardiac sodium channel expression and gating. *Cardiovascular Research*, **2010**, 85, 691-700	9.9	53
126	A connexin40 mutation associated with a malignant variant of progressive familial heart block type I. *Circulation: Arrhythmia and Electrophysiology*, **2012**, 5, 163-72	6.4	53
125	Na+ channel mutation leading to loss of function and non-progressive cardiac conduction defects. *Journal of Molecular and Cellular Cardiology*, **2003**, 35, 549-57	5.8	53
124	Inherited cardiac arrhythmias. *Nature Reviews Disease Primers*, **2020**, 6, 58	51.1	53
123	Genetics of sudden cardiac death caused by ventricular arrhythmias. *Nature Reviews Cardiology*, **2014**, 11, 96-111	14.8	52
122	Polymorphisms in human connexin40 gene promoter are associated with increased risk of hypertension in men. *Journal of Hypertension*, **2006**, 24, 325-30	1.9	52
121	Combined reduction of intercellular coupling and membrane excitability differentially affects transverse and longitudinal cardiac conduction. *Cardiovascular Research*, **2009**, 83, 52-60	9.9	51
120	Role of sequence variations in the human ether-a-go-go-related gene (HERG, KCNH2) in the Brugada syndrome. *Cardiovascular Research*, **2005**, 68, 441-53	9.9	51
119	hiPSC-derived cardiomyocytes from Brugada Syndrome patients without identified mutations do not exhibit clear cellular electrophysiological abnormalities. *Scientific Reports*, **2016**, 6, 30967	4.9	50

118	Genome wide analysis of drug-induced torsades de pointes: lack of common variants with large effect sizes. *PLoS ONE*, **2013**, 8, e78511	3.7	48
117	Developmental aspects of long QT syndrome type 3 and Brugada syndrome on the basis of a single SCN5A mutation in childhood. *Journal of the American College of Cardiology*, **2005**, 46, 331-7	15.1	46
116	Coxsackie and adenovirus receptor is a modifier of cardiac conduction and arrhythmia vulnerability in the setting of myocardial ischemia. *Journal of the American College of Cardiology*, **2014**, 63, 549-59	15.1	45
115	Exclusion of multiple candidate genes and large genomic rearrangements in SCN5A in a Dutch Brugada syndrome cohort. *Heart Rhythm*, **2007**, 4, 752-5	6.7	43
114	Common genetic variation modulating cardiac ECG parameters and susceptibility to sudden cardiac death. *Journal of Molecular and Cellular Cardiology*, **2012**, 52, 620-9	5.8	42
113	Natural genetic variation of the cardiac transcriptome in non-diseased donors and patients with dilated cardiomyopathy. *Genome Biology*, **2017**, 18, 170	18.3	40
112	Genetics of congenital heart disease: the contribution of the noncoding regulatory genome. *Journal of Human Genetics*, **2016**, 61, 13-9	4.3	36
111	Patch-Clamp Recording from Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes: Improving Action Potential Characteristics through Dynamic Clamp. *International Journal of Molecular Sciences*, **2017**, 18,	6.3	35
110	Dissection of a quantitative trait locus for PR interval duration identifies Tnni3k as a novel modulator of cardiac conduction. *PLoS Genetics*, **2012**, 8, e1003113	6	35
109	Genome-wide identification of expression quantitative trait loci (eQTLs) in human heart. *PLoS ONE*, **2014**, 9, e97380	3.7	35
108	Shared genetic pathways contribute to risk of hypertrophic and dilated cardiomyopathies with opposite directions of effect. *Nature Genetics*, **2021**, 53, 128-134	36.3	35
107	The Brugada Syndrome Susceptibility Gene Modulates Cardiac Transmural Ion Channel Patterning and Electrical Heterogeneity. *Circulation Research*, **2017**, 121, 537-548	15.7	34
106	GNB5 Mutations Cause an Autosomal-Recessive Multisystem Syndrome with Sinus Bradycardia and Cognitive Disability. *American Journal of Human Genetics*, **2016**, 99, 704-710	11	34
