

# Bo Zhu

## List of Publications by Year in descending order

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39  
papers

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citations

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times ranked

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#	ARTICLE	IF	CITATIONS
1	Engineering Broad-Spectrum Bacterial Blight Resistance by Simultaneously Disrupting Variable TALE-Binding Elements of Multiple Susceptibility Genes in Rice. <i>Molecular Plant</i> , 2019, 12, 1434-1446.	8.3	207
2	Genome Sequence of <i>Stenotrophomonas maltophilia</i> RR-10, Isolated as an Endophyte from Rice Root. <i>Journal of Bacteriology</i> , 2012, 194, 1280-1281.	2.2	59
3	<i>Enterobacter mori</i> sp. nov., associated with bacterial wilt on <i>Morus alba</i> L.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 2769-2774.	1.7	51
4	Genome Sequence of the Rice-Pathogenic Bacterium <i>Acidovorax avenae</i> subsp. <i>avenae</i> RS-1. <i>Journal of Bacteriology</i> , 2011, 193, 5013-5014.	2.2	47
5	Horizontal gene transfer in silkworm, <i>Bombyx mori</i> . <i>BMC Genomics</i> , 2011, 12, 248.	2.8	45
6	<i>Enterobacter sacchari</i> sp. nov., a nitrogen-fixing bacterium associated with sugar cane ( <i>Saccharum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222	1.7	43
7	Multi-omics analysis of niche specificity provides new insights into ecological adaptation in bacteria. <i>ISME Journal</i> , 2016, 10, 2072-2075.	9.8	40
8	Identification and characterization of the <i>Enterobacter</i> complex causing mulberry ( <i>Morus alba</i> ) wilt disease in China. <i>European Journal of Plant Pathology</i> , 2010, 126, 465-478.	1.7	38
9	Complete genome sequence of <i>Kosakonia sacchari</i> type strain SP1T. <i>Standards in Genomic Sciences</i> , 2014, 9, 1311-1318.	1.5	35
10	Regulatory role of <i>tetR</i> gene in a novel gene cluster of <i>Acidovorax avenae</i> subsp. <i>avenae</i> RS-1 under oxidative stress. <i>Frontiers in Microbiology</i> , 2014, 5, 547.	3.5	34
11	Genome Sequence of <i>Enterobacter</i> sp. Strain SP1, an Endophytic Nitrogen-Fixing Bacterium Isolated from Sugarcane. <i>Journal of Bacteriology</i> , 2012, 194, 6963-6964.	2.2	26
12	<i>Enterobacter</i> spp.: A new evidence causing bacterial wilt on mulberry. <i>Science China Life Sciences</i> , 2010, 53, 292-300.	4.9	25
13	Characterization of <i>pilP</i> , a gene required for twitching motility, pathogenicity, and biofilm formation of <i>Acidovorax avenae</i> subsp. <i>avenae</i> RS-1. <i>European Journal of Plant Pathology</i> , 2012, 134, 551-560.	1.7	24
14	Effect of chitosan solution on the bacterial septicemia disease of <i>Bombyx mori</i> (Lepidoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222	1.2	22
15	A-to-I RNA editing in bacteria increases pathogenicity and tolerance to oxidative stress. <i>PLoS Pathogens</i> , 2020, 16, e1008740.	4.7	22
16	<i>Bacillus subtilis</i> Y16 and biogas slurry enhanced potassium to sodium ratio and physiology of sunflower ( <i>Helianthus annuus</i> L.) to mitigate salt stress. <i>Environmental Science and Pollution Research</i> , 2021, 28, 38637-38647.	5.3	19
17	Tal1NXtc01 in <i>Xanthomonas translucens</i> pv. <i>cerealis</i> Contributes to Virulence in Bacterial Leaf Streak of Wheat. <i>Frontiers in Microbiology</i> , 2019, 10, 2040.	3.5	15
18	Genome Sequence Resource for <i>Ilyonectria mors-panacis</i> , Causing Rusty Root Rot of <i>Panax notoginseng</i> . <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 1468-1471.	2.6	13

