Nathan R Tucker

List of Publications by Year
in descending order

34 papers	3,523 citations	257450 24 h-index	395702 33 g-index
44 all docs	44 docs citations	44 times ranked	7218 citing authors

#	Article	IF	Citations
1	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	21.4	552
2	Transcriptional and Cellular Diversity of the Human Heart. Circulation, 2020, 142, 466-482.	1.6	326
3	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	21.4	279
4	Single-cell meta-analysis of SARS-CoV-2 entry genes across tissues and demographics. Nature Medicine, 2021, 27, 546-559.	30.7	261
5	COVID-19 and Cardiovascular Disease. Circulation Research, 2021, 128, 1214-1236.	4.5	232
6	Integrating Genetic, Transcriptional, and Functional Analyses to Identify 5 Novel Genes for Atrial Fibrillation. Circulation, 2014, 130, 1225-1235.	1.6	183
7	PHACTR1 Is a Genetic Susceptibility Locus for Fibromuscular Dysplasia Supporting Its Complex Genetic Pattern of Inheritance. PLoS Genetics, 2016, 12, e1006367.	3.5	146
8	Association Between Titin Loss-of-Function Variants and Early-Onset Atrial Fibrillation. JAMA - Journal of the American Medical Association, 2018, 320, 2354.	7.4	144
9	Discovery and validation of sub-threshold genome-wide association study loci using epigenomic signatures. ELife, 2016, 5, .	6.0	115
10	Single-nucleus profiling of human dilated and hypertrophic cardiomyopathy. Nature, 2022, 608, 174-180.	27.8	115
11	Emerging Directions in the Genetics of Atrial Fibrillation. Circulation Research, 2014, 114, 1469-1482.	4.5	106
12	Genetic association analyses highlight biological pathways underlying mitral valve prolapse. Nature Genetics, 2015, 47, 1206-1211.	21.4	103
13	Deep learning enables genetic analysis of the human thoracic aorta. Nature Genetics, 2022, 54, 40-51.	21.4	90
14	Myocyte Specific Upregulation of ACE2 in Cardiovascular Disease: Implications for SARS-CoV-2 Mediated Myocarditis. Circulation, 2020, 142, 708-710.	1.6	73
15	A novel trafficking-defective HCN4 mutation is associated with early-onset atrial fibrillation. Heart Rhythm, 2014, 11, 1055-1062.	0.7	64
16	Novel Mutation in FLNC (Filamin C) Causes Familial Restrictive Cardiomyopathy. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	62
17	A Functional Variant Associated with Atrial Fibrillation Regulates PITX2c Expression through TFAP2a. American Journal of Human Genetics, 2016, 99, 1281-1291.	6.2	59
18	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59

#	Article	IF	Citations
19	Common variation in atrial fibrillation: navigating the path from genetic association to mechanism. Cardiovascular Research, 2016, 109, 493-501.	3.8	54
20	Epigenetic and Transcriptional Networks Underlying Atrial Fibrillation. Circulation Research, 2020, 127, 34-50.	4.5	48
21	Long-range Pitx2c enhancerâ€“promoter interactions prevent predisposition to atrial fibrillation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 22692-22698.	7.1	46
22	Diminished PRRX1 Expression Is Associated With Increased Risk of Atrial Fibrillation and Shortening of the Cardiac Action Potential. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	33
23	Identification of Functional Variant Enhancers Associated With Atrial Fibrillation. Circulation Research, 2020, 127, 229-243.	4.5	33
24	Genome-Wide Association Studyâ€“Driven Gene-Set Analyses, Genetic, and Functional Follow-Up Suggest GLIS1 as a Susceptibility Gene for Mitral Valve Prolapse. Circulation Genomic and Precision Medicine, 2019, 12, e002497.	3.6	31
25	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	3.6	19
26	Single-cell technologies to decipher cardiovascular diseases. European Heart Journal, 2022, 43, 4536-4547.	2.2	19
27	Mutation of a common amino acid in NKX2.5 results in dilated cardiomyopathy in two large families. BMC Medical Genetics, 2016, 17, 83.	2.1	14
28	Epigenetic Analyses of Human Left Atrial Tissue Identifies Gene Networks Underlying Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2020, 13, e003085.	3.6	14
29	Clinico-histopathologic and single-nuclei RNA-sequencing insights into cardiac injury and microthrombi in critical COVID-19. JCI Insight, 2022, 7, .	5.0	14
30	Cardioprotective Effects of MTSS1 Enhancer Variants. Circulation, 2019, 139, 2073-2076.	1.6	12
31	Increased atrial effectiveness of flecainide conferred by altered biophysical properties of sodium channels. Journal of Molecular and Cellular Cardiology, 2022, 166, 23-35.	1.9	12
32	Genetic Reduction in Left Ventricular Protein Kinase C-Î± and Adverse Ventricular Remodeling in Human Subjects. Circulation Genomic and Precision Medicine, 2018, 11, e001901.	3.6	10
33	SnRNA sequencing defines signaling by RBC-derived extracellular vesicles in the murine heart. Life Science Alliance, 2021, 4, e202101048.	2.8	9
34	Response by Ma et al to Letter Regarding Article, â€œNovel Mutation in FLNC (Filamin C) Causes Familial Restrictive Cardiomyopathyâ€. Circulation Genomic and Precision Medicine, 2018, 11, e002140.	3.6	0