

Gustav Ahlberg

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

1,104
citations

686830

13
h-index

525886

27
g-index

30
all docs

30
docs citations

30
times ranked

2662
citing authors

#	ARTICLE	IF	CITATIONS
1	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018, 50, 1225-1233.	9.4	552
2	Rare truncating variants in the sarcomeric protein titin associate with familial and early-onset atrial fibrillation. <i>Nature Communications</i> , 2018, 9, 4316.	5.8	93
3	Rare genetic variants previously associated with congenital forms of long QT syndrome have little or no effect on the QT interval. <i>European Heart Journal</i> , 2015, 36, 2523-2529.	1.0	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. <i>Cardiovascular Research</i> , 2020, 116, 1147-1160.	1.8	50
5	Integration of 60,000 exomes and ACMG guidelines question the role of Catecholaminergic Polymorphic Ventricular Tachycardia-associated variants. <i>Clinical Genetics</i> , 2017, 91, 63-72.	1.0	31
6	DeepFake electrocardiograms using generative adversarial networks are the beginning of the end for privacy issues in medicine. <i>Scientific Reports</i> , 2021, 11, 21896.	1.6	31
7	Genome-wide association study identifies 18 novel loci associated with left atrial volume and function. <i>European Heart Journal</i> , 2021, 42, 4523-4534.	1.0	30
8	Analyses of more than 60,000 exomes questions the role of numerous genes previously associated with dilated cardiomyopathy. <i>Molecular Genetics & Genomic Medicine</i> , 2016, 4, 617-623.	0.6	29
9	Early sarcomere and metabolic defects in a zebrafish <i>pitx2c</i> cardiac arrhythmia model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24115-24121.	3.3	28
10	Numerous Brugada syndrome-associated genetic variants have no effect on J-point elevation, syncope susceptibility, malignant cardiac arrhythmia, and all-cause mortality. <i>Genetics in Medicine</i> , 2017, 19, 521-528.	1.1	26
11	Explaining deep neural networks for knowledge discovery in electrocardiogram analysis. <i>Scientific Reports</i> , 2021, 11, 10949.	1.6	26
12	Distinguishing pathogenic mutations from background genetic noise in cardiology: The use of large genome databases for genetic interpretation. <i>Clinical Genetics</i> , 2018, 93, 459-466.	1.0	20
13	A Novel Familial Cardiac Arrhythmia Syndrome with Widespread ST-Segment Depression. <i>New England Journal of Medicine</i> , 2018, 379, 1780-1781.	13.9	17
14	Loss-of-Function Variants in Cytoskeletal Genes Are Associated with Early-Onset Atrial Fibrillation. <i>Journal of Clinical Medicine</i> , 2020, 9, 372.	1.0	14
15	Genome-wide association study identifies locus at chromosome 2q32.1 associated with syncope and collapse. <i>Cardiovascular Research</i> , 2020, 116, 138-148.	1.8	13
16	Deep sequencing of atrial fibrillation patients with mitral valve regurgitation shows no evidence of mosaicism but reveals novel rare germline variants. <i>Heart Rhythm</i> , 2017, 14, 1531-1538.	0.3	12
17	Next-generation sequencing of AV nodal reentrant tachycardia patients identifies broad spectrum of variants in ion channel genes. <i>European Journal of Human Genetics</i> , 2018, 26, 660-668.	1.4	12
18	Early-onset atrial fibrillation patients show reduced left ventricular ejection fraction and increased atrial fibrosis. <i>Scientific Reports</i> , 2020, 10, 10039.	1.6	12

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19	Association of Variants Near the Bradykinin Receptor B2 Gene With Angioedema in Patients Taking ACE-Inhibitors. <i>Journal of the American College of Cardiology</i> , 2021, 78, 696-709.	1.2	10
20	A Novel Loss-of-Function Variant in the Chloride Ion Channel Gene <i>Clcn2</i> Associates with Atrial Fibrillation. <i>Scientific Reports</i> , 2020, 10, 1453.	1.6	10
21	Reappraisal of variants previously linked with sudden infant death syndrome: results from three population-based cohorts. <i>European Journal of Human Genetics</i> , 2019, 27, 1427-1435.	1.4	9
22	Analysis of 60,706 Exomes Questions the Role of De Novo Variants Previously Implicated in Cardiac Disease. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	7
23	Polygenic risk score for ACE-inhibitor-associated cough based on the discovery of new genetic loci. <i>European Heart Journal</i> , 2022, 43, 4707-4718.	1.0	5
24	Association of Common and Rare Genetic Variation in the 3-Hydroxy-3-Methylglutaryl Coenzyme A Reductase Gene and Cataract Risk. <i>Journal of the American Heart Association</i> , 2022, 11, .	1.6	4
25	Brugada Syndrome-Associated Genetic Loci Are Associated With J-Point Elevation and an Increased Risk of Cardiac Arrest. <i>Frontiers in Physiology</i> , 2018, 9, 894.	1.3	2
26	Effect of Loss-of-Function Genetic Variants in <i>PCSK9</i> on Glycemic Traits, Neurocognitive Impairment, and Hepatobiliary Function. <i>Diabetes Care</i> , 2022, 45, 251-254.	4.3	1
27	Whole-Exome Sequencing Implicates Neuronal Calcium Channel with Familial Atrial Fibrillation. <i>Frontiers in Genetics</i> , 2022, 13, 806429.	1.1	1
28	Clinical Implications of <i>SCN10A</i> Loss-of-Function Variants in 169,610 Exomes Representing the General Population. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, CIRCGEN121003574.	1.6	1