

Yang Bai

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

19,684
citations

201385

27
h-index

377514

34
g-index

41
all docs

41
docs citations

41
times ranked

24750
citing authors

#	ARTICLE	IF	CITATIONS
1	The root microbiome: Community assembly and its contributions to plant fitness. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 230-243.	4.1	99
2	Bio-organic soil amendment promotes the suppression of <i>Ralstonia solanacearum</i> by inducing changes in the functionality and composition of rhizosphere bacterial communities. <i>New Phytologist</i> , 2022, 235, 1558-1574.	3.5	57
3	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
4	Biochar stimulates tomato roots to recruit a bacterial assemblage contributing to disease resistance against <i>Fusarium</i> wilt. , 2022, 1, .		9
5	A practical guide to amplicon and metagenomic analysis of microbiome data. <i>Protein and Cell</i> , 2021, 12, 315-330.	4.8	376
6	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
7	High-throughput cultivation and identification of bacteria from the plant root microbiota. <i>Nature Protocols</i> , 2021, 16, 988-1012.	5.5	91
8	Stuck on you: Bacterial-auxin-mediated bacterial colonization of plant roots. <i>Cell Host and Microbe</i> , 2021, 29, 1471-1473.	5.1	0
9	Rbec: a tool for analysis of amplicon sequencing data from synthetic microbial communities. <i>ISME Communications</i> , 2021, 1, .	1.7	6
10	Host-Associated Quantitative Abundance Profiling Reveals the Microbial Load Variation of Root Microbiome. <i>Plant Communications</i> , 2020, 1, 100003.	3.6	38
11	From signaling to function: how strigolactones regulate plant development. <i>Science China Life Sciences</i> , 2020, 63, 1768-1770.	2.3	6
12	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.	5.1	66
13	Variation in rhizosphere microbial communities and its association with the symbiotic efficiency of rhizobia in soybean. <i>ISME Journal</i> , 2020, 14, 1915-1928.	4.4	154
14	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
15	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
16	Reductionist synthetic community approaches in root microbiome research. <i>Current Opinion in Microbiology</i> , 2019, 49, 97-102.	2.3	105
17	Contribution of Microbial Inter-kingdom Balance to Plant Health. <i>Molecular Plant</i> , 2019, 12, 148-149.	3.9	12
18	Plant-derived coumarins shape the composition of an <i>Arabidopsis</i> synthetic root microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12558-12565.	3.3	313

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19	A specialized metabolic network selectively modulates <i>Arabidopsis</i> root microbiota. <i>Science</i> , 2019, 364, .	6.0	470
20	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
21	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
22	Generation of herbicide tolerance traits and a new selectable marker in wheat using base editing. <i>Nature Plants</i> , 2019, 5, 480-485.	4.7	210
23	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
24	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
25	Core microbiomes for sustainable agroecosystems. <i>Nature Plants</i> , 2018, 4, 247-257.	4.7	639
26	Root exudates drive the soil-borne legacy of aboveground pathogen infection. <i>Microbiome</i> , 2018, 6, 156.	4.9	354
27	Critical Assessment of Metagenome Interpretation—a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	9.0	635
28	Taxonomic structure and functional association of foxtail millet root microbiome. <i>GigaScience</i> , 2017, 6, 1-12.	3.3	1,228
29	The Plant Microbiota: Systems-Level Insights and Perspectives. <i>Annual Review of Genetics</i> , 2016, 50, 211-234.	3.2	627
30	Rhizobacterial volatiles and photosynthesis-related signals coordinate MYB72 expression in <i>Arabidopsis</i> roots during onset of induced systemic resistance and iron deficiency responses. <i>Plant Journal</i> , 2015, 84, 309-322.	2.8	171
31	Functional overlap of the <i>Arabidopsis</i> leaf and root microbiota. <i>Nature</i> , 2015, 528, 364-369.	13.7	1,062
32	ANGUSTIFOLIA is a central component of tissue morphogenesis mediated by the atypical receptor-like kinase STRUBBELIG. <i>BMC Plant Biology</i> , 2013, 13, 16.	1.6	30
33	Tissue layer specific regulation of leaf length and width in <i>Arabidopsis</i> as revealed by the cell autonomous action of ANGUSTIFOLIA. <i>Plant Journal</i> , 2010, 61, 191-199.	2.8	31