

# Tianxiao Huan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/402419/publications.pdf>

Version: 2024-02-01

62  
papers

5,329  
citations

136950

32  
h-index

118850

62  
g-index

73  
all docs

73  
docs citations

73  
times ranked

11032  
citing authors

#	ARTICLE	IF	CITATIONS
1	Higher diet quality relates to decelerated epigenetic aging. American Journal of Clinical Nutrition, 2022, 115, 163-170.	4.7	42
2	Association of 71 cardiovascular disease-related plasma proteins with pulmonary function in the community. PLoS ONE, 2022, 17, e0266523.	2.5	0
3	Integrative analysis of clinical and epigenetic biomarkers of mortality. Aging Cell, 2022, 21, e13608.	6.7	8
4	Mir-30d Regulates Cardiac Remodeling by Intracellular and Paracrine Signaling. Circulation Research, 2021, 128, e1-e23.	4.5	81
5	JEM: A joint test to estimate the effect of multiple genetic variants on DNA methylation. Genetic Epidemiology, 2021, 45, 280-292.	1.3	0
6	Associations of Alcohol Consumption with Cardiovascular Disease-Related Proteomic Biomarkers: The Framingham Heart Study. Journal of Nutrition, 2021, 151, 2574-2582.	2.9	5
7	Epigenome-wide association study of mitochondrial genome copy number. Human Molecular Genetics, 2021, 31, 309-319.	2.9	6
8	Proteins as Mediators of the Association Between Diet Quality and Incident Cardiovascular Disease and All-Cause Mortality: The Framingham Heart Study. Journal of the American Heart Association, 2021, 10, e021245.	3.7	11
9	Longitudinal change in blood DNA epigenetic signature after smoking cessation. Epigenetics, 2021, , 1-12.	2.7	5
10	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
11	Whole Blood DNA Methylation Signatures of Diet Are Associated With Cardiovascular Disease Risk Factors and All-Cause Mortality. Circulation Genomic and Precision Medicine, 2020, 13, e002766.	3.6	42
12	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. Aging, 2020, 12, 14092-14124.	3.1	15
13	Whole blood microRNA expression associated with stroke: Results from the Framingham Heart Study. PLoS ONE, 2019, 14, e0219261.	2.5	19
14	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. Circulation, 2019, 140, 645-657.	1.6	151
15	Genome-wide identification of DNA methylation QTLs in whole blood highlights pathways for cardiovascular disease. Nature Communications, 2019, 10, 4267.	12.8	139
16	Integrative Genomics Analysis Unravels Tissue-Specific Pathways, Networks, and Key Regulators of Blood Pressure Regulation. Frontiers in Cardiovascular Medicine, 2019, 6, 21.	2.4	15
17	A Peripheral Blood DNA Methylation Signature of Hepatic Fat Reveals a Potential Causal Pathway for Nonalcoholic Fatty Liver Disease. Diabetes, 2019, 68, 1073-1083.	0.6	41
18	Evidence for a Causal Role of the SH2B3 M Axis in Blood Pressure Regulation. Hypertension, 2019, 73, 497-503.	2.7	11

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19	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor $\pm$ . <i>JAMA Cardiology</i> , 2018, 3, 463.	6.1	33
20	Genetic and Environmental Effects on Gene Expression Signatures of Blood Pressure. <i>Hypertension</i> , 2018, 71, 457-464.	2.7	16
21	Age-associated microRNA expression in human peripheral blood is associated with all-cause mortality and age-related traits. <i>Aging Cell</i> , 2018, 17, e12687.	6.7	114
22	Epigenome-Wide Association Study of Soluble Tumor Necrosis Factor Receptor 2 Levels in the Framingham Heart Study. <i>Frontiers in Pharmacology</i> , 2018, 9, 207.	3.5	11
23	Micro RNAs from DNA Viruses are Found Widely in Plasma in a Large Observational Human Population. <i>Scientific Reports</i> , 2018, 8, 6397.	3.3	6
24	Genome-wide mapping of plasma protein QTLs identifies putatively causal genes and pathways for cardiovascular disease. <i>Nature Communications</i> , 2018, 9, 3268.	12.8	221
25	Associations of Circulating Extracellular RNAs With Myocardial Remodeling and Heart Failure. <i>JAMA Cardiology</i> , 2018, 3, 871.	6.1	33
26	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. <i>Nature Communications</i> , 2018, 9, 2976.	12.8	85
27	Integrated genome-wide analysis of expression quantitative trait loci aids interpretation of genomic association studies. <i>Genome Biology</i> , 2017, 18, 16.	8.8	151
28	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: Cardiovascular Genetics</i> , 2017, 10, .	5.1	104
29	Dynamic Role of trans Regulation of Gene Expression in Relation to Complex Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 571-580.	6.2	101
30	Cross-sectional relations of whole blood microRNA expression levels and hand grip strength in a community sample. <i>Aging Cell</i> , 2017, 16, 888-894.	6.7	13
31	MicroRNA Signature of Cigarette Smoking and Evidence for a Putative Causal Role of MicroRNAs in Smoking-Related Inflammation and Target Organ Damage. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	45
32	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017, 101, 888-902.	6.2	154
33	Messenger RNA and MicroRNA transcriptomic signatures of cardiometabolic risk factors. <i>BMC Genomics</i> , 2017, 18, 139.	2.8	33
34	Shared genetic regulatory networks for cardiovascular disease and type 2 diabetes in multiple populations of diverse ethnicities in the United States. <i>PLoS Genetics</i> , 2017, 13, e1007040.	3.5	82
35	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.	8.4	246
36	Whole blood gene expression and white matter Hyperintensities. <i>Molecular Neurodegeneration</i> , 2017, 12, 67.	10.8	28

