

Connie R Bezzina

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2697891/publications.pdf>

Version: 2024-02-01

206
papers

15,994
citations

14644

66
h-index

18633

119
g-index

215
all docs

215
docs citations

215
times ranked

13765
citing authors

#	ARTICLE	IF	CITATIONS
1	Maturation of hiPSC-derived cardiomyocytes promotes adult alternative splicing of SCN5A and reveals changes in sodium current associated with cardiac arrhythmia. Cardiovascular Research, 2023, 119, 167-182.	1.8	13
2	Chronically elevated branched chain amino acid levels are pro-arrhythmic. Cardiovascular Research, 2022, 118, 1742-1757.	1.8	24
3	Minor hypertrophic cardiomyopathy genes, major insights into the genetics of cardiomyopathies. Nature Reviews Cardiology, 2022, 19, 151-167.	6.1	50
4	Exploring the Relationship Between Schizophrenia and Cardiovascular Disease: A Genetic Correlation and Multivariable Mendelian Randomization Study. Schizophrenia Bulletin, 2022, 48, 463-473.	2.3	28
5	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, 118, 3016-3051.	1.8	30
6	Common Genetic Variants Contribute to Risk of Transposition of the Great Arteries. Circulation Research, 2022, 130, 166-180.	2.0	15
7	Genome-wide association analyses identify new Brugada syndrome risk loci and highlight a new mechanism of sodium channel regulation in disease susceptibility. Nature Genetics, 2022, 54, 232-239.	9.4	55
8	First Steps of Population Genomic Medicine in the Arrhythmia World: Pros and Cons. Circulation, 2022, 145, 892-895.	1.6	2
9	European Heart Rhythm Association (EHRA)/Heart Rhythm Society (HRS)/Asia Pacific Heart Rhythm Society (APHRS)/Latin American Heart Rhythm Society (LAHRS) Expert Consensus Statement on the state of genetic testing for cardiac diseases. Europace, 2022, 24, 1307-1367.	0.7	108
10	European Heart Rhythm Association (EHRA)/Heart Rhythm Society (HRS)/Asia Pacific Heart Rhythm Society (APHRS)/Latin American Heart Rhythm Society (LAHRS) Expert Consensus Statement on the State of Genetic Testing for Cardiac Diseases. Heart Rhythm, 2022, 19, e1-e60.	0.3	78
11	European Heart Rhythm Association (<sc>EHRA</sc>)/Heart Rhythm Society (<sc>HRS</sc>)/Asia Pacific Heart Rhythm Society (<sc>APHRS</sc>)/Latin American Heart Rhythm Society (<sc>LAHRS</sc>) Expert Consensus Statement on the state of genetic testing for cardiac diseases. Journal of Arrhythmia, 2022, 38, 491-553.	0.5	24
12	A deep learning approach identifies new ECG features in congenital long QT syndrome. BMC Medicine, 2022, 20, 162.	2.3	13
13	Enhancing rare variant interpretation in inherited arrhythmias through quantitative analysis of consortium disease cohorts and population controls. Genetics in Medicine, 2021, 23, 47-58.	1.1	57
14	Common genetic variants and modifiable risk factors underpin hypertrophic cardiomyopathy susceptibility and expressivity. Nature Genetics, 2021, 53, 135-142.	9.4	165
15	Illuminating the path from genetics to clinical outcome in Brugada syndrome. European Heart Journal, 2021, 42, 1091-1093.	1.0	12
16	Biallelic loss-of-function variants in PLD1 cause congenital right-sided cardiac valve defects and neonatal cardiomyopathy. Journal of Clinical Investigation, 2021, 131, .	3.9	16
17	Genetics and genomics of arrhythmic risk: current and future strategies to prevent sudden cardiac death. Nature Reviews Cardiology, 2021, 18, 774-784.	6.1	15
18	Clinical Characteristics of <i>SCN5A</i> p.R965C Carriers: A Common Founder Variant Predisposing to Brugada Syndrome in Thailand. Circulation Genomic and Precision Medicine, 2021, 14, e003229.	1.6	3

