CITATION REPORT List of articles citing

Spectrum and prevalence of mutations from the first 2,500 consecutive unrelated patients referred for the FAMILION long QT syndrome genetic test

DOI: 10.1016/j.hrthm.2009.05.021 Heart Rhythm, 2009, 6, 1297-303.

Source: https://exaly.com/paper-pdf/47125180/citation-report.pdf

Version: 2024-04-28

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

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

#	Paper	IF	Citations
359			
358	Closer look at genetic testing in long-QT syndrome: will DNA diagnostics ever be enough?. 2009 , 120, 1745-8		16
357	Is it time to develop a "pathogenicity" score to distinguish long QT syndrome causing mutations from "background" genetic noise?. <i>Heart Rhythm</i> , 2009 , 6, 1304-5	6.7	7
356	Rescue of mutated cardiac ion channels in inherited arrhythmia syndromes. 2010 , 56, 113-22		21
355	Genetic testing in cardiovascular diseases. 2010 , 25, 243-8		11
354	HERG1 channelopathies. 2010 , 460, 265-76		63
353	Cardiac sodium channelopathies. 2010 , 460, 223-37		136
352	KvDB; mining and mapping sequence variants in voltage-gated potassium channels. 2010 , 31, 908-17		3
351	LQTS gene LOVD database. 2010 , 31, E1801-10		22
350	An Examination of KCNE1 Mutations and Common Variants in Chronic Tinnitus. 2010 , 1, 23-37		17
349	Impact of gene patents and licensing practices on access to genetic testing for long QT syndrome. 2010 , 12, S111-54		13
348	The year in arrhythmias-2009 part II. Heart Rhythm, 2010, 7, 538-48	6.7	
347	An international compendium of mutations in the SCN5A-encoded cardiac sodium channel in patients referred for Brugada syndrome genetic testing. <i>Heart Rhythm</i> , 2010 , 7, 33-46	6.7	515
346	Long QT syndrome with compound mutations is associated with a more severe phenotype: a Japanese multicenter study. <i>Heart Rhythm</i> , 2010 , 7, 1411-8	6.7	89
345	Gain-of-function mutation S422L in the KCNJ8-encoded cardiac K(ATP) channel Kir6.1 as a pathogenic substrate for J-wave syndromes. <i>Heart Rhythm</i> , 2010 , 7, 1466-71	6.7	208
344	Only Connect. <i>Molecular Diagnosis and Therapy</i> , 2010 , 14, 67-72	4.5	1
343	Origin of the Swedish long QT syndrome Y111C/KCNQ1 founder mutation. <i>Heart Rhythm</i> , 2011 , 8, 541-	76. ₇	25

342	R231C mutation in KCNQ1 causes long QT syndrome type 1 and familial atrial fibrillation. <i>Heart Rhythm</i> , 2011 , 8, 48-55	53
341	Screening for copy number variation in genes associated with the long QT syndrome: clinical relevance. 2011 , 57, 40-7	69
340	HRS/EHRA expert consensus statement on the state of genetic testing for the channelopathies and cardiomyopathies this document was developed as a partnership between the Heart Rhythm 6.7 Society (HRS) and the European Heart Rhythm Association (EHRA). <i>Heart Rhythm</i> , 2011 , 8, 1308-39	737
339	Development of a high resolution melting method for the detection of genetic variations in Long QT Syndrome. 2011 , 412, 203-7	9
338	Exome sequencing of ion channel genes reveals complex profiles confounding personal risk assessment in epilepsy. 2011 , 145, 1036-48	240
337	Guidelines for genetic testing of inherited cardiac disorders. 2011 , 20, 681-7	56
336	Inhibition of nonsense-mediated mRNA decay by antisense morpholino oligonucleotides restores functional expression of hERG nonsense and frameshift mutations in long-QT syndrome. 2011 , 50, 223-9	22
335	HRS/EHRA expert consensus statement on the state of genetic testing for the channelopathies and cardiomyopathies: this document was developed as a partnership between the Heart Rhythm Society (HRS) and the European Heart Rhythm Association (EHRA). 2011 , 13, 1077-109	557
334	[Progress in cardiac electrophysiology and arrhythmias]. 2011 , 64 Suppl 1, 81-90	6
333	Sudden infant death syndrome and cardiac channelopathies: from mechanisms to prevention of avoidable tragedies. 2011 , 1,	3
332	Inherited Heart Diseases. 2011 , 295-337	
331	Recurrent and Founder Mutations in the Netherlands: the Long-QT Syndrome. 2011 , 19, 10-16	6
330	Prevalence of HCM and long QT syndrome mutations in young sudden cardiac death-related cases. 2011 , 125, 565-72	22
329	Gating-related molecular motions in the extracellular domain of the IKs channel: implications for IKs channelopathy. 2011 , 239, 137-56	20
328	Phenotypical manifestations of mutations in the genes encoding subunits of the cardiac voltage-dependent L-type calcium channel. 2011 , 108, 607-18	60
327	MOG1: a new susceptibility gene for Brugada syndrome. 2011 , 4, 261-8	124
326	Defining the disconnect between in vitro models and human arrhythmogenic disease: context matters. 2011 , 124, 993-5	4
325	The voltage-gated channel accessory protein KCNE2: multiple ion channel partners, multiple ways to long QT syndrome. 2011 , 13, e38	18

324	Genetic testing for potentially lethal, highly treatable inherited cardiomyopathies/channelopathies in clinical practice. 2011 , 123, 1021-37	151
323	The QT and corrected QT interval in recovery after exercise in children. 2011 , 4, 448-55	16
322	KCNE1 enhances phosphatidylinositol 4,5-bisphosphate (PIP2) sensitivity of IKs to modulate channel activity. 2011 , 108, 9095-100	87
321	Multiple splicing defects caused by hERG splice site mutation 2592+1G>A associated with long QT syndrome. 2011 , 300, H312-8	8
320	A presumably benign human ether-a-go-go-related gene mutation (R176W) with a malignant primary manifestation of long QT syndrome. 2012 , 22, 360-3	3
319	Phylogenetic and physicochemical analyses enhance the classification of rare nonsynonymous single nucleotide variants in type 1 and 2 long-QT syndrome. 2012 , 5, 519-28	48
318	Long-QT syndrome: from genetics to management. 2012 , 5, 868-77	349
317	A public resource facilitating clinical use of genomes. 2012 , 109, 11920-7	154
316	Cardiac ion channelopathies and the sudden infant death syndrome. 2012 , 2012, 846171	33
315	Clinical utility of chromosomal microarray analysis. 2012 , 130, e1085-95	39
314	Prevalence, mutation spectrum, and cardiac phenotype of the Jervell and Lange-Nielsen syndrome in Sweden. 2012 , 14, 1799-806	23
313	The prevalence of mutations in KCNQ1, KCNH2, and SCN5A in an unselected national cohort of young sudden unexplained death cases. <i>Journal of Cardiovascular Electrophysiology</i> , 2012 , 23, 1092-8	57
312	Arrhythmias: Epinephrine test for sudden cardiac deathis it too early?. 2012 , 9, 675-6	
311	Ion channel associated diseases: overview of molecular mechanisms. 2012 , 112, 6319-33	28
310	The compound mutation, a model for acquire long QT syndrome. 2012 , 6, e187-e188	1
309	Early LQT2 nonsense mutation generates N-terminally truncated hERG channels with altered gating properties by the reinitiation of translation. 2012 , 53, 725-33	16
308	Genotype-phenotype analysis of three Chinese families with Jervell and Lange-Nielsen syndrome. 2012 , 3, 67-75	5
307	High-risk long QT syndrome mutations in the Kv7.1 (KCNQ1) pore disrupt the molecular basis for rapid K(+) permeation. 2012 , 51, 9076-85	14

