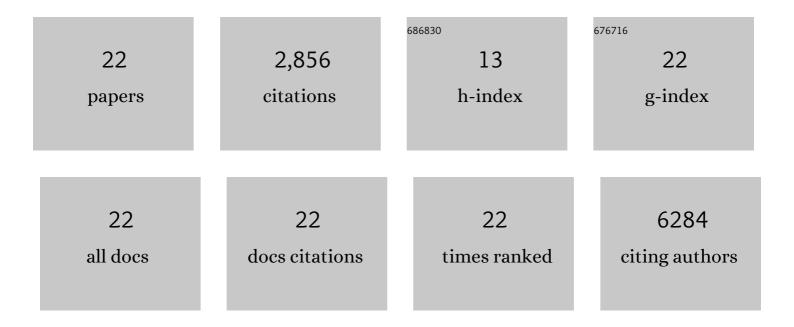
Yun-Zeng Zhang

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8929895/publications.pdf

Version: 2024-02-01



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

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