#	ARTICLE	IF	CITATIONS
19	Rare variants in KDR, encoding VEGF Receptor 2, are associated with tetralogy of Fallot. <i>Genetics in Medicine</i> , 2021, 23, 1952-1960.	1.1	7
20	Targeting the Microtubule EB1-CLASP2 Complex Modulates Na ^v 1.5 at Intercalated Discs. <i>Circulation Research</i> , 2021, 129, 349-365.	2.0	23
21	Variant Intronic Enhancer Controls <i>SCN10A-short</i> Expression and Heart Conduction. <i>Circulation</i> , 2021, 144, 229-242.	1.6	20
22	ALPK3: a full spectrum cardiomyopathy gene?. <i>European Heart Journal</i> , 2021, 42, 3074-3077.	1.0	4
23	Novel pathogenic role for galectin-3 in early disease stages of arrhythmogenic cardiomyopathy. <i>Heart Rhythm</i> , 2021, 18, 1394-1403.	0.3	8
24	Shared genetic pathways contribute to risk of hypertrophic and dilated cardiomyopathies with opposite directions of effect. <i>Nature Genetics</i> , 2021, 53, 128-134.	9.4	155
25	Systematic large-scale assessment of the genetic architecture of left ventricular noncompaction reveals diverse etiologies. <i>Genetics in Medicine</i> , 2021, 23, 856-864.	1.1	45
26	Sequential Defects in Cardiac Lineage Commitment and Maturation Cause Hypoplastic Left Heart Syndrome. <i>Circulation</i> , 2021, 144, 1409-1428.	1.6	29
27	Two siblings with early repolarization syndrome: clinical and genetic characterization by whole-exome sequencing. <i>Europace</i> , 2021, 23, 775-780.	0.7	1
28	The yield of postmortem genetic testing in sudden death cases with structural findings at autopsy. <i>European Journal of Human Genetics</i> , 2020, 28, 17-22.	1.4	38
29	Epidemiology of inherited arrhythmias. <i>Nature Reviews Cardiology</i> , 2020, 17, 205-215.	6.1	37
30	Scientists on the Spot: The complex inheritance of cardiac disorders. <i>Cardiovascular Research</i> , 2020, 116, e11-e11.	1.8	0
31	Inherited cardiac arrhythmias. <i>Nature Reviews Disease Primers</i> , 2020, 6, 58.	18.1	146
32	Functional modulation of atrio-ventricular conduction by enhanced late sodium current and calcium-dependent mechanisms in <i>Scn5a1798insD/+</i> mice. <i>Europace</i> , 2020, 22, 1579-1589.	0.7	9
33	<i>SCN5A</i> Mutation Type and a Genetic Risk Score Associate Variably With Brugada Syndrome Phenotype in <i>SCN5A</i> Families. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002911.	1.6	41
34	Sibling history is associated with heart failure after a first myocardial infarction. <i>Open Heart</i> , 2020, 7, e001143.	0.9	1
35	When genetic burden reaches threshold. <i>European Heart Journal</i> , 2020, 41, 3849-3855.	1.0	40
36	Transethnic Genome-Wide Association Study Provides Insights in the Genetic Architecture and Heritability of Long QT Syndrome. <i>Circulation</i> , 2020, 142, 324-338.	1.6	83

#	ARTICLE	IF	CITATIONS
37	Genome-wide association studies of cardiac electrical phenotypes. <i>Cardiovascular Research</i> , 2020, 116, 1620-1634.	1.8	18
38	Common and rare susceptibility genetic variants predisposing to Brugada syndrome in Thailand. <i>Heart Rhythm</i> , 2020, 17, 2145-2153.	0.3	23
39	Seasonality of ventricular fibrillation at first myocardial infarction and association with viral exposure. <i>PLoS ONE</i> , 2020, 15, e0226936.	1.1	4
40	Electrophysiological Abnormalities in VLCAD Deficient hiPSC-Cardiomyocytes Can Be Improved by Lowering Accumulation of Fatty Acid Oxidation Intermediates. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2589.	1.8	24
41	SARS-CoV-2, COVID-19, and inherited arrhythmia syndromes. <i>Heart Rhythm</i> , 2020, 17, 1456-1462.	0.3	162
42	Electrophysiological Abnormalities in VLCAD Deficient hiPSC-Cardiomyocytes Do not Improve with Carnitine Supplementation. <i>Frontiers in Pharmacology</i> , 2020, 11, 616834.	1.6	5
43	Research in understudied populations offers local and global insights into the genetics of hypertrophic cardiomyopathy. <i>Polish Archives of Internal Medicine</i> , 2020, 130, 76-78.	0.3	1
44	Title is missing!. , 2020, 15, e0226936.		0
45	Title is missing!. , 2020, 15, e0226936.		0
46	Supraventricular tachycardias, conduction disease, and cardiomyopathy in 3 families with the same rare variant in TNNI3K (p.Glu768Lys). <i>Heart Rhythm</i> , 2019, 16, 98-105.	0.3	18
47	Beyond the One Gene—One Disease Paradigm. <i>Circulation</i> , 2019, 140, 595-610.	1.6	101
48	<i>GATA6</i> mutations: Characterization of two novel patients and a comprehensive overview of the <i>GATA6</i> genotypic and phenotypic spectrum. <i>American Journal of Medical Genetics, Part A</i> , 2019, 179, 1836-1845.	0.7	16
49	Functional Consequences of the SCN5A-p.Y1977N Mutation within the PY Ubiquitylation Motif: Discrepancy between HEK293 Cells and Transgenic Mice. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5033.	1.8	11
50	Blood Pressure-Associated Genetic Variants in the Natriuretic Peptide Receptor 1 Gene Modulate Guanylate Cyclase Activity. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, e002472.	1.6	10
51	Predicting cardiac electrical response to sodium-channel blockade and Brugada syndrome using polygenic risk scores. <i>European Heart Journal</i> , 2019, 40, 3097-3107.	1.0	55
52	Genetic variation in <i>GNB5</i> causes bradycardia by increasing IK,ACh augmenting cholinergic response. <i>DMM Disease Models and Mechanisms</i> , 2019, 12, .	1.2	19
53	Calmodulin mutations and life-threatening cardiac arrhythmias: insights from the International Calmodulinopathy Registry. <i>European Heart Journal</i> , 2019, 40, 2964-2975.	1.0	116
54	Subsequent Event Risk in Individuals With Established Coronary Heart Disease. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, e002470.	1.6	17