105	Switch From Fetal to Adult Isoform in Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes Unmasks the Cellular Phenotype of a Conduction Disease-Causing Mutation. *Journal of the American Heart Association*, **2017**, 6,	6	34
104	Predicting cardiac electrical response to sodium-channel blockade and Brugada syndrome using polygenic risk scores. *European Heart Journal*, **2019**, 40, 3097-3107	9.5	33
103	Characterization of a novel SCN5A mutation associated with Brugada syndrome reveals involvement of DIIIS4-S5 linker in slow inactivation. *Cardiovascular Research*, **2007**, 76, 418-29	9.9	33
102	Common genetic variants and modifiable risk factors underpin hypertrophic cardiomyopathy susceptibility and expressivity. *Nature Genetics*, **2021**, 53, 135-142	36.3	33
101	Dilated cardiomyopathy due to sodium channel dysfunction: what is the connection?. *Circulation: Arrhythmia and Electrophysiology*, **2008**, 1, 80-2	6.4	32

100	Analysis for Genetic Modifiers of Disease Severity in Patients With Long-QT Syndrome Type 2. *Circulation: Cardiovascular Genetics*, **2015**, 8, 447-456		31
99	Voltage-gated sodium channels: action players with many faces. *Annals of Medicine*, **2006**, 38, 472-82	1.5	31
98	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. *European Heart Journal*, **2018**, 39, 3961-3969	9.5	31
97	Sudden cardiac arrest associated with use of a non-cardiac drug that reduces cardiac excitability: evidence from bench, bedside, and community. *European Heart Journal*, **2013**, 34, 1506-16	9.5	30
96	The primary arrhythmia syndromes: same mutation, different manifestations. Are we starting to understand why?. *Journal of Cardiovascular Electrophysiology*, **2008**, 19, 445-52	2.7	30
95	Anti-arrhythmic potential of the late sodium current inhibitor GS-458967 in murine Scn5a-1798insD+/- and human SCN5A-1795insD+/- iPSC-derived cardiomyocytes. *Cardiovascular Research*, **2017**, 113, 829-838	9.9	28
94	Genome-Wide Polyadenylation Maps Reveal Dynamic mRNA 3REnd Formation in the Failing Human Heart. *Circulation Research*, **2016**, 118, 433-8	15.7	28
93	Arrhythmogenic cardiomyopathy: transgenic animal models provide novel insights into disease pathobiology. *Circulation: Cardiovascular Genetics*, **2011**, 4, 318-26		28
92	Transethnic Genome-Wide Association Study Provides Insights in the Genetic Architecture and Heritability of Long QT Syndrome. *Circulation*, **2020**, 142, 324-338	16.7	27
91	Gain-of-function mutation in SCN5A causes ventricular arrhythmias and early onset atrial fibrillation. *International Journal of Cardiology*, **2017**, 236, 187-193	3.2	23
90	The role of renin-angiotensin-aldosterone system polymorphisms in phenotypic expression of MYBPC3-related hypertrophic cardiomyopathy. *European Journal of Human Genetics*, **2012**, 20, 1071-7	5.3	23
89	A complex double deletion in LMNA underlies progressive cardiac conduction disease, atrial arrhythmias, and sudden death. *Circulation: Cardiovascular Genetics*, **2011**, 4, 280-7		23
88	Sudden Cardiac Arrest and Rare Genetic Variants in the Community. *Circulation: Cardiovascular Genetics*, **2016**, 9, 147-53		22
87	Sodium Channel Remodeling in Subcellular Microdomains of Murine Failing Cardiomyocytes. *Journal of the American Heart Association*, **2017**, 6,	6	21
86	Readthrough-Promoting Drugs Gentamicin and PTC124 Fail to Rescue Nav1.5 Function of Human-Induced Pluripotent Stem Cell-Derived Cardiomyocytes Carrying Nonsense Mutations in the Sodium Channel Gene SCN5A. *Circulation: Arrhythmia and Electrophysiology*, **2016**, 9,	6.4	20
85	Identification of an I-dependent and I-mediated proarrhythmic mechanism in cardiomyocytes derived from pluripotent stem cells of a Brugada syndrome patient. *Scientific Reports*, **2018**, 8, 11246	4.9	20
