Yichuan Liu

List of Publications by Year in Descending Order

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	Improved Genetic Risk Scoring Algorithm (GRS2) for Type 1 Diabetes Prediction.. *Pediatric Diabetes*, **2022**,	3.6	3
51	Expansion of Schizophrenia Gene Network Knowledge Using Machine Learning Selected Signals From Dorsolateral Prefrontal Cortex and Amygdala RNA-seq Data.. *Frontiers in Psychiatry*, **2022**, 13, 797329	5	0
50	Burden of rare coding variants reveals genetic heterogeneity between obese and non-obese asthma patients in the African American population.. *Respiratory Research*, **2022**, 23, 116	7.3	0
49	Saudi Arabian CML patient with a novel four-way translocation at t(9;22;5;2)(q34;q11.2;p13;q44).. *Molecular Genetics & Genomic Medicine*, **2022**, e1865	2.3	
48	Rare neurological manifestations in a Saudi Arabian patient with Ehlers-Danlos syndrome and a novel homozygous variant in the TNXB gene. *American Journal of Medical Genetics, Part A*, **2021**, 188, 618	2.5	
47	Machine Learning Reduced Gene/Non-Coding RNA Features That Classify Schizophrenia Patients Accurately and Highlight Insightful Gene Clusters. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	1
46	Facilitates ErbB2-Mammary Adenocarcinoma in Mice. *Cancers*, **2021**, 13,	6.6	3
45	Serum levels of the IgA isotype switch factor TGF-β1 are elevated in patients with COVID-19. *FEBS Letters*, **2021**, 595, 1819-1824	3.8	4
44	Deep learning prediction of attention-deficit hyperactivity disorder in African Americans by copy number variation. *Experimental Biology and Medicine*, **2021**, 246, 2317-2323	3.7	2
43	FLNC and MYLK2 Gene Mutations in a Chinese Family with Different Phenotypes of Cardiomyopathy. *International Heart Journal*, **2021**, 62, 127-134	1.8	1
42	Association of novel rare coding variants with juvenile idiopathic arthritis. *Annals of the Rheumatic Diseases*, **2021**, 80, 626-631	2.4	2
41	Rare Recurrent Variants in Noncoding Regions Impact Attention-Deficit Hyperactivity Disorder (ADHD) Gene Networks in Children of both African American and European American Ancestry. *Genes*, **2021**, 12,	4.2	2
40	MONTAGE: a new tool for high-throughput detection of mosaic copy number variation. *BMC Genomics*, **2021**, 22, 133	4.5	0
39	A genome-wide association meta-analysis identifies new eosinophilic esophagitis loci. *Journal of Allergy and Clinical Immunology*, **2021**,	11.5	1
38	Mitochondrial DNA haplogroups and risk of attention deficit and hyperactivity disorder in European Americans. *Translational Psychiatry*, **2020**, 10, 370	8.6	0
37	Circulating and tissue matricellular RNA and protein expression in calcific aortic valve disease. *Physiological Genomics*, **2020**, 52, 191-199	3.6	6
36	Mitochondrial DNA Haplogroups and Susceptibility to Neuroblastoma. *Journal of the National Cancer Institute*, **2020**, 112, 1259-1266	9.7	5

