

Yichuan Liu

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

1,357
citations

430874

18
h-index

395702

33
g-index

70
all docs

70
docs citations

70
times ranked

3008
citing authors

#	ARTICLE	IF	CITATIONS
1	RNA-Seq identifies novel myocardial gene expression signatures of heart failure. <i>Genomics</i> , 2015, 105, 83-89.	2.9	220
2	ARAF recurrent mutation causes central conducting lymphatic anomaly treatable with a MEK inhibitor. <i>Nature Medicine</i> , 2019, 25, 1116-1122.	30.7	136
3	Comprehensive analysis of gene expression in human retina and supporting tissues. <i>Human Molecular Genetics</i> , 2014, 23, 4001-4014.	2.9	109
4	Tissue-Specific RNA-Seq in Human Evoked Inflammation Identifies Blood and Adipose LincRNA Signatures of Cardiometabolic Diseases. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2014, 34, 902-912.	2.4	75
5	Pathogenic variant in EPHB4 results in central conducting lymphatic anomaly. <i>Human Molecular Genetics</i> , 2018, 27, 3233-3245.	2.9	73
6	RNA-seq analysis of amygdala tissue reveals characteristic expression profiles in schizophrenia. <i>Translational Psychiatry</i> , 2017, 7, e1203-e1203.	4.8	63
7	Evaluating the Impact of Sequencing Depth on Transcriptome Profiling in Human Adipose. <i>PLoS ONE</i> , 2013, 8, e66883.	2.5	60
8	Non-coding RNA dysregulation in the amygdala region of schizophrenia patients contributes to the pathogenesis of the disease. <i>Translational Psychiatry</i> , 2018, 8, 44.	4.8	55
9	A Functional Synonymous Coding Variant in the <i>IL1RN</i> Gene Is Associated with Survival in Septic Shock. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2014, 190, 656-664.	5.6	42
10	PennSeq: accurate isoform-specific gene expression quantification in RNA-Seq by modeling non-uniform read distribution. <i>Nucleic Acids Research</i> , 2014, 42, e20-e20.	14.5	33
11	The Long Noncoding RNA Landscape in Amygdala Tissues from Schizophrenia Patients. <i>EBioMedicine</i> , 2018, 34, 171-181.	6.1	32
12	Combining targeted panel-based resequencing and copy-number variation analysis for the diagnosis of inherited syndromic retinopathies and associated ciliopathies. <i>Scientific Reports</i> , 2018, 8, 5285.	3.3	28
13	Expression Pattern of the SARS-CoV-2 Entry Genes ACE2 and TMPRSS2 in the Respiratory Tract. <i>Viruses</i> , 2020, 12, 1174.	3.3	27
14	Common and Rare Genetic Risk Factors Converge in Protein Interaction Networks Underlying Schizophrenia. <i>Frontiers in Genetics</i> , 2018, 9, 434.	2.3	26
15	A genome-wide association study of anorexia nervosa suggests a risk locus implicated in dysregulated leptin signaling. <i>Scientific Reports</i> , 2017, 7, 3847.	3.3	23
16	Bayesian integration of genetics and epigenetics detects causal regulatory SNPs underlying expression variability. <i>Nature Communications</i> , 2015, 6, 8555.	12.8	22
17	Common variants in MMP20 at 11q22.2 predispose to 11q deletion and neuroblastoma risk. <i>Nature Communications</i> , 2017, 8, 569.	12.8	22
18	A genome-wide association meta-analysis identifies new eosinophilic esophagitis loci. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 149, 988-998.	2.9	19

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19	Application of Whole Exome Sequencing in Six Families with an Initial Diagnosis of Autosomal Dominant Retinitis Pigmentosa: Lessons Learned. <i>PLoS ONE</i> , 2015, 10, e0133624.	2.5	19
20	Integrative genomics identifies 7p11.2 as a novel locus for fever and clinical stress response in humans. <i>Human Molecular Genetics</i> , 2015, 24, 1801-1812.	2.9	18
21	Serum levels of the IgA isotype switch factor TGF β 1 are elevated in patients with COVID-19. <i>FEBS Letters</i> , 2021, 595, 1819-1824.	2.8	16
22	Common variants at 5q33.1 predispose to migraine in African-American children. <i>Journal of Medical Genetics</i> , 2018, 55, 831-836.	3.2	15
23	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> , 2019, 10, 819.	2.3	15
24	Application of deep learning algorithm on whole genome sequencing data uncovers structural variants associated with multiple mental disorders in African American patients. <i>Molecular Psychiatry</i> , 2022, 27, 1469-1478.	7.9	13
25	Mitochondrial DNA haplogroups and risk of attention deficit and hyperactivity disorder in European Americans. <i>Translational Psychiatry</i> , 2020, 10, 370.	4.8	11
26	Circulating and tissue matricellular RNA and protein expression in calcific aortic valve disease. <i>Physiological Genomics</i> , 2020, 52, 191-199.	2.3	11
27	Improved genetic risk scoring algorithm for type 1 diabetes prediction. <i>Pediatric Diabetes</i> , 2022, 23, 320-323.	2.9	11
28	Mitochondrial DNA Haplogroups and Susceptibility to Neuroblastoma. <i>Journal of the National Cancer Institute</i> , 2020, 112, 1259-1266.	6.3	10
29	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> , 2021, 12, 310.	2.4	10
30	Copy number variation in CEP57L1 predisposes to congenital absence of bilateral ACL and PCL ligaments. <i>Human Genomics</i> , 2015, 9, 31.	2.9	9
31	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> , 2022, 13, 797329.	2.6	9
32	Testing Genetic Association With Rare Variants in Admixed Populations. <i>Genetic Epidemiology</i> , 2013, 37, 38-47.	1.3	8
33	Deep learning prediction of attention-deficit hyperactivity disorder in African Americans by copy number variation. <i>Experimental Biology and Medicine</i> , 2021, 246, 2317-2323.	2.4	8
34	Modular composition predicts kinase/substrate interactions. <i>BMC Bioinformatics</i> , 2010, 11, 349.	2.6	7
35	Mapping Splicing Quantitative Trait Loci in RNA-Seq. <i>Cancer Informatics</i> , 2015, 14s1, CIN.S24832.	1.9	7
36	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> , 2019, 47, 2768-2777.	1.0	7