84	Quantitative trait loci for electrocardiographic parameters and arrhythmia in the mouse. *Journal of Molecular and Cellular Cardiology*, **2011**, 50, 380-9	5.8	20
83	Dilation of the Aorta Ascendens Forms Part of the Clinical Spectrum of HCN4 Mutations. *Journal of the American College of Cardiology*, **2016**, 67, 2313-2315	15.1	20

82	Impact of Selection Bias on Estimation of Subsequent Event Risk. *Circulation: Cardiovascular Genetics*, **2017**, 10,		19
81	Homozygous frameshift mutations in FAT1 cause a syndrome characterized by colobomatous-microphthalmia, ptosis, nephropathy and syndactyly. *Nature Communications*, **2019**, 10, 1180	17.4	19
80	Yield and Pitfalls of Ajmaline Testing in the Evaluation of Unexplained Cardiac Arrest and Sudden Unexplained Death: Single-Center Experience With 482 Families. *JACC: Clinical Electrophysiology*, **2017**, 3, 1400-1408	4.6	19
79	Variants in the SCN5A Promoter Associated With Various Arrhythmia Phenotypes. *Journal of the American Heart Association*, **2016**, 5,	6	18
78	Epidemiology of inherited arrhythmias. *Nature Reviews Cardiology*, **2020**, 17, 205-215	14.8	18
77	Exome sequencing identifies primary carnitine deficiency in a family with cardiomyopathy and sudden death. *European Journal of Human Genetics*, **2017**, 25, 783-787	5.3	16
76	Developmental aspects of cardiac arrhythmogenesis. *Cardiovascular Research*, **2011**, 91, 243-51	9.9	16
75	The yield of postmortem genetic testing in sudden death cases with structural findings at autopsy. *European Journal of Human Genetics*, **2020**, 28, 17-22	5.3	16
74	A heterozygous deletion mutation in the cardiac sodium channel gene SCN5A with loss- and gain-of-function characteristics manifests as isolated conduction disease, without signs of Brugada or long QT syndrome. *PLoS ONE*, **2013**, 8, e67963	3.7	15
73	Association of Chromosome 9p21 With Subsequent Coronary Heart Disease Events. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002471	5.2	14
72	A novel LQT3 mutation implicates the human cardiac sodium channel domain IVS6 in inactivation kinetics. *Cardiovascular Research*, **2003**, 57, 1072-8	9.9	14
71	Subsequent Event Risk in Individuals With Established Coronary Heart Disease. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002470	5.2	13
70	Mutation Type and a Genetic Risk Score Associate Variably With Brugada Syndrome Phenotype in Families. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002911	5.2	13
69	Electrophysiological Abnormalities in VLCAD Deficient hiPSC-Cardiomyocytes Can Be Improved by Lowering Accumulation of Fatty Acid Oxidation Intermediates. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	13
68	Early repolarization pattern: its ECG characteristics, arrhythmogeneity and heritability. *Journal of Interventional Cardiac Electrophysiology*, **2014**, 39, 185-92	2.4	13
67	Substitution of a conserved alanine in the domain IIIS4-S5 linker of the cardiac sodium channel causes long QT syndrome. *Cardiovascular Research*, **2005**, 67, 459-66	9.9	13
66	Next-Generation Sequencing in Post-mortem Genetic Testing of Young Sudden Cardiac Death Cases. *Frontiers in Cardiovascular Medicine*, **2016**, 3, 13	5.4	13
65	Enhancing rare variant interpretation in inherited arrhythmias through quantitative analysis of consortium disease cohorts and population controls. *Genetics in Medicine*, **2021**, 23, 47-58	8.1	13

64	When genetic burden reaches threshold. *European Heart Journal*, **2020**, 41, 3849-3855	9.5	12
63	A common co-morbidity modulates disease expression and treatment efficacy in inherited cardiac sodium channelopathy. *European Heart Journal*, **2018**, 39, 2898-2907	9.5	12
62	Genomic organisation and chromosomal localisation of two members of the KCND ion channel family, KCND2 and KCND3. *Human Genetics*, **2000**, 106, 614-9	6.3	12
