Kun Zuo

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/5030671/kun-zuo-publications-by-year.pdf

Version: 2024-04-20

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

20	198	9	14
papers	citations	h-index	g-index
22 ext. papers	342 ext. citations	3.8 avg, IF	2.9 L-index

#	Paper	IF	Citations
20	Patients with end-stage renal disease requiring hemodialysis benefit from percutaneous coronary intervention after non-ST-segment elevation myocardial infarction <i>Internal and Emergency Medicine</i> , 2022 , 1	3.7	
19	Distal Transradial Access: a Safe and Feasible Approach for Coronary Catheterization in Cases of Total Radial Artery Occlusion <i>Journal of Cardiovascular Translational Research</i> , 2022 , 1	3.3	О
18	Dysbiosis of Gut Microbiota and Metabolite Phenylacetylglutamine in Coronary Artery Disease Patients With Stent Stenosis <i>Frontiers in Cardiovascular Medicine</i> , 2022 , 9, 832092	5.4	1
17	Elevated plasma Ninjurin-1 levels in atrial fibrillation is associated with atrial remodeling and thromboembolic risk <i>BMC Cardiovascular Disorders</i> , 2022 , 22, 153	2.3	
16	Association between Gut Microbiota Dysbiosis and the CHA2DS2-VASc Score in Atrial Fibrillation Patients. <i>International Journal of Clinical Practice</i> , 2022 , 2022, 1-10	2.9	O
15	Characteristics and variation of fecal bacterial communities and functions in isolated systolic and diastolic hypertensive patients. <i>BMC Microbiology</i> , 2021 , 21, 128	4.5	5
14	Cigarette smoking status alters dysbiotic gut microbes in hypertensive patients. <i>Journal of Clinical Hypertension</i> , 2021 , 23, 1431-1446	2.3	5
13	Altered synthesis of genes associated with short-chain fatty acids in the gut of patients with atrial fibrillation. <i>BMC Genomics</i> , 2021 , 22, 634	4.5	4
12	p38/JNK Is Required for the Proliferation and Phenotype Changes of Vascular Smooth Muscle Cells Induced by in Essential Hypertension. <i>International Journal of Hypertension</i> , 2020 , 2020, 3123968	2.4	1
11	Different Types of Atrial Fibrillation Share Patterns of Gut Microbiota Dysbiosis. <i>MSphere</i> , 2020 , 5,	5	17
10	Shifts in gut microbiome and metabolome are associated with risk of recurrent atrial fibrillation. <i>Journal of Cellular and Molecular Medicine</i> , 2020 , 24, 13356-13369	5.6	11
9	MicroRNA-122 aggravates angiotensin II-mediated apoptosis and autophagy imbalance in rat aortic adventitial fibroblasts via the modulation of SIRT6-elabela-ACE2 signaling. <i>European Journal of Pharmacology</i> , 2020 , 883, 173374	5.3	25
8	Metagenomic data-mining reveals enrichment of trimethylamine-N-oxide synthesis in gut microbiome in atrial fibrillation patients. <i>BMC Genomics</i> , 2020 , 21, 526	4.5	11
7	Myofibroblast-Derived Exosomes Contribute to Development of a Susceptible Substrate for Atrial Fibrillation. <i>Cardiology</i> , 2020 , 145, 324-332	1.6	11
6	Disordered gut microbiota and alterations in metabolic patterns are associated with atrial fibrillation. <i>GigaScience</i> , 2019 , 8,	7.6	47
5	Dysbiotic gut microbes may contribute to hypertension by limiting vitamin D production. <i>Clinical Cardiology</i> , 2019 , 42, 710-719	3.3	28
4	Study on the relationship between telomere length changes and recurrence of atrial fibrillation after radiofrequency catheter ablation. <i>Journal of Cardiovascular Electrophysiology</i> , 2019 , 30, 1117-112	4 ^{2.7}	5

LIST OF PUBLICATIONS

3	Duration of Persistent Atrial Fibrillation Is Associated with Alterations in Human Gut Microbiota and Metabolic Phenotypes. <i>MSystems</i> , 2019 , 4,	7.6	15
2	Correlation between cardiac rhythm, left atrial appendage flow velocity, and CHA DS -VASc score: Study based on transesophageal echocardiography and 2-dimensional speckle tracking. <i>Clinical Cardiology</i> , 2017 , 40, 120-125	3.3	10
1	Shifts in gut microbiome and metabolome are associated with risk of recurrent atrial fibrillation		1