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19	Genome Sequence of the Pathogenic <i>Herbaspirillum seropedicae</i> Strain Os45, Isolated from Rice Roots. <i>Journal of Bacteriology</i> , 2012, 194, 6995-6996.	2.2	11
20	Characterization and Inference of Gene Gain/Loss along <i>Burkholderia</i> Evolutionary History. <i>Evolutionary Bioinformatics</i> , 2011, 7, EBO.S7510.	1.2	10
21	TALE-triggered and iTALE-suppressed Xa1-mediated resistance to bacterial blight is independent of rice transcription factor subunits OsTFIIA131 or OsTFIIA135. <i>Journal of Experimental Botany</i> , 2021, 72, 3249-3262.	4.8	10
22	Interkingdom Gene Transfer May Contribute to the Evolution of Phytopathogenicity in <i>Botrytis Cinerea</i> . <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S8486.	1.2	8
23	<i>Pseudomonas bijieensis</i> sp. nov., isolated from cornfield soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	1.7	8
24	Transcriptome analysis of <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> exposed to H2O2 reveals horizontal gene transfer contributes to its oxidative stress response. <i>PLoS ONE</i> , 2019, 14, e0218844.	2.5	7
25	Genome Resource of a Hypervirulent Strain LN4 of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Causing Bacterial Blight of Rice. <i>Plant Disease</i> , 2020, 104, 2764-2767.	1.4	7
26	Genome Sequence of the <i>Enterobacter mori</i> Type Strain, LMG 25706, a Pathogenic Bacterium of <i>Morus alba</i> L. <i>Journal of Bacteriology</i> , 2011, 193, 3670-3671.	2.2	6
27	Complete Genome Sequence of <i>Massilia oculi</i> sp. nov. CCUG 43427T (=DSM 26321T), the Type Strain of <i>M. oculi</i> , and Comparison with Genome Sequences of Other <i>Massilia</i> Strains. <i>Current Microbiology</i> , 2019, 76, 1082-1086.	2.2	6
28	Genome Sequence of <i>Micromonospora terminaliae</i> TMS7 <sup>T</sup> , a New Endophytic Actinobacterium Isolated from the Medicinal Plant <i>Terminalia mucronata</i> . <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 721-723.	2.6	5
29	Genome Resource for <i>Pseudomonas</i> sp. Strain L22-9: A Potential Novel Species with Antifungal Activity. <i>Phytopathology</i> , 2021, 111, 425-428.	2.2	5
30	Genome Sequence and Adaptation Analysis of the Human and Rice Pathogenic Strain <i>Burkholderia glumae</i> AU6208. <i>Pathogens</i> , 2021, 10, 87.	2.8	5
31	Genome Resource of <i>Ancylobacter pratisalsi</i> E130 <sup>T</sup> : A Novel Plant-Growth-Promoting Bacterium Isolated from the Rhizosphere. <i>Phytopathology</i> , 2022, 112, 729-731.	2.2	5
32	A-to-I mRNA Editing in a Ferric Siderophore Receptor Improves Competition for Iron in <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0157121.	3.0	5
33	A <i>Xanthomonas</i> transcription activator-like effector is trapped in nonhost plants for immunity. <i>Plant Communications</i> , 2022, 3, 100249.	7.7	4
34	Microsynteny conservation analysis revealed the evolutionary history of bacterial biphenyl degradation pathway. <i>Environmental Microbiology Reports</i> , 2022, 14, 494-505.	2.4	4
35	A key antisense sRNA modulates the oxidative stress response and virulence in <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> . <i>PLoS Pathogens</i> , 2021, 17, e1009762.	4.7	3
36	Complete Genomic Data of <i>Burkholderia glumae</i> Strain GX Associated with Bacterial Panicle Blight of Rice in China. <i>Plant Disease</i> , 2020, 104, 1578-1580.	1.4	2

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37	Identification and Characterization of Rice Circular RNAs Responding to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Invasion. <i>Phytopathology</i> , 2022, 112, 492-500.	2.2	2
38	Distributed Community Detection on Overlapping Stochastic Block Model. , 2020, , .		0
39	Genome Resource of <i>Pseudomonas chlororaphis</i> L5734: A Bacterium Antagonistic to the Mulberry Gray Mold Pathogen <i>Botrytis cinerea</i> . <i>Plant Disease</i> , 2022, 106, 1049-1051.	1.4	0