

Brett M Kroncke

List of Publications by Year in descending order

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times ranked

1374
citing authors

#	ARTICLE	IF	CITATIONS
1	Veratridine Can Bind to a Site at the Mouth of the Channel Pore at Human Cardiac Sodium Channel NaV1.5. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2225.	1.8	2
2	Arrhythmia Variant Associations and Reclassifications in the eMERGE-III Sequencing Study. <i>Circulation</i> , 2022, 145, 877-891.	1.6	18
3	A massively parallel assay accurately discriminates between functionally normal and abnormal variants in a hotspot domain of KCNH2. <i>American Journal of Human Genetics</i> , 2022, 109, 1208-1216.	2.6	15
4	Estimating the Posttest Probability of Long QT Syndrome Diagnosis for Rare <i>KCNH2</i> Variants. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003289.	1.6	10
5	High-Throughput Reclassification of SCN5A Variants. <i>American Journal of Human Genetics</i> , 2020, 107, 111-123.	2.6	88
6	A Bayesian method to estimate variant-induced disease penetrance. <i>PLoS Genetics</i> , 2020, 16, e1008862.	1.5	11
7	High-throughput discovery of trafficking-deficient variants in the cardiac potassium channel KV11.1. <i>Heart Rhythm</i> , 2020, 17, 2180-2189.	0.3	42
8	Deep Mutational Scan of an <i>SCN5A</i> Voltage Sensor. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002786.	1.6	33
9	A Bayesian method to estimate variant-induced disease penetrance. , 2020, 16, e1008862.		0
10	A Bayesian method to estimate variant-induced disease penetrance. , 2020, 16, e1008862.		0
11	A Bayesian method to estimate variant-induced disease penetrance. , 2020, 16, e1008862.		0
12	A Bayesian method to estimate variant-induced disease penetrance. , 2020, 16, e1008862.		0
13	A Bayesian method to estimate variant-induced disease penetrance. , 2020, 16, e1008862.		0
14	A Bayesian method to estimate variant-induced disease penetrance. , 2020, 16, e1008862.		0
15	Association of Thyroid Function Genetic Predictors With Atrial Fibrillation. <i>JAMA Cardiology</i> , 2019, 4, 136.	3.0	23
16	SCN5A variant R222Q generated abnormal changes in cardiac sodium current and action potentials in murine myocytes and Purkinje cells. <i>Heart Rhythm</i> , 2019, 16, 1676-1685.	0.3	15
17	Patient-independent human induced pluripotent stem cell model: A new tool for rapid determination of genetic variant pathogenicity in long QT syndrome. <i>Heart Rhythm</i> , 2019, 16, 1686-1695.	0.3	32
18	Protein structure aids predicting functional perturbation of missense variants in SCN5A and KCNQ1. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 206-214.	1.9	19

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19	Multiple mechanisms underlie increased cardiac late sodium current. <i>Heart Rhythm</i> , 2019, 16, 1091-1097.	0.3	8
20	Exploiting ion channel structure to assess rare variant pathogenicity. <i>Heart Rhythm</i> , 2018, 15, 890-894.	0.3	4
21	A Mechanism of Calmodulin Modulation of the Human Cardiac Sodium Channel. <i>Structure</i> , 2018, 26, 683-694.e3.	1.6	43
22	<i>SCN5A</i> (Na ^V 1.5) Variant Functional Perturbation and Clinical Presentation. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002095.	1.6	36
23	Arrhythmia genetics: Not dark and lite, but 50 shades of gray. <i>Heart Rhythm</i> , 2018, 15, 1231-1232.	0.3	2
24	Structural and biochemical differences between the Notch and the amyloid precursor protein transmembrane domains. <i>Science Advances</i> , 2017, 3, e1602794.	4.7	38
25	Predicting the Functional Impact of KCNQ1 Variants of Unknown Significance. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	40
26	Structural basis for KCNE3 modulation of potassium recycling in epithelia. <i>Science Advances</i> , 2016, 2, e1501228.	4.7	45
27	Documentation of an Imperative To Improve Methods for Predicting Membrane Protein Stability. <i>Biochemistry</i> , 2016, 55, 5002-5009.	1.2	46
28	Structural Basis for KCNQ1 Long-QT Syndrome Disease causing Mutations. <i>Biophysical Journal</i> , 2016, 110, 230a.	0.2	0
29	Solution NMR Structure Determination of Polytopic α -Helical Membrane Proteins. <i>Methods in Enzymology</i> , 2015, 557, 329-348.	0.4	4
30	Personalized Biochemistry and Biophysics. <i>Biochemistry</i> , 2015, 54, 2551-2559.	1.2	31
31	Probing Structural Dynamics and Topology of the KCNE1 Membrane Protein in Lipid Bilayers via Site-Directed Spin Labeling and Electron Paramagnetic Resonance Spectroscopy. <i>Biochemistry</i> , 2015, 54, 6402-6412.	1.2	26
32	Structural Investigation of the Transmembrane Domain of KCNE1 in Proteoliposomes. <i>Biochemistry</i> , 2014, 53, 6392-6401.	1.2	42
33	Structure of the Neisserial Outer Membrane Protein Opa ₆₀ : α -Loop Flexibility Essential to Receptor Recognition and Bacterial Engulfment. <i>Journal of the American Chemical Society</i> , 2014, 136, 9938-9946.	6.6	52
34	Mapping Membrane Protein Backbone Dynamics: A Comparison of Site-Directed Spin Labeling with NMR 15N-Relaxation Measurements. <i>Biophysical Journal</i> , 2014, 107, 1697-1702.	0.2	6
35	Interaction Between KCNQ1 Gain-of-Function Residues. <i>Biophysical Journal</i> , 2014, 106, 141a.	0.2	2
36	Backbone 1H, 13C and 15N resonance assignments of the α -helical membrane protein TM0026 from <i>Thermotoga maritima</i> . <i>Biomolecular NMR Assignments</i> , 2013, 7, 203-206.	0.4	2

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37	MAPK Phosphorylation of Connexin 43 Promotes Binding of Cyclin E and Smooth Muscle Cell Proliferation. <i>Circulation Research</i> , 2012, 111, 201-211.	2.0	89
38	Identification and removal of nitroxide spin label contaminant: Impact on PRE studies of α -helical membrane proteins in detergent. <i>Protein Science</i> , 2012, 21, 589-595.	3.1	6
39	Nitroxide Spin Label Side Chain Dynamics of Solvent Exposed Sites on Membrane Proteins. <i>Biophysical Journal</i> , 2011, 100, 143a-144a.	0.2	0