Morten Salling Olesen

List of Publications by Year
in descending order

68	2,503	304602	223716
papers	citations	22 h-index	46 g-index

69	69	69	4666
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.	9.4	552
2	Implantable loop recorder detection of atrial fibrillation to prevent stroke (The LOOP Study): a randomised controlled trial. Lancet, The, 2021, 398, 1507-1516.	6.3	251
3	P-wave duration and the risk of atrial fibrillation: Results from the Copenhagen ECG Study. Heart Rhythm, 2015, 12, 1887-1895.	0.3	152
4	Risk prediction of cardiovascular death based on the QTc interval: evaluating age and gender differences in a large primary care population. European Heart Journal, 2014, 35, 1335-1344.	1.0	98
5	Atrial fibrillation: the role of common and rare genetic variants. European Journal of Human Genetics, 2014, 22, 297-306.	1.4	96
6	Rare truncating variants in the sarcomeric protein titin associate with familial and early-onset atrial fibrillation. Nature Communications, 2018, 9, 4316.	5.8	93
7	Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development. American Journal of Human Genetics, 2018, 102, 103-115.	2.6	86
8	Transethnic Genome-Wide Association Study Provides Insights in the Genetic Architecture and Heritability of Long QT Syndrome. Circulation, 2020, 142, 324-338.	1.6	83
9	Very early-onset lone atrial fibrillation patients have a high prevalence of rare variants in genes previously associated with atrial fibrillation. Heart Rhythm, 2014, 11, 246-251.	0.3	54
10	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.	1.0	53
11	Genetic Loci on Chromosomes 4q25, 7p31, and 12p12 Are Associated With Onset of Lone Atrial Fibrillation Before the Age of 40 Years. Canadian Journal of Cardiology, 2012, 28, 191-195.	0.8	50
12	Common and Rare Variants in SCN10A Modulate the Risk of Atrial Fibrillation. Circulation: Cardiovascular Genetics, 2015, 8, 64-73.	5.1	50
13	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.	1.8	50
14	A Novel Nonsense Variant in Nav1.5 Cofactor MOG1 Eliminates Its Sodium Current Increasing Effect and May Increase the Risk of Arrhythmias. Canadian Journal of Cardiology, 2011, 27, 523.e17-523.e23.	0.8	45
15	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	5.8	39
16	Visit-to-Visit Variability of Hemoglobin A1c in People Without Diabetes and Risk of Major Adverse Cardiovascular Events and All-Cause Mortality. Diabetes Care, 2019, 42, 134-141.	4.3	36
17	Electrocardiographic Tpeakâ€“Tend interval and risk of cardiovascular morbidity and mortality: Results from the Copenhagen ECG study. Heart Rhythm, 2016, 13, 915-924.	0.3	34
18	Risk Prediction of Atrial Fibrillation Based on Electrocardiographic Interatrial Block. Journal of the American Heart Association, 2018, 7, .	1.6	32

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19	Effect of diabetes duration on the relationship between glycaemic control and risk of death in older adults with type 2 diabetes. Diabetes, Obesity and Metabolism, 2020, 22, 231-242.	2.2	32
20	Multifocal atrial and ventricular premature contractions with an increased risk of dilated cardiomyopathy caused by a Na v 1.5 gain-of-function mutation (G213D). International Journal of Cardiology, 2018, 257, 160-167.	0.8	31
21	Atrial fibrillationâ€"a complex polygenetic disease. European Journal of Human Genetics, 2021, 29, 1051-1060.	1.4	30
22	Genome-wide association study identifies 18 novel loci associated with left atrial volume and function. European Heart Journal, 2021, 42, 4523-4534.	1.0	30
23	Electrocardiographic PR Interval Duration and Cardiovascular Risk: Results From the Copenhagen ECG Study. Canadian Journal of Cardiology, 2017, 33, 674-681.	0.8	29
24	The role of the sodium current complex in a nonreferred nationwide cohort of sudden infant death syndrome. Heart Rhythm, 2015, 12, 1241-1249.	0.3	26
25	Quantitative Proteomics of Human Heart Samples Collected In Vivo Reveal the Remodeled Protein Landscape of Dilated Left Atrium Without Atrial Fibrillation. Molecular and Cellular Proteomics, 2020, 19, 1132-1144.	2.5	24
26	Nationwide (Denmark) Study of Symptoms Preceding Sudden Death due to Arrhythmogenic Right Ventricular Cardiomyopathy. American Journal of Cardiology, 2014, 113, 1250-1254.	0.7	23
27	Quantitative proteome comparison of human hearts with those of model organisms. PLoS Biology, 2021, 19, e3001144.	2.6	23
28	Left Atrial Late Gadolinium Enhancement is Associated With Incident Atrial Fibrillation as Detected by Continuous Monitoring With Implantable Loop Recorders. JACC: Cardiovascular Imaging, 2020, 13, 1690-1700.	2.3	22
29	Association Between Heart Rate at Rest and Incident Atrial Fibrillation (from the Copenhagen) Tj ETQq1 1 0.784314 rgBT /Overlock 1	0.7	21
30	Electrocardiographic Preexcitation and Risk of Cardiovascular Morbidity and Mortality. Circulation: Arrhythmia and Electrophysiology, 2017, 10, .	2.1	20
31	Atrial fibrillation and cardiac fibrosis: A review on the potential of extracellular matrix proteins as biomarkers. Matrix Biology, 2020, 91-92, 188-203.	1.5	20
32	The role of common genetic variants in atrial fibrillation. Journal of Electrocardiology, 2016, 49, 864-870.	0.4	19
33	A Novel Familial Cardiac Arrhythmia Syndrome with Widespread ST-Segment Depression. New England Journal of Medicine, 2018, 379, 1780-1781.	13.9	17
34	Verification of threshold for image intensity ratio analyses of late gadolinium enhancement magnetic resonance imaging of left atrial fibrosis in 1.5T scans. International Journal of Cardiovascular Imaging, 2020, 36, 513-520.	0.7	17
35	Loss-of-Function Variants in the SYNPO2L Gene Are Associated With Atrial Fibrillation. Frontiers in Cardiovascular Medicine, 2021, 8, 650667.	1.1	17
36	Clinical implications of electrocardiographic bundle branch block in primary care. Heart, 2019, 105, heartjnl-2018-314295.	1.2	15