306	hERG K(+) channels: structure, function, and clinical significance. 2012 , 92, 1393-478	426
305	A KCNE1 missense variant (V47I) causing exercise-induced long QT syndrome (Romano Ward). 2012 , 156, e33-5	4
304	End-recovery QTc: a useful metric for assessing genetic variants of unknown significance in long-QT syndrome. <i>Journal of Cardiovascular Electrophysiology</i> , 2012 , 23, 637-42	6
303	Multifocal ectopic Purkinje-related premature contractions: a new SCN5A-related cardiac channelopathy. 2012 , 60, 144-56	109
302	Impaired ion channel function related to a common KCNQ1 mutation - implications for risk stratification in long QT syndrome 1. 2012 , 511, 26-33	5
301	Concealed long QT syndrome and intractable partial epilepsy: a case report. 2012 , 87, 1128-31	9
300	Comparative analytical utility of DNA derived from alternative human specimens for molecular autopsy and diagnostics. 2012 , 14, 451-7	10
299	Prevalence of Significant Genetic Variants in Congenital Long QT Syndrome is Largely Underestimated. 2012 , 3, 72	11
298	Opposite Effects of the S4-S5 Linker and PIP(2) on Voltage-Gated Channel Function: KCNQ1/KCNE1 and Other Channels. 2012 , 3, 125	22
297	Congenital long-QT syndrome in AddisonMdisease: a novel association. 2012 , 33, 652-5	
296	Long QT Syndromes: Genetic Basis. 2012 , 4, 1-16	5
295	How to Interpret Results of Genetic Testing and Counsel Families. 2012 , 4, 97-101	
294	Impact of genetics on the clinical management of channelopathies. 2013 , 62, 169-180	216
293	Visual automated fluorescence electrophoresis provides simultaneous quality, quantity, and molecular weight spectra for genomic DNA from archived neonatal blood spots. 2013 , 15, 283-90	3
292	Left cardiac sympathetic denervation in long QT syndrome: analysis of therapeutic nonresponders. 2013 , 6, 705-11	76
291	Prolongation of the QTc interval predicts appropriate implantable cardioverter-defibrillator therapies in hypertrophic cardiomyopathy. 2013 , 1, 149-55	34
290	Interpreting secondary cardiac disease variants in an exome cohort. 2013 , 6, 337-46	59
289	Conundrum of sudden cardiac death: making sense of missense. 2013 , 6, e58-63	2

288	Novel deletion mutation in the cardiac sodium channel inactivation gate causes long QT syndrome. 2013 , 165, 362-5		7
287	L539 fs/47, a truncated mutation of human ether-a-go-go-related gene (hERG), decreases hERG ion channel currents in HEK 293 cells. 2013 , 40, 28-36		7
286	An adolescent with possible arrhythmogenic right ventricular dysplasia and long QT syndrome: evaluation and management. 2013 , 18, 75-8		
285	Iron-deficiency anaemia, gastric hyperplasia, and elevated gastrin levels due to potassium channel dysfunction in the Jervell and Lange-Nielsen Syndrome. 2013 , 23, 325-34		20
284	Cardiac channelopathies: genetic and molecular mechanisms. 2013, 517, 1-11		83
283	Clinical utility gene card for: long-QT syndrome (types 1-13). 2013 , 21,		7
282	Results of genetic testing in 855 consecutive unrelated patients referred for long QT syndrome in a clinical laboratory. 2013 , 17, 553-61		26
281	Mechanisms of Cardiac Arrhythmia. 2013 , 93-128		
280	Case records of the Massachusetts General Hospital. Case 18-2013: a 32-year-old woman with recurrent episodes of altered consciousness. 2013 , 368, 2304-12		5
279	Long QT syndrome: beyond the causal mutation. 2013 , 591, 4125-39		44
²⁷⁹	Characterization of 2 genetic variants of Na(v) 1.5-arginine 689 found in patients with cardiac	2.7	8
	Characterization of 2 genetic variants of Na(v) 1.5-arginine 689 found in patients with cardiac	2.7	
278	Characterization of 2 genetic variants of Na(v) 1.5-arginine 689 found in patients with cardiac arrhythmias. <i>Journal of Cardiovascular Electrophysiology</i> , 2013 , 24, 1037-46	2.7	8
278 277	Characterization of 2 genetic variants of Na(v) 1.5-arginine 689 found in patients with cardiac arrhythmias. <i>Journal of Cardiovascular Electrophysiology</i> , 2013 , 24, 1037-46 Quantitative PCR as an alternative in the diagnosis of long-QT syndrome. 2013 , 2013, 418604 Pharmacological and non-pharmacological therapy for arrhythmias in the pediatric population:	2.7	8
278 277 276	Characterization of 2 genetic variants of Na(v) 1.5-arginine 689 found in patients with cardiac arrhythmias. <i>Journal of Cardiovascular Electrophysiology</i> , 2013 , 24, 1037-46 Quantitative PCR as an alternative in the diagnosis of long-QT syndrome. 2013 , 2013, 418604 Pharmacological and non-pharmacological therapy for arrhythmias in the pediatric population: EHRA and AEPC-Arrhythmia Working Group joint consensus statement. 2013 , 15, 1337-82	2.7	8 1 190
278 277 276 275	Characterization of 2 genetic variants of Na(v) 1.5-arginine 689 found in patients with cardiac arrhythmias. <i>Journal of Cardiovascular Electrophysiology</i> , 2013 , 24, 1037-46 Quantitative PCR as an alternative in the diagnosis of long-QT syndrome. 2013 , 2013, 418604 Pharmacological and non-pharmacological therapy for arrhythmias in the pediatric population: EHRA and AEPC-Arrhythmia Working Group joint consensus statement. 2013 , 15, 1337-82 Arrhythmia risk in long QT syndrome: beyond the disease-causative mutation. 2013 , 6, 313-6	2.7	8 1 190 10
278 277 276 275	Characterization of 2 genetic variants of Na(v) 1.5-arginine 689 found in patients with cardiac arrhythmias. <i>Journal of Cardiovascular Electrophysiology</i> , 2013 , 24, 1037-46 Quantitative PCR as an alternative in the diagnosis of long-QT syndrome. 2013 , 2013, 418604 Pharmacological and non-pharmacological therapy for arrhythmias in the pediatric population: EHRA and AEPC-Arrhythmia Working Group joint consensus statement. 2013 , 15, 1337-82 Arrhythmia risk in long QT syndrome: beyond the disease-causative mutation. 2013 , 6, 313-6 Genetic testing in cardiovascular medicine: current landscape and future horizons. 2013 , 28, 317-25 Exome sequencing and systems biology converge to identify novel mutations in the L-type calcium	2.7	8 1 190 10 32

