Yichuan Liu

List of Publications by Year
in descending order

57	1,357	430754	395590
papers	citations	18 h-index	33 g-index

70	70	70	3008
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	RNA-Seq identifies novel myocardial gene expression signatures of heart failure. Genomics, 2015, 105, 83-89.	1.3	220
2	ARAF recurrent mutation causes central conducting lymphatic anomaly treatable with a MEK inhibitor. Nature Medicine, 2019, 25, 1116-1122.	15.2	136
3	Comprehensive analysis of gene expression in human retina and supporting tissues. Human Molecular Genetics, 2014, 23, 4001-4014.	1.4	109
4	Tissue-Specific RNA-Seq in Human Evoked Inflammation Identifies Blood and Adipose LincRNA Signatures of Cardiometabolic Diseases. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 902-912.	1.1	75
5	Pathogenic variant in EPHB4 results in central conducting lymphatic anomaly. Human Molecular Genetics, 2018, 27, 3233-3245.	1.4	73
6	RNA-seq analysis of amygdala tissue reveals characteristic expression profiles in schizophrenia. Translational Psychiatry, 2017, 7, e1203-e1203.	2.4	63
7	Evaluating the Impact of Sequencing Depth on Transcriptome Profiling in Human Adipose. PLoS ONE, 2013, 8, e66883.	1.1	60
8	Non-coding RNA dysregulation in the amygdala region of schizophrenia patients contributes to the pathogenesis of the disease. Translational Psychiatry, 2018, 8, 44.	2.4	55
9	A Functional Synonymous Coding Variant in theIL1RNGene Is Associated with Survival in Septic Shock. American Journal of Respiratory and Critical Care Medicine, 2014, 190, 656-664.	2.5	42
10	PennSeq: accurate isoform-specific gene expression quantification in RNA-Seq by modeling non-uniform read distribution. Nucleic Acids Research, 2014, 42, e20-e20.	6.5	33
11	The Long Noncoding RNA Landscape in Amygdala Tissues from Schizophrenia Patients. EBioMedicine, 2018, 34, 171-181.	2.7	32
12	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.	1.6	28
13	Expression Pattern of the SARS-CoV-2 Entry Genes ACE2 and TMPRSS2 in the Respiratory Tract. Viruses, 2020, 12, 1174.	1.5	27
14	Common and Rare Genetic Risk Factors Converge in Protein Interaction Networks Underlying Schizophrenia. Frontiers in Genetics, 2018, 9, 434.	1.1	26
15	A genome-wide association study of anorexia nervosa suggests a risk locus implicated in dysregulated leptin signaling. Scientific Reports, 2017, 7, 3847.	1.6	23
16	Bayesian integration of genetics and epigenetics detects causal regulatory SNPs underlying expression variability. Nature Communications, 2015, 6, 8555.	5.8	22
17	Common variants in MMP20 at 11q22.2 predispose to 11q deletion and neuroblastoma risk. Nature Communications, 2017, 8, 569.	5.8	22
18	A genome-wide association meta-analysis identifies new eosinophilic esophagitis loci. Journal of Allergy and Clinical Immunology, 2022, 149, 988-998.	1.5	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. PLoS ONE, 2015, 10, e0133624.	1.1	19
20	Integrative genomics identifies 7p11.2 as a novel locus for fever and clinical stress response in humans. Human Molecular Genetics, 2015, 24, 1801-1812.	1.4	18
21	Serum levels of the IgA isotype switch factor TGFâ€Î²1 are elevated in patients with COVIDâ€19. FEBS Letters, 2021, 595, 1819-1824.	1.3	16
22	Common variants at 5q33.1 predispose to migraine in African-American children. Journal of Medical Genetics, 2018, 55, 831-836.	1.5	15
23	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.	1.1	15
24	Application of deep learning algorithm on whole genome sequencing data uncovers structural variants associated with multiple mental disorders in African American patients. Molecular Psychiatry, 2022, 27, 1469-1478.	4.1	13
25	Mitochondrial DNA haplogroups and risk of attention deficit and hyperactivity disorder in European Americans. Translational Psychiatry, 2020, 10, 370.	2.4	11
26	Circulating and tissue matricellular RNA and protein expression in calcific aortic valve disease. Physiological Genomics, 2020, 52, 191-199.	1.0	11
27	Improved genetic risk scoring algorithm for type 1 diabetes prediction. Pediatric Diabetes, 2022, 23, 320-323.	1.2	11
28	Mitochondrial DNA Haplogroups and Susceptibility to Neuroblastoma. Journal of the National Cancer Institute, 2020, 112, 1259-1266.	3.0	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. Genes, 2021, 12, 310.	1.0	10
30	Copy number variation in CEP57L1 predisposes to congenital absence of bilateral ACL and PCL ligaments. Human Genomics, 2015, 9, 31.	1.4	9
31	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.	1.3	9
32	Testing Genetic Association With Rare Variants in Admixed Populations. Genetic Epidemiology, 2013, 37, 38-47.	0.6	8
33	Deep learning prediction of attention-deficit hyperactivity disorder in African Americans by copy number variation. Experimental Biology and Medicine, 2021, 246, 2317-2323.	1.1	8
34	Modular composition predicts kinase/substrate interactions. BMC Bioinformatics, 2010, 11, 349.	1.2	7
35	Mapping Splicing Quantitative Trait Loci in RNA-Seq. Cancer Informatics, 2015, 14s1, CIN.S24832.	0.9	7
36	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.	0.4	7

