

# Tianxiao Huan

## List of Publications by Citations

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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.

62

papers

3,406

citations

28

h-index

58

g-index

73

ext. papers

4,610

ext. citations

9.5

avg, IF

4.14

L-index

| #  | Paper  | IF   | Citations |
|----|--|------|-----------|
| 62 | Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , <b>2016</b> , 9, 436-447   |      | 442       |
| 61 | The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , <b>2015</b> , 6, 8570   | 17.4 | 335       |
| 60 | DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , <b>2016</b> , 17, 255   | 18.3 | 171       |
| 59 | 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> , <b>2017</b> , 14, e1002215 | 11.6 | 162       |
| 58 | Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , <b>2016</b> , 48, 1162-70   | 36.3 | 152       |
| 57 | Integrative genomics reveals novel molecular pathways and gene networks for coronary artery disease. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004502   | 6    | 147       |
| 56 | A systems biology framework identifies molecular underpinnings of coronary heart disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , <b>2013</b> , 33, 1427-34  | 9.4  | 125       |
| 55 | Genome-wide mapping of plasma protein QTLs identifies putatively causal genes and pathways for cardiovascular disease. <i>Nature Communications</i> , <b>2018</b> , 9, 3268  | 17.4 | 111       |
| 54 | Integrated genome-wide analysis of expression quantitative trait loci aids interpretation of genomic association studies. <i>Genome Biology</i> , <b>2017</b> , 18, 16   | 18.3 | 108       |
| 53 | Genome-wide identification of microRNA expression quantitative trait loci. <i>Nature Communications</i> , <b>2015</b> , 6, 6601  | 17.4 | 104       |
| 52 | Lymphocyte adaptor protein LNK deficiency exacerbates hypertension and end-organ inflammation. <i>Journal of Clinical Investigation</i> , <b>2015</b> , 125, 1189-202  | 15.9 | 102       |
| 51 | Atrial natriuretic peptide is negatively regulated by microRNA-425. <i>Journal of Clinical Investigation</i> , <b>2013</b> , 123, 3378-82  | 15.9 | 92        |
| 50 | A meta-analysis of gene expression signatures of blood pressure and hypertension. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005035  | 6    | 83        |
| 49 | DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , <b>2017</b> , 101, 888-902   | 11   | 83        |
| 48 | Gene expression signatures of coronary heart disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , <b>2013</b> , 33, 1418-26  | 9.4  | 80        |
| 47 | Identification of common genetic variants controlling transcript isoform variation in human whole blood. <i>Nature Genetics</i> , <b>2015</b> , 47, 345-52   | 36.3 | 77        |
| 46 | Age-associated microRNA expression in human peripheral blood is associated with all-cause mortality and age-related traits. <i>Aging Cell</i> , <b>2018</b> , 17, e12687   | 9.9  | 75        |

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| 45 | 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> , <b>2017</b> , 10, |      | 72 |
| 44 | Integrative network analysis reveals molecular mechanisms of blood pressure regulation. <i>Molecular Systems Biology</i> , <b>2015</b> , 11, 799  | 12.2 | 72 |
| 43 | Genome-wide identification of DNA methylation QTLs in whole blood highlights pathways for cardiovascular disease. <i>Nature Communications</i> , <b>2019</b> , 10, 4267   | 17.4 | 65 |
| 42 | Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. <i>Circulation</i> , <b>2019</b> , 140, 645-657   | 16.7 | 65 |
| 41 | A whole-blood transcriptome meta-analysis identifies gene expression signatures of cigarette smoking. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 4611-4623   | 5.6  | 58 |
| 40 | Dynamic Role of trans Regulation of Gene Expression in Relation to Complex Traits. <i>American Journal of Human Genetics</i> , <b>2017</b> , 100, 571-580   | 11   | 50 |
| 39 | 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> , <b>2017</b> , 13, e1007040                                    | 6    | 48 |
| 38 | Sex- and age-interacting eQTLs in human complex diseases. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 1947-56   | 5.6  | 48 |
| 37 | Integromic analysis of genetic variation and gene expression identifies networks for cardiovascular disease phenotypes. <i>Circulation</i> , <b>2015</b> , 131, 536-49  | 16.7 | 46 |
| 36 | Dissecting the roles of microRNAs in coronary heart disease via integrative genomic analyses. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , <b>2015</b> , 35, 1011-21   | 9.4  | 46 |
| 35 | Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. <i>Nature Communications</i> , <b>2018</b> , 9, 2976   | 17.4 | 45 |
| 34 | 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> , <b>2017</b> , 10,                       |      | 28 |
| 33 | Mir-30d Regulates Cardiac Remodeling by Intracellular and Paracrine Signaling. <i>Circulation Research</i> , <b>2021</b> , 128, e1-e23  | 15.7 | 27 |
| 32 | A Peripheral Blood DNA Methylation Signature of Hepatic Fat Reveals a Potential Causal Pathway for Nonalcoholic Fatty Liver Disease. <i>Diabetes</i> , <b>2019</b> , 68, 1073-1083  | 0.9  | 25 |
| 31 | Messenger RNA and MicroRNA transcriptomic signatures of cardiometabolic risk factors. <i>BMC Genomics</i> , <b>2017</b> , 18, 139   | 4.5  | 25 |
| 30 | Associations of Circulating Extracellular RNAs With Myocardial Remodeling and Heart Failure. <i>JAMA Cardiology</i> , <b>2018</b> , 3, 871-876  | 16.2 | 22 |
| 29 | Domain combination of the vertebrate-like TLR gene family: implications for their origin and evolution. <i>Journal of Genetics</i> , <b>2011</b> , 90, 401-8  | 1.2  | 21 |
| 28 | 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> , <b>2020</b> , 13, e002766                               | 5.2  | 18 |

