

Yun-Zeng Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

2,856
citations

686830

13
h-index

676716

22
g-index

22
all docs

22
docs citations

22
times ranked

6284
citing authors

#	ARTICLE	IF	CITATIONS
1	Taxonomic structure and functional association of foxtail millet root microbiome. <i>GigaScience</i> , 2017, 6, 1-12.	3.3	1,228
2	Genome editing of the disease susceptibility gene <i>LOB1</i> in citrus confers resistance to citrus canker. <i>Plant Biotechnology Journal</i> , 2017, 15, 817-823.	4.1	371
3	The structure and function of the global citrus rhizosphere microbiome. <i>Nature Communications</i> , 2018, 9, 4894.	5.8	304
4	The <i>Candidatus</i> <i>Liberibacter</i> "Host Interface: Insights into Pathogenesis Mechanisms and Disease Control. <i>Annual Review of Phytopathology</i> , 2017, 55, 451-482.	3.5	246
5	Huanglongbing impairs the rhizosphere-to-rhizoplane enrichment process of the citrus root-associated microbiome. <i>Microbiome</i> , 2017, 5, 97.	4.9	177
6	Editing Citrus Genome via SaCas9/sgRNA System. <i>Frontiers in Plant Science</i> , 2017, 8, 2135.	1.7	87
7	Tale of the Huanglongbing Disease Pyramid in the Context of the Citrus Microbiome. <i>Phytopathology</i> , 2017, 107, 380-387.	1.1	79
8	SEC-Translocon Dependent Extracytoplasmic Proteins of <i>Candidatus</i> <i>Liberibacter asiaticus</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1989.	1.5	72
9	The phyllosphere microbiome shifts toward combating melanose pathogen. <i>Microbiome</i> , 2022, 10, 56.	4.9	54
10	Characterization of Antimicrobial-Producing Beneficial Bacteria Isolated from Huanglongbing Escape Citrus Trees. <i>Frontiers in Microbiology</i> , 2017, 8, 2415.	1.5	48
11	Positive selection is the main driving force for evolution of citrus canker-causing <i>Xanthomonas</i> . <i>ISME Journal</i> , 2015, 9, 2128-2138.	4.4	35
12	Diffusible signal factor (DSF)-mediated quorum sensing modulates expression of diverse traits in <i>Xanthomonas citri</i> and responses of citrus plants to promote disease. <i>BMC Genomics</i> , 2019, 20, 55.	1.2	35
13	Origin and diversification of <i>Xanthomonas citri</i> subsp. <i>citri</i> pathotypes revealed by inclusive phylogenomic, dating, and biogeographic analyses. <i>BMC Genomics</i> , 2019, 20, 700.	1.2	33
14	The Citrus Microbiome: From Structure and Function to Microbiome Engineering and Beyond. <i>Phytobiomes Journal</i> , 2021, 5, 249-262.	1.4	16
15	Transcriptome analysis of root response to citrus blight based on the newly assembled Swingle citrumelo draft genome. <i>BMC Genomics</i> , 2016, 17, 485.	1.2	15
16	Mechanisms Underlying the Rhizosphere-To-Rhizoplane Enrichment of <i>Cellvibrio</i> Unveiled by Genome-Centric Metagenomics and Metatranscriptomics. <i>Microorganisms</i> , 2020, 8, 583.	1.6	14
17	Temporal Transcription Profiling of Sweet Orange in Response to PthA4-Mediated <i>Xanthomonas citri</i> subsp. <i>citri</i> Infection. <i>Phytopathology</i> , 2016, 106, 442-451.	1.1	12
18	<i>Salmonella Pullorum</i> <i>spiC</i> mutant is a desirable LASV candidate with proper virulence, high immune protection and easy-to-use oral administration. <i>Vaccine</i> , 2021, 39, 1383-1391.	1.7	8

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19	Gut microbiota mediates cognitive impairment in young mice after multiple neonatal exposures to sevoflurane. <i>Aging</i> , 2021, 13, 16733-16748.	1.4	8
20	Implication of immune cell signature of tumor microenvironment in diffuse large Bâ€cell lymphoma. <i>Hematological Oncology</i> , 2021, 39, 616-624.	0.8	7
21	Closely related Salmonella Derby strains triggered distinct gut microbiota alteration. <i>Gut Pathogens</i> , 2022, 14, 6.	1.6	5
22	Transcriptomic Analysis of <i>Streptococcus suis</i> in Response to Ferrous Iron and Cobalt Toxicity. <i>Genes</i> , 2020, 11, 1035.	1.0	2