Gustav Ahlberg

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7212642/publications.pdf

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28	1,104	687363 13	526287 27
papers	citations	h-index	g-index

30	30	30	2662
all docs	docs citations	times ranked	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	Rare truncating variants in the sarcomeric protein titin associate with familial and early-onset atrial fibrillation. Nature Communications, 2018, 9, 4316.	12.8	93
3	Rare genetic variants previously associated with congenital forms of long QT syndrome have little or no effect on the QT interval. European Heart Journal, 2015, 36, 2523-2529.	2.2	53
4	Human iPSC modelling of a familial form of atrial fibrillation reveals a gain of function of If and ICaL in patient-derived cardiomyocytes. Cardiovascular Research, 2020, 116, 1147-1160.	3.8	50
5	Integration of 60,000 exomes and <scp>ACMG</scp> guidelines question the role of Catecholaminergic Polymorphic Ventricular Tachycardiaâ€associated variants. Clinical Genetics, 2017, 91, 63-72.	2.0	31
6	DeepFake electrocardiograms using generative adversarial networks are the beginning of the end for privacy issues in medicine. Scientific Reports, 2021, 11, 21896.	3.3	31
7	Genome-wide association study identifies 18 novel loci associated with left atrial volume and function. European Heart Journal, 2021, 42, 4523-4534.	2.2	30
8	Analyses of more than 60,000 exomes questions the role of numerous genes previously associated with dilated cardiomyopathy. Molecular Genetics & Genomic Medicine, 2016, 4, 617-623.	1.2	29
9	Early sarcomere and metabolic defects in a zebrafish pitx2c cardiac arrhythmia model. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 24115-24121.	7.1	28
10	Numerous Brugada syndromeâ€“associated genetic variants have no effect on J-point elevation, syncope susceptibility, malignant cardiac arrhythmia, and all-cause mortality. Genetics in Medicine, 2017, 19, 521-528.	2.4	26
11	Explaining deep neural networks for knowledge discovery in electrocardiogram analysis. Scientific Reports, 2021, 11, 10949.	3.3	26
12	Distinguishing pathogenic mutations from background genetic noise in cardiology: The use of large genome databases for genetic interpretation. Clinical Genetics, 2018, 93, 459-466.	2.0	20
13	A Novel Familial Cardiac Arrhythmia Syndrome with Widespread ST-Segment Depression. New England Journal of Medicine, 2018, 379, 1780-1781.	27.0	17
14	Loss-of-Function Variants in Cytoskeletal Genes Are Associated with Early-Onset Atrial Fibrillation. Journal of Clinical Medicine, 2020, 9, 372.	2.4	14
15	Genome-wide association study identifies locus at chromosome 2q32.1 associated with syncope and collapse. Cardiovascular Research, 2020, 116, 138-148.	3.8	13
16	Deep sequencing of atrial fibrillation patients with mitral valve regurgitation shows no evidence of mosaicism but reveals novel rare germline variants. Heart Rhythm, 2017, 14, 1531-1538.	0.7	12
17	Next-generation sequencing of AV nodal reentrant tachycardia patients identifies broad spectrum of variants in ion channel genes. European Journal of Human Genetics, 2018, 26, 660-668.	2.8	12
18	Early-onset atrial fibrillation patients show reduced left ventricular ejection fraction and increased atrial fibrosis. Scientific Reports, 2020, 10, 10039.	3.3	12

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19	Association of Variants Near the Bradykinin Receptor B2 Gene With Angioedema in Patients Taking ACEÂInhibitors. Journal of the American College of Cardiology, 2021, 78, 696-709.	2.8	10
20	A Novel Loss-of-Function Variant in the Chloride Ion Channel Gene Clcn2 Associates with Atrial Fibrillation. Scientific Reports, 2020, 10, 1453.	3.3	10
21	Reappraisal of variants previously linked with sudden infant death syndrome: results from three population-based cohorts. European Journal of Human Genetics, 2019, 27, 1427-1435.	2.8	9
22	Analysis of 60â€‰706 Exomes Questions the Role of De Novo Variants Previously Implicated in Cardiac Disease. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	7
23	Polygenic risk score for ACE-inhibitor-associated cough based on the discovery of new genetic loci. European Heart Journal, 2022, 43, 4707-4718.	2.2	5
24	Association of Common and Rare Genetic Variation in the 3â€Hydroxyâ€3â€Methylglutaryl Coenzyme A Reductase Gene and Cataract Risk. Journal of the American Heart Association, 2022, 11, .	3.7	4
25	Brugada Syndrome-Associated Genetic Loci Are Associated With J-Point Elevation and an Increased Risk of Cardiac Arrest. Frontiers in Physiology, 2018, 9, 894.	2.8	2
26	Effect of Loss-of-Function Genetic Variants in PCSK9 on Glycemic Traits, Neurocognitive Impairment, and Hepatobiliary Function. Diabetes Care, 2022, 45, 251-254.	8.6	1
27	Whole-Exome Sequencing Implicates Neuronal Calcium Channel with Familial Atrial Fibrillation. Frontiers in Genetics, 2022, 13, 806429.	2.3	1
28	Clinical Implications of SCN10A Loss-of-Function Variants in 169â€‰610 Exomes Representing the General Population. Circulation Genomic and Precision Medicine, 2022, 15, CIRCGEN121003574.	3.6	1