

# Yichuan Liu

## 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.

52

papers

818

citations

16

h-index

27

g-index

70

ext. papers

1,136

ext. citations

6.6

avg, IF

3.69

L-index

#	Paper	IF	Citations
52	RNA-Seq identifies novel myocardial gene expression signatures of heart failure. <i>Genomics</i> , <b>2015</b> , 105, 83-9	4.3	129
51	Comprehensive analysis of gene expression in human retina and supporting tissues. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 4001-14	5.6	86
50	ARAF recurrent mutation causes central conducting lymphatic anomaly treatable with a MEK inhibitor. <i>Nature Medicine</i> , <b>2019</b> , 25, 1116-1122	50.5	70
49	Tissue-specific RNA-Seq in human evoked inflammation identifies blood and adipose LincRNA signatures of cardiometabolic diseases. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , <b>2014</b> , 34, 902-12	9.4	60
48	Evaluating the impact of sequencing depth on transcriptome profiling in human adipose. <i>PLoS ONE</i> , <b>2013</b> , 8, e66883	3.7	44
47	Pathogenic variant in EPHB4 results in central conducting lymphatic anomaly. <i>Human Molecular Genetics</i> , <b>2018</b> , 27, 3233-3245	5.6	42
46	Non-coding RNA dysregulation in the amygdala region of schizophrenia patients contributes to the pathogenesis of the disease. <i>Translational Psychiatry</i> , <b>2018</b> , 8, 44	8.6	36
45	RNA-seq analysis of amygdala tissue reveals characteristic expression profiles in schizophrenia. <i>Translational Psychiatry</i> , <b>2017</b> , 7, e1203	8.6	29
44	PennSeq: accurate isoform-specific gene expression quantification in RNA-Seq by modeling non-uniform read distribution. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, e20	20.1	29
43	A functional synonymous coding variant in the IL1RN gene is associated with survival in septic shock. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2014</b> , 190, 656-64	10.2	28
42	Bayesian integration of genetics and epigenetics detects causal regulatory SNPs underlying expression variability. <i>Nature Communications</i> , <b>2015</b> , 6, 8555	17.4	20
41	Common variants in MMP20 at 11q22.2 predispose to 11q deletion and neuroblastoma risk. <i>Nature Communications</i> , <b>2017</b> , 8, 569	17.4	19
40	Common and Rare Genetic Risk Factors Converge in Protein Interaction Networks Underlying Schizophrenia. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 434	4.5	19
39	The Long Noncoding RNA Landscape in Amygdala Tissues from Schizophrenia Patients. <i>EBioMedicine</i> , <b>2018</b> , 34, 171-181	8.8	18
38	Combining targeted panel-based resequencing and copy-number variation analysis for the diagnosis of inherited syndromic retinopathies and associated ciliopathies. <i>Scientific Reports</i> , <b>2018</b> , 8, 5285	4.9	17
37	Application of Whole Exome Sequencing in Six Families with an Initial Diagnosis of Autosomal Dominant Retinitis Pigmentosa: Lessons Learned. <i>PLoS ONE</i> , <b>2015</b> , 10, e0133624	3.7	17
36	A genome-wide association study of anorexia nervosa suggests a risk locus implicated in dysregulated leptin signaling. <i>Scientific Reports</i> , <b>2017</b> , 7, 3847	4.9	16

35	Integrative genomics identifies 7p11.2 as a novel locus for fever and clinical stress response in humans. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 1801-12	5.6	16
34	Expression Pattern of the SARS-CoV-2 Entry Genes and in the Respiratory Tract. <i>Viruses</i> , <b>2020</b> , 12,	6.2	12
33	Common variants at 5q33.1 predispose to migraine in African-American children. <i>Journal of Medical Genetics</i> , <b>2018</b> , 55, 831-836	5.8	10
32	Testing genetic association with rare variants in admixed populations. <i>Genetic Epidemiology</i> , <b>2013</b> , 37, 38-47	2.6	8
31	Association of Rare Recurrent Copy Number Variants With Congenital Heart Defects Based on Next-Generation Sequencing Data From Family Trios. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 819	4.5	6
30	Microduplications at the 15q11.2 BP1-BP2 locus are enriched in patients with anorexia nervosa. <i>Journal of Psychiatric Research</i> , <b>2019</b> , 113, 34-38	5.2	6
29	Circulating and tissue matricellular RNA and protein expression in calcific aortic valve disease. <i>Physiological Genomics</i> , <b>2020</b> , 52, 191-199	3.6	6
28	Mapping Splicing Quantitative Trait Loci in RNA-Seq. <i>Cancer Informatics</i> , <b>2015</b> , 14, 45-53	2.4	6
27	Mapping Splicing Quantitative Trait Loci in RNA-Seq. <i>Cancer Informatics</i> , <b>2014</b> , 13, 35-43	2.4	6
26	Modular composition predicts kinase/substrate interactions. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 349	3.6	6
25	Dual-targeting strategy using trastuzumab and lapatinib in a patient with HER2 gene amplification in recurrent metachronous metastatic gallbladder carcinoma. <i>Journal of International Medical Research</i> , <b>2019</b> , 47, 2768-2777	1.4	5
24	Mitochondrial DNA Haplogroups and Susceptibility to Neuroblastoma. <i>Journal of the National Cancer Institute</i> , <b>2020</b> , 112, 1259-1266	9.7	5
23	Copy number variation in CEP57L1 predisposes to congenital absence of bilateral ACL and PCL ligaments. <i>Human Genomics</i> , <b>2015</b> , 9, 31	6.8	5
22	Domain altering SNPs in the human proteome and their impact on signaling pathways. <i>PLoS ONE</i> , <b>2010</b> , 5, e12890	3.7	5
21	Heterozygous Deletion Impacting SMARCD1 in the Original Kindred with Absent Dermatoglyphs and Associated Features (Baird, 1964). <i>Journal of Pediatrics</i> , <b>2018</b> , 194, 248-252.e2	3.6	4
20	Non-coding structural variation differentially impacts attention-deficit hyperactivity disorder (ADHD) gene networks in African American vs Caucasian children. <i>Scientific Reports</i> , <b>2020</b> , 10, 15252	4.9	4
19	Serum levels of the IgA isotype switch factor TGF- $\beta$ are elevated in patients with COVID-19. <i>FEBS Letters</i> , <b>2021</b> , 595, 1819-1824	3.8	4
18	Regulation of Janus Kinase 2 by an Inflammatory Bowel Disease Causal Non-coding Single Nucleotide Polymorphism. <i>Journal of Crohn's and Colitis</i> , <b>2020</b> , 14, 646-653	1.5	3

