

# Tianxiao Huan

## List of Publications by Year in descending order

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Version: 2024-02-01

62  
papers

5,329  
citations

136740

32  
h-index

118652

62  
g-index

73  
all docs

73  
docs citations

73  
times ranked

11032  
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 436-447.	5.1	678
2	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015, 6, 8570.	5.8	533
3	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016, 17, 255.	3.8	251
4	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.	3.9	246
5	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , 2016, 48, 1162-1170.	9.4	223
6	Genome-wide mapping of plasma protein QTLs identifies putatively causal genes and pathways for cardiovascular disease. <i>Nature Communications</i> , 2018, 9, 3268.	5.8	221
7	Integrative Genomics Reveals Novel Molecular Pathways and Gene Networks for Coronary Artery Disease. <i>PLoS Genetics</i> , 2014, 10, e1004502.	1.5	192
8	A Systems Biology Framework Identifies Molecular Underpinnings of Coronary Heart Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013, 33, 1427-1434.	1.1	157
9	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017, 101, 888-902.	2.6	154
10	Integrated genome-wide analysis of expression quantitative trait loci aids interpretation of genomic association studies. <i>Genome Biology</i> , 2017, 18, 16.	3.8	151
11	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. <i>Circulation</i> , 2019, 140, 645-657.	1.6	151
12	Genome-wide identification of DNA methylation QTLs in whole blood highlights pathways for cardiovascular disease. <i>Nature Communications</i> , 2019, 10, 4267.	5.8	139
13	Genome-wide identification of microRNA expression quantitative trait loci. <i>Nature Communications</i> , 2015, 6, 6601.	5.8	134
14	Lymphocyte adaptor protein LNK deficiency exacerbates hypertension and end-organ inflammation. <i>Journal of Clinical Investigation</i> , 2015, 125, 1189-1202.	3.9	128
15	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.	3.0	114
16	Atrial natriuretic peptide is negatively regulated by microRNA-425. <i>Journal of Clinical Investigation</i> , 2013, 123, 3378-3382.	3.9	109
17	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. <i>PLoS Genetics</i> , 2015, 11, e1005035.	1.5	107
18	Gene Expression Signatures of Coronary Heart Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013, 33, 1418-1426.	1.1	105

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19	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
20	Identification of common genetic variants controlling transcript isoform variation in human whole blood. <i>Nature Genetics</i> , 2015, 47, 345-352.	9.4	103
21	Integrative network analysis reveals molecular mechanisms of blood pressure regulation. <i>Molecular Systems Biology</i> , 2015, 11, 799.	3.2	102
22	Dynamic Role of trans Regulation of Gene Expression in Relation to Complex Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 571-580.	2.6	101
23	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. <i>Nature Communications</i> , 2018, 9, 2976.	5.8	85
24	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.	1.5	82
25	Mir-30d Regulates Cardiac Remodeling by Intracellular and Paracrine Signaling. <i>Circulation Research</i> , 2021, 128, e1-e23.	2.0	81
26	A Whole-Blood Transcriptome Meta-Analysis Identifies Gene Expression Signatures of Cigarette Smoking. <i>Human Molecular Genetics</i> , 2016, 25, ddw288.	1.4	76
27	Sex- and age-interacting eQTLs in human complex diseases. <i>Human Molecular Genetics</i> , 2014, 23, 1947-1956.	1.4	66
28	Integromic Analysis of Genetic Variation and Gene Expression Identifies Networks for Cardiovascular Disease Phenotypes. <i>Circulation</i> , 2015, 131, 536-549.	1.6	65
29	Dissecting the Roles of MicroRNAs in Coronary Heart Disease via Integrative Genomic Analyses. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 1011-1021.	1.1	53
30	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
31	Whole Blood DNA Methylation Signatures of Diet Are Associated With Cardiovascular Disease Risk Factors and All-Cause Mortality. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002766.	1.6	42
32	Higher diet quality relates to decelerated epigenetic aging. <i>American Journal of Clinical Nutrition</i> , 2022, 115, 163-170.	2.2	42
33	A Peripheral Blood DNA Methylation Signature of Hepatic Fat Reveals a Potential Causal Pathway for Nonalcoholic Fatty Liver Disease. <i>Diabetes</i> , 2019, 68, 1073-1083.	0.3	41
34	A systematic heritability analysis of the human whole blood transcriptome. <i>Human Genetics</i> , 2015, 134, 343-358.	1.8	35
35	Messenger RNA and MicroRNA transcriptomic signatures of cardiometabolic risk factors. <i>BMC Genomics</i> , 2017, 18, 139.	1.2	33
36	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor $\alpha$ . <i>JAMA Cardiology</i> , 2018, 3, 463.	3.0	33

