

# Ming Hu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2985716/publications.pdf>

Version: 2024-02-01

15  
papers

227  
citations

1478505

6  
h-index

1058476

14  
g-index

15  
all docs

15  
docs citations

15  
times ranked

114  
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Dickeya zeae</i> strains isolated from rice, banana and clivia rot plants show great virulence differentials. <i>BMC Microbiology</i> , 2018, 18, 136.	3.3	43
2	A two-component regulatory system VfmIH modulates multiple virulence traits in <i>Dickeya zeae</i> . <i>Molecular Microbiology</i> , 2019, 111, 1493-1509.	2.5	32
3	Screening, Identification and Efficacy Evaluation of Antagonistic Bacteria for Biocontrol of Soft Rot Disease Caused by <i>Dickeya zeae</i> . <i>Microorganisms</i> , 2020, 8, 697.	3.6	29
4	<i>Enterobacter asburiae</i> and <i>Pantoea ananatis</i> Causing Rice Bacterial Blight in China. <i>Plant Disease</i> , 2021, 105, 2078-2088.	1.4	23
5	Five Fungal Pathogens Are Responsible for Bayberry Twig Blight and Fungicides Were Screened for Disease Control. <i>Microorganisms</i> , 2020, 8, 689.	3.6	17
6	Virulence Factor Identification in the Banana Pathogen <i>Dickeya zeae</i> MS2. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	15
7	<i>Dickeya</i> Manipulates Multiple Quorum Sensing Systems to Control Virulence and Collective Behaviors. <i>Frontiers in Plant Science</i> , 2022, 13, 838125.	3.6	10
8	Isolation, Characterization, and Genomic Investigation of a Phytopathogenic Strain of <i>Stenotrophomonas maltophilia</i> . <i>Phytopathology</i> , 2021, 111, 2088-2099.	2.2	8
9	Microbial Diversity Analysis and Genome Sequencing Identify <i>Xanthomonas perforans</i> as the Pathogen of Bacterial Leaf Canker of Water Spinach ( <i>Ipomoea aquatic</i> ). <i>Frontiers in Microbiology</i> , 2021, 12, 752760.	3.5	8
10	Genomic and Functional Dissections of <i>Dickeya zeae</i> Shed Light on the Role of Type III Secretion System and Cell Wall-Degrading Enzymes to Host Range and Virulence. <i>Microbiology Spectrum</i> , 2022, 10, e0159021.	3.0	8
11	Isolation and Genome Analysis of <i>Pectobacterium colocasium</i> sp. nov. and <i>Pectobacterium aroidearum</i> , Two New Pathogens of Taro. <i>Frontiers in Plant Science</i> , 2022, 13, 852750.	3.6	8
12	First Report of Bacterial Soft Rot Disease on Taro Caused by <i>Dickeya fangzhongdai</i> in China. <i>Plant Disease</i> , 2021, 105, 3737.	1.4	7
13	OhrR is a central transcriptional regulator of virulence in <i>Dickeya zeae</i> . <i>Molecular Plant Pathology</i> , 2022, 23, 45-59.	4.2	7
14	Five Plant Natural Products Are Potential Type III Secretion System Inhibitors to Effectively Control Soft-Rot Disease Caused by <i>Dickeya</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 839025.	3.5	7
15	The integration host factor regulates multiple virulence pathways in bacterial pathogen <i>Dickeya zeae</i> MS2. <i>Molecular Plant Pathology</i> , 2022, 23, 1487-1507.	4.2	5