#	ARTICLE	IF	CITATIONS
55	Association of Chromosome 9p21 With Subsequent Coronary Heart Disease Events. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, e002471.	1.6	22
56	Homozygous frameshift mutations in FAT1 cause a syndrome characterized by colobomatous-microphthalmia, ptosis, nephropathy and syndactyly. <i>Nature Communications</i> , 2019, 10, 1180.	5.8	27
57	Câ€...Identification of the major genetic contributors to tetralogy of fallot. , 2019, , .		0
58	Predicting Risk for Adult-Onset Sudden Cardiac Death in the Population. <i>Journal of the American College of Cardiology</i> , 2019, 74, 2635-2637.	1.2	3
59	Whole Exome Sequencing Reveals the Major Genetic Contributors to Nonsyndromic Tetralogy of Fallot. <i>Circulation Research</i> , 2019, 124, 553-563.	2.0	118
60	A common co-morbidity modulates disease expression and treatment efficacy in inherited cardiac sodium channelopathy. <i>European Heart Journal</i> , 2018, 39, 2898-2907.	1.0	17
61	Bioinformatic analysis of a plakophilin-2-dependent transcription network: implications for the mechanisms of arrhythmogenic right ventricular cardiomyopathy in humans and in boxer dogs. <i>Europace</i> , 2018, 20, iii125-iii132.	0.7	16
62	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. <i>European Heart Journal</i> , 2018, 39, 3961-3969.	1.0	59
63	Systems Genetics Approaches in Rat Identify Novel Genes and Gene Networks Associated With Cardiac Conduction. <i>Journal of the American Heart Association</i> , 2018, 7, e009243.	1.6	18
64	Enhanced late sodium current underlies pro-arrhythmic intracellular sodium and calcium dysregulation in murine sodium channelopathy. <i>International Journal of Cardiology</i> , 2018, 263, 54-62.	0.8	16
65	Genomic approaches for the elucidation of genes and gene networks underlying cardiovascular traits. <i>Biophysical Reviews</i> , 2018, 10, 1053-1060.	1.5	5
66	Identification of an INa-dependent and Ito-mediated proarrhythmic mechanism in cardiomyocytes derived from pluripotent stem cells of a Brugada syndrome patient. <i>Scientific Reports</i> , 2018, 8, 11246.	1.6	31
67	Inherited dilated cardiomyopathy in a large Moroccan family caused by LMNA mutation. <i>Anatolian Journal of Cardiology</i> , 2018, 20, 65-68.	0.5	3
68	Multilevel analyses of SCN5A mutations in arrhythmogenic right ventricular dysplasia/cardiomyopathy suggest non-canonical mechanisms for disease pathogenesis. <i>Cardiovascular Research</i> , 2017, 113, 102-111.	1.8	148
69	Gain-of-function mutation in SCN5A causes ventricular arrhythmias and early onset atrial fibrillation. <i>International Journal of Cardiology</i> , 2017, 236, 187-193.	0.8	30
70	Utility of Post-Mortem Genetic Testing in Cases of Sudden Arrhythmic Death Syndrome. <i>Journal of the American College of Cardiology</i> , 2017, 69, 2134-2145.	1.2	219
71	Pacing Discovery. <i>Circulation Research</i> , 2017, 120, 1524-1526.	2.0	0
72	Anti-arrhythmic potential of the late sodium current inhibitor GS-458967 in murine Scn5a-1798insD+/âˆ“ and human SCN5A-1795insD+/âˆ“ iPSC-derived cardiomyocytes. <i>Cardiovascular Research</i> , 2017, 113, 829-838.	1.8	41