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37	Reevaluation of genetic variants previously associated with arrhythmogenic right ventricular cardiomyopathy integrating populationâ€based cohorts and proteomics data. Clinical Genetics, 2019, 96, 506-514.	1.0	14
38	Dilated cardiomyopathy caused by truncating titin variants: long-term outcomes, arrhythmias, response to treatment and sex differences. Journal of Medical Genetics, 2021, 58, 832-841.	1.5	14
39	Investigating gene-microRNA networks in atrial fibrillation patients with mitral valve regurgitation. PLoS ONE, 2020, 15, e0232719.	1.1	14
40	Loss-of-Function Variants in Cytoskeletal Genes Are Associated with Early-Onset Atrial Fibrillation. Journal of Clinical Medicine, 2020, 9, 372.	1.0	14
41	Brugada syndrome risk loci seem protective against atrial fibrillation. European Journal of Human Genetics, 2014, 22, 1357-1361.	1.4	13
42	Genome-wide association study identifies locus at chromosome 2q32.1 associated with syncope and collapse. Cardiovascular Research, 2020, 116, 138-148.	1.8	13
43	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.	0.3	12
44	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.	1.4	12
45	Early-onset atrial fibrillation patients show reduced left ventricular ejection fraction and increased atrial fibrosis. Scientific Reports, 2020, 10, 10039.	1.6	12
46	Genetic Aspects of Lone Atrial Fibrillation: What Do We Know?. Current Pharmaceutical Design, 2014, 21, 667-678.	0.9	12
47	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.	1.2	10
48	A Novel Loss-of-Function Variant in the Chloride Ion Channel Gene Clcn2 Associates with Atrial Fibrillation. Scientific Reports, 2020, 10, 1453.	1.6	10
49	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.	1.4	9
50	Electrocardiographic T-wave morphology and risk of mortality. International Journal of Cardiology, 2021, 328, 199-205.	0.8	9
51	Fascicular heart blocks and risk of adverse cardiovascular outcomes: Results from a large primary care population. Heart Rhythm, 2022, 19, 252-259.	0.3	8
52	Generation of induced pluripotent stem cells (iPSC) from an atrial fibrillation patient carrying a PITX2 p.M200V mutation. Stem Cell Research, 2017, 24, 8-11.	0.3	7
53	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
54	Role of PR-Interval In Predicting the Occurrence of Atrial Fibrillation. Journal of Atrial Fibrillation, 2013, 6, 956.	0.5	6

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55	Cardiac magnetic resonance systematically overestimates mitral regurgitations by the indirect method. Open Heart, 2020, 7, e001323.	0.9	5
56	Electrocardiographic Findings, Arrhythmias, and Left Ventricular Involvement in Familial ST-Depression Syndrome. Circulation: Arrhythmia and Electrophysiology, 2022, , 101161CIRCEP121010688.	2.1	5
57	Polygenic risk score for ACE-inhibitor-associated cough based on the discovery of new genetic loci. European Heart Journal, 2022, 43, 4707-4718.	1.0	5
58	Natural History and Clinical Characteristics of the First 10 Danish Families With Familial ST-Depression Syndrome. Journal of the American College of Cardiology, 2021, 77, 2617-2619.	1.2	4
59	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, .	1.6	4
60	Mutation analysis of the candidate genes SCN1B-4B, FHL1, and LMNA in patients with arrhythmogenic right ventricular cardiomyopathy. Applied & Translational Genomics, 2012, 1, 44-46.	2.1	3
61	Generation of induced pluripotent stem cells (iPSC) from an atrial fibrillation patient carrying a KCNA5 p.D322H mutation. Stem Cell Research, 2017, 24, 29-32.	0.3	3
62	Early glycaemic changes after initiation of oral antidiabetic medication and risk of major adverse cardiovascular events: results from a large primary care population of patients with type 2 diabetes. European Heart Journal - Cardiovascular Pharmacotherapy, 2021, 7, 486-495.	1.4	3
63	KCNE1 G38S polymorphism is not the cause of long QT syndrome. Journal of Electrocardiology, 2016, 49, 249-250.	0.4	2
64	Effect of Loss-of-Function Genetic Variants in PCSK9 on Glycemic Traits, Neurocognitive Impairment, and Hepatobiliary Function. Diabetes Care, 2022, 45, 251-254.	4.3	1
65	Whole-Exome Sequencing Implicates Neuronal Calcium Channel with Familial Atrial Fibrillation. Frontiers in Genetics, 2022, 13, 806429.	1.1	1
66	Clinical Implications of SCN10A Loss-of-Function Variants in 169â€‰610 Exomes Representing the General Population. Circulation Genomic and Precision Medicine, 2022, 15, CIRCGEN121003574.	1.6	1
67	Hundreds of new murine genes cause CVD. , 2022, 1, 104-104.		0
68	Left Atrial Remodeling and Cerebrovascular Disease Assessed by Magnetic Resonance Imaging in Continuously Monitored Patients. Cerebrovascular Diseases, 2022, 51, 403-412.	0.8	0