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37	Microduplications at the 15q11.2 BP1â€“BP2 locus are enriched in patients with anorexia nervosa. Journal of Psychiatric Research, 2019, 113, 34-38.	1.5	7
38	Genetic correlations between COVID-19 and a variety of traits and diseases. Innovation(China), 2021, 2, 100112.	5.2	7
39	Mapping Splicing Quantitative Trait Loci in RNA-Seq. Cancer Informatics, 2014, 13s4, CIN.S13971.	0.9	6
40	Heterozygous Deletion Impacting SMARCAD1 in the Original Kindred with Absent Dermatoglyphs and Associated Features (Baird, 1964). Journal of Pediatrics, 2018, 194, 248-252.e2.	0.9	6
41	<i>FLNC</i> and <i>MYLK2</i> Gene Mutations in a Chinese Family with Different Phenotypes of Cardiomyopathy. International Heart Journal, 2021, 62, 127-134.	0.5	6
42	Association of novel rare coding variants with juvenile idiopathic arthritis. Annals of the Rheumatic Diseases, 2021, 80, 626-631.	0.5	6
43	Domain Altering SNPs in the Human Proteome and Their Impact on Signaling Pathways. PLoS ONE, 2010, 5, e12890.	1.1	5
44	Non-coding structural variation differentially impacts attention-deficit hyperactivity disorder (ADHD) gene networks in African American vs Caucasian children. Scientific Reports, 2020, 10, 15252.	1.6	5
45	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.	0.6	5
46	PparÎ³1 Facilitates ErbB2-Mammary Adenocarcinoma in Mice. Cancers, 2021, 13, 2171.	1.7	5
47	MONTAGE: a new tool for high-throughput detection of mosaic copy number variation. BMC Genomics, 2021, 22, 133.	1.2	4
48	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, 3364.	1.8	4
49	Identification of Mitochondrial DNA Variants Associated With Risk of Neuroblastoma. Journal of the National Cancer Institute, 2022, 114, 910-913.	3.0	4
50	Mutation burden analysis of six common mental disorders in African Americans by whole genome sequencing. Human Molecular Genetics, 2022, 31, 3769-3776.	1.4	4
51	Role of the ADCY9 gene in cardiac abnormalities of the Rubinstein-Taybi syndrome. Orphanet Journal of Rare Diseases, 2020, 15, 101.	1.2	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. JMIR Biomedical Engineering, 2020, 5, e20506.	0.7	2
53	Genome-wide association study reveals two loci for serum magnesium concentrations in European-American children. Scientific Reports, 2015, 5, 18792.	1.6	1
54	Rare neurological manifestations in a Saudi Arabian patient with <scp>Ehlersâ€“Danlos</scp> syndrome and a novel homozygous variant in the <scp>TNXB</scp> gene. American Journal of Medical Genetics, Part A, 2022, 188, 618-623.	0.7	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. Respiratory Research, 2022, 23, 116.	1.4	1
56	Saudi Arabian CML patient with a novel fourâ€way translocation at t(9;22;5;2)(q34;q11.2;p13;q44). Molecular Genetics & Genomic Medicine, 2022, , e1865.	0.6	1
57	Microduplications at the 15q11.2 BP1-BP2 Locus are Enriched in Patients with Anorexia Nervosa. SSRN Electronic Journal, 0, , .	0.4	0