#	ARTICLE	IF	CITATIONS
73	The Brugada Syndrome Susceptibility Gene <i>HEY2</i> Modulates Cardiac Transmural Ion Channel Patterning and Electrical Heterogeneity. <i>Circulation Research</i> , 2017, 121, 537-548.	2.0	63
74	Exome sequencing identifies primary carnitine deficiency in a family with cardiomyopathy and sudden death. <i>European Journal of Human Genetics</i> , 2017, 25, 783-787.	1.4	21
75	Familial Disease Is Not Always Genetic: A Family With Atrioventricular Block and Mitral Regurgitation. <i>Canadian Journal of Cardiology</i> , 2017, 33, 554.e9-554.e11.	0.8	0
76	Impact of Selection Bias on Estimation of Subsequent Event Risk. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	28
77	Arrhythmogenic cardiomyopathy: pathology, genetics, and concepts in pathogenesis. <i>Cardiovascular Research</i> , 2017, 113, 1521-1531.	1.8	98
78	Response by Veerman et al to Letter Regarding Article, "The Brugada Syndrome Susceptibility Gene <i>HEY2</i> Modulates Cardiac Transmural Ion Channel Patterning and Electrical Heterogeneity" <i>Circulation Research</i> , 2017, 121, e21.	2.0	0
79	Dissecting the Genetic Basis of the ECG as a Means of Understanding Mechanisms of Arrhythmia. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	2
80	Sodium Channel Remodeling in Subcellular Microdomains of Murine Failing Cardiomyocytes. <i>Journal of the American Heart Association</i> , 2017, 6, .	1.6	31
81	Yield and Pitfalls of Ajmaline Testing in the Evaluation of Unexplained Cardiac Arrest and Sudden Unexplained Death. <i>JACC: Clinical Electrophysiology</i> , 2017, 3, 1400-1408.	1.3	34
82	Heart failure following STEMI: a contemporary cohort study of incidence and prognostic factors. <i>Open Heart</i> , 2017, 4, e000551.	0.9	26
83	Patch-Clamp Recording from Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes: Improving Action Potential Characteristics through Dynamic Clamp. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1873.	1.8	55
84	Natural genetic variation of the cardiac transcriptome in non-diseased donors and patients with dilated cardiomyopathy. <i>Genome Biology</i> , 2017, 18, 170.	3.8	70
85	Complex Genetics of Cardiovascular Traits in Mice: F2-Mapping of QTLs and Their Underlying Genes. <i>Methods in Molecular Biology</i> , 2017, 1488, 431-454.	0.4	4
86	Switch From Fetal to Adult <i>SCN5A</i> Isoform in Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes Unmasks the Cellular Phenotype of a Conduction Disease-Causing Mutation. <i>Journal of the American Heart Association</i> , 2017, 6, .	1.6	54
87	Next-Generation Sequencing in Post-mortem Genetic Testing of Young Sudden Cardiac Death Cases. <i>Frontiers in Cardiovascular Medicine</i> , 2016, 3, 13.	1.1	20
88	Genome-wide association of multiple complex traits in outbred mice by ultra-low-coverage sequencing. <i>Nature Genetics</i> , 2016, 48, 912-918.	9.4	124
89	Dilation of the Aorta Ascendens Forms Part of the Clinical Spectrum of HCN4 Mutations. <i>Journal of the American College of Cardiology</i> , 2016, 67, 2313-2315.	1.2	25
90	Clinical Aspects of Type 3 Long-QT Syndrome. <i>Circulation</i> , 2016, 134, 872-882.	1.6	162

#	ARTICLE	IF	CITATIONS
91	GNB5 Mutations Cause an Autosomal-Recessive Multisystem Syndrome with Sinus Bradycardia and Cognitive Disability. American Journal of Human Genetics, 2016, 99, 704-710.	2.6	58
92	52 Genetic Loci Influencing Myocardial Mass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
93	Variants in the <i>SCN5A</i> Promoter Associated With Various Arrhythmia Phenotypes. Journal of the American Heart Association, 2016, 5, .	1.6	22
94	hiPSC-derived cardiomyocytes from Brugada Syndrome patients without identified mutations do not exhibit clear cellular electrophysiological abnormalities. Scientific Reports, 2016, 6, 30967.	1.6	64
95	Readthrough-Promoting Drugs Gentamicin and PTC124 Fail to Rescue Na ^v 1.5 Function of Human-Induced Pluripotent Stem Cell-Derived Cardiomyocytes Carrying Nonsense Mutations in the Sodium Channel Gene <i>SCN5A</i> . Circulation: Arrhythmia and Electrophysiology, 2016, 9, .	2.1	28
96	Sudden Cardiac Arrest and Rare Genetic Variants in the Community. Circulation: Cardiovascular Genetics, 2016, 9, 147-153.	5.1	27
97	Cardiac dyssynchrony and response to cardiac resynchronisation therapy in heart failure: can genetic predisposition play a role?. Netherlands Heart Journal, 2016, 24, 11-15.	0.3	1
98	Genome-Wide Polyadenylation Maps Reveal Dynamic mRNA 3'-End Formation in the Failing Human Heart. Circulation Research, 2016, 118, 433-438.	2.0	41
99	Genetics of congenital heart disease: the contribution of the noncoding regulatory genome. Journal of Human Genetics, 2016, 61, 13-19.	1.1	52
100	Chemokine ligand 9 modulates cardiac repolarization via Cxcr3 receptor binding. International Journal of Cardiology, 2015, 201, 49-52.	0.8	2
101	Analysis for Genetic Modifiers of Disease Severity in Patients With Long-QT Syndrome Type 2. Circulation: Cardiovascular Genetics, 2015, 8, 447-456.	5.1	51
102	Genetics of Sudden Cardiac Death. Circulation Research, 2015, 116, 1919-1936.	2.0	211
103	Role of common and rare variants in <i>SCN10A</i> : results from the Brugada syndrome QRS locus gene discovery collaborative study. Cardiovascular Research, 2015, 106, 520-529.	1.8	108
104	TNNI3K in cardiovascular disease and prospects for therapy. Journal of Molecular and Cellular Cardiology, 2015, 82, 167-173.	0.9	15
105	Integrative Genomic Approach Identifies Multiple Genes Involved in Cardiac Collagen Deposition. Circulation: Cardiovascular Genetics, 2014, 7, 790-798.	5.1	10
106	Genomics of cardiac electrical function. Briefings in Functional Genomics, 2014, 13, 39-50.	1.3	1
107	Common genetic variation and risk for sudden cardiac death in acquired cardiac disease. Heart Rhythm, 2014, 11, 653-654.	0.3	1
108	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

