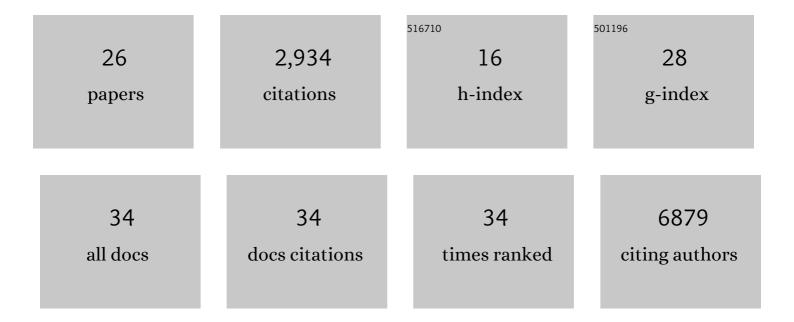
Chen Yao

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4284420/publications.pdf Version: 2024-02-01



<u>CHEN ΥΛΟ</u>

#	Article	IF	CITATIONS
1	An Integrative Genomic Strategy Identifies sRAGE as a Causal and Protective Biomarker of Lung Function. Chest, 2022, 161, 76-84.	0.8	5
2	Cardiovascular disease related circulating biomarkers and cancer incidence and mortality: is there an association?. Cardiovascular Research, 2022, 118, 2317-2328.	3.8	15
3	Integrative analysis of clinical and epigenetic biomarkers of mortality. Aging Cell, 2022, 21, e13608.	6.7	8
4	Cardiovascular disease protein biomarkers are associated with kidney function: The Framingham Heart Study. PLoS ONE, 2022, 17, e0268293.	2.5	2
5	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. Clinical Epigenetics, 2021, 13, 60.	4.1	14
6	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. Nature Communications, 2021, 12, 3987.	12.8	18
7	Associations of Alcohol Consumption with Cardiovascular Disease-Related Proteomic Biomarkers: The Framingham Heart Study. Journal of Nutrition, 2021, 151, 2574-2582.	2.9	5
8	Proteins as Mediators of the Association Between Diet Quality and Incident Cardiovascular Disease and Allâ€Cause Mortality: The Framingham Heart Study. Journal of the American Heart Association, 2021, 10, e021245.	3.7	11
9	Epigenome-wide association study of DNA methylation and microRNA expression highlights novel pathways for human complex traits. Epigenetics, 2020, 15, 183-198.	2.7	15
10	Integrative Genomic Analysis Reveals Four Protein Biomarkers for Platelet Traits. Circulation Research, 2020, 127, 1182-1194.	4.5	7
11	Adipsin preserves beta cells in diabetic mice and associates with protection from type 2 diabetes in humans. Nature Medicine, 2019, 25, 1739-1747.	30.7	100
12	Genome-wide identification of DNA methylation QTLs in whole blood highlights pathways for cardiovascular disease. Nature Communications, 2019, 10, 4267.	12.8	139
13	The role of platelets in mediating a response to human influenza infection. Nature Communications, 2019, 10, 1780.	12.8	199
14	Evidence for a Causal Role of the <i>SH2B3</i> -l² ₂ M Axis in Blood Pressure Regulation. Hypertension, 2019, 73, 497-503.	2.7	11
15	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor α. JAMA Cardiology, 2018, 3, 463.	6.1	33
16	Genomeâ€wide mapping of plasma protein QTLs identifies putatively causal genes and pathways for cardiovascular disease. Nature Communications, 2018, 9, 3268.	12.8	221
17	Integrated genome-wide analysis of expression quantitative trait loci aids interpretation of genomic association studies. Genome Biology, 2017, 18, 16.	8.8	151
18	Epigenetic Patterns in Blood Associated With Lipid Traits Predict Incident Coronary Heart Disease Events and Are Enriched for Results From Genome-Wide Association Studies. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	104

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#	Article	lF	CITATIONS
19	Dynamic Role of trans Regulation of Gene Expression in Relation to Complex Traits. American Journal of Human Genetics, 2017, 100, 571-580.	6.2	101
20	Epigenome-wide association studies identify DNA methylation associated with kidney function. Nature Communications, 2017, 8, 1286.	12.8	145
21	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. PLoS Medicine, 2017, 14, e1002215.	8.4	246
22	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	8.8	251
23	Epigenetic Signatures of Cigarette Smoking. Circulation: Cardiovascular Genetics, 2016, 9, 436-447.	5.1	678
24	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. PLoS Genetics, 2015, 11, e1005035.	3.5	107
25	Genome-wide identification of microRNA expression quantitative trait loci. Nature Communications, 2015, 6, 6601.	12.8	134
26	Epigenome-Wide Association Study of Fasting Blood Lipids in the Genetics of Lipid-Lowering Drugs and Diet Network Study. Circulation, 2014, 130, 565-572.	1.6	190