

# Huijun Qian

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6305666/publications.pdf>

Version: 2024-02-01

9  
papers

1,077  
citations

1163117

8  
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1474206

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docs citations

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times ranked

3007  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	28.9	388
2	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , 2020, 182, 1198-1213.e14.	28.9	353
3	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations. <i>PLoS Genetics</i> , 2019, 15, e1008500.	3.5	203
4	Common genetic risk variants identified in the SPARK cohort support DDHD2 as a candidate risk gene for autism. <i>Translational Psychiatry</i> , 2020, 10, 265.	4.8	56
5	Association of <i>APOL1</i> With Heart Failure With Preserved Ejection Fraction in Postmenopausal African American Women. <i>JAMA Cardiology</i> , 2018, 3, 712.	6.1	17
6	SMNN: batch effect correction for single-cell RNA-seq data via supervised mutual nearest neighbor detection. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	17
7	Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. <i>EBioMedicine</i> , 2021, 63, 103157.	6.1	14
8	Transcriptome-Wide Association Study of Blood Cell Traits in African Ancestry and Hispanic/Latino Populations. <i>Genes</i> , 2021, 12, 1049.	2.4	11
9	Genome-Wide Association of Kidney Traits in Hispanics/Latinos Using Dense Imputed Whole-Genome Sequencing Data. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002891.	3.6	6