#	ARTICLE	IF	CITATIONS
109	Early repolarization pattern: its ECG characteristics, arrhythmogeneity and heritability. <i>Journal of Interventional Cardiac Electrophysiology</i> , 2014, 39, 185-192.	0.6	15
110	Coxsackie and Adenovirus Receptor Is a Modifier of Cardiac Conduction and Arrhythmia Vulnerability in the Setting of Myocardial Ischemia. <i>Journal of the American College of Cardiology</i> , 2014, 63, 549-559.	1.2	58
111	A Mutation in CALM1 Encoding Calmodulin in Familial Idiopathic Ventricular Fibrillation in Childhood and Adolescence. <i>Journal of the American College of Cardiology</i> , 2014, 63, 259-266.	1.2	160
112	Genetics of sudden cardiac death caused by ventricular arrhythmias. <i>Nature Reviews Cardiology</i> , 2014, 11, 96-111.	6.1	59
113	PDZ Domain Binding Motif Regulates Cardiomyocyte Compartment-Specific Na ^v 1.5 Channel Expression and Function. <i>Circulation</i> , 2014, 130, 147-160.	1.6	113
114	Role of Rare and Common Genetic Variation in SCN5A in Cardiac Electrical Function and Arrhythmia. <i>Cardiac Electrophysiology Clinics</i> , 2014, 6, 665-677.	0.7	1
115	HCN4 Mutations in Multiple Families With Bradycardia and Left Ventricular Noncompaction Cardiomyopathy. <i>Journal of the American College of Cardiology</i> , 2014, 64, 745-756.	1.2	173
116	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014, 46, 826-836.	9.4	281
117	A common genetic variant within SCN10A modulates cardiac SCN5A expression. <i>Journal of Clinical Investigation</i> , 2014, 124, 1844-1852.	3.9	168
118	Genome-Wide Identification of Expression Quantitative Trait Loci (eQTLs) in Human Heart. <i>PLoS ONE</i> , 2014, 9, e97380.	1.1	44
119	Genome-wide association study of multiple congenital heart disease phenotypes identifies a susceptibility locus for atrial septal defect at chromosome 4p16. <i>Nature Genetics</i> , 2013, 45, 822-824.	9.4	123
120	Common variants at SCN5A-SCN10A and HEY2 are associated with Brugada syndrome, a rare disease with high risk of sudden cardiac death. <i>Nature Genetics</i> , 2013, 45, 1044-1049.	9.4	467
121	Sudden cardiac arrest associated with use of a non-cardiac drug that reduces cardiac excitability: evidence from bench, bedside, and community. <i>European Heart Journal</i> , 2013, 34, 1506-1516.	1.0	47
122	Reduced Sodium Channel Function Unmasks Residual Embryonic Slow Conduction in the Adult Right Ventricular Outflow Tract. <i>Circulation Research</i> , 2013, 113, 137-141.	2.0	87
123	Arrhythmogenic Right Ventricular Cardiomyopathy: Growing Evidence for Complex Inheritance. <i>Circulation: Cardiovascular Genetics</i> , 2013, 6, 525-527.	5.1	11
124	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. <i>PLoS ONE</i> , 2013, 8, e57216.	1.1	9
125	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. <i>PLoS ONE</i> , 2013, 8, e67963.	1.1	23
126	Genome Wide Analysis of Drug-Induced Torsades de Pointes: Lack of Common Variants with Large Effect Sizes. <i>PLoS ONE</i> , 2013, 8, e78511.	1.1	57