(2014-2013)

270	Modification by KCNE1 variants of the hERG potassium channel response to premature stimulation and to pharmacological inhibition. 2013 , 1, e00175	16
269	Molecular and genetic basis of sudden cardiac death. 2013 , 123, 75-83	54
268	The disease-specific phenotype in cardiomyocytes derived from induced pluripotent stem cells of two long QT syndrome type 3 patients. 2013 , 8, e83005	60
267	Long QT syndrome, cardiovascular anomaly and findings in ECG-guided genetic testing. 2014 , 4, 122-128	4
266	Paralogue annotation identifies novel pathogenic variants in patients with Brugada syndrome and catecholaminergic polymorphic ventricular tachycardia. 2014 , 51, 35-44	31
265	Translational toxicology and rescue strategies of the hERG channel dysfunction: biochemical and molecular mechanistic aspects. 2014 , 35, 1473-84	18
264	Genetic characteristics of children and adolescents with long-QT syndrome diagnosed by school-based electrocardiographic screening programs. 2014 , 7, 107-12	19
263	Position of premature termination codons determines susceptibility of hERG mutations to nonsense-mediated mRNA decay in long QT syndrome. 2014 , 539, 190-7	11
262	Loss-of-function of the voltage-gated sodium channel NaV1.5 (channelopathies) in patients with irritable bowel syndrome. 2014 , 146, 1659-1668	93
261	A missense mutation in the sodium channel ¶b subunit reveals SCN1B as a susceptibility gene underlying long QT syndrome. <i>Heart Rhythm</i> , 2014 , 11, 1202-9	28
260	Genetics of sudden cardiac death caused by ventricular arrhythmias. 2014 , 11, 96-111	52
259	Sodium channels, cardiac arrhythmia, and therapeutic strategy. 2014 , 70, 367-92	8
258	Double trouble, stick to the basics should be the rule!. <i>Heart Rhythm</i> , 2014 , 11, 2105-6	
257	The Role of the Cardiac Sodium Channel in Perinatal Early Infant Mortality. 2014, 6, 749-759	5
256	Novel Kv7.1-phosphatidylinositol 4,5-bisphosphate interaction sites uncovered by charge neutralization scanning. 2014 , 289, 22749-22758	25
255	Phenotype, origin and estimated prevalence of a common long QT syndrome mutation: a clinical, genealogical and molecular genetics study including Swedish R518X/KCNQ1 families. 2014 , 14, 22	18
254	Mutations in Danish patients with long QT syndrome and the identification of a large founder family with p.F29L in KCNH2. 2014 , 15, 31	11
253	Next generation sequencing challenges in the analysis of cardiac sudden death due to arrhythmogenic disorders. 2014 , 35, 3111-6	17

252	Genetic variants for long QT syndrome among infants and children from a statewide newborn hearing screening program cohort. 2014 , 164, 590-5.e1-3	8
251	Computer-Based Early Warning System for Potentially Life-Threatening QT Prolongation. 2014 , 3, e235-e244	1
250	The variant hERG/R148W associated with LQTS is a mutation that reduces current density on co-expression with the WT. 2014 , 536, 348-56	4
249	Exome analysis-based molecular autopsy in cases of sudden unexplained death in the young. <i>Heart Rhythm</i> , 2014 , 11, 655-62	101
248	High prevalence of the SCN5A E1784K mutation in school children with long QT syndrome living on the Okinawa islands. 2014 , 78, 1974-9	16
247	The safety of modern anesthesia for children with long QT syndrome. 2014 , 119, 932-938	16
246	SCN5A mutations and polymorphisms in patients with ventricular fibrillation during acute myocardial infarction. 2014 , 10, 2039-44	11
245	Contribution of Cardiac Sodium Channel Ebubunit Variants to Brugada Syndrome. 2015 , 79, 2118-29	7
244	A Common Mutation of Long QT Syndrome Type 1 in Japan. 2015 , 79, 2026-30	13
243	Mutation Analysis of KCNQ1, KCNH2 and SCN5A Genes in Taiwanese Long QT Syndrome Patients. 2015 , 56, 450-3	10
242	Comprehensive Genetic Characterization of a Spanish Brugada Syndrome Cohort. 2015 , 10, e0132888	19
241	Next-generation sequencing for the diagnosis of cardiac arrhythmia syndromes. <i>Heart Rhythm</i> , 2015 , 12, 1062-70	23
240	CALM3 mutation associated with long QT syndrome. <i>Heart Rhythm</i> , 2015 , 12, 419-22 6.7	79
239	Bayesian models for syndrome- and gene-specific probabilities of novel variant pathogenicity. 2015 , 7, 5	19
238	Distinctive malfunctions of calmodulin mutations associated with heart RyR2-mediated arrhythmic disease. 2015 , 1850, 2168-76	22
237	Targeted next generation sequencing application in cardiac channelopathies: Analysis of a cohort of autopsy-negative sudden unexplained deaths. 2015 , 254, 5-11	25
236	Genetic purgatory and the cardiac channelopathies: Exposing the variants of uncertain/unknown significance issue. <i>Heart Rhythm</i> , 2015 , 12, 2325-31	112
235	Enhanced Classification of Brugada Syndrome-Associated and Long-QT Syndrome-Associated Genetic Variants in the SCN5A-Encoded Na(v)1.5 Cardiac Sodium Channel. 2015 , 8, 582-95	65

(2016-2015)

