

# 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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43  
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1083  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | 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         |
| 2  | 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         |
| 3  | 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         |
| 4  | 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         |
| 5  | Micro-synteny conservation analysis revealed the evolutionary history of bacterial biphenyl degradation pathway. <i>Environmental Microbiology Reports</i> , 2022, 14, 494-505.   | 2.4 | 4         |
| 6  | 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         |
| 7  | 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         |
| 8  | TALE-triggered and iTALE-suppressed Xa1-mediated resistance to bacterial blight is independent of rice transcription factor subunits OsTFIIA <sup>3</sup> 1 or OsTFIIA <sup>3</sup> 5. <i>Journal of Experimental Botany</i> , 2021, 72, 3249-3262. | 4.8 | 10        |
| 9  | <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        |
| 10 | 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         |
| 11 | 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         |
| 12 | 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         |
| 13 | A-to-I RNA editing in bacteria increases pathogenicity and tolerance to oxidative stress. <i>PLoS Pathogens</i> , 2020, 16, e1008740.   | 4.7 | 22        |
| 14 | 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         |
| 15 | 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         |
| 16 | Distributed Community Detection on Overlapping Stochastic Block Model. , 2020, , .  |     | 0         |
| 17 | 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        |
| 18 | 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       |

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|----|--|-----|-----------|
| 19 | Transcriptome analysis of <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> exposed to H <sub>2</sub> O <sub>2</sub> reveals horizontal gene transfer contributes to its oxidative stress response. <i>PLoS ONE</i> , 2019, 14, e0218844.               | 2.5 | 7         |
| 20 | 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        |
| 21 | 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         |
| 22 | <i>Pseudomonas bijieensis</i> sp. nov., isolated from cornfield soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .   | 1.7 | 8         |
| 23 | 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        |
| 24 | Complete genome sequence of <i>Kosakonia sacchari</i> type strain SP1T. <i>Standards in Genomic Sciences</i> , 2014, 9, 1311-1318.   | 1.5 | 35        |
| 25 | 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        |
| 26 | <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 5   | 1.7 | 48        |
| 27 | 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        |
| 28 | 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        |
| 29 | 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        |
| 30 | 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         |
| 31 | 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        |
| 32 | <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        |
| 33 | Horizontal gene transfer in silkworm, <i>Bombyx mori</i> . <i>BMC Genomics</i> , 2011, 12, 248.  | 2.8 | 45        |
| 34 | Characterization and Inference of Gene Gain/Loss along <i>Burkholderia</i> Evolutionary History. <i>Evolutionary Bioinformatics</i> , 2011, 7, EBO.S7510.  | 1.2 | 10        |
| 35 | 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        |
| 36 | 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         |

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| 37 | Effect of chitosan solution on the bacterial septicemia disease of Bombyx mori (Lepidoptera: Tj ETQq1 1 0.784314,rgBT /Overlock 10  | 1.2 | 22        |
| 38 | Enterobacter spp.: A new evidence causing bacterial wilt on mulberry. Science China Life Sciences, 2010, 53, 292-300.   | 4.9 | 25        |
| 39 | Identification and characterization of the Enterobacter complex causing mulberry (Morus alba) wilt disease in China. European Journal of Plant Pathology, 2010, 126, 465-478. | 1.7 | 38        |