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| 27 | ProteoLens: a visual analytic tool for multi-scale database-driven biological network data mining. <i>BMC Bioinformatics</i> , <b>2008</b> , 9 Suppl 9, S5   | 3.6  | 18 |
| 26 | Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor $\square$ <i>JAMA Cardiology</i> , <b>2018</b> , 3, 463-472 | 16.2 | 17 |
| 25 | A systematic heritability analysis of the human whole blood transcriptome. <i>Human Genetics</i> , <b>2015</b> , 134, 343-58   | 6.3  | 15 |
| 24 | Cross-sectional relations of whole-blood miRNA expression levels and hand grip strength in a community sample. <i>Aging Cell</i> , <b>2017</b> , 16, 888-894   | 9.9  | 12 |
| 23 | Whole blood microRNA expression associated with stroke: Results from the Framingham Heart Study. <i>PLoS ONE</i> , <b>2019</b> , 14, e0219261  | 3.7  | 12 |
| 22 | Genetic and Environmental Effects on Gene Expression Signatures of Blood Pressure: A Transcriptome-Wide Twin Study. <i>Hypertension</i> , <b>2018</b> , 71, 457-464                                      | 8.5  | 9  |
| 21 | Epigenome-Wide Association Study of Soluble Tumor Necrosis Factor Receptor 2 Levels in the Framingham Heart Study. <i>Frontiers in Pharmacology</i> , <b>2018</b> , 9, 207                               | 5.6  | 8  |
| 20 | Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. <i>PLoS ONE</i> , <b>2017</b> , 12, e0182472                                      | 3.7  | 8  |
| 19 | Integrative Genomics Analysis Unravels Tissue-Specific Pathways, Networks, and Key Regulators of Blood Pressure Regulation. <i>Frontiers in Cardiovascular Medicine</i> , <b>2019</b> , 6, 21            | 5.4  | 7  |
| 18 | Finding fractal patterns in molecular interaction networks: a case study in Alzheimer's disease. <i>International Journal of Computational Biology and Drug Design</i> , <b>2009</b> , 2, 340-52         | 0.4  | 6  |
| 17 | Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. <i>Aging</i> , <b>2020</b> , 12, 14092-14124  | 5.6  | 6  |
| 16 | Systems biology visualization tools for drug target discovery. <i>Expert Opinion on Drug Discovery</i> , <b>2010</b> , 5, 425-39   | 6.2  | 5  |
| 15 | Higher diet quality relates to decelerated epigenetic aging. <i>American Journal of Clinical Nutrition</i> , <b>2021</b> ,   | 7    | 5  |
| 14 | Epigenome-wide association study of DNA methylation and microRNA expression highlights novel pathways for human complex traits. <i>Epigenetics</i> , <b>2020</b> , 15, 183-198                           | 5.7  | 5  |
| 13 | Whole blood gene expression and white matter Hyperintensities. <i>Molecular Neurodegeneration</i> , <b>2017</b> , 12, 67   | 19   | 4  |
| 12 | Micro RNAs from DNA Viruses are Found Widely in Plasma in a Large Observational Human Population. <i>Scientific Reports</i> , <b>2018</b> , 8, 6397  | 4.9  | 4  |
| 11 | Genome-wide Association Study Of Plasma Proteins Identifies Putatively Causal Genes, Proteins, And Pathways For Cardiovascular Disease   |      | 4  |
| 10 | Evidence for a Causal Role of the SH2B3-M Axis in Blood Pressure Regulation. <i>Hypertension</i> , <b>2019</b> , 73, 497-503   | 8.5  | 4  |

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| 9 | Seed-weighted random walk ranking for cancer biomarker prioritisation: a case study in leukaemia. <i>International Journal of Data Mining and Bioinformatics</i> , <b>2014</b> , 9, 135-48   | 0.5 | 3 |
| 8 | 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> , <b>2010</b> , 77, 115-28 | 3.6 | 2 |
| 7 | 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> , <b>2009</b> , 19, 705-712       | 3.6 | 2 |
| 6 | 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> , <b>2021</b> , 10, e021245      | 6   | 1 |
| 5 | Integrative analysis of clinical and epigenetic biomarkers of mortality.. <i>Aging Cell</i> , <b>2022</b> , e13608   | 9.9 | 1 |
| 4 | Associations of Alcohol Consumption with Cardiovascular Disease-Related Proteomic Biomarkers: The Framingham Heart Study. <i>Journal of Nutrition</i> , <b>2021</b> , 151, 2574-2582   | 4.1 | 0 |
| 3 | Longitudinal change in blood DNA epigenetic signature after smoking cessation. <i>Epigenetics</i> , <b>2021</b> , 1-12   | 5.7 | 0 |
| 2 | JEM: A joint test to estimate the effect of multiple genetic variants on DNA methylation. <i>Genetic Epidemiology</i> , <b>2021</b> , 45, 280-292  | 2.6 |   |
| 1 | Association of 71 cardiovascular disease-related plasma proteins with pulmonary function in the community.. <i>PLoS ONE</i> , <b>2022</b> , 17, e0266523   | 3.7 |   |