61	Systematic large-scale assessment of the genetic architecture of left ventricular noncompaction reveals diverse etiologies. *Genetics in Medicine*, **2021**, 23, 856-864	8.1	12
60	TNNI3K in cardiovascular disease and prospects for therapy. *Journal of Molecular and Cellular Cardiology*, **2015**, 82, 167-73	5.8	11
59	Heart failure following STEMI: a contemporary cohort study of incidence and prognostic factors. *Open Heart*, **2017**, 4, e000551	3	10
58	Enhanced late sodium current underlies pro-arrhythmic intracellular sodium and calcium dysregulation in murine sodium channelopathy. *International Journal of Cardiology*, **2018**, 263, 54-62	3.2	10
57	Supraventricular tachycardias, conduction disease, and cardiomyopathy in 3 families with the same rare variant in TNNI3K (p.Glu768Lys). *Heart Rhythm*, **2019**, 16, 98-105	6.7	9
56	SNPs identified as modulators of ECG traits in the general population do not markedly affect ECG traits during acute myocardial infarction nor ventricular fibrillation risk in this condition. *PLoS ONE*, **2013**, 8, e57216	3.7	9
55	Bioinformatic analysis of a plakophilin-2-dependent transcription network: implications for the mechanisms of arrhythmogenic right ventricular cardiomyopathy in humans and in boxer dogs. *Europace*, **2018**, 20, iii125-iii132	3.9	9
54	Systems Genetics Approaches in Rat Identify Novel Genes and Gene Networks Associated With Cardiac Conduction. *Journal of the American Heart Association*, **2018**, 7, e009243	6	9
53	Common and rare susceptibility genetic variants predisposing to Brugada syndrome in Thailand. *Heart Rhythm*, **2020**, 17, 2145-2153	6.7	8
52	Functional Consequences of the -p.Y1977N Mutation within the PY Ubiquitylation Motif: Discrepancy between HEK293 Cells and Transgenic Mice. *International Journal of Molecular Sciences* , **2019**, 20,	6.3	8
51	Integrative genomic approach identifies multiple genes involved in cardiac collagen deposition. *Circulation: Cardiovascular Genetics*, **2014**, 7, 790-8		8
50	Pharmacological rescue of mutant ion channels. *Cardiovascular Research*, **2002**, 55, 229-32	9.9	8
49	Genetic variation in causes bradycardia by augmenting the cholinergic response via increased acetylcholine-activated potassium current ( ). *DMM Disease Models and Mechanisms*, **2019**, 12,	4.1	7
48	The chemical compound PTC124 does not affect cellular electrophysiology of cardiac ventricular myocytes. *Cardiovascular Drugs and Therapy*, **2012**, 26, 41-5	3.9	7
47	GATA6 mutations: Characterization of two novel patients and a comprehensive overview of the GATA6 genotypic and phenotypic spectrum. *American Journal of Medical Genetics, Part A*, **2019**, 179, 1836-1845	2.5	6

46	Cardiac desmosomal (dys)function and myocyte viability. *Cell Cycle*, **2010**, 9, 1246-52	4.7	6
45	Sequential Defects in Cardiac Lineage Commitment and Maturation Cause Hypoplastic Left Heart Syndrome. *Circulation*, **2021**, 144, 1409-1428	16.7	6
44	Chronically elevated branched chain amino acid levels are pro-arrhythmic. *Cardiovascular Research*, **2021**,	9.9	6
43	Illuminating the path from genetics to clinical outcome in Brugada syndrome. *European Heart Journal*, **2021**, 42, 1091-1093	9.5	6
42	Minor hypertrophic cardiomyopathy genes, major insights into the genetics of cardiomyopathies. *Nature Reviews Cardiology*, **2021**,	14.8	5
41	Blood Pressure-Associated Genetic Variants in the Natriuretic Peptide Receptor 1 Gene Modulate Guanylate Cyclase Activity. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002472	5.2	4
40	Genome-wide association studies of cardiac electrical phenotypes. *Cardiovascular Research*, **2020**, 116, 1620-1634	9.9	4
39	Genomic organisation and chromosomal localisation of two members of the KCND ion channel family, KCND2 and KCND3. *Human Genetics*, **2000**, 106, 614-619	6.3	4
