

Yong-Xin Liu

List of Publications by Year in Descending Order

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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.

33
papers

5,598
citations

18
h-index

51
g-index

51
ext. papers

10,522
ext. citations

9.4
avg, IF

5.01
L-index

#	Paper	IF	Citations
33	ImageGP: An easy-to-use data visualization web server for scientific researchers 2022 , 1,		10
32	Erratum for Zhang et al., "Source Tracking and Global Distribution of the Tigecycline-Nonsusceptible Tet(X)". <i>Microbiology Spectrum</i> , 2022 , e0113122	8.9	0
31	A practical guide to amplicon and metagenomic analysis of microbiome data. <i>Protein and Cell</i> , 2021 , 12, 315-330	7.2	100
30	Active ammonia-oxidizing bacteria and archaea in wastewater treatment systems. <i>Journal of Environmental Sciences</i> , 2021 , 102, 273-282	6.4	6
29	The rice histone methylation regulates hub species of the root microbiota. <i>Journal of Genetics and Genomics</i> , 2021 , 48, 836-843	4	1
28	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
27	The role of genotype and diet in shaping gut microbiome in a genetic vitamin A deficient mouse model. <i>Journal of Genetics and Genomics</i> , 2021 , 49, 155-155	4	0
26	High-throughput cultivation and identification of bacteria from the plant root microbiota. <i>Nature Protocols</i> , 2021 , 16, 988-1012	18.8	22
25	Source Tracking and Global Distribution of the Tigecycline Non-Susceptible (X).. <i>Microbiology Spectrum</i> , 2021 , e0116421	8.9	2
24	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
23	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
22	Host-Associated Quantitative Abundance Profiling Reveals the Microbial Load Variation of Root Microbiome. <i>Plant Communications</i> , 2020 , 1, 100003	9	20
21	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
20	Analysis of rice root bacterial microbiota of Nipponbare and IR24. <i>Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji</i> , 2020 , 42, 506-518	1.4	
19	A specialized metabolic network selectively modulates root microbiota. <i>Science</i> , 2019 , 364,	33.3	211
18	Recently duplicated sesquiterpene (C25) gene clusters in <i>Arabidopsis thaliana</i> modulate root microbiota. <i>Science China Life Sciences</i> , 2019 , 62, 947-958	8.5	25
17	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

16	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050
15	Reductionist synthetic community approaches in root microbiome research. <i>Current Opinion in Microbiology</i> , 2019 , 49, 97-102	7.9	39
14	N ₂ O 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
13	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
12	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
11	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 2018 ,		78
10	Dynamic chromatin changes associated with de novo centromere formation in maize euchromatin. <i>Plant Journal</i> , 2016 , 88, 854-866	6.9	15
9	Endogenous small RNA clusters in plants. <i>Genomics, Proteomics and Bioinformatics</i> , 2014 , 12, 64-71	6.5	20
8	MicroRNA Primary Transcripts and Promoter Elements Analysis in Soybean (<i>Glycine max</i> L. Merrill). <i>Journal of Integrative Agriculture</i> , 2013 , 12, 1522-1529	3.2	5
7	In silico Detection of Novel MicroRNAs Genes in Soybean Genome. <i>Agricultural Sciences in China</i> , 2011 , 10, 1336-1345		13
6	Genomic Analysis of MicroRNA Promoters and Their Cis-Acting Elements in Soybean. <i>Agricultural Sciences in China</i> , 2010 , 9, 1561-1570		10
5	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
4	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
3	Small RNA expression pattern in multiply inbred lines and their hybrids of maize embryo		1
2	Recovery of high-qualified Genomes from a deep-inland Salt Lake Using BASALT		4
1	Source tracking and global distribution of the mobilized tetracycline resistant gene tet(X)		1