Andrew M Glazer

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4281418/publications.pdf

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41	1,721	331538	395590
papers	citations	21 h-index	33 g-index

49	49	49	3763
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Phenotype risk scores identify patients with unrecognized Mendelian disease patterns. Science, 2018, 359, 1233-1239.	6.0	164
2	Clinical and Biological Insights Into Combined Post- and Pre-Capillary Pulmonary Hypertension. Journal of the American College of Cardiology, 2016, 68, 2525-2536.	1.2	160
3	Modular Skeletal Evolution in Sticklebacks Is Controlled by Additive and Clustered Quantitative Trait Loci. Genetics, 2014, 197, 405-420.	1.2	122
4	Genome Assembly Improvement and Mapping Convergently Evolved Skeletal Traits in Sticklebacks with Genotyping-by-Sequencing. G3: Genes, Genomes, Genetics, 2015, 5, 1463-1472.	0.8	112
5	Phenome-wide scanning identifies multiple diseases and disease severity phenotypes associated with HLA variants. Science Translational Medicine, 2017, 9, .	5.8	105
6	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. American Journal of Human Genetics, 2019, 105, 588-605.	2.6	99
7	High-Throughput Reclassification of SCN5A Variants. American Journal of Human Genetics, 2020, 107, 111-123.	2.6	88
8	The Zn Finger protein Iguana impacts Hedgehog signaling by promoting ciliogenesis. Developmental Biology, 2010, 337, 148-156.	0.9	87
9	Androgenic Effects on Ventricular Repolarization. Circulation, 2019, 140, 1070-1080.	1.6	67
10	Early-Onset Atrial Fibrillation and the Prevalence of Rare Variants in Cardiomyopathy and Arrhythmia Genes. JAMA Cardiology, 2021, 6, 1371.	3.0	66
11	Comparison of HLA allelic imputation programs. PLoS ONE, 2017, 12, e0172444.	1.1	58
12	Hypogonadism as a Reversible Cause of Torsades de Pointes in Men. Circulation, 2018, 138, 110-113.	1.6	57
13	Genome-wide association and pathway analysis of left ventricular function after anthracycline exposure in adults. Pharmacogenetics and Genomics, 2017, 27, 247-254.	0.7	54
14	Distinct developmental and genetic mechanisms underlie convergently evolved tooth gain in sticklebacks. Development (Cambridge), 2015, 142, 2442-51.	1.2	53
15	A Mechanism of Calmodulin Modulation of the Human Cardiac Sodium Channel. Structure, 2018, 26, 683-694.e3.	1.6	43
16	High-throughput discovery of trafficking-deficient variants in the cardiac potassium channel KV11.1. Heart Rhythm, 2020, 17, 2180-2189.	0.3	42
17	Increased long QT and torsade de pointes reporting on tamoxifen compared with aromatase inhibitors. Heart, 2018, 104, 1859-1863.	1.2	37
18	Parallel developmental genetic features underlie stickleback gill raker evolution. EvoDevo, 2014, 5, 19.	1.3	36

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19	SCN5A (Na _V 1.5) Variant Functional Perturbation and Clinical Presentation. Circulation Genomic and Precision Medicine, 2018, 11, e002095.	1.6	36
20	Partially repeatable genetic basis of benthic adaptation in threespine sticklebacks. Evolution; International Journal of Organic Evolution, 2016, 70, 887-902.	1.1	33
21	Deep Mutational Scan of an SCN5A Voltage Sensor. Circulation Genomic and Precision Medicine, 2020, 13, e002786.	1.6	33
22	Patient-independent human induced pluripotent stem cell model: A new tool for rapid determination of genetic variant pathogenicity in long QT syndrome. Heart Rhythm, 2019, 16, 1686-1695.	0.3	32
23	Association of Thyroid Function Genetic Predictors With Atrial Fibrillation. JAMA Cardiology, 2019, 4, 136.	3.0	23
24	Arrhythmia Variant Associations and Reclassifications in the eMERGE-III Sequencing Study. Circulation, 2022, 145, 877-891.	1.6	18
25	Two developmentally temporal quantitative trait loci underlie convergent evolution of increased branchial bone length in sticklebacks. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20140822.	1.2	17
26	Mortality Among Patients With Early-Onset Atrial Fibrillation and Rare Variants in Cardiomyopathy and Arrhythmia Genes. JAMA Cardiology, 2022, 7, 733.	3.0	14
27	Common Ancestry-Specific Ion Channel Variants Predispose to Drug-Induced Arrhythmias. Circulation, 2022, 145, 299-308.	1.6	12
28	A Bayesian method to estimate variant-induced disease penetrance. PLoS Genetics, 2020, 16, e1008862.	1.5	11
29	Estimating the Posttest Probability of Long QT Syndrome Diagnosis for Rare KCNH2 Variants. Circulation Genomic and Precision Medicine, 2021, 14, e003289.	1.6	10
30	Dominant negative effects of SCN5A missense variants. Genetics in Medicine, 2022, 24, 1238-1248.	1.1	9
31	KCNQ1 and Long QT Syndrome in 1/45 Amish. Circulation Genomic and Precision Medicine, 2020, 13, e003133.	1.6	7
32	Arrhythmia genetics: Not dark and lite, but 50 shades of gray. Heart Rhythm, 2018, 15, 1231-1232.	0.3	2
33	Veratridine Can Bind to a Site at the Mouth of the Channel Pore at Human Cardiac Sodium Channel NaV1.5. International Journal of Molecular Sciences, 2022, 23, 2225.	1.8	2
34	Exploring the Genetic Basis of Variation in Gene Predictions with a Synthetic Association Study. PLoS ONE, 2010, 5, e11645.	1.1	0
35	Incessant atrial and ventricular tachycardias associated with an SCN5A mutation. HeartRhythm Case Reports, 2021, 7, 806-811.	0.2	0
36	A Bayesian method to estimate variant-induced disease penetrance. , 2020, 16, e1008862.		0

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37	A Bayesian method to estimate variant-induced disease penetrance. , 2020, 16, e1008862.		0
38	A Bayesian method to estimate variant-induced disease penetrance. , 2020, 16, e1008862.		0
39	A Bayesian method to estimate variant-induced disease penetrance. , 2020, 16, e1008862.		0
40	A Bayesian method to estimate variant-induced disease penetrance. , 2020, 16, e1008862.		0
41	A Bayesian method to estimate variant-induced disease penetrance. , 2020, 16, e1008862.		0