

Yong-Xin Liu

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

15,210
citations

393982

19
h-index

433756

31
g-index

51
all docs

51
docs citations

51
times ranked

17583
citing authors

#	ARTICLE	IF	CITATIONS
1	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> , 2022, 49, 155-164.	1.7	6
2	ImageGP: An easy-to-use data visualization web server for scientific researchers. , 2022, 1, .		206
3	iMeta: Integrated meta-omics for biology and environments. , 2022, 1, .		13
4	Dietary licorice enhances in vivo cadmium detoxification and modulates gut microbial metabolism in mice. , 2022, 1, .		8
5	Erratum for Zhang et al., "Source Tracking and Global Distribution of the Tigecycline-Nonsusceptible Tet(X) Microbiology Spectrum, 2022, 10, e0113122.	1.2	1
6	Fusarium fruiting body microbiome member <i>Pantoea agglomerans</i> inhibits fungal pathogenesis by targeting lipid rafts. <i>Nature Microbiology</i> , 2022, 7, 831-843.	5.9	44
7	Antioxidant potential of <i>Pediococcus pentosaceus</i> strains from the sow milk bacterial collection in weaned piglets. <i>Microbiome</i> , 2022, 10, .	4.9	16
8	ggClusterNet: An R package for microbiome network analysis and modularity-based multiple network layouts. , 2022, 1, .		75
9	A practical guide to amplicon and metagenomic analysis of microbiome data. <i>Protein and Cell</i> , 2021, 12, 315-330.	4.8	376
10	Active ammonia-oxidizing bacteria and archaea in wastewater treatment systems. <i>Journal of Environmental Sciences</i> , 2021, 102, 273-282.	3.2	16
11	é~éšé†â†ç »âŸ1â...â'CEé%â'šæç%©æ1ç3»ç»†èCE. <i>Bio-protocol</i> , 2021, , .	0.2	0
12	âŸâ°Zæ%©âçžâæ°æ©çš,,ç3»ç»Ÿâè,2æ'çš,,æž,,â»°â'CEâ±•ç°. <i>Bio-protocol</i> , 2021, , .	0.2	1
13	ä1/2ç"QIIME 2â†æžâ3/4©ç"Ÿç%©ç»,16S rRNAâŸâ>æ%©âçžâæµ<â°æ°æ°. <i>Bio-protocol</i> , 2021, , .	0.2	2
14	â©ç"æ-èCEæç%©â'CEââŸ1â...»ç»†èCEâ1/2"ç3»ç"ç©Ÿæ1ç3»â3/4©ç"Ÿç%©ç»,âŸŸèf1/2. <i>Bio-protocol</i> , 2021, , .	0.2	0
15	æ°ç"æ1ç3»â3/4©ç"Ÿç%©ç»,ç"ç©Ÿäçš,,æ:æœ-çšæââ-æâ'CE16S rRNA âŸâ>æ%©âçžâæ-†â°â^Ÿâ†æ-1æ3°. <i>Bio-protocol</i> , 2021, , .		
16	The rice histone methylation regulates hub species of the root microbiota. <i>Journal of Genetics and Genomics</i> , 2021, 48, 836-843.	1.7	9
17	EVEN: Easy to create repeatable and editable Venn diagrams and Venn networks online. <i>Journal of Genetics and Genomics</i> , 2021, 48, 863-866.	1.7	171
18	High-throughput cultivation and identification of bacteria from the plant root microbiota. <i>Nature Protocols</i> , 2021, 16, 988-1012.	5.5	91

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19	æ~“æ%©åçžârl/4šæ~“ç””ã€â-é†ââ’CEè..â13ââçš,,æ%©åçžââ^†æžæµç”. Bio-protocol, 2021, , .	0.2	0
20	ImageGPåœ..â3/4@ç”ÿç%©ç»,â~è\$†âCE-ä,çš,,â”ç””. Bio-protocol, 2021, , .	0.2	0
21	Source Tracking and Global Distribution of the Tigecycline Non-Susceptible <i>tet(X)</i> . Microbiology Spectrum, 2021, 9, e0116421.	1.2	16
22	Host-Associated Quantitative Abundance Profiling Reveals the Microbial Load Variation of Root Microbiome. Plant Communications, 2020, 1, 100003.	3.6	38
23	A guide to human microbiome research: study design, sample collection, and bioinformatics analysis. Chinese Medical Journal, 2020, 133, 1844-1855.	0.9	55
24	An Arabidopsis Secondary Metabolite Directly Targets Expression of the Bacterial Type III Secretion System to Inhibit Bacterial Virulence. Cell Host and Microbe, 2020, 27, 601-613.e7.	5.1	66
25	Gut microbiota in children with juvenile idiopathic arthritis: characteristics, biomarker identification, and usefulness in clinical prediction. BMC Genomics, 2020, 21, 286.	1.2	30
26	éšœœ°â®âÿ°â>ç»,æµ<â°œ°æ°è~é†æžšâ^†â’CEâž»â®žâ»çš,,â^†æžæµç”<â’CEâ„èšé—®éç~Analysis Pipeline and Frequently Asked Questions Metagenomic Sequencing. Bio-protocol, 2020, , .	0.2	0
27	Analysis of rice root bacterial microbiota of Nipponbare and IR24. Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji, 2020, 42, 506-518.	0.1	1
28	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	9.4	11,167
29	Reductionist synthetic community approaches in root microbiome research. Current Opinion in Microbiology, 2019, 49, 97-102.	2.3	105
30	A specialized metabolic network selectively modulates <i>Arabidopsis</i> root microbiota. Science, 2019, 364, .	6.0	470
31	Recently duplicated sesterterpene (C25) gene clusters in <i>Arabidopsis thaliana</i> modulate root microbiota. Science China Life Sciences, 2019, 62, 947-958.	2.3	52
32	NRT1.1B is associated with root microbiota composition and nitrogen use in field-grown rice. Nature Biotechnology, 2019, 37, 676-684.	9.4	641
33	N2O and NO emission from a biological aerated filter treating coking wastewater: Main source and microbial community. Journal of Cleaner Production, 2019, 213, 365-374.	4.6	74
34	Expression of the Nitrate Transporter Gene <i>OsNRT1.1A/OsNPF6.3</i> Confers High Yield and Early Maturation in Rice. Plant Cell, 2018, 30, 638-651.	3.1	227
35	Root microbiota shift in rice correlates with resident time in the field and developmental stage. Science China Life Sciences, 2018, 61, 613-621.	2.3	204
36	Dynamic chromatin changes associated with <i>de novo</i> centromere formation in maize euchromatin. Plant Journal, 2016, 88, 854-866.	2.8	23

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37	Endogenous Small RNA Clusters in Plants. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 64-71.	3.0	24
38	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.	1.7	5
39	In silico Detection of Novel MicroRNAs Genes in Soybean Genome. <i>Agricultural Sciences in China</i> , 2011, 10, 1336-1345.	0.6	15
40	Genomic Analysis of MicroRNA Promoters and Their Cis-Acting Elements in Soybean. <i>Agricultural Sciences in China</i> , 2010, 9, 1561-1570.	0.6	11
41	Microbial community roles and chemical mechanisms in the parasitic development of <i>Orobancha cumana</i> .		3