234	Enhancing the Predictive Power of Mutations in the C-Terminus of the KCNQ1-Encoded Kv7.1 Voltage-Gated Potassium Channel. 2015 , 8, 187-97	14
233	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. 2015 , 47, 717-726	244
232	IKs Gain- and Loss-of-Function in Early-Onset Lone Atrial Fibrillation. <i>Journal of Cardiovascular Electrophysiology</i> , 2015 , 26, 715-23	22
231	Heterogeneous Phenotype of Long QT Syndrome Caused by the KCNH2-H562R Mutation: Importance of Familial Genetic Testing. 2015 , 68, 861-8	2
230	Assessment of the predictive accuracy of five in silico prediction tools, alone or in combination, and two metaservers to classify long QT syndrome gene mutations. 2015 , 16, 34	52
229	Fenotipo heterogfieo del sfidrome de QT largo causado por la mutacifi KCNH2-H562R: importancia del estudio genfico familiar. 2015 , 68, 861-868	5
228	A Systematic Review on the Cost-Effectiveness of Genetic and Electrocardiogram Testing for Long QT Syndrome in Infants and Young Adults. 2015 , 18, 700-8	8
227	Screen-based identification and validation of four new ion channels as regulators of renal ciliogenesis. 2015 , 128, 4550-9	12
226	Genetic analysis, in silico prediction, and family segregation in long QT syndrome. 2015, 23, 79-85	12
225	A comparison of genetic findings in sudden cardiac death victims and cardiac patients: the importance of phenotypic classification. 2015 , 17, 350-7	16
224	Reduced Uptake of Family Screening in Genotype-Negative Versus Genotype-Positive Long QT Syndrome. 2015 , 24, 558-64	8
223	Physiological and Pathophysiological Insights of Nav1.4 and Nav1.5 Comparison. 2015 , 6, 314	27
222	J Wave Syndrome-Susceptibility Mutations Versus Benign Rare Variants: How Do We Decide?. 2016 , 91-120	
221	Exome-based analysis of cardiac arrhythmia, respiratory control, and epilepsy genes in sudden unexpected death in epilepsy. 2016 , 79, 522-34	162
220	Genetic Testing for Cardiovascular Conditions Predisposing to Sudden Death. 2016 , 175-186	1
219	Cardiac sodium channel palmitoylation regulates channel availability and myocyte excitability with implications for arrhythmia generation. 2016 , 7, 12035	31
218	The KCNE Family of Ion Channel Regulatory Subunits. 2016 , 1-24	1
217	Role of Genetic Testing in Patients with Ventricular Arrhythmias in Apparently Normal Hearts. 2016 , 8, 515-23	O

216	Pore size matters for potassium channel conductance. 2016 , 148, 277-91	20
215	Genetic basis of dilated cardiomyopathy. 2016 , 224, 461-472	50
214	Genetic investigation of 100 heart genes in sudden unexplained death victims in a forensic setting. 2016 , 24, 1797-1802	41
213	Aggregate penetrance of genomic variants for actionable disorders in European and African Americans. 2016 , 8, 364ra151	41
212	KCNQ1 mutations associated with Jervell and Lange-Nielsen syndrome and autosomal recessive Romano-Ward syndrome in India-expanding the spectrum of long QT syndrome type 1. 2016 , 170, 1510-9	7
211	Genotype-based clinical manifestation and treatment of Chinese long QT syndrome patients with KCNQ1 mutations - R380S and W305L. 2016 , 26, 754-63	4
210	Clinical and genetic features of Australian families with long QT syndrome: A registry-based study. 2016 , 32, 456-461	7
209	Semiconductor Whole Exome Sequencing for the Identification of Genetic Variants in Colombian Patients Clinically Diagnosed with Long QT Syndrome. <i>Molecular Diagnosis and Therapy</i> , 2016 , 20, 353-62 ⁴⁻⁵	O
208	Founder Mutation Genotyping and Sudden Cardiac Arrest: The Promise of Precision Medicine Fulfilled or the Next Step Into Precise Uncertainty. 2016 , 9, 107-9	1
207	Phenotype guided characterization and molecular analysis of Indian patients with long QT syndromes. 2016 , 16, 8-18	8
206	J Wave Syndromes. 2016 ,	
205	Sudden unexpected death in epilepsy genetics: Molecular diagnostics and prevention. <i>Epilepsia</i> , 2016 , 57 Suppl 1, 17-25	52
204	Common Genotypes of Long QT Syndrome in China and the Role of ECG Prediction. 2016 , 133, 73-8	11
203	Genetic Control of Potassium Channels. 2016 , 8, 285-306	5
202	Exercise restrictions for patients with inherited cardiac conditions: Current guidelines, challenges and limitations. 2016 , 209, 234-41	16
201	The impact of recent advances in genetics in understanding disease mechanisms underlying the long QT syndromes. 2016 , 397, 679-93	8
200	The role of hereditary KCNQ1 mutations in water-related death. 2016 , 130, 361-3	2
199	Patient Outcomes From a Specialized Inherited Arrhythmia Clinic. 2016 , 9, e003440	14

198	KCNE1 and KCNE3: The yin and yang of voltage-gated K(+) channel regulation. 2016 , 576, 1-13	50
197	Calmodulin and Ca(2+) control of voltage gated Na(+) channels. 2016 , 10, 45-54	25
196	Phenotype-driven molecular autopsy for sudden cardiac death. 2017 , 91, 22-29	21
195	Epilepsy-related sudden unexpected death: targeted molecular analysis of inherited heart disease genes using next-generation DNA sequencing. 2017 , 27, 292-304	29
194	Calmodulin limits pathogenic Na+ channel persistent current. 2017 , 149, 277-293	39
193	Mutation Load of Multiple Ion Channel Gene Mutations in Brugada Syndrome. 2017 , 137, 256-260	14
192	Anesthesia for children with long QT syndrome: Challenges and solutions from pediatric studies. 2017 , 14, 3-8	О
191	Relevance of molecular testing in patients with a family history of sudden death. 2017 , 276, 18-23	6
190	Systematic ajmaline challenge in patients with long QT 3 syndrome caused by the most common mutation: a multicentre study. 2017 , 19, 1723-1729	6
189	Using high-resolution variant frequencies to empower clinical genome interpretation. 2017 , 19, 1151-1158	208
189	Using high-resolution variant frequencies to empower clinical genome interpretation. 2017 , 19, 1151-1158 Genotype-phenotype dilemma in a case of sudden cardiac death with the E1053K mutation and a deletion in the SCN5A gene. 2017 , 275, 187-194	208
	Genotype-phenotype dilemma in a case of sudden cardiac death with the E1053K mutation and a	
188	Genotype-phenotype dilemma in a case of sudden cardiac death with the E1053K mutation and a deletion in the SCN5A gene. 2017 , 275, 187-194	10
188	Genotype-phenotype dilemma in a case of sudden cardiac death with the E1053K mutation and a deletion in the SCN5A gene. 2017 , 275, 187-194 Issues and Challenges in Diagnostic Sequencing for Inherited Cardiac Conditions. 2017 , 63, 116-128 Care in Specialized Centers and Data Sharing Increase Agreement in Hypertrophic Cardiomyopathy	10
188 187 186	Genotype-phenotype dilemma in a case of sudden cardiac death with the E1053K mutation and a deletion in the SCN5A gene. 2017, 275, 187-194 Issues and Challenges in Diagnostic Sequencing for Inherited Cardiac Conditions. 2017, 63, 116-128 Care in Specialized Centers and Data Sharing Increase Agreement in Hypertrophic Cardiomyopathy Genetic Test Interpretation. 2017, 10, Repeat genetic testing with targeted capture sequencing in primary arrhythmia syndrome and	10 6 27
188 187 186	Genotype-phenotype dilemma in a case of sudden cardiac death with the E1053K mutation and a deletion in the SCN5A gene. 2017, 275, 187-194 Issues and Challenges in Diagnostic Sequencing for Inherited Cardiac Conditions. 2017, 63, 116-128 Care in Specialized Centers and Data Sharing Increase Agreement in Hypertrophic Cardiomyopathy Genetic Test Interpretation. 2017, 10, Repeat genetic testing with targeted capture sequencing in primary arrhythmia syndrome and cardiomyopathy. 2017, 25, 1313-1323 Clinical Yield of Familial Screening After Sudden Death in Young Subjects: The French Experience.	10 6 27 9
188 187 186 185	Genotype-phenotype dilemma in a case of sudden cardiac death with the E1053K mutation and a deletion in the SCN5A gene. 2017, 275, 187-194 Issues and Challenges in Diagnostic Sequencing for Inherited Cardiac Conditions. 2017, 63, 116-128 Care in Specialized Centers and Data Sharing Increase Agreement in Hypertrophic Cardiomyopathy Genetic Test Interpretation. 2017, 10, Repeat genetic testing with targeted capture sequencing in primary arrhythmia syndrome and cardiomyopathy. 2017, 25, 1313-1323 Clinical Yield of Familial Screening After Sudden Death in Young Subjects: The French Experience. 2017, 10,	10 6 27 9

