Jan Haas

List of Publications by Year
in descending order

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61	4,523	147801 31	128289 60
papers	citations	h-index	g-index

63	63	63	7700
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Atlas of the clinical genetics of human dilated cardiomyopathy. European Heart Journal, 2015, 36, 1123-1135.	2.2	456
2	A blood based 12-miRNA signature of Alzheimer disease patients. Genome Biology, 2013, 14, R78.	9.6	438
3	Toward the blood-borne miRNome of human diseases. Nature Methods, 2011, 8, 841-843.	19.0	339
4	Non-coding RNAs in cardiovascular diseases: diagnostic and therapeutic perspectives. European Heart Journal, 2018, 39, 2704-2716.	2.2	300
5	MicroRNA signatures in total peripheral blood as novel biomarkers for acute myocardial infarction. Basic Research in Cardiology, 2011, 106, 13-23.	5.9	242
6	Alterations in cardiac DNA methylation in human dilated cardiomyopathy. EMBO Molecular Medicine, 2013, 5, 413-429.	6.9	210
7	Clinical genetics and outcome of left ventricular non-compaction cardiomyopathy. European Heart Journal, 2017, 38, 3449-3460.	2.2	168
8	Genotype-phenotype associations in dilated cardiomyopathy: meta-analysis on more than 8000 individuals. Clinical Research in Cardiology, 2017, 106, 127-139.	3.3	156
9	Targeted Next-Generation Sequencing for the Molecular Genetic Diagnostics of Cardiomyopathies. Circulation: Cardiovascular Genetics, 2011, 4, 110-122.	5.1	155
10	Epigenome-Wide Association Study Identifies Cardiac Gene Patterning and a Novel Class of Biomarkers for Heart Failure. Circulation, 2017, 136, 1528-1544.	1.6	139
11	A genome-wide association study identifies 6p21 as novel risk locus for dilated cardiomyopathy. European Heart Journal, 2014, 35, 1069-1077.	2.2	137
12	The Symptom Complex of Familial Sinus Node Dysfunction and Myocardial Noncompaction Is Associated With Mutations in the HCN4 Channel. Journal of the American College of Cardiology, 2014, 64, 757-767.	2.8	128
13	Catecholamine-Dependent Î²-Adrenergic Signaling in a Pluripotent Stem Cell ModelÂof Takotsubo Cardiomyopathy. Journal of the American College of Cardiology, 2017, 70, 975-991.	2.8	124
14	Clinical outcomes associated with sarcomere mutations in hypertrophic cardiomyopathy: a meta-analysis on 7675 individuals. Clinical Research in Cardiology, 2018, 107, 30-41.	3.3	99
15	A mutation in the glutamate-rich region of RNA-binding motif protein 20 causes dilated cardiomyopathy through missplicing of titin and impaired Frankâ€“Starling mechanism. Cardiovascular Research, 2016, 112, 452-463.	3.8	97
16	Immune system-mediated atherosclerosis caused by deficiency of long non-coding RNAMALAT1in ApoEâ^'/â^'mice. Cardiovascular Research, 2019, 115, 302-314.	3.8	89
17	Long noncoding RNA NEAT1 modulates immune cell functions and is suppressed in early onset myocardial infarction patients. Cardiovascular Research, 2019, 115, 1886-1906.	3.8	86
18	Influence of the Confounding Factors Age and Sex on MicroRNA Profiles from Peripheral Blood. Clinical Chemistry, 2014, 60, 1200-1208.	3.2	84

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19	Severe DCM phenotype of patient harboring RBM20 mutation S635A can be modeled by patient-specific induced pluripotent stem cell-derived cardiomyocytes. Journal of Molecular and Cellular Cardiology, 2017, 113, 9-21.	1.9	84
20	Towards Personalized Cardiology: Multi-Scale Modeling of the Failing Heart. PLoS ONE, 2015, 10, e0134869.	2.5	65
21	Web-based NGS data analysis using miRMaster: a large-scale meta-analysis of human miRNAs. Nucleic Acids Research, 2017, 45, 8731-8744.	14.5	63
22	Identification and Functional Characterization of Hypoxia-Induced Endoplasmic Reticulum Stress Regulating lncRNA (HypERlnc) in Pericytes. Circulation Research, 2017, 121, 368-375.	4.5	61
23	Clinical and genetic insights into non-compaction: a meta-analysis and systematic review on 7598 individuals. Clinical Research in Cardiology, 2019, 108, 1297-1308.	3.3	61
24	Long noncoding RNAMALAT1-derived mascRNA is involved in cardiovascular innate immunity. Journal of Molecular Cell Biology, 2016, 8, 178-181.	3.3	55
25	The cardiac microenvironment uses nonâ€canonical <scp>WNT</scp> signaling to activate monocytes after myocardial infarction. EMBO Molecular Medicine, 2017, 9, 1279-1293.	6.9	55
26	Validating Alzheimer's disease micro RNAs using nextâ€generation sequencing. Alzheimer's and Dementia, 2016, 12, 565-576.	0.8	53
27	Prioritizing and selecting likely novel miRNAs from NGS data. Nucleic Acids Research, 2016, 44, e53-e53.	14.5	52
28	Genomic structural variations lead to dysregulation of important coding and nonâ€coding RNA species in dilated cardiomyopathy. EMBO Molecular Medicine, 2018, 10, 107-120.	6.9	43
29	Data-driven estimation of cardiac electrical diffusivity from 12-lead ECG signals. Medical Image Analysis, 2014, 18, 1361-1376.	11.6	42
30	Familial Recurrent Myocarditis Triggered by Exercise in Patients With a Truncating Variant of the Desmoplakin Gene. Journal of the American Heart Association, 2020, 9, e015289.	3.7	39
31	miRTrail - a comprehensive webserver for analyzing gene and miRNA patterns to enhance the understanding of regulatory mechanisms in diseases. BMC Bioinformatics, 2012, 13, 36.	2.6	36
32	Next-generation sequencing entering the clinical arena. Molecular and Cellular Probes, 2011, 25, 206-211.	2.1	30
33	Next-generation sequencing identifies altered whole blood microRNAs in neuromyelitis optica spectrum disorder which may permit discrimination from multiple sclerosis. Journal of Neuroinflammation, 2015, 12, 196.	7.2	27
34	Silencing the CSF-1 Axis Using Nanoparticle Encapsulated siRNA Mitigates Viral and Autoimmune Myocarditis. Frontiers in Immunology, 2018, 9, 2303.	4.8	26
35	A high-resolution map of the human small non-coding transcriptome. Bioinformatics, 2018, 34, 1621-1628.	4.1	24
36	Systematic permutation testing in GWAS pathway analyses: identification of genetic networks in dilated cardiomyopathy and ulcerative colitis. BMC Genomics, 2014, 15, 622.	2.8	23