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37	Associations of Circulating Extracellular RNAs With Myocardial Remodeling and Heart Failure. <i>JAMA Cardiology</i> , 2018, 3, 871.	3.0	33
38	ProteoLens: a visual analytic tool for multi-scale database-driven biological network data mining. <i>BMC Bioinformatics</i> , 2008, 9, S5.	1.2	30
39	Whole blood gene expression and white matter Hyperintensities. <i>Molecular Neurodegeneration</i> , 2017, 12, 67.	4.4	28
40	Domain combination of the vertebrate-like TLR gene family: implications for their origin and evolution. <i>Journal of Genetics</i> , 2011, 90, 401-408.	0.4	24
41	Whole blood microRNA expression associated with stroke: Results from the Framingham Heart Study. <i>PLoS ONE</i> , 2019, 14, e0219261.	1.1	19
42	Genetic and Environmental Effects on Gene Expression Signatures of Blood Pressure. <i>Hypertension</i> , 2018, 71, 457-464.	1.3	16
43	Integrative Genomics Analysis Unravels Tissue-Specific Pathways, Networks, and Key Regulators of Blood Pressure Regulation. <i>Frontiers in Cardiovascular Medicine</i> , 2019, 6, 21.	1.1	15
44	Epigenome-wide association study of DNA methylation and microRNA expression highlights novel pathways for human complex traits. <i>Epigenetics</i> , 2020, 15, 183-198.	1.3	15
45	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. <i>Aging</i> , 2020, 12, 14092-14124.	1.4	15
46	Cross-sectional relations of whole-blood miRNA expression levels and hand grip strength in a community sample. <i>Aging Cell</i> , 2017, 16, 888-894.	3.0	13
47	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.	1.6	11
48	Evidence for a Causal Role of the SH2B3- $\beta$ 2 M Axis in Blood Pressure Regulation. <i>Hypertension</i> , 2019, 73, 497-503.	1.3	11
49	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.	1.6	11
50	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. <i>PLoS ONE</i> , 2017, 12, e0182472.	1.1	10
51	Systems biology visualization tools for drug target discovery. <i>Expert Opinion on Drug Discovery</i> , 2010, 5, 425-439.	2.5	8
52	Integrative analysis of clinical and epigenetic biomarkers of mortality. <i>Aging Cell</i> , 2022, 21, e13608.	3.0	8
53	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
54	Micro RNAs from DNA Viruses are Found Widely in Plasma in a Large Observational Human Population. <i>Scientific Reports</i> , 2018, 8, 6397.	1.6	6

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55	Epigenome-wide association study of mitochondrial genome copy number. <i>Human Molecular Genetics</i> , 2021, 31, 309-319.	1.4	6
56	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
57	Associations of Alcohol Consumption with Cardiovascular Disease-Related Proteomic Biomarkers: The Framingham Heart Study. <i>Journal of Nutrition</i> , 2021, 151, 2574-2582.	1.3	5
58	Longitudinal change in blood DNA epigenetic signature after smoking cessation. <i>Epigenetics</i> , 2021, , 1-12.	1.3	5
59	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.	1.8	4
60	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.	1.9	3
61	JEM: A joint test to estimate the effect of multiple genetic variants on DNA methylation. <i>Genetic Epidemiology</i> , 2021, 45, 280-292.	0.6	0
62	Association of 71 cardiovascular disease-related plasma proteins with pulmonary function in the community. <i>PLoS ONE</i> , 2022, 17, e0266523.	1.1	0