35	Regulation of Janus Kinase 2 by an Inflammatory Bowel Disease Causal Non-coding Single Nucleotide Polymorphism. *Journal of Crohn's and Colitis*, **2020**, 14, 646-653	1.5	3
34	Interpretation of Maturity-Onset Diabetes of the Young Genetic Variants Based on American College of Medical Genetics and Genomics Criteria: Machine-Learning Model Development. *JMIR Biomedical Engineering*, **2020**, 5, e20506	1.3	0
33	Expression Pattern of the SARS-CoV-2 Entry Genes and in the Respiratory Tract. *Viruses*, **2020**, 12,	6.2	12
32	Non-coding structural variation differentially impacts attention-deficit hyperactivity disorder (ADHD) gene networks in African American vs Caucasian children. *Scientific Reports*, **2020**, 10, 15252	4.9	4
31	Role of the ADCY9 gene in cardiac abnormalities of the Rubinstein-Taybi syndrome. *Orphanet Journal of Rare Diseases*, **2020**, 15, 101	4.2	1
30	Association of Rare Recurrent Copy Number Variants With Congenital Heart Defects Based on Next-Generation Sequencing Data From Family Trios. *Frontiers in Genetics*, **2019**, 10, 819	4.5	6
29	Dual-targeting strategy using trastuzumab and lapatinib in a patient with HER2 gene amplification in recurrent metachronous metastatic gallbladder carcinoma. *Journal of International Medical Research*, **2019**, 47, 2768-2777	1.4	5
28	Microduplications at the 15q11.2 BP1-BP2 locus are enriched in patients with anorexia nervosa. *Journal of Psychiatric Research*, **2019**, 113, 34-38	5.2	6
27	ARAF recurrent mutation causes central conducting lymphatic anomaly treatable with a MEK inhibitor. *Nature Medicine*, **2019**, 25, 1116-1122	50.5	70
26	Combining targeted panel-based resequencing and copy-number variation analysis for the diagnosis of inherited syndromic retinopathies and associated ciliopathies. *Scientific Reports*, **2018**, 8, 5285	4.9	17
25	Non-coding RNA dysregulation in the amygdala region of schizophrenia patients contributes to the pathogenesis of the disease. *Translational Psychiatry*, **2018**, 8, 44	8.6	36
24	Heterozygous Deletion Impacting SMARCAD1 in the Original Kindred with Absent Dermatoglyphs and Associated Features (Baird, 1964). *Journal of Pediatrics*, **2018**, 194, 248-252.e2	3.6	4
23	The Long Noncoding RNA Landscape in Amygdala Tissues from Schizophrenia Patients. *EBioMedicine*, **2018**, 34, 171-181	8.8	18
22	Pathogenic variant in EPHB4 results in central conducting lymphatic anomaly. *Human Molecular Genetics*, **2018**, 27, 3233-3245	5.6	42
21	Common variants at 5q33.1 predispose to migraine in African-American children. *Journal of Medical Genetics*, **2018**, 55, 831-836	5.8	10
20	Common and Rare Genetic Risk Factors Converge in Protein Interaction Networks Underlying Schizophrenia. *Frontiers in Genetics*, **2018**, 9, 434	4.5	19
19	A genome-wide association study of anorexia nervosa suggests a risk locus implicated in dysregulated leptin signaling. *Scientific Reports*, **2017**, 7, 3847	4.9	16
18	Common variants in MMP20 at 11q22.2 predispose to 11q deletion and neuroblastoma risk. *Nature Communications*, **2017**, 8, 569	17.4	19

17	RNA-seq analysis of amygdala tissue reveals characteristic expression profiles in schizophrenia. *Translational Psychiatry*, **2017**, 7, e1203	8.6	29
16	Integrative genomics identifies 7p11.2 as a novel locus for fever and clinical stress response in humans. *Human Molecular Genetics*, **2015**, 24, 1801-12	5.6	16
15	Bayesian integration of genetics and epigenetics detects causal regulatory SNPs underlying expression variability. *Nature Communications*, **2015**, 6, 8555	17.4	20
14	RNA-Seq identifies novel myocardial gene expression signatures of heart failure. *Genomics*, **2015**, 105, 83-9	4.3	129
13	Genome-wide association study reveals two loci for serum magnesium concentrations in European-American children. *Scientific Reports*, **2015**, 5, 18792	4.9	1
12	Mapping Splicing Quantitative Trait Loci in RNA-Seq. *Cancer Informatics*, **2015**, 14, 45-53	2.4	6
11	Copy number variation in CEP57L1 predisposes to congenital absence of bilateral ACL and PCL ligaments. *Human Genomics*, **2015**, 9, 31	6.8	5
10	Application of Whole Exome Sequencing in Six Families with an Initial Diagnosis of Autosomal Dominant Retinitis Pigmentosa: Lessons Learned. *PLoS ONE*, **2015**, 10, e0133624	3.7	17
9	Comprehensive analysis of gene expression in human retina and supporting tissues. *Human Molecular Genetics*, **2014**, 23, 4001-14	5.6	86
8	Mapping Splicing Quantitative Trait Loci in RNA-Seq. *Cancer Informatics*, **2014**, 13, 35-43	2.4	6
7	Tissue-specific RNA-Seq in human evoked inflammation identifies blood and adipose LincRNA signatures of cardiometabolic diseases. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2014**, 34, 902-12	9.4	60
6	A functional synonymous coding variant in the IL1RN gene is associated with survival in septic shock. *American Journal of Respiratory and Critical Care Medicine*, **2014**, 190, 656-64	10.2	28
5	PennSeq: accurate isoform-specific gene expression quantification in RNA-Seq by modeling non-uniform read distribution. *Nucleic Acids Research*, **2014**, 42, e20	20.1	29
4	Testing genetic association with rare variants in admixed populations. *Genetic Epidemiology*, **2013**, 37, 38-47	2.6	8
3	Evaluating the impact of sequencing depth on transcriptome profiling in human adipose. *PLoS ONE*, **2013**, 8, e66883	3.7	44
2	Domain altering SNPs in the human proteome and their impact on signaling pathways. *PLoS ONE*, **2010**, 5, e12890	3.7	5
1	Modular composition predicts kinase/substrate interactions. *BMC Bioinformatics*, **2010**, 11, 349	3.6	6