

Wenxiong Lin

List of Publications by Year in descending order

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130
papers

3,706
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docs citations

144
times ranked

3037
citing authors

#	ARTICLE	IF	CITATIONS
1	Bio-fertilizer Amendment Alleviates the Replanting Disease under Consecutive Monoculture Regimes by Reshaping Leaf and Root Microbiome. <i>Microbial Ecology</i> , 2022, 84, 452-464.	2.8	9
2	A sugarcane smut fungus effector simulates the host endogenous elicitor peptide to suppress plant immunity. <i>New Phytologist</i> , 2022, 233, 919-933.	7.3	21
3	The combination of biochar and PGPBs stimulates the differentiation in rhizosphere soil microbiome and metabolites to suppress soil-borne pathogens under consecutive monoculture regimes. <i>GCB Bioenergy</i> , 2022, 14, 84-103.	5.6	15
4	Sugarcane cultivar-dependent changes in assemblage of soil rhizosphere fungal communities in subtropical ecosystem. <i>Environmental Science and Pollution Research</i> , 2022, 29, 20795-20807.	5.3	10
5	Bio-fertilizer Affects Structural Dynamics, Function, and Network Patterns of the Sugarcane Rhizospheric Microbiota. <i>Microbial Ecology</i> , 2022, 84, 1195-1211.	2.8	14
6	Evaluation of maize/peanut intercropping effects on microbial assembly, root exudates and peanut nitrogen uptake. <i>Plant Physiology and Biochemistry</i> , 2022, 171, 75-83.	5.8	20
7	Deciphering the Molecular Mechanisms of Chilling Tolerance in Lsi1-Overexpressing Rice. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4667.	4.1	4
8	Consecutive monoculture regimes differently affected the diversity of the rhizosphere soil viral community and accumulated soil-borne plant viruses. <i>Agriculture, Ecosystems and Environment</i> , 2022, 337, 108076.	5.3	5
9	First Report of <i>Mucor</i> spp. Causing Root Rot of <i>Radix pseudostellariae</i> in Guizhou Province of China. <i>Plant Disease</i> , 2021, 105, 1200.	1.4	1
10	The soybean plasma membrane-localized cation/H ⁺ exchanger GmCHX20a plays a negative role under salt stress. <i>Physiologia Plantarum</i> , 2021, 171, 714-727.	5.2	15
11	Antagonistic Activity of <i>Trichoderma</i> spp. Against <i>Fusarium oxysporum</i> in Rhizosphere of <i>Radix pseudostellariae</i> Triggers the Expression of Host Defense Genes and Improves Its Growth Under Long-Term Monoculture System. <i>Frontiers in Microbiology</i> , 2021, 12, 579920.	3.5	23
12	Soil Metagenomics Reveals Effects of Continuous Sugarcane Cropping on the Structure and Functional Pathway of Rhizospheric Microbial Community. <i>Frontiers in Microbiology</i> , 2021, 12, 627569.	3.5	80
13	Replanting disease alters the faunal community composition and diversity in the rhizosphere soil of <i>Radix pseudostellariae</i> . <i>Agriculture, Ecosystems and Environment</i> , 2021, 310, 107304.	5.3	10
14	Sugarcane monoculture drives microbial community composition, activity and abundance of agricultural-related microorganisms. <i>Environmental Science and Pollution Research</i> , 2021, 28, 48080-48096.	5.3	28
15	Revealing Microbiome Structure and Assembly Process in Three Rhizocompartments of <i>Achyranthes bidentata</i> Under Continuous Monoculture Regimes. <i>Frontiers in Microbiology</i> , 2021, 12, 677654.	3.5	4
16	Proteomic analysis reveals a role of ADP-glucose pyrophosphorylase in the asynchronous filling of rice superior and inferior spikelets. <i>Protein Expression and Purification</i> , 2021, 183, 105875.	1.3	8
17	Silicon Modulates Molecular and Physiological Activities in Lsi1 Transgenic and Wild Lemont Rice Seedlings under Arsenic Stress. <i>Agronomy</i> , 2021, 11, 1532.	3.0	4
18	<sc>SIPHL1</sc>, a <sc>MYB</sc> transcription factor identified from tomato, positively regulates the phosphate starvation response. <i>Physiologia Plantarum</i> , 2021, 173, 1063-1077.	5.2	13

