

Yang Bai

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

8,723
citations

22
h-index

41
g-index

41
ext. papers

14,541
ext. citations

14.9
avg, IF

5.65
L-index

#	Paper	IF	Citations
33	Rbec: a tool for analysis of amplicon sequencing data from synthetic microbial communities. <i>ISME Communications</i> , 2021 , 1,		1
32	Stuck on you: Bacterial-auxin-mediated bacterial colonization of plant roots. <i>Cell Host and Microbe</i> , 2021 , 29, 1471-1473	23.4	
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	The rice histone methylation regulates hub species of the root microbiota. <i>Journal of Genetics and Genomics</i> , 2021 , 48, 836-843	4	1
29	High-throughput cultivation and identification of bacteria from the plant root microbiota. <i>Nature Protocols</i> , 2021 , 16, 988-1012	18.8	22
28	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
27	Variation in rhizosphere microbial communities and its association with the symbiotic efficiency of rhizobia in soybean. <i>ISME Journal</i> , 2020 , 14, 1915-1928	11.9	49
26	From signaling to function: how strigolactones regulate plant development. <i>Science China Life Sciences</i> , 2020 , 63, 1768-1770	8.5	2
25	Host-Associated Quantitative Abundance Profiling Reveals the Microbial Load Variation of Root Microbiome. <i>Plant Communications</i> , 2020 , 1, 100003	9	20
24	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	
23	Contribution of Microbial Inter-kingdom Balance to Plant Health. <i>Molecular Plant</i> , 2019 , 12, 148-149	14.4	6
22	Plant-derived coumarins shape the composition of an synthetic root microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 12558-12565	11.5	141
21	A specialized metabolic network selectively modulates root microbiota. <i>Science</i> , 2019 , 364,	33.3	211
20	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
19	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
18	Generation of herbicide tolerance traits and a new selectable marker in wheat using base editing. <i>Nature Plants</i> , 2019 , 5, 480-485	11.5	116
17	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050

16	Reductionist synthetic community approaches in root microbiome research. <i>Current Opinion in Microbiology</i> , 2019 , 49, 97-102	7.9	39
15	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
14	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
13	Core microbiomes for sustainable agroecosystems. <i>Nature Plants</i> , 2018 , 4, 247-257	11.5	328
12	Root exudates drive the soil-borne legacy of aboveground pathogen infection. <i>Microbiome</i> , 2018 , 6, 156-166	16.6	163
11	Critical Assessment of Metagenome Interpretation-a benchmark of metagenomics software. <i>Nature Methods</i> , 2017 , 14, 1063-1071	21.6	412
10	Taxonomic structure and functional association of foxtail millet root microbiome. <i>GigaScience</i> , 2017 , 6, 1-12	7.6	1155
9	The Plant Microbiota: Systems-Level Insights and Perspectives. <i>Annual Review of Genetics</i> , 2016 , 50, 211-234	234	353
8	Functional overlap of the Arabidopsis leaf and root microbiota. <i>Nature</i> , 2015 , 528, 364-9	50.4	612
7	Rhizobacterial volatiles and photosynthesis-related signals coordinate MYB72 expression in Arabidopsis roots during onset of induced systemic resistance and iron-deficiency responses. <i>Plant Journal</i> , 2015 , 84, 309-22	6.9	110
6	ANGUSTIFOLIA is a central component of tissue morphogenesis mediated by the atypical receptor-like kinase STRUBBELIG. <i>BMC Plant Biology</i> , 2013 , 13, 16	5.3	17
5	Tissue layer specific regulation of leaf length and width in Arabidopsis as revealed by the cell autonomous action of ANGUSTIFOLIA. <i>Plant Journal</i> , 2010 , 61, 191-9	6.9	26
4	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
3	Critical Assessment of Metagenome Interpretation a benchmark of computational metagenomics software		17
2	Plant-derived coumarins shape the composition of an Arabidopsis synthetic root microbiome		3
1	Rbec: a tool for analysis of amplicon sequencing data from synthetic microbial communities		1