38	Complex Genetics of Cardiovascular Traits in Mice: F2-Mapping of QTLs and Their Underlying Genes. *Methods in Molecular Biology*, **2017**, 1488, 431-454	1.4	4
37	Biallelic loss-of-function variants in PLD1 cause congenital right-sided cardiac valve defects and neonatal cardiomyopathy. *Journal of Clinical Investigation*, **2021**, 131,	15.9	4
36	Genetic Basis of Ventricular Arrhythmias. *Current Cardiovascular Risk Reports*, **2010**, 4, 454-460	0.9	3
35	Animal models and animal-free innovations for cardiovascular research: current status and routes to be explored. Consensus document of the ESC working group on myocardial function and the ESC Working Group on Cellular Biology of the Heart.. *Cardiovascular Research*, **2022**,	9.9	3
34	Functional modulation of atrio-ventricular conduction by enhanced late sodium current and calcium-dependent mechanisms in Scn5a1798insD/+ mice. *Europace*, **2020**, 22, 1579-1589	3.9	3
33	Genomic approaches for the elucidation of genes and gene networks underlying cardiovascular traits. *Biophysical Reviews*, **2018**, 10, 1053-1060	3.7	3
32	Seasonality of ventricular fibrillation at first myocardial infarction and association with viral exposure. *PLoS ONE*, **2020**, 15, e0226936	3.7	2
31	Chemokine ligand 9 modulates cardiac repolarization via Cxcr3 receptor binding. *International Journal of Cardiology*, **2015**, 201, 49-52	3.2	2
30	Genetics of lone atrial fibrillation. *Europace*, **2010**, 12, 1351-2	3.9	2
29	Genetic Background Determines Magnitude of Late Sodium Current, Extent of Intracellular Na+ and Ca2+ Dysregulation, and Severity of Cardiomyopathy in Murine Sodium Channelopathy. *Heart Rhythm*, **2009**, 6, 1686	6.7	2

28	Common Genetic Variants Contribute to Risk of Transposition of the Great Arteries. *Circulation Research*, **2021**,	15.7	2
27	Inherited dilated cardiomyopathy in a large Moroccan family caused by LMNA mutation. *Anatolian Journal of Cardiology*, **2018**, 20, 65-68	0.8	2
26	Targeting the Microtubule EB1-CLASP2 Complex Modulates Na1.5 at Intercalated Discs. *Circulation Research*, **2021**, 129, 349-365	15.7	2
25	Electrophysiological Abnormalities in VLCAD Deficient hiPSC-Cardiomyocytes Do not Improve with Carnitine Supplementation. *Frontiers in Pharmacology*, **2020**, 11, 616834	5.6	2
24	Sibling history is associated with heart failure after a first myocardial infarction. *Open Heart*, **2020**, 7, e001143	3	1
23	Cardiac dyssynchrony and response to cardiac resynchronisation therapy in heart failure: can genetic predisposition play a role?. *Netherlands Heart Journal*, **2016**, 24, 11-5	2.2	1
22	Role of Rare and Common Genetic Variation in SCN5A in Cardiac Electrical Function and Arrhythmia. *Cardiac Electrophysiology Clinics*, **2014**, 6, 665-677	1.4	1
21	Genomics of cardiac electrical function. *Briefings in Functional Genomics*, **2014**, 13, 39-50	4.9	1
20	Genetic predisposition for sudden cardiac death in myocardial ischaemia: the Arrhythmia Genetics in the NEtherlandS study. *Netherlands Heart Journal*, **2011**, 19, 96-100	2.2	1
19	Complex inheritance for susceptibility to sudden cardiac death. *Current Pharmaceutical Design*, **2013**, 19, 6864-72	3.3	1
18	Exploring the Relationship Between Schizophrenia and Cardiovascular Disease: A Genetic Correlation and Multivariable Mendelian Randomization Study. *Schizophrenia Bulletin*, **2021**,	1.3	1
17	The genetic architecture of left ventricular non-compaction reveals both substantial overlap with other cardiomyopathies and a distinct aetiology in a subset of cases		1
16	Genetics and genomics of arrhythmic risk: current and future strategies to prevent sudden cardiac death. *Nature Reviews Cardiology*, **2021**, 18, 774-784	14.8	1
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