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37	Microduplications at the 15q11.2 BP1&BP2 locus are enriched in patients with anorexia nervosa. <i>Journal of Psychiatric Research</i> , 2019, 113, 34-38.	3.1	7
38	Genetic correlations between COVID-19 and a variety of traits and diseases. <i>Innovation(China)</i> , 2021, 2, 100112.	9.1	7
39	Mapping Splicing Quantitative Trait Loci in RNA-Seq. <i>Cancer Informatics</i> , 2014, 13s4, CIN.S13971.	1.9	6
40	Heterozygous Deletion Impacting SMARCAD1 in the Original Kindred with Absent Dermatoglyphs and Associated Features (Baird, 1964). <i>Journal of Pediatrics</i> , 2018, 194, 248-252.e2.	1.8	6
41	<i>FLNC</i> and <i>MYLK2</i> Gene Mutations in a Chinese Family with Different Phenotypes of Cardiomyopathy. <i>International Heart Journal</i> , 2021, 62, 127-134.	1.0	6
42	Association of novel rare coding variants with juvenile idiopathic arthritis. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, 626-631.	0.9	6
43	Domain Altering SNPs in the Human Proteome and Their Impact on Signaling Pathways. <i>PLoS ONE</i> , 2010, 5, e12890.	2.5	5
44	Non-coding structural variation differentially impacts attention-deficit hyperactivity disorder (ADHD) gene networks in African American vs Caucasian children. <i>Scientific Reports</i> , 2020, 10, 15252.	3.3	5
45	Regulation of Janus Kinase 2 by an Inflammatory Bowel Disease Causal Non-coding Single Nucleotide Polymorphism. <i>Journal of Crohn's and Colitis</i> , 2020, 14, 646-653.	1.3	5
46	Ppar ^β 1 Facilitates ErbB2-Mammary Adenocarcinoma in Mice. <i>Cancers</i> , 2021, 13, 2171.	3.7	5
47	MONTAGE: a new tool for high-throughput detection of mosaic copy number variation. <i>BMC Genomics</i> , 2021, 22, 133.	2.8	4
48	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> , 2021, 22, 3364.	4.1	4
49	Identification of Mitochondrial DNA Variants Associated With Risk of Neuroblastoma. <i>Journal of the National Cancer Institute</i> , 2022, 114, 910-913.	6.3	4
50	Mutation burden analysis of six common mental disorders in African Americans by whole genome sequencing. <i>Human Molecular Genetics</i> , 2022, 31, 3769-3776.	2.9	4
51	Role of the ADCY9 gene in cardiac abnormalities of the Rubinstein-Taybi syndrome. <i>Orphanet Journal of Rare Diseases</i> , 2020, 15, 101.	2.7	2
52	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> , 2020, 5, e20506.	1.2	2
53	Genome-wide association study reveals two loci for serum magnesium concentrations in European-American children. <i>Scientific Reports</i> , 2015, 5, 18792.	3.3	1
54	Rare neurological manifestations in a Saudi Arabian patient with <sc>Ehlers&Danlos</sc> syndrome and a novel homozygous variant in the <sc><i>TNXB</i></sc> gene. <i>American Journal of Medical Genetics, Part A</i> , 2022, 188, 618-623.	1.2	1

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55	Burden of rare coding variants reveals genetic heterogeneity between obese and non-obese asthma patients in the African American population. <i>Respiratory Research</i> , 2022, 23, 116.	3.6	1
56	Saudi Arabian CML patient with a novel four-way translocation at t(9;22;5;2)(q34;q11.2;p13;q44). <i>Molecular Genetics & Genomic Medicine</i> , 2022, , e1865.	1.2	1
57	Microduplications at the 15q11.2 BP1-BP2 Locus are Enriched in Patients with Anorexia Nervosa. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0