180	Loss-of-Function Variants: True Monogenic Culprits of Long-QT Syndrome or Proarrhythmic Variants Requiring Secondary Provocation?. 2017 , 10,		21
179	Cancer drugs and QT prolongation: weighing risk against benefit. 2017 , 16, 1099-1102		9
178	An Autopsy Case of Sudden Unexpected Death of a Young Adult in a Hot Bath: Molecular Analysis Using Next-Generation DNA Sequencing. 2017 , 10, 1179547617702884		4
177	Contribution of a KCNH2 variant in genotyped long QT syndrome: Romano-Ward syndrome under double mutations and acquired long QT syndrome under heterozygote. 2017 , 70, 74-79		5
176	Molecular Pathophysiology of Congenital Long QT Syndrome. 2017 , 97, 89-134		92
175	Regulation of KCNQ/Kv7 family voltage-gated K channels by lipids. 2017 , 1859, 586-597		25
174	Long noncoding RNA (lincRNA), a new paradigm in gene expression control. 2017, 17, 135-143		141
173	Considerations when using next-generation sequencing for genetic diagnosis of long-QT syndrome in the clinical testing laboratory. 2017 , 464, 128-135		5
172	Targeted Cancer Therapies and QT Interval Prolongation: Unveiling the Mechanisms Underlying Arrhythmic Complications and the Need for Risk Stratification Strategies. 2017 , 37, 121-134		7
171	Sudden death in a young patient with atrial fibrillation. 2017 , 7,		O
170	Cardiac Channelopathies and Sudden Death: Recent Clinical and Genetic Advances. 2017, 6,		63
169	Allelic Complexity in Long QT Syndrome: A Family-Case Study. <i>International Journal of Molecular Sciences</i> , 2017 , 18,	6.3	2
168	"Homozygous, and compound heterozygous mutation in 3 Turkish family with Jervell and Lange-Nielsen syndrome: case reports". 2017 , 18, 114		
167	Gene-Targeted Analysis of Clinically Diagnosed Long QT Russian Families. 2017, 58, 81-87		13
166	KCNQ1 Gene Variants in Large Asymptomatic Populations: Considerations for Genomic Screening of Military Cohorts. 2017 , 182, e1795-e1800		2
165	Yield of the Genetic Test in Suspected Catecholaminergic Polymorphic Ventricular Tachycardia and Implications for Test Interpretation. 2018 , 11, e001424		20
164	The phenotype is equally important in promoting variants from benign to pathogenic as well as in demoting variants from pathogenic to benign. <i>Heart Rhythm</i> , 2018 , 15, 562-563	6.7	1
163	Exploiting ion channel structure to assess rare variant pathogenicity. <i>Heart Rhythm</i> , 2018 , 15, 890-894	6.7	1

162	CardioClassifier: disease- and gene-specific computational decision support for clinical genome interpretation. 2018 , 20, 1246-1254	45
161	Targeted next generation sequencing in a young population with suspected inherited malignant cardiac arrhythmias. 2018 , 26, 303-313	6
160	Using the genome aggregation database, computational pathogenicity prediction tools, and patch clamp heterologous expression studies to demote previously published long QT syndrome type 1 mutations from pathogenic to benign. <i>Heart Rhythm</i> , 2018 , 15, 555-561	11
159	A New Approach to Rare Diseases of Children: The Undiagnosed Diseases Network. 2018 , 196, 291-297.e2	12
158	The long-QT syndrome and exercise practice: The never-ending debate. <i>Journal of Cardiovascular Electrophysiology</i> , 2018 , 29, 489-496	9
157	The genetic architecture of long QT syndrome: A critical reappraisal. 2018 , 28, 453-464	58
156	The voltage-gated sodium channel EF-hands form an interaction with the III-IV linker that is disturbed by disease-causing mutations. 2018 , 8, 4483	19
155	Unexplained cardiac arrest: a tale of conflicting interpretations of KCNQ1 genetic test results. 2018 , 107, 670-678	5
154	Cardiac Genetic Predisposition in Sudden înfant Death Syndrome. 2018, 71, 1217-1227	43
153	Mechanisms in Heritable Sodium Channel Diseases. 2018 , 473-482	
152	Inheritable Potassium Channel Diseases. 2018 , 494-503	1
151	High-Throughput Functional Evaluation of KCNQ1 Decrypts Variants of Unknown Significance. 2018 , 11, e002345	40
150	Mutational and phenotypic spectra of KCNE1 deficiency in Jervell and Lange-Nielsen Syndrome and Romano-Ward Syndrome. 2019 , 40, 162-176	18
149	Variants: Association With Cardiac Disorders. 2018 , 9, 1372	47
148	From Genotype to Phenotype. 2018 , 11, e002316	5
147	Cardiac voltage-sodium channel mutations association with primary electrical diseases: AuthorsM reply. 2018 , 20, 1707-1708	O
146	Genetic and Phenotypic Characterization of Community Hospital Patients With QT Prolongation. 2018 , 7, e009706	5
145	Role of genetic heart disease in sentinel sudden cardiac arrest survivors across the age spectrum. 2018 , 270, 214-220	17

