

Nathan R Tucker

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

3,523
citations

293460

24
h-index

445137

33
g-index

44
all docs

44
docs citations

44
times ranked

7859
citing authors

#	ARTICLE	IF	CITATIONS
1	Deep learning enables genetic analysis of the human thoracic aorta. <i>Nature Genetics</i> , 2022, 54, 40-51.	9.4	90
2	Clinico-histopathologic and single-nuclei RNA-sequencing insights into cardiac injury and microthrombi in critical COVID-19. <i>JCI Insight</i> , 2022, 7, .	2.3	14
3	Increased atrial effectiveness of flecainide conferred by altered biophysical properties of sodium channels. <i>Journal of Molecular and Cellular Cardiology</i> , 2022, 166, 23-35.	0.9	12
4	Single-cell technologies to decipher cardiovascular diseases. <i>European Heart Journal</i> , 2022, 43, 4536-4547.	1.0	19
5	Single-nucleus profiling of human dilated and hypertrophic cardiomyopathy. <i>Nature</i> , 2022, 608, 174-180.	13.7	115
6	Single-cell meta-analysis of SARS-CoV-2 entry genes across tissues and demographics. <i>Nature Medicine</i> , 2021, 27, 546-559.	15.2	261
7	COVID-19 and Cardiovascular Disease. <i>Circulation Research</i> , 2021, 128, 1214-1236.	2.0	232
8	SnRNA sequencing defines signaling by RBC-derived extracellular vesicles in the murine heart. <i>Life Science Alliance</i> , 2021, 4, e202101048.	1.3	9
9	Epigenetic Analyses of Human Left Atrial Tissue Identifies Gene Networks Underlying Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e003085.	1.6	14
10	Transcriptional and Cellular Diversity of the Human Heart. <i>Circulation</i> , 2020, 142, 466-482.	1.6	326
11	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.	5.8	59
12	Myocyte Specific Upregulation of ACE2 in Cardiovascular Disease: Implications for SARS-CoV-2 Mediated Myocarditis. <i>Circulation</i> , 2020, 142, 708-710.	1.6	73
13	Epigenetic and Transcriptional Networks Underlying Atrial Fibrillation. <i>Circulation Research</i> , 2020, 127, 34-50.	2.0	48
14	Identification of Functional Variant Enhancers Associated With Atrial Fibrillation. <i>Circulation Research</i> , 2020, 127, 229-243.	2.0	33
15	Long-range Pitx2c enhancerâ€‘promoter interactions prevent predisposition to atrial fibrillation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22692-22698.	3.3	46
16	Cardioprotective Effects of <i>MTSS1</i> Enhancer Variants. <i>Circulation</i> , 2019, 139, 2073-2076.	1.6	12
17	Genome-Wide Association Studyâ€‘Driven Gene-Set Analyses, Genetic, and Functional Follow-Up Suggest <i>GLIS1</i> as a Susceptibility Gene for Mitral Valve Prolapse. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, e002497.	1.6	31
18	Response by Ma et al to Letter Regarding Article, â€œNovel Mutation in FLNC (Filamin C) Causes Familial Restrictive Cardiomyopathyâ€‘. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002140.	1.6	0

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19	Association Between Titin Loss-of-Function Variants and Early-Onset Atrial Fibrillation. <i>JAMA - Journal of the American Medical Association</i> , 2018, 320, 2354.	3.8	144
20	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002037.	1.6	19
21	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018, 50, 1225-1233.	9.4	552
22	Genetic Reduction in Left Ventricular Protein Kinase C- β and Adverse Ventricular Remodeling in Human Subjects. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e001901.	1.6	10
23	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , 2017, 49, 946-952.	9.4	279
24	Diminished <i>PRRX1</i> Expression Is Associated With Increased Risk of Atrial Fibrillation and Shortening of the Cardiac Action Potential. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	33
25	Novel Mutation in <i>FLNC</i> (Filamin C) Causes Familial Restrictive Cardiomyopathy. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	62
26	Mutation of a common amino acid in NKX2.5 results in dilated cardiomyopathy in two large families. <i>BMC Medical Genetics</i> , 2016, 17, 83.	2.1	14
27	A Functional Variant Associated with Atrial Fibrillation Regulates PITX2c Expression through TFAP2a. <i>American Journal of Human Genetics</i> , 2016, 99, 1281-1291.	2.6	59
28	Common variation in atrial fibrillation: navigating the path from genetic association to mechanism. <i>Cardiovascular Research</i> , 2016, 109, 493-501.	1.8	54
29	PHACTR1 Is a Genetic Susceptibility Locus for Fibromuscular Dysplasia Supporting Its Complex Genetic Pattern of Inheritance. <i>PLoS Genetics</i> , 2016, 12, e1006367.	1.5	146
30	Discovery and validation of sub-threshold genome-wide association study loci using epigenomic signatures. <i>ELife</i> , 2016, 5, .	2.8	115
31	Genetic association analyses highlight biological pathways underlying mitral valve prolapse. <i>Nature Genetics</i> , 2015, 47, 1206-1211.	9.4	103
32	Integrating Genetic, Transcriptional, and Functional Analyses to Identify 5 Novel Genes for Atrial Fibrillation. <i>Circulation</i> , 2014, 130, 1225-1235.	1.6	183
33	Emerging Directions in the Genetics of Atrial Fibrillation. <i>Circulation Research</i> , 2014, 114, 1469-1482.	2.0	106
34	A novel trafficking-defective HCN4 mutation is associated with early-onset atrial fibrillation. <i>Heart Rhythm</i> , 2014, 11, 1055-1062.	0.3	64