17	Improved Genetic Risk Scoring Algorithm (GRS2) for Type 1 Diabetes Prediction.. <i>Pediatric Diabetes</i> , <b>2022</b> ,	3.6	3
16	Facilitates ErbB2-Mammary Adenocarcinoma in Mice. <i>Cancers</i> , <b>2021</b> , 13,	6.6	3
15	Deep learning prediction of attention-deficit hyperactivity disorder in African Americans by copy number variation. <i>Experimental Biology and Medicine</i> , <b>2021</b> , 246, 2317-2323	3.7	2
14	Association of novel rare coding variants with juvenile idiopathic arthritis. <i>Annals of the Rheumatic Diseases</i> , <b>2021</b> , 80, 626-631	2.4	2
13	Rare Recurrent Variants in Noncoding Regions Impact Attention-Deficit Hyperactivity Disorder (ADHD) Gene Networks in Children of both African American and European American Ancestry. <i>Genes</i> , <b>2021</b> , 12,	4.2	2
12	Genome-wide association study reveals two loci for serum magnesium concentrations in European-American children. <i>Scientific Reports</i> , <b>2015</b> , 5, 18792	4.9	1
11	Machine Learning Reduced Gene/Non-Coding RNA Features That Classify Schizophrenia Patients Accurately and Highlight Insightful Gene Clusters. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	6.3	1
10	Role of the ADCY9 gene in cardiac abnormalities of the Rubinstein-Taybi syndrome. <i>Orphanet Journal of Rare Diseases</i> , <b>2020</b> , 15, 101	4.2	1
9	FLNC and MYLK2 Gene Mutations in a Chinese Family with Different Phenotypes of Cardiomyopathy. <i>International Heart Journal</i> , <b>2021</b> , 62, 127-134	1.8	1
8	A genome-wide association meta-analysis identifies new eosinophilic esophagitis loci. <i>Journal of Allergy and Clinical Immunology</i> , <b>2021</b> ,	11.5	1
7	Mitochondrial DNA haplogroups and risk of attention deficit and hyperactivity disorder in European Americans. <i>Translational Psychiatry</i> , <b>2020</b> , 10, 370	8.6	0
6	Interpretation of Maturity-Onset Diabetes of the Young Genetic Variants Based on American College of Medical Genetics and Genomics Criteria: Machine-Learning Model Development. <i>JMIR Biomedical Engineering</i> , <b>2020</b> , 5, e20506	1.3	0
5	MONTAGE: a new tool for high-throughput detection of mosaic copy number variation. <i>BMC Genomics</i> , <b>2021</b> , 22, 133	4.5	0
4	Expansion of Schizophrenia Gene Network Knowledge Using Machine Learning Selected Signals From Dorsolateral Prefrontal Cortex and Amygdala RNA-seq Data.. <i>Frontiers in Psychiatry</i> , <b>2022</b> , 13, 797329	5.5	0
3	Burden of rare coding variants reveals genetic heterogeneity between obese and non-obese asthma patients in the African American population.. <i>Respiratory Research</i> , <b>2022</b> , 23, 116	7.3	0
2	Rare neurological manifestations in a Saudi Arabian patient with Ehlers-Danlos syndrome and a novel homozygous variant in the TNXB gene. <i>American Journal of Medical Genetics, Part A</i> , <b>2021</b> , 188, 618	2.5	
1	Saudi Arabian CML patient with a novel four-way translocation at t(9;22;5;2)(q34;q11.2;p13;q44).. <i>Molecular Genetics &amp; Genomic Medicine</i> , <b>2022</b> , e1865	2.3	