144	New onset seizures in a patient with Long QT Syndrome (LQTS2) and a pathogenic carboxyl-terminus frameshift variant of the KCNH2 gene. 2018 , 53, 253-255	1
143	Genome Editing of Induced Pluripotent Stem Cells to Decipher Cardiac Channelopathy Variant. 2018 , 72, 62-75	61
142	Guidelines for Heart Disease Screening in Schools (JCS 2016/JSPCCS 2016) - Digest Version. 2018 , 82, 2385-2444	10
141	Role of the voltage sensor module in Na domain IV on fast inactivation in sodium channelopathies: The implication of closed-state inactivation. 2019 , 13, 331-343	11
140	A Rare Case of the Digenic Inheritance of Long QT Syndrome Type 2 and Type 6. 2019 , 2019, 1384139	2
139	Next-generation sequencing using microfluidic PCR enrichment for molecular autopsy. 2019 , 19, 174	5
138	Specific Therapy Based on the Genotype in a Malignant Form of Long QT3, Carrying the V411M Mutation. 2019 , 60, 979-982	4
137	Functional Consequences of the -p.Y1977N Mutation within the PY Ubiquitylation Motif: Discrepancy between HEK293 Cells and Transgenic Mice. <i>International Journal of Molecular Sciences</i> 6.3, 2019, 20,	8
136	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. 2019 , 105, 588-605	63
135	Characterization of a novel LQT3 variant with a selective efficacy of mexiletine treatment. 2019 , 9, 12997	3
134	Disease modeling of cardiac arrhythmias using human induced pluripotent stem cells. 2019 , 19, 313-333	4
133	Enhanced closed-state inactivation of mutant cardiac sodium channels (SCN5A N1541D and R1632C) through different mechanisms. 2019 , 130, 88-95	9
132	Association of Genetic and Clinical Aspects of Congenital Long QT Syndrome With Life-Threatening Arrhythmias in Japanese Patients. 2019 , 4, 246-254	15
131	Structures of human Na1.7 channel in complex with auxiliary subunits and animal toxins. 2019 , 363, 1303-130	18193
130	Systematic re-evaluation of SCN5A variants associated with Brugada syndrome. <i>Journal of Cardiovascular Electrophysiology</i> , 2019 , 30, 118-127	24
129	Transcription alterations of KCNQ1 associated with imprinted methylation defects in the Beckwith-Wiedemann locus. 2019 , 21, 1808-1820	28
128	Emerging Implications of Genetic Testing in Inherited Primary Arrhythmia Syndromes. 2019 , 27, 23-33	8
127	Genetic arrhythmias complicating patients with dilated cardiomyopathy. <i>Heart Rhythm</i> , 2020 , 17, 305-31 & .7	4

(2020-2020)

126	Utilization of the genome aggregation database, in silico tools, and heterologous expression patch-clamp studies to identify and demote previously published type 2 long QT syndrome: Causative variants from pathogenic to likely benign. <i>Heart Rhythm</i> , 2020 , 17, 315-323	6.7	1
125	Improving long QT syndrome diagnosis by a polynomial-based T-wave morphology characterization. <i>Heart Rhythm</i> , 2020 , 17, 752-758	6.7	10
124	Alterations of Nedd4-2-binding capacity in PY-motif of Na 1.5 channel underlie long QT syndrome and Brugada syndrome. 2020 , 229, e13438		3
123	Functional phenotype variations of two novel K 7.1 mutations identified in patients with Long QT syndrome. 2020 , 43, 210-216		2
122	Suppression of cardiac memory-related severe form of torsades de pointes by landiolol in a patient with congenital long QT syndrome type 2. <i>HeartRhythm Case Reports</i> , 2020 , 6, 407-410	1	0
121	Genetic testing in Polynesian long QT syndrome probands reveals a lower diagnostic yield and an increased prevalence of rare variants. <i>Heart Rhythm</i> , 2020 , 17, 1304-1311	6.7	1
120	Low resolution protein mapping and KB-R7943 drug-protein molecular interaction analysis of long-QT syndrome linked KCNH2 mutations. 2020 , 13, 183-193		3
119	Clinical Implications and Gender Differences of KCNQ1 p.Gly168Arg Pathogenic Variant in Long QT Syndrome. 2020 , 9,		О
118	Systematic Evaluation of Variant Using ACMG/AMP Guidelines and Risk Stratification in Long QT Syndrome Type 1. 2020 ,		О
117	and Long QT Syndrome in 1/45 Amish: The Road From Identification to Implementation of Culturally Appropriate Precision Medicine. 2020 , 13, e003133		2
116	Transethnic Genome-Wide Association Study Provides Insights in the Genetic Architecture and Heritability of Long QT Syndrome. 2020 , 142, 324-338		27
115	Frequency of KCNQ1 variants causing loss of methylation of Imprinting Centre 2 in Beckwith-Wiedemann syndrome. 2020 , 12, 63		5
114	Chemical modification of proteins by insertion of synthetic peptides using tandem protein trans-splicing. 2020 , 11, 2284		15
113	Genetic homozygosity in a diverse population: An experience of long QT syndrome. 2020 , 316, 117-124		1
112	High-Throughput Reclassification of SCN5A Variants. 2020 , 107, 111-123		32
111	Roles for Countercharge in the Voltage Sensor Domain of Ion Channels. 2020 , 11, 160		7
110	In silico systems for predicting chemical-induced side effects using known and potential chemical protein interactions, enabling mechanism estimation. 2020 , 45, 137-149		3
109	Palmitoylation: A Fatty Regulator of Myocardial Electrophysiology. 2020 , 11, 108		10