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37	A self-taught artificial agent for multi-physics computational model personalization. Medical Image Analysis, 2016, 34, 52-64.	11.6	20
38	Energy Metabolites as Biomarkers in Ischemic and Dilated Cardiomyopathy. International Journal of Molecular Sciences, 2021, 22, 1999.	4.1	20
39	Reduction of A-to-I RNA editing in the failing human heart regulates formation of circular RNAs. Basic Research in Cardiology, 2022, 117, .	5.9	19
40	RNA splicing regulated by RBFOX1 is essential for cardiac function in zebrafish. Journal of Cell Science, 2015, 128, 3030-40.	2.0	16
41	Identification of SCN5a p.C335R Variant in a Large Family with Dilated Cardiomyopathy and Conduction Disease. International Journal of Molecular Sciences, 2021, 22, 12990.	4.1	16
42	Deep characterization of blood cell miRNomes by NGS. Cellular and Molecular Life Sciences, 2016, 73, 3169-3181.	5.4	15
43	Robust Image-Based Estimation of Cardiac Tissue Parameters and Their Uncertainty from Noisy Data. Lecture Notes in Computer Science, 2014, 17, 9-16.	1.3	13
44	Clinical and Genetic Investigations of 109 Index Patients With Dilated Cardiomyopathy and 445 of Their Relatives. Circulation: Heart Failure, 2020, 13, e006701.	3.9	12
45	Epigenetic Regulation of Alternative mRNA Splicing in Dilated Cardiomyopathy. Journal of Clinical Medicine, 2020, 9, 1499.	2.4	11
46	miFRame: analysis and visualization of miRNA sequencing data in neurological disorders. Journal of Translational Medicine, 2015, 13, 224.	4.4	10
47	The chameleon of cardiology: cardiac sarcoidosis before and after heart transplantation. ESC Heart Failure, 2020, 7, 692-696.	3.1	10
48	Doxorubicin induces cardiotoxicity in a pluripotent stem cell model of aggressive B cell lymphoma cancer patients. Basic Research in Cardiology, 2022, 117, 13.	5.9	10
49	The Role of Quality Control in Targeted Next-generation Sequencing Library Preparation. Genomics, Proteomics and Bioinformatics, 2016, 14, 200-206.	6.9	9
50	Extracellular NLRP3 inflammasome particles are internalized by human coronary artery smooth muscle cells and induce pro-atherogenic effects. Scientific Reports, 2021, 11, 15156.	3.3	8
51	Fast Data-Driven Calibration of a Cardiac Electrophysiology Model from Images and ECG. Lecture Notes in Computer Science, 2013, 16, 1-8.	1.3	8
52	Missense Variant E1295K of Sodium Channel SCN5A Associated With Recurrent Ventricular Fibrillation and Myocardial Inflammation. JACC: Case Reports, 2022, 4, 280-286.	0.6	7
53	microRNA neural networks improve diagnosis of acute coronary syndrome (ACS). Journal of Molecular and Cellular Cardiology, 2021, 151, 155-162.	1.9	6
54	ANK2 functionally interacts with KCNH2 aggravating long QT syndrome in a double mutation carrier. Biochemical and Biophysical Research Communications, 2019, 512, 845-851.	2.1	5

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55	Targeted next-generation sequencing: the clinicianâ€™s stethoscope for genetic disorders. Personalized Medicine, 2014, 11, 581-592.	1.5	4
56	SLM2 Is A Novel Cardiac Splicing Factor Involved in Heart Failure due to Dilated Cardiomyopathy. Genomics, Proteomics and Bioinformatics, 2022, 20, 129-146.	6.9	4
57	Marathon-Induced Cardiac Strain as Model for the Evaluation of Diagnostic microRNAs for Acute Myocardial Infarction. Journal of Clinical Medicine, 2022, 11, 5.	2.4	4
58	Automatic image-to-model framework for patient-specific electromechanical modeling of the heart. , 2014, , .		3
59	Controlling my genome with my smartphone: first clinical experiences of the PROMISE system. Clinical Research in Cardiology, 2021, , 1.	3.3	3
60	Hide and Seek: Protein-coding Sequences Inside â€œNon-codingâ€•RNAs. Genomics, Proteomics and Bioinformatics, 2016, 14, 179-180.	6.9	2
61	From Single Variants to Protein Cascades. Journal of Biological Chemistry, 2016, 291, 1582-1590.	3.4	2