#	ARTICLE	IF	CITATIONS
127	Complex Inheritance for Susceptibility to Sudden Cardiac Death. <i>Current Pharmaceutical Design</i> , 2013, 19, 6864-6872.	0.9	3
128	Dissection of a Quantitative Trait Locus for PR Interval Duration Identifies Tnni3k as a Novel Modulator of Cardiac Conduction. <i>PLoS Genetics</i> , 2012, 8, e1003113.	1.5	45
129	A Connexin40 Mutation Associated With a Malignant Variant of Progressive Familial Heart Block Type I. <i>Circulation: Arrhythmia and Electrophysiology</i> , 2012, 5, 163-172.	2.1	58
130	A Large Candidate Gene Survey Identifies the <i>KCNE1</i> D85N Polymorphism as a Possible Modulator of Drug-Induced Torsades de Pointes. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 91-99.	5.1	150
131	Variants in the 5' untranslated region of the <i>KCNQ1</i> -encoded Kv7.1 potassium channel modify disease severity in patients with type 1 long QT syndrome in an allele-specific manner. <i>European Heart Journal</i> , 2012, 33, 714-723.	1.0	130
132	Intercalated disc abnormalities, reduced Na ⁺ current density, and conduction slowing in desmoglein-2 mutant mice prior to cardiomyopathic changes. <i>Cardiovascular Research</i> , 2012, 95, 409-418.	1.8	180
133	Functional Na ^v 1.8 Channels in Intracardiac Neurons. <i>Circulation Research</i> , 2012, 111, 333-343.	2.0	131
134	Common genetic variation modulating cardiac ECG parameters and susceptibility to sudden cardiac death. <i>Journal of Molecular and Cellular Cardiology</i> , 2012, 52, 620-629.	0.9	51
135	Induced pluripotent stem cell derived cardiomyocytes as models for cardiac arrhythmias. <i>Frontiers in Physiology</i> , 2012, 3, 346.	1.3	168
136	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. <i>American Journal of Human Genetics</i> , 2012, 91, 823-838.	2.6	227
137	The role of renin-angiotensin-aldosterone system polymorphisms in phenotypic expression of MYBPC3-related hypertrophic cardiomyopathy. <i>European Journal of Human Genetics</i> , 2012, 20, 1071-1077.	1.4	28
138	Cardiomyocytes Derived From Pluripotent Stem Cells Recapitulate Electrophysiological Characteristics of an Overlap Syndrome of Cardiac Sodium Channel Disease. <i>Circulation</i> , 2012, 125, 3079-3091.	1.6	245
139	The Chemical Compound PTC124 Does Not Affect Cellular Electrophysiology of Cardiac Ventricular Myocytes. <i>Cardiovascular Drugs and Therapy</i> , 2012, 26, 41-45.	1.3	8
140	Genetic variation in T-box binding element functionally affects SCN5A/SCN10A enhancer. <i>Journal of Clinical Investigation</i> , 2012, 122, 2519-2530.	3.9	167
141	KCND3 mutations in Brugada syndrome: The plot thickens. <i>Heart Rhythm</i> , 2011, 8, 1033-1035.	0.3	5
142	Inherited Cardiac Arrhythmia Syndromes: Role of the Sodium Channel. <i>Cardiac Electrophysiology Clinics</i> , 2011, 3, 93-112.	0.7	0
143	Quantitative trait loci for electrocardiographic parameters and arrhythmia in the mouse. <i>Journal of Molecular and Cellular Cardiology</i> , 2011, 50, 380-389.	0.9	22
144	Genetic predisposition for sudden cardiac death in myocardial ischaemia: the Arrhythmia Genetics in the NetherlandS study. <i>Netherlands Heart Journal</i> , 2011, 19, 96-100.	0.3	5

#	ARTICLE	IF	CITATIONS
145	Arrhythmogenic Cardiomyopathy. <i>Circulation: Cardiovascular Genetics</i> , 2011, 4, 318-326.	5.1	35
146	A Complex Double Deletion in <i>LMNA</i> Underlies Progressive Cardiac Conduction Disease, Atrial Arrhythmias, and Sudden Death. <i>Circulation: Cardiovascular Genetics</i> , 2011, 4, 280-287.	5.1	24
147	Developmental aspects of cardiac arrhythmogenesis. <i>Cardiovascular Research</i> , 2011, 91, 243-251.	1.8	25
148	Identification of a Sudden Cardiac Death Susceptibility Locus at 2q24.2 through Genome-Wide Association in European Ancestry Individuals. <i>PLoS Genetics</i> , 2011, 7, e1002158.	1.5	117
149	Familial Idiopathic Ventricular Fibrillation Linked to Chromosome 7q36 Harboring DPP6. <i>Journal of Arrhythmia</i> , 2011, 27, OP59_4.	0.5	0
150	Genetic Basis of Ventricular Arrhythmias. <i>Current Cardiovascular Risk Reports</i> , 2010, 4, 454-460.	0.8	3
151	Identification of FOXP1 deletions in three unrelated patients with mental retardation and significant speech and language deficits. <i>Human Mutation</i> , 2010, 31, E1851-E1860.	1.1	130
152	Genetic variation in SCN10A influences cardiac conduction. <i>Nature Genetics</i> , 2010, 42, 149-152.	9.4	248
153	Genome-wide association study identifies a susceptibility locus at 21q21 for ventricular fibrillation in acute myocardial infarction. <i>Nature Genetics</i> , 2010, 42, 688-691.	9.4	170
154	Cardiac desmosomal (dys)function and myocyte viability. <i>Cell Cycle</i> , 2010, 9, 1246-1252.	1.3	7
155	Tubulin polymerization modifies cardiac sodium channel expression and gating. <i>Cardiovascular Research</i> , 2010, 85, 691-700.	1.8	68
156	Genetics of lone atrial fibrillation. <i>Europace</i> , 2010, 12, 1351-1352.	0.7	3
157	Mechanism of right precordial ST-segment elevation in structural heart disease: Excitation failure by current-to-load mismatch. <i>Heart Rhythm</i> , 2010, 7, 238-248.	0.3	117
158	REVIEW: Sodium Channel (Dys)Function and Cardiac Arrhythmias. <i>Cardiovascular Therapeutics</i> , 2010, 28, 287-294.	1.1	128
159	Genetically Determined Differences in Sodium Current Characteristics Modulate Conduction Disease Severity in Mice With Cardiac Sodium Channelopathy. <i>Circulation Research</i> , 2009, 104, 1283-1292.	2.0	86
160	Combined reduction of intercellular coupling and membrane excitability differentially affects transverse and longitudinal cardiac conduction. <i>Cardiovascular Research</i> , 2009, 83, 52-60.	1.8	54
161	Myocyte necrosis underlies progressive myocardial dystrophy in mouse <i>dsg2</i> -related arrhythmogenic right ventricular cardiomyopathy. <i>Journal of Experimental Medicine</i> , 2009, 206, 1787-1802.	4.2	184
162	Haplotype-Sharing Analysis Implicates Chromosome 7q36 Harboring DPP6 in Familial Idiopathic Ventricular Fibrillation. <i>American Journal of Human Genetics</i> , 2009, 84, 468-476.	2.6	158

