

Yong-Xin Liu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8058702/publications.pdf>

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	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
2	NRT1.1B is associated with root microbiota composition and nitrogen use in field-grown rice. <i>Nature Biotechnology</i> , 2019, 37, 676-684.	9.4	641
3	A specialized metabolic network selectively modulates <i>Arabidopsis</i> root microbiota. <i>Science</i> , 2019, 364, .	6.0	470
4	A practical guide to amplicon and metagenomic analysis of microbiome data. <i>Protein and Cell</i> , 2021, 12, 315-330.	4.8	376
5	Expression of the Nitrate Transporter Gene <i>OsNRT1.1A/OsNPF6.3</i> Confers High Yield and Early Maturation in Rice. <i>Plant Cell</i> , 2018, 30, 638-651.	3.1	227
6	ImageGP: An easy-to-use data visualization web server for scientific researchers. , 2022, 1, .		206
7	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.	2.3	204
8	EVenn: 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
9	Reductionist synthetic community approaches in root microbiome research. <i>Current Opinion in Microbiology</i> , 2019, 49, 97-102.	2.3	105
10	High-throughput cultivation and identification of bacteria from the plant root microbiota. <i>Nature Protocols</i> , 2021, 16, 988-1012.	5.5	91
11	ggClusterNet: An R package for microbiome network analysis and modularity-based multiple network layouts. , 2022, 1, .		75
12	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.	4.6	74
13	An <i>Arabidopsis</i> 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.	5.1	66
14	A guide to human microbiome research: study design, sample collection, and bioinformatics analysis. <i>Chinese Medical Journal</i> , 2020, 133, 1844-1855.	0.9	55
15	Recently duplicated sesterterpene (C25) gene clusters in <i>Arabidopsis thaliana</i> modulate root microbiota. <i>Science China Life Sciences</i> , 2019, 62, 947-958.	2.3	52
16	<i>Fusarium</i> 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
17	Host-Associated Quantitative Abundance Profiling Reveals the Microbial Load Variation of Root Microbiome. <i>Plant Communications</i> , 2020, 1, 100003.	3.6	38
18	Gut microbiota in children with juvenile idiopathic arthritis: characteristics, biomarker identification, and usefulness in clinical prediction. <i>BMC Genomics</i> , 2020, 21, 286.	1.2	30

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19	Endogenous Small RNA Clusters in Plants. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 64-71.	3.0	24
20	Dynamic chromatin changes associated with <i>de novo</i> centromere formation in maize euchromatin. <i>Plant Journal</i> , 2016, 88, 854-866.	2.8	23
21	Active ammonia-oxidizing bacteria and archaea in wastewater treatment systems. <i>Journal of Environmental Sciences</i> , 2021, 102, 273-282.	3.2	16
22	Source Tracking and Global Distribution of the Tigecycline Non-Susceptible <i>tet(X)</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0116421.	1.2	16
23	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
24	In silico Detection of Novel MicroRNAs Genes in Soybean Genome. <i>Agricultural Sciences in China</i> , 2011, 10, 1336-1345.	0.6	15
25	iMeta: Integrated meta-omics for biology and environments. , 2022, 1, .		13
26	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
27	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
28	Dietary licorice enhances in vivo cadmium detoxification and modulates gut microbial metabolism in mice. , 2022, 1, .		8
29	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
30	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
31	Microbial community roles and chemical mechanisms in the parasitic development of <i>Orobanche cumana</i> . , 0, , .		3
32	1/2 QiIME 2 4 16S rRNA. Bio-protocol, 2021, , .	0.2	2
33	2 3 3 2. Bio-protocol, 2021, , .	0.2	1
34	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.	0.1	1
35	Erratum for Zhang et al., Source Tracking and Global Distribution of the Tigecycline-Nonsusceptible Tet(X). <i>Microbiology Spectrum</i> , 2022, 10, e0113122.	1.2	1
36	1 3 3. Bio-protocol, 2021, , .	0.2	0

#	ARTICLE	IF	CITATIONS
37	âˆ©ç””æ—èÆæç%â’Æâ-âÿ!â...»ç»†èÆä1/2“ç³»ç”ç©¶æ¹ç³»â³/4©ç”ÿç%©ç»,âŠÿèf1/2. Bio-protocol, 2021, , .	0.2	0
38	æ”ç”»æ¹ç³»â³/4©ç”ÿç%©ç»,ç”ç©¶ä,çš,,æ·æœ-çšæâ€â-æ-â’Æ16S rRNA âÿ°â»æ%â©çžâæ-†â“â^¶â†æ-¹æ³. Bio-protocol, 2021, , .	0.2	0
39	æ”æ%â©çžââ/4šæ”ç””â€â-é†ââ’Æè-â¹â³çš,,æ%â©çžââ^†æžæµç”ç”. Bio-protocol, 2021, , .	0.2	0
40	ImageGPâœ”â³/4©ç”ÿç%©ç»,â-èš†âÆ-ä,çš,,â²”ç””. Bio-protocol, 2021, , .	0.2	0
41	éšæœ°â©âÿ°â»ç»,æµçâ°æ°æ”è”é†æžšâ^¶â’Æâž»â©çžâ»çš,,â^†æžæµç”ç”â’Æâ„èšé—©éç”Analysis Pipeline and Frequently Asked Questions for Metagenomic Sequencing. Bio-protocol, 2020, , .	0.2	0