Chen Yao

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 1,846 15 34 g-index

34 2,501 13.1 3.67 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
26	Integrative analysis of clinical and epigenetic biomarkers of mortality Aging Cell, 2022, e13608	9.9	1
25	Cardiovascular disease protein biomarkers are associated with kidney function: The Framingham Heart Study <i>PLoS ONE</i> , 2022 , 17, e0268293	3.7	
24	Epigenome-wide association study of whole blood gene expression in Framingham Heart Study participants provides molecular insight into the potential role of CHRNA5 in cigarette smoking-related lung diseases. <i>Clinical Epigenetics</i> , 2021 , 13, 60	7.7	3
23	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021 , 12, 3987	17.4	3
22	Associations of Alcohol Consumption with Cardiovascular Disease-Related Proteomic Biomarkers: The Framingham Heart Study. <i>Journal of Nutrition</i> , 2021 , 151, 2574-2582	4.1	O
21	An Integrative Genomic Strategy Identifies sRAGE as a Causal and Protective Biomarker of Lung Function. <i>Chest</i> , 2021 ,	5.3	1
20	Proteins as Mediators of the Association Between Diet Quality and Incident Cardiovascular Disease and All-Cause Mortality: The Framingham Heart Study. <i>Journal of the American Heart Association</i> , 2021 , 10, e021245	6	1
19	Cardiovascular disease related circulating biomarkers and cancer incidence and mortality: is there an association?. <i>Cardiovascular Research</i> , 2021 ,	9.9	1
18	Integrative Genomic Analysis Reveals Four Protein Biomarkers for Platelet Traits. <i>Circulation Research</i> , 2020 , 127, 1182-1194	15.7	3
17	Epigenome-wide association study of DNA methylation and microRNA expression highlights novel pathways for human complex traits. <i>Epigenetics</i> , 2020 , 15, 183-198	5.7	5
16	Genome-wide identification of DNA methylation QTLs in whole blood highlights pathways for cardiovascular disease. <i>Nature Communications</i> , 2019 , 10, 4267	17.4	65
15	The role of platelets in mediating a response to human influenza infection. <i>Nature Communications</i> , 2019 , 10, 1780	17.4	126
14	Adipsin preserves beta cells in diabetic mice and associates with protection from type 2 diabetes in humans. <i>Nature Medicine</i> , 2019 , 25, 1739-1747	50.5	52
13	Evidence for a Causal Role of the SH2B3-M Axis in Blood Pressure Regulation. <i>Hypertension</i> , 2019 , 73, 497-503	8.5	4
12	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor [] JAMA Cardiology, 2018, 3, 463-472	16.2	17
11	Genome-wide mapping of plasma protein QTLs identifies putatively causal genes and pathways for cardiovascular disease. <i>Nature Communications</i> , 2018 , 9, 3268	17.4	111
10	Integrated genome-wide analysis of expression quantitative trait loci aids interpretation of genomic association studies. <i>Genome Biology</i> , 2017 , 18, 16	18.3	108

LIST OF PUBLICATIONS

9	Epigenetic Patterns in Blood Associated With Lipid Traits Predict Incident Coronary Heart Disease Events and Are Enriched for Results From Genome-Wide Association Studies. <i>Circulation:</i> Cardiovascular Genetics, 2017, 10,		72
8	Dynamic Role of trans Regulation of Gene Expression in Relation to Complex Traits. <i>American Journal of Human Genetics</i> , 2017 , 100, 571-580	11	50
7	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. <i>PLoS Medicine</i> , 2017 , 14, e1002215	11.6	162
6	Epigenome-wide association studies identify DNA methylation associated with kidney function. <i>Nature Communications</i> , 2017 , 8, 1286	17.4	92
5	Epigenetic Signatures of Cigarette Smoking. Circulation: Cardiovascular Genetics, 2016, 9, 436-447		442
4	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016 , 17, 255	18.3	171
3	A meta-analysis of gene expression signatures of blood pressure and hypertension. <i>PLoS Genetics</i> , 2015 , 11, e1005035	6	83
2	Genome-wide identification of microRNA expression quantitative trait loci. <i>Nature Communications</i> , 2015 , 6, 6601	17.4	104
1	Epigenome-wide association study of fasting blood lipids in the Genetics of Lipid-lowering Drugs and Diet Network study. <i>Circulation</i> , 2014 , 130, 565-72	16.7	161