#	ARTICLE	IF	CITATIONS
163	Genetic Background Determines Magnitude of Late Sodium Current, Extent of Intracellular Na ⁺ and Ca ²⁺ Dysregulation, and Severity of Cardiomyopathy in Murine Sodium Channelopathy. <i>Heart Rhythm</i> , 2009, 6, 1686.	0.3	2
164	Type of SCN5A mutation determines clinical severity and degree of conduction slowing in loss-of-function sodium channelopathies. <i>Heart Rhythm</i> , 2009, 6, 341-348.	0.3	224
165	Myocyte necrosis underlies progressive myocardial dystrophy in mouse <i>dsg2</i> -related arrhythmogenic right ventricular cardiomyopathy. <i>Journal of Cell Biology</i> , 2009, 186, i5-i5.	2.3	0
166	The Primary Arrhythmia Syndromes: Same Mutation, Different Manifestations. Are We Starting to Understand Why?. <i>Journal of Cardiovascular Electrophysiology</i> , 2008, 19, 445-452.	0.8	33
167	Cardiac Sodium Channel Overlap Syndromes: Different Faces of SCN5A Mutations. <i>Trends in Cardiovascular Medicine</i> , 2008, 18, 78-87.	2.3	182
168	Dilated Cardiomyopathy due to Sodium Channel Dysfunction. <i>Circulation: Arrhythmia and Electrophysiology</i> , 2008, 1, 80-82.	2.1	38
169	Sodium channel β 1 subunit mutations associated with Brugada syndrome and cardiac conduction disease in humans. <i>Journal of Clinical Investigation</i> , 2008, 118, 2260-8.	3.9	400
170	Fever-induced QTc prolongation and ventricular arrhythmias in individuals with type 2 congenital long QT syndrome. <i>Journal of Clinical Investigation</i> , 2008, 118, 2552-61.	3.9	73
171	Characterization of a novel SCN5A mutation associated with Brugada syndrome reveals involvement of D1154S linker in slow inactivation. <i>Cardiovascular Research</i> , 2007, 76, 418-429.	1.8	40
172	Genetic modulation of cardiac repolarization reserve. <i>Heart Rhythm</i> , 2007, 4, 608-610.	0.3	15
173	Exclusion of multiple candidate genes and large genomic rearrangements in SCN5A in a Dutch Brugada syndrome cohort. <i>Heart Rhythm</i> , 2007, 4, 752-755.	0.3	48
174	Genetic Basis for Cardiac Arrhythmias. , 2007, , 2577-2598.		0
175	Long QT syndrome caused by a large duplication in the KCNH2 (HERG) gene undetectable by current polymerase chain reaction-based exon-scanning methodologies. <i>Heart Rhythm</i> , 2006, 3, 52-55.	0.3	65
176	Voltage-gated sodium channels: Action players with many faces. <i>Annals of Medicine</i> , 2006, 38, 472-482.	1.5	33
177	Polymorphisms in human connexin40 gene promoter are associated with increased risk of hypertension in men. <i>Journal of Hypertension</i> , 2006, 24, 325-330.	0.3	64
178	Diagnostic Value of Flecainide Testing in Unmasking SCN5A-Related Brugada Syndrome. <i>Journal of Cardiovascular Electrophysiology</i> , 2006, 17, 857-864.	0.8	120
179	Overlap Syndrome of Cardiac Sodium Channel Disease in Mice Carrying the Equivalent Mutation of Human SCN5A -1795insD. <i>Circulation</i> , 2006, 114, 2584-2594.	1.6	174
180	Familial Sudden Death Is an Important Risk Factor for Primary Ventricular Fibrillation. <i>Circulation</i> , 2006, 114, 1140-1145.	1.6	258

