Yong-Xin 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.

18 5,598 51 33 h-index g-index citations papers 10,522 5.01 51 9.4 avg, IF L-index ext. citations ext. papers

#	Paper	IF	Citations
33	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050
32	NRT1.1B is associated with root microbiota composition and nitrogen use in field-grown rice. <i>Nature Biotechnology</i> , 2019 , 37, 676-684	44.5	276
31	A specialized metabolic network selectively modulates root microbiota. <i>Science</i> , 2019 , 364,	33.3	211
30	Expression of the Nitrate Transporter Gene Confers High Yield and Early Maturation in Rice. <i>Plant Cell</i> , 2018 , 30, 638-651	11.6	145
29	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
28	A practical guide to amplicon and metagenomic analysis of microbiome data. <i>Protein and Cell</i> , 2021 , 12, 315-330	7.2	100
27	Root microbiota shift in rice correlates with resident time in the field and developmental stage. <i>Science China Life Sciences</i> , 2018 , 61, 613-621	8.5	98
26	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 2018,		78
25	N2O and NO emission from a biological aerated filter treating coking wastewater: Main source and microbial community. <i>Journal of Cleaner Production</i> , 2019 , 213, 365-374	10.3	48
24	Reductionist synthetic community approaches in root microbiome research. <i>Current Opinion in Microbiology</i> , 2019 , 49, 97-102	7.9	39
23	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
22	An Arabidopsis Secondary Metabolite Directly Targets Expression of the Bacterial Type III Secretion System to Inhibit Bacterial Virulence. <i>Cell Host and Microbe</i> , 2020 , 27, 601-613.e7	23.4	29
21	Recently duplicated sesterterpene (C25) gene clusters in Arabidopsis thaliana modulate root microbiota. <i>Science China Life Sciences</i> , 2019 , 62, 947-958	8.5	25
20	EVenn: Easy to create repeatable and editable Venn diagrams and Venn networks online. <i>Journal of Genetics and Genomics</i> , 2021 , 48, 863-866	4	22
19	High-throughput cultivation and identification of bacteria from the plant root microbiota. <i>Nature Protocols</i> , 2021 , 16, 988-1012	18.8	22
18	Endogenous small RNA clusters in plants. <i>Genomics, Proteomics and Bioinformatics</i> , 2014 , 12, 64-71	6.5	20
17	Host-Associated Quantitative Abundance Profiling Reveals the Microbial Load Variation of Root Microbiome. <i>Plant Communications</i> , 2020 , 1, 100003	9	20

LIST OF PUBLICATIONS

	Gut microbiota in children with juvenile idiopathic arthritis: characteristics, biomarker identification, and usefulness in clinical prediction. <i>BMC Genomics</i> , 2020 , 21, 286	4.5	17
15	Dynamic chromatin changes associated with de novo centromere formation in maize euchromatin. <i>Plant Journal</i> , 2016 , 88, 854-866	6.9	15
14	In silico Detection of Novel MicroRNAs Genes in Soybean Genome. <i>Agricultural Sciences in China</i> , 2011 , 10, 1336-1345		13
13	A guide to human microbiome research: study design, sample collection, and bioinformatics analysis. <i>Chinese Medical Journal</i> , 2020 , 133, 1844-1855	2.9	13
12	Genomic Analysis of MicroRNA Promoters and Their Cis-Acting Elements in Soybean. <i>Agricultural Sciences in China</i> , 2010 , 9, 1561-1570		10
11	ImageGP: An easy-to-use data visualization web server for scientific researchers 2022, 1,		10
10	Active ammonia-oxidizing bacteria and archaea in wastewater treatment systems. <i>Journal of Environmental Sciences</i> , 2021 , 102, 273-282	6.4	6
9	MicroRNA Primary Transcripts and Promoter Elements Analysis in Soybean (Glycine max L. Merril.). <i>Journal of Integrative Agriculture</i> , 2013 , 12, 1522-1529	3.2	5
8	Recovery of high-qualitied Genomes from a deep-inland Salt Lake Using BASALT		4
7	Source Tracking and Global Distribution of the Tigecycline Non-Susceptible (X) <i>Microbiology Spectrum</i> , 2021 , e0116421	8.9	2
7		8.9	2
	Spectrum, 2021 , e0116421	8.9 4	
6	Spectrum, 2021, e0116421 Small RNA expression pattern in multiply inbred lines and their hybrids of maize embryo The rice histone methylation regulates hub species of the root microbiota. <i>Journal of Genetics and</i>		1
6 5	Small RNA expression pattern in multiply inbred lines and their hybrids of maize embryo The rice histone methylation regulates hub species of the root microbiota. <i>Journal of Genetics and Genomics</i> , 2021 , 48, 836-843		1
654	Small RNA expression pattern in multiply inbred lines and their hybrids of maize embryo The rice histone methylation regulates hub species of the root microbiota. <i>Journal of Genetics and Genomics</i> , 2021, 48, 836-843 Source tracking and global distribution of the mobilized tigecycline resistant gene tet(X) The role of genotype and diet in shaping gut microbiome in a genetic vitamin A deficient mouse	4	1 1