108	Explaining sudden infant death with cardiac arrhythmias: Complete exon sequencing of nine cardiac arrhythmia genes in Dutch SIDS cases highlights new and known DNA variants. 2020 , 46, 102266		4
107	A rare coincidence: the long QT syndrome and cardio-facio-cutaneous syndrome. 2020 , 30, 1209-1211		
106	High-throughput discovery of trafficking-deficient variants in the cardiac potassium channel K11.1. Heart Rhythm, 2020 , 17, 2180-2189	ó.7	12
105	The Emergence of Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes (hiPSC-CMs) as a Platform to Model Arrhythmogenic Diseases. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	5.3	10
104	Deep Mutational Scan of an Voltage Sensor. 2020 , 13, e002786		10
103	Targeted next generation sequencing revealed a novel deletion-frameshift mutation of KCNH2 gene in a Chinese Han family with long QT syndrome: A case report and review of Chinese cases. 2020 , 99, e19749		2
102	Understanding the personal and community impact of long QT syndrome: A perspective from Gitxsan women. 2020 , 29, 562-573		1
101	Pseudopolymorphic Wide Complex Tachycardia in a Child With Long QT Syndrome. 2020 , 2, 591-594		
100	Structural Basis for the Modulation of Human KCNQ4 by Small-Molecule Drugs. 2021, 81, 25-37.e4		17
99	Off-label use of chloroquine, hydroxychloroquine, azithromycin and lopinavir/ritonavir in COVID-19 risks prolonging the QT interval by targeting the hERG channel. 2021 , 893, 173813		14
98	Enhancing rare variant interpretation in inherited arrhythmias through quantitative analysis of consortium disease cohorts and population controls. 2021 , 23, 47-58		13
97	Ca-saturated calmodulin binds tightly to the N-terminal domain of A-type fibroblast growth factor homologous factors. 2021 , 296, 100458		2
96	Disease-linked supertrafficking of a potassium channel. 2021 , 296, 100423		2
95	Unusual Overlapping Cardiac Sarcoidosis and Long-QT Type 3 Induced Ventricular Fibrillation. 2021 , 60, 85-89		
94	Modulation of the IKS channel by PIP2 requires two binding sites per monomer.		Ο
93	Calmodulinopathy in inherited arrhythmia syndromes. 2021 , 33, 339-344		
92	Proteomic and functional mapping of cardiac NaV1.5 channel phosphorylation sites. 2021 , 153,		3
91	Long-QT founder variant T309I-Kv7.1 with dominant negative pattern may predispose delayed afterdepolarizations under Eadrenergic stimulation. 2021 , 11, 3573		O

90	Identifying the causes of recurrent pregnancy loss in consanguineous couples using whole exome sequencing on the products of miscarriage with no chromosomal abnormalities. 2021 , 11, 6952		3
89	Multiple arrhythmic and cardiomyopathic phenotypes associated with an SCN5A A735E mutation. 2021 , 65, 122-127		3
88	Molecular Diagnosis of Inherited Cardiac Diseases in the Era of Next-Generation Sequencing: A Single CenterMExperience Over 5 Years. <i>Molecular Diagnosis and Therapy</i> , 2021 , 25, 373-385	4.5	1
87	Inherited arrhythmia syndrome predisposing to sudden cardiac death. 2021 , 36, 527-538		4
86	TNNI3 and KCNQ1 co-inherited variants in a family with hypertrophic cardiomyopathy and long QT phenotypes: A case report. 2021 , 27, 100743		О
85	Long QT-Syndrome With Torsades de Pointes Managed Considering Financial Constraints Faced by the Patient. <i>Cureus</i> , 2021 , 13, e15892	1.2	
84	Genetic variants associated with inherited cardiovascular disorders among 13,131 asymptomatic older adults of European descent. 2021 , 6, 51		3
83	Functional cross-talk between phosphorylation and disease-causing mutations in the cardiac sodium channel Na1.5. 2021 , 118,		2
82	Genomic Autopsy of Sudden Deaths in Young Individuals. 2021 , 6, 1247-1256		2
81	A missense KCNQ1 Mutation Impairs Insulin Secretion in Neonatal Diabetes.		O
80	Artificial Intelligence, Machine Learning and Deep Learning in Ion Channel Bioinformatics. 2021 , 11,		1
79	Long QT syndrome with potassium voltage-gated channel subfamily H member 2 gene mutation mimicking refractory epilepsy: case report. 2021 , 21, 338		1
78	Molecular determinants of the modulation of the VSD-PD coupling mechanism of the KV7.1 channel by the KCNE1 ancillary subunits.		
77	Compendium of causative genes and their encoded proteins for common monogenic disorders. 2021 ,		2
76	Calmodulin Interactions with Voltage-Gated Sodium Channels. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	1
75	Ligand modulation of KCNQ-encoded (K7) potassium channels in the heart and nervous system. 2021 , 906, 174278		1
74	Genetics of Adult and Fetal Forms of Long QT Syndrome. Cardiac and Vascular Biology, 2019, 1-43	0.2	1
73	Structural basis of cytoplasmic NaV1.5 and NaV1.4 regulation. 2021 , 153,		7

72	Arrhythmia Mechanisms in Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes. 2020 , 77, 300-316	5
71	Using high-resolution variant frequencies to empower clinical genome interpretation.	4
7º	Functional crosstalk between phosphorylation and disease-causing mutations in the cardiac sodium channel Nav1.5.	1
69	High Throughput Functional Evaluation of KCNQ1 Decrypts Variants of Unknown Significance.	1
68	High-throughput reclassification of SCN5A variants.	О
67	Catheter ablation of ventricular fibrillation storm in a long QT syndrome genotype carrier with normal QT interval. 2013 , 54, e1-e4	9
66	Genetic testing for long QT syndrome and the category of cardiac ion channelopathies. 2012 , e4f9995f69e60	7 6
65	Long QT interval in Turner syndromea high prevalence of LQTS gene mutations. 2013 , 8, e69614	23
64	Mutation in BMPR2 Promoter: A M econd HitMor Manifestation of Pulmonary Arterial Hypertension?. 2015 , 10, e0133042	20
63	Upgraded molecular models of the human KCNQ1 potassium channel. 2019 , 14, e0220415	13
62	Splice Site Variants in the and Genes: Transcript Analysis as a Tool in Supporting Pathogenicity. 2017 , 9, 709-718	4
61	Long QT Syndrome Modelling with Cardiomyocytes Derived from Human-induced Pluripotent Stem Cells. 2019 , 8, 105-110	25
60	GENETIC REASONS OF SUDDEN CARDIAC DEATH. 2017 , 19, 15-22	1
59	Long QT syndrome in South Africa: the results of comprehensive genetic screening. <i>Cardiovascular Journal of Africa</i> , 2013 , 24, 231-7	6
58	Genetics of Cardiac Arrhythmias. 2012 , 81-90	2
57	Ion Channelopathies. 2012 , 85-97	
56	Sodium Ion Channelopathies. 2013 , 193-207	
55	Recurrent and Founder Mutations in the Netherlands: the Long-QT Syndrome*. 2013, 13-19	

54	?????. Japanese Journal of Electrocardiology, 2013 , 33, 193-194	О	
53	Ventricular Tachycardiac and Sudden Arrhythmic Death. 2014 , 2971-2998		
52	Mechanisms in Heritable Sodium Channel Diseases. 2014 , 491-500		
51	Inheritable Potassium Channel Disease. 2014 , 501-509		
50	CardioClassifier Idemonstrating the power of disease- and gene-specific computational decision support for clinical genome interpretation.		1
49	Multi-Disciplinary Management of Inherited Cardiovascular Conditions. 2018, 817-838		
48	Genetic Testing for Inheritable Cardiac Channelopathies. Cardiac and Vascular Biology, 2018, 323-358	0.2	
47	Harmonizing Clinical Sequencing And Interpretation For The Emerge III Network.		
46	Upgraded molecular models of the human KCNQ1 potassium channel.		
45	Genome sequencing for early-onset dementia: high diagnostic yield and frequent observation of multiple contributory alleles.		1
44	Deep Mutational Scan of a cardiac sodium channel voltage sensor.		0
43	Chemical modification of proteins by insertion of synthetic peptides using tandem protein trans-splicing.		
42	High-throughput discovery of trafficking-deficient variants in the cardiac potassium channel KCNH2: Deep mutational scan of KCNH2 trafficking.		
41	Simultaneous Catecholaminergic Polymorphic Ventricular Tachycardia and Long QT Syndrome Gene Mutations. <i>Cureus</i> , 2021 , 13, e19195	1.2	
40	Mechanisms of Cardiac Arrhythmias. 2020 , 1-29		
39	Mechanisms of Cardiac Arrhythmias. 2020 , 1-29 Disease-Linked Super-Trafficking of a Mutant Potassium Channel.		