#	ARTICLE	IF	CITATIONS
181	Common Sodium Channel Promoter Haplotype in Asian Subjects Underlies Variability in Cardiac Conduction. <i>Circulation</i> , 2006, 113, 338-344.	1.6	215
182	Substitution of a conserved alanine in the domain IIS4â€“S5 linker of the cardiac sodium channel causes long QT syndrome. <i>Cardiovascular Research</i> , 2005, 67, 459-466.	1.8	16
183	The molecular genetics of arrhythmias. <i>Cardiovascular Research</i> , 2005, 67, 343-346.	1.8	10
184	Genetics of cardiac arrhythmias. <i>Heart</i> , 2005, 91, 1352-1358.	1.2	122
185	Right Ventricular Fibrosis and Conduction Delay in a Patient With Clinical Signs of Brugada Syndrome. <i>Circulation</i> , 2005, 112, 2769-2777.	1.6	401
186	Role of sequence variations in the human ether-a-go-go-related gene (HERG, KCNH2) in the Brugada syndrome. <i>Cardiovascular Research</i> , 2005, 68, 441-453.	1.8	63
187	A mutation in the human cardiac sodium channel (E161K) contributes to sick sinus syndrome, conduction disease and Brugada syndrome in two families. <i>Journal of Molecular and Cellular Cardiology</i> , 2005, 38, 969-981.	0.9	184
188	Developmental Aspects of Long QT Syndrome Type 3 and Brugada Syndrome on the Basis of a Single SCN5A Mutation in Childhood. <i>Journal of the American College of Cardiology</i> , 2005, 46, 331-337.	1.2	52
189	Mutation in the KCNQ1 Gene Leading to the Short QT-Interval Syndrome. <i>Circulation</i> , 2004, 109, 2394-2397.	1.6	603
190	Genetic control of sodium channel function. <i>Cardiovascular Research</i> , 2003, 57, 961-973.	1.8	157
191	Na ⁺ channel mutation leading to loss of function and non-progressive cardiac conduction defects. <i>Journal of Molecular and Cellular Cardiology</i> , 2003, 35, 549-557.	0.9	56
192	A Cardiac Sodium Channel Mutation Cosegregates With a Rare Connexin40 Genotype in Familial Atrial Standstill. <i>Circulation Research</i> , 2003, 92, 14-22.	2.0	261
193	Compound Heterozygosity for Mutations (W156X and R225W) in SCN5A Associated With Severe Cardiac Conduction Disturbances and Degenerative Changes in the Conduction System. <i>Circulation Research</i> , 2003, 92, 159-168.	2.0	222
194	A novel LQT3 mutation implicates the human cardiac sodium channel domain IVS6 in inactivation kinetics. <i>Cardiovascular Research</i> , 2003, 57, 1072-1078.	1.8	21
195	A common polymorphism in KCNH2 (HERG) hastens cardiac repolarization. <i>Cardiovascular Research</i> , 2003, 59, 27-36.	1.8	156
196	Contribution of Sodium Channel Mutations to Bradycardia and Sinus Node Dysfunction in LQT3 Families. <i>Circulation Research</i> , 2003, 92, 976-983.	2.0	140
197	Ion Channel Disease as a Cause of the Brugada Syndrome. <i>Contemporary Cardiology</i> , 2003, , 187-200.	0.0	0
198	Pharmacological rescue of mutant ion channels. <i>Cardiovascular Research</i> , 2002, 55, 229-232.	1.8	11

#	ARTICLE	IF	CITATIONS
199	Genotype-phenotype relationship in Brugada syndrome: electrocardiographic features differentiate SCN5A-related patients from non-SCN5A-related patients. <i>Journal of the American College of Cardiology</i> , 2002, 40, 350-356.	1.2	360
200	Possible Bradycardic Mode of Death and Successful Pacemaker Treatment in a Large Family with Features of Long QT Syndrome Type 3 and Brugada Syndrome. <i>Journal of Cardiovascular Electrophysiology</i> , 2001, 12, 630-636.	0.8	140
201	A sodium-channel mutation causes isolated cardiac conduction disease. <i>Nature</i> , 2001, 409, 1043-1047.	13.7	377
202	Gating-Dependent Mechanisms for Flecainide Action in SCN5A-Linked Arrhythmia Syndromes. <i>Circulation</i> , 2001, 104, 1200-1205.	1.6	85
203	Genomic organisation and chromosomal localisation of two members of the KCND ion channel family, KCND2 and KCND3. <i>Human Genetics</i> , 2000, 106, 614-619.	1.8	4
204	Two Distinct Congenital Arrhythmias Evoked by a Multidysfunctional Na ⁺ Channel. <i>Circulation Research</i> , 2000, 86, E91-7.	2.0	279
205	Genomic organisation and chromosomal localisation of two members of the KCND ion channel family, KCND2 and KCND3. <i>Human Genetics</i> , 2000, 106, 614-619.	1.8	19
206	A Single Na ⁺ Channel Mutation Causing Both Long-QT and Brugada Syndromes. <i>Circulation Research</i> , 1999, 85, 1206-1213.	2.0	612