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37	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. <i>PLoS ONE</i> , 2017, 12, e0182472.	2.5	10
38	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016, 17, 255.	8.8	251
39	A Whole-Blood Transcriptome Meta-Analysis Identifies Gene Expression Signatures of Cigarette Smoking. <i>Human Molecular Genetics</i> , 2016, 25, ddw288.	2.9	76
40	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 436-447.	5.1	678
41	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , 2016, 48, 1162-1170.	21.4	223
42	Dissecting the Roles of MicroRNAs in Coronary Heart Disease via Integrative Genomic Analyses. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 1011-1021.	2.4	53
43	Identification of common genetic variants controlling transcript isoform variation in human whole blood. <i>Nature Genetics</i> , 2015, 47, 345-352.	21.4	103
44	A systematic heritability analysis of the human whole blood transcriptome. <i>Human Genetics</i> , 2015, 134, 343-358.	3.8	35
45	Integromic Analysis of Genetic Variation and Gene Expression Identifies Networks for Cardiovascular Disease Phenotypes. <i>Circulation</i> , 2015, 131, 536-549.	1.6	65
46	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. <i>PLoS Genetics</i> , 2015, 11, e1005035.	3.5	107
47	Genome-wide identification of microRNA expression quantitative trait loci. <i>Nature Communications</i> , 2015, 6, 6601.	12.8	134
48	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015, 6, 8570.	12.8	533
49	Integrative network analysis reveals molecular mechanisms of blood pressure regulation. <i>Molecular Systems Biology</i> , 2015, 11, 799.	7.2	102
50	Lymphocyte adaptor protein LNK deficiency exacerbates hypertension and end-organ inflammation. <i>Journal of Clinical Investigation</i> , 2015, 125, 1189-1202.	8.2	128
51	Integrative Genomics Reveals Novel Molecular Pathways and Gene Networks for Coronary Artery Disease. <i>PLoS Genetics</i> , 2014, 10, e1004502.	3.5	192
52	Sex- and age-interacting eQTLs in human complex diseases. <i>Human Molecular Genetics</i> , 2014, 23, 1947-1956.	2.9	66
53	Seed-weighted random walk ranking for cancer biomarker prioritisation: a case study in leukaemia. <i>International Journal of Data Mining and Bioinformatics</i> , 2014, 9, 135.	0.1	5
54	A Systems Biology Framework Identifies Molecular Underpinnings of Coronary Heart Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013, 33, 1427-1434.	2.4	157

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55	Gene Expression Signatures of Coronary Heart Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013, 33, 1418-1426.	2.4	105
56	Atrial natriuretic peptide is negatively regulated by microRNA-425. <i>Journal of Clinical Investigation</i> , 2013, 123, 3378-3382.	8.2	109
57	Domain combination of the vertebrate-like TLR gene family: implications for their origin and evolution. <i>Journal of Genetics</i> , 2011, 90, 401-408.	0.7	24
58	Prolonged Survival of Human Hepatocarcinoma Cells in the Liver of Newborn C57BL/6 Mice and Resulting Cellular Xenorejection, Especially the Activation of Hepatic Natural Killer T Cells. <i>Pathobiology</i> , 2010, 77, 115-128.	3.8	3
59	Systems biology visualization tools for drug target discovery. <i>Expert Opinion on Drug Discovery</i> , 2010, 5, 425-439.	5.0	8
60	Growth potential of human hepatocarcinoma cells in the liver of neonatal immunocompetent mice and its relation to immunological tolerance. <i>Progress in Natural Science: Materials International</i> , 2009, 19, 705-712.	4.4	4
61	Finding fractal patterns in molecular interaction networks: a case study in Alzheimer's disease. <i>International Journal of Computational Biology and Drug Design</i> , 2009, 2, 340.	0.3	7
62	ProteoLens: a visual analytic tool for multi-scale database-driven biological network data mining. <i>BMC Bioinformatics</i> , 2008, 9, S5.	2.6	30