

Gustav Ahlberg

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

26

papers

580

citations

9

h-index

24

g-index

30

ext. papers

870

ext. citations

9.7

avg, IF

2.9

L-index

#	Paper	IF	Citations
26	Whole-Exome Sequencing Implicates Neuronal Calcium Channel with Familial Atrial Fibrillation.. <i>Frontiers in Genetics</i> , 2022 , 13, 806429	4.5	
25	DeepFake electrocardiograms using generative adversarial networks are the beginning of the end for privacy issues in medicine. <i>Scientific Reports</i> , 2021 , 11, 21896	4.9	6
24	Explaining deep neural networks for knowledge discovery in electrocardiogram analysis. <i>Scientific Reports</i> , 2021 , 11, 10949	4.9	9
23	Genome-wide association study identifies 18 novel loci associated with left atrial volume and function. <i>European Heart Journal</i> , 2021 , 42, 4523-4534	9.5	4
22	Association of Variants Near the Bradykinin Receptor B Gene With Angioedema in Patients Taking ACEInhibitors. <i>Journal of the American College of Cardiology</i> , 2021 , 78, 696-709	15.1	2
21	Early-onset atrial fibrillation patients show reduced left ventricular ejection fraction and increased atrial fibrosis. <i>Scientific Reports</i> , 2020 , 10, 10039	4.9	3
20	Loss-of-Function Variants in Cytoskeletal Genes Are Associated with Early-Onset Atrial Fibrillation. <i>Journal of Clinical Medicine</i> , 2020 , 9,	5.1	7
19	A Novel Loss-of-Function Variant in the Chloride Ion Channel Gene Clcn2 Associates with Atrial Fibrillation. <i>Scientific Reports</i> , 2020 , 10, 1453	4.9	4
18	Genome-wide association study identifies locus at chromosome 2q32.1 associated with syncope and collapse. <i>Cardiovascular Research</i> , 2020 , 116, 138-148	9.9	6
17	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	9.9	27
16	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	5.3	4
15	Early sarcomere and metabolic defects in a zebrafish cardiac arrhythmia model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 24115-24121	11.5	14
14	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	5.3	6
13	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	4	16
12	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	4.6	1
11	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018 , 50, 1225-1233	36.3	277
10	A Novel Familial Cardiac Arrhythmia Syndrome with Widespread ST-Segment Depression. <i>New England Journal of Medicine</i> , 2018 , 379, 1780-1781	59.2	7

9	Rare truncating variants in the sarcomeric protein titin associate with familial and early-onset atrial fibrillation. <i>Nature Communications</i> , 2018 , 9, 4316	17.4	58
8	Analysis of 60 706 Exomes Questions the Role of De Novo Variants Previously Implicated in Cardiac Disease. <i>Circulation: Cardiovascular Genetics</i> , 2017 , 10,		3
7	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	6.7	7
6	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	4	26
5	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	8.1	20
4	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	2.3	24
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, 2523-9	9.5	45
2	DeepFake electrocardiograms: the key for open science for artificial intelligence in medicine		2
1	Explaining Deep Neural Networks for Knowledge Discovery in Electrocardiogram Analysis		2