

Jianchi Chen

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Evaluation of Olive as a Host of <i>Xylella fastidiosa</i> and Associated Sharpshooter Vectors. <i>Plant Disease</i> , 2014, 98, 1186-1193.	1.4	66
2	Historical Perspectives, Management, and Current Research of Citrus HLB in Guangdong Province of China, Where the Disease has been Endemic for Over a Hundred Years. <i>Phytopathology</i> , 2018, 108, 1224-1236.	2.2	56
3	Unusual Five Copies and Dual Forms of <i>nrdB</i> in <i>Candidatus Liberibacter asiaticus</i> : Biological Implications and PCR Detection Application. <i>Scientific Reports</i> , 2016, 6, 39020.	3.3	54
4	A Type 3 Prophage of <i>Candidatus Liberibacter asiaticus</i> ™ Carrying a Restriction-Modification System. <i>Phytopathology</i> , 2018, 108, 454-461.	2.2	46
5	Analysis of a Prophage Gene Frequency Revealed Population Variation of <i>Candidatus Liberibacter asiaticus</i> ™ from Two Citrus-Growing Provinces in China. <i>Plant Disease</i> , 2011, 95, 431-435.	1.4	42
6	Enhancing PCR Capacity To Detect <i>Candidatus Liberibacter asiaticus</i> ™ Utilizing Whole Genome Sequence Information. <i>Plant Disease</i> , 2020, 104, 527-532.	1.4	37
7	Prophage Diversity of <i>Candidatus Liberibacter asiaticus</i> ™ Strains in California. <i>Phytopathology</i> , 2019, 109, 551-559.	2.2	34
8	Winter curing of <i>Prunus dulcis</i> cv 'Butte', P. webbii and their interspecific hybrid in response to <i>Xylella fastidiosa</i> infections. <i>Euphytica</i> , 2009, 169, 113-122.	1.2	23
9	Plasmids of <i>Xylella fastidiosa</i> mulberry-infecting strains share extensive sequence identity and gene complement with pVEIS01 from the earthworm symbiont <i>Verminephrobacter eiseniae</i> . <i>Physiological and Molecular Plant Pathology</i> , 2010, 74, 238-245.	2.5	19
10	Preliminary research on soil conditioner mediated citrus Huanglongbing mitigation in the field in Guangdong, China. <i>European Journal of Plant Pathology</i> , 2013, 137, 283-293.	1.7	19
11	Genetic Discovery in <i>Xylella fastidiosa</i> Through Sequence Analysis of Selected Randomly Amplified Polymorphic DNAs. <i>Current Microbiology</i> , 2005, 50, 78-83.	2.2	12
12	Morphological evidence for phages in <i>Xylella fastidiosa</i> . <i>Virology Journal</i> , 2008, 5, 75.	3.4	12
13	High throughput PCR detection of <i>Xylella fastidiosa</i> directly from almond tissues. <i>Journal of Microbiological Methods</i> , 2008, 73, 57-61.	1.6	11
14	Population diversity of <i>Diaphorina citri</i> (Hemiptera: Liviidae) in China based on whole mitochondrial genome sequences. <i>Pest Management Science</i> , 2018, 74, 2569-2577.	3.4	10
15	Genome Sequence Resource of <i>Candidatus Liberibacter asiaticus</i> ™ strain 9PA From Brazil. <i>Plant Disease</i> , 2021, 105, 199-201.	1.4	9
16	A Novel Microviridae Phage (CLasMV1) From <i>Candidatus Liberibacter asiaticus</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 754245.	3.5	9
17	Colony morphology of <i>Xylella fastidiosa</i> almond leaf scorch strains. <i>Canadian Journal of Plant Pathology</i> , 2007, 29, 225-231.	1.4	8
18	Genome analysis of <i>Spiroplasma citri</i> strains from different host plants and its leafhopper vectors. <i>BMC Genomics</i> , 2021, 22, 373.	2.8	8

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19	Scanning electron microscopy and in vitro cultivation of endophytic bacteria from potato tubers afflicted with zebra chip disease. <i>Canadian Journal of Plant Pathology</i> , 2013, 35, 192-199.	1.4	7
20	Genome Sequence Resource of <i>Candidatus Liberibacter asiaticus</i> ™ from Thailand. <i>Plant Disease</i> , 2020, 104, 624-626.	1.4	7
21	Genome Sequence Resources of Two <i>Candidatus Liberibacter asiaticus</i> ™ Strains from Pakistan. <i>Plant Disease</i> , 2020, 104, 2048-2050.	1.4	7
22	Genome Sequence Resource for <i>Spiroplasma citri</i> , Strain CC-2, Associated with Citrus Stubborn Disease in California. <i>Phytopathology</i> , 2020, 110, 254-256.	2.2	6
23	Detection of a Single-Copy Plasmid, pXFSL21, in <i>Xylella fastidiosa</i> Strain Stag's Leap with Two Toxin-Antitoxin Systems Using Next-Generation Sequencing. <i>Phytopathology</i> , 2019, 109, 240-247.	2.2	5
24	Bacteriomic Analyses of Asian Citrus Psyllid and Citrus Samples Infected With <i>Candidatus Liberibacter asiaticus</i> in Southern California and Huanglongbing Management Implications. <i>Frontiers in Microbiology</i> , 2021, 12, 683481.	3.5	5
25	Identification of a Novel 1033 Nucleotide Deletion Polymorphism in the Prophage Region of <i>Candidatus Liberibacter asiaticus</i> ™: Potential Applications for Bacterial Epidemiology. <i>Journal of Phytopathology</i> , 2015, 163, 681-685.	1.0	4
26	Whole genome sequence of five strains of <i>Spiroplasma citri</i> isolated from different host plants and its leafhopper vector. <i>BMC Research Notes</i> , 2020, 13, 320.	1.4	3
27	Mitochondrial Genome Resource of a Grapevine Strain of <i>Trichoderma harzianum</i> , a Potential Biological Control Agent for Fungal Canker Diseases. <i>PhytoFrontiers</i> , 2022, 2, 143-146.	1.6	3
28	Investigation of Citrus HLB Symptom Variations Associated with <i>Candidatus Liberibacter asiaticus</i> Strains Harboring Different Phages in Southern China. <i>Agronomy</i> , 2021, 11, 2262.	3.0	3
29	Complete Genome Sequence of <i>Curtobacterium</i> sp. Strain TXMA1, Isolated from a Grapevine in Texas, USA. <i>Microbiology Resource Announcements</i> , 2022, 11, e0096821.	0.6	0