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19	Rhizospheric pathogen proliferation and ROS production is associated with premature senescence of the osvha-a1 rice mutant. <i>Journal of Experimental Botany</i> , 2021, 72, 7247-7263.	4.8	2
20	The appearance of volatile aromas in Tieguanyin tea with different elevations. <i>Journal of Food Science</i> , 2021, 86, 4405-4416.	3.1	6
21	Continuous Sugarcane Planting Negatively Impacts Soil Microbial Community Structure, Soil Fertility, and Sugarcane Agronomic Parameters. <i>Microorganisms</i> , 2021, 9, 2008.	3.6	25
22	Genome-wide identification and molecular evolution analysis of the heat shock transcription factor (HSF) gene family in four diploid and two allopolyploid <i>Gossypium</i> species. <i>Genomics</i> , 2021, 113, 3112-3127.	2.9	13
23	Diversity of microbial communities and soil nutrients in sugarcane rhizosphere soil under water soluble fertilizer. <i>PLoS ONE</i> , 2021, 16, e0245626.	2.5	27
24	Comparison of Silicon-Evoked Responses on Arsenic Stress between Different Dular Rice Genotypes. <i>Plants</i> , 2021, 10, 2210.	3.5	4
25	Sugarcaneâ€Peanut Intercropping System Enhances Bacteria Abundance, Diversity, and Sugarcane Parameters in Rhizospheric and Bulk Soils. <i>Frontiers in Microbiology</i> , 2021, 12, 815129.	3.5	20
26	Modification of Rhizosphere Bacterial Community Structure and Functional Potentials to Control <i>Pseudostellaria heterophylla</i> Replant Disease. <i>Plant Disease</i> , 2020, 104, 25-34.	1.4	20
27	Biochar mediates microbial communities and their metabolic characteristics under continuous monoculture. <i>Chemosphere</i> , 2020, 246, 125835.	8.2	24
28	MYB57 transcriptionally regulates MAPK11 to interact with PAL2;3 and modulate rice allelopathy. <i>Journal of Experimental Botany</i> , 2020, 71, 2127-2141.	4.8	14
29	The LysR-Type Transcriptional Regulator YeeY Plays Important Roles in the Regulatory of Furazolidone Resistance in <i>Aeromonas hydrophila</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 577376.	3.5	7
30	Molecular Evolution and Expansion of the KUP Family in the Allopolyploid Cotton Species <i>Gossypium hirsutum</i> and <i>Gossypium barbadense</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 545042.	3.6	3
31	Metagenomic Analysis Exploring Taxonomic and Functional Diversity of Soil Microbial Communities in Sugarcane Fields Applied with Organic Fertilizer. <i>BioMed Research International</i> , 2020, 2020, 1-11.	1.9	13
32	Plant-mediated rhizospheric interactions in intraspecific intercropping alleviate the replanting disease of <i>Radix pseudostellariae</i> . <i>Plant and Soil</i> , 2020, 454, 411-430.	3.7	24
33	Serine hydroxymethyltransferase localised in the endoplasmic reticulum plays a role in scavenging H ₂ O ₂ to enhance rice chilling tolerance. <i>BMC Plant Biology</i> , 2020, 20, 236.	3.6	15
34	OsPAL2-1 Mediates Allelopathic Interactions Between Rice and Specific Microorganisms in the Rhizosphere Ecosystem. <i>Frontiers in Microbiology</i> , 2020, 11, 1411.	3.5	6
35	Metabolite profiling of rhizosphere soil of different allelopathic potential rice accessions. <i>BMC Plant Biology</i> , 2020, 20, 265.	3.6	13
36	Underlying Mechanism of Wild <i>Radix pseudostellariae</i> in Tolerance to Disease Under the Natural Forest Cover. <i>Frontiers in Microbiology</i> , 2020, 11, 1142.	3.5	12