36	Novel frameshift mutation in the gene responsible for Jervell and Lange-Nielsen syndrome. <i>Iranian Journal of Basic Medical Sciences</i> , 2018 , 21, 108-111	1.8	4
35	A standardised hERG phenotyping pipeline to evaluate KCNH2 genetic variant pathogenicity. <i>Clinical and Translational Medicine</i> , 2021 , 11, e609	5.7	O
34	Mechanistic insights into the interaction of cardiac sodium channel Na1.5 with MOG1 and a new molecular mechanism for Brugada syndrome. <i>Heart Rhythm</i> , 2021 ,	6.7	2
33	Structural Modelling of KCNQ1 and KCNH2 Double Mutant Proteins, Identified in Two Severe Long QT Syndrome Cases, Reveals New Insights into Cardiac Channelopathies. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	O
32	A High-throughput Assay to Identify Drugs that can Treat Long QT Syndrome Caused by Trafficking-deficient K11.1 (hERG) Variants <i>Molecular Pharmacology</i> , 2022 ,	4.3	
31	Physiological Functions, Biophysical Properties, and Regulation of KCNQ1 (K7.1) Potassium Channels <i>Advances in Experimental Medicine and Biology</i> , 2021 , 1349, 335-353	3.6	1
30	Strategies for prevention and management of QT interval prolongation and torsades de pointes. 2022 , 303-333		
29	Case Report: Biventricular Noncompaction Cardiomyopathy With Pulmonary Stenosis and Bradycardia in a Fetus With KCNH2 Mutation <i>Frontiers in Genetics</i> , 2022 , 13, 821226	4.5	O
28	Bilateral Reappearance of the N20 Potential in a Normothermic Young Woman Post-Anoxic Brain Injury <i>Journal of Clinical Neurophysiology</i> , 2022 ,	2.2	0
27	Novel presentation of nonsense mutation as SCN5A overlap syndrome <i>HeartRhythm Case Reports</i> , 2022 , 8, 209-213	1	
26	p.Gly262AlafsTer98: A New Threatening Variant Associated with Long QT Syndrome in a Spanish Cohort <i>Life</i> , 2022 , 12,	3	2
25	Mutational Spectrum of Congenital Long QT Syndrome in Turkey; Identification of Twelve Novel Mutations Across KCNQ1, KCNH2, SCN5A, KCNJ2, CACNA1C, CALM1. <i>Journal of Cardiovascular Electrophysiology</i> , 2021 ,	2.7	
24	Predicting the Functional Impact of KCNQ1 Variants with Artificial Neural Networks.		
23	Predicting the functional impact of KCNQ1 variants with artificial neural networks <i>PLoS Computational Biology</i> , 2022 , 18, e1010038	5	O
22	Rare SUDEP SCN5A variants cause changes in channel function implicating cardiac arrhythmia as a cause of death <i>Epilepsia</i> , 2022 ,	6.4	0
21	Association of QTc Interval and V4-S Wave With Appropriate ICD Therapy in Hypertrophic Cardiomyopathy. <i>Frontiers in Cardiovascular Medicine</i> , 2022 , 9,	5.4	
20	The ERG1 K+ Channel and Its Role in Neuronal Health and Disease. <i>Frontiers in Molecular Neuroscience</i> , 2022 , 15,	6.1	1
19	The Genetics and Epigenetics of Ventricular Arrhythmias in Patients Without Structural Heart Disease. <i>Frontiers in Cardiovascular Medicine</i> , 9,	5.4	О

18	Proactive functional classification of all possible missense single-nucleotide variants in KCNQ4. <i>Genome Research</i> , gr.276562.122	9.7	О
17	Continuous Bayesian Variant Interpretation Accounts for Incomplete Penetrance among Mendelian Cardiac Channelopathies.		
16	Genotype-Specific ECG-Based Risk Stratification Approaches in Patients With Long-QT Syndrome. <i>Frontiers in Cardiovascular Medicine</i> , 9,	5.4	
15	The Advantages, Challenges, and Future of Human-Induced Pluripotent Stem Cell Lines in Type 2 Long QT Syndrome.		
14	Whole exome sequencing in Brugada and long QT syndromes revealed novel rare and potential pathogenic mutations related to the dysfunction of the cardiac sodium channel. 2022 , 17,		О
13	Same family, same mutation, different ECG.		O
12	Pharmacological rescue of specific long QT variants of KCNQ1/KCNE1 channels. 13,		О
11	Continuous Bayesian Variant Interpretation Accounts for Incomplete Penetrance among Mendelian Cardiac Channelopathies. 2022 ,		О
10	Modeling long QT syndrome type 2 on-a-chip via in-depth assessment of isogenic gene-edited 3D cardiac tissues. 2022 , 8,		1
9	Functional Characterization of a Spectrum of Novel Romano-Ward Syndrome KCNQ1 Variants. 2023 , 24, 1350		O
8	Modulation of the IKS channel by PIP2 requires two binding sites per monomer. 2023, 3, 100073		О
7	Beyond gene-disease validity: capturing structured data on inheritance, allelic-requirement, disease-relevant variant classes, and disease mechanism for inherited cardiac conditions.		Ο
6	Clinical and functional characterisation of a recurrent KCNQ1 variant in the Belgian population. 2023 , 18,		O
5	In silico analysis of the dynamic regulation of cardiac electrophysiology by K v 11.1 ion-channel trafficking.		O
4	First report of genetic variants detected in Argentinian patients with clinical Long QT Syndrome diagnosis.		О
3	IKs Activator ML277 Mildly Affects Repolarization and Arrhythmic Outcome in the CAVB Dog Model. 2023 , 11, 1147		O
2	Identification of a novel pathogenic variant in KCNH2 in an Iranian family with long QT syndrome 2 by whole-exome sequencing.		О
1	High-throughput functional mapping of variants in an arrhythmia gene,KCNE1, reveals novel biology.		O