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37	Soil Sickness in Aged Tea Plantation Is Associated With a Shift in Microbial Communities as a Result of Plant Polyphenol Accumulation in the Tea Gardens. <i>Frontiers in Plant Science</i> , 2020, 11, 601.	3.6	54
38	Linking Short-Chain N-Acyl Homoserine Lactone-Mediated Quorum Sensing and Replant Disease: A Case Study of <i>Rehmannia glutinosa</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 787.	3.6	12
39	Pervasive duplication, biased molecular evolution and comprehensive functional analysis of the PP2C family in <i>Glycine max</i> . <i>BMC Genomics</i> , 2020, 21, 465.	2.8	9
40	Ectopic Expression of Gs5PTase8, a Soybean Inositol Polyphosphate 5-Phosphatase, Enhances Salt Tolerance in Plants. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1023.	4.1	9
41	Lsi1 plays an active role in enhancing the chilling tolerance of rice roots. <i>Plant Growth Regulation</i> , 2020, 90, 529-543.	3.4	7
42	nifH Gene Sequencing Reveals the Effects of Successive Monoculture on the Soil Diazotrophic Microbial Community in <i>Casuarina equisetifolia</i> Plantations. <i>Frontiers in Plant Science</i> , 2020, 11, 578812.	3.6	8
43	Four LysR-type transcriptional regulator family proteins (LTTRs) involved in antibiotic resistance in <i>Aeromonas hydrophila</i> . <i>World Journal of Microbiology and Biotechnology</i> , 2019, 35, 127.	3.6	12
44	Long-Term Monoculture Negatively Regulates Fungal Community Composition and Abundance of Tea Orchards. <i>Agronomy</i> , 2019, 9, 466.	3.0	43
45	Molecular evolution and lineage-specific expansion of the PP2C family in <i>Zea mays</i> . <i>Planta</i> , 2019, 250, 1521-1538.	3.2	51
46	Properties of bacterial community in the rhizosphere soils of <i>Achyranthes bidentata</i> tolerant to consecutive monoculture. <i>Plant Growth Regulation</i> , 2019, 89, 167-178.	3.4	17
47	Exploring the Potential of Overexpressed OsCIPK2 Rice as a Nitrogen Utilization Efficient Crop and Analysis of Its Associated Rhizo-Compartmental Microbial Communities. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3636.	4.1	15
48	The Function of Inositol Phosphatases in Plant Tolerance to Abiotic Stress. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3999.	4.1	64
49	Nitrogen Fertilizer Amendment Alter the Bacterial Community Structure in the Rhizosphere of Rice (<i>Oryza sativa</i> L.) and Improve Crop Yield. <i>Frontiers in Microbiology</i> , 2019, 10, 2623.	3.5	16
50	Purification and characterization of <i>Inonotus hispidus</i> exopolysaccharide and its protective effect on acute alcoholic liver injury in mice. <i>International Journal of Biological Macromolecules</i> , 2019, 129, 41-49.	7.5	49
51	The effects of chemical and organic fertilizer usage on rhizosphere soil in tea orchards. <i>PLoS ONE</i> , 2019, 14, e0217018.	2.5	188
52	Restoration of Long-Term Monoculture Degraded Tea Orchard by Green and Goat Manures Applications System. <i>Sustainability</i> , 2019, 11, 1011.	3.2	16
53	Comparative Extracellular Proteomics of <i>Aeromonas hydrophila</i> Reveals Iron-Regulated Secreted Proteins as Potential Vaccine Candidates. <i>Frontiers in Immunology</i> , 2019, 10, 256.	4.8	54
54	Physiological and Transcriptome Analyses of Early Leaf Senescence for <i>ospls1</i> Mutant Rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT./Overlock 10 Tf 50	4.1	17

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55	Gibberellins play dual roles in response to phosphate starvation of tomato seedlings, negatively in shoots but positively in roots. <i>Journal of Plant Physiology</i> , 2019, 234-235, 145-153.	3.5	22
56	Short-Term Effects of Different Organic Amendments on Soil Fungal Composition. <i>Sustainability</i> , 2019, 11, 198.	3.2	36
57	H2O2 as a Feedback Signal on Dual-Located WHIRLY1 Associates with Leaf Senescence in Arabidopsis. <i>Cells</i> , 2019, 8, 1585.	4.1	22
58	Extraction, characterization and antioxidant activity analysis of the polysaccharide from the solid-state fermentation substrate of <i>Inonotus hispidus</i> . <i>International Journal of Biological Macromolecules</i> , 2019, 123, 468-476.	7.5	25
59	SWATH based quantitative proteomics analysis reveals Hfq2 play an important role on pleiotropic physiological functions in <i>Aeromonas hydrophila</i> . <i>Journal of Proteomics</i> , 2019, 195, 1-10.	2.4	14
60	Rhizosphere responses to environmental conditions in <i>Radix pseudostellariae</i> under continuous monoculture regimes. <i>Agriculture, Ecosystems and Environment</i> , 2019, 270-271, 19-31.	5.3	47
61	Characterization of the physicochemical properties and extraction optimization of natural melanin from <i>Inonotus hispidus</i> mushroom. <i>Food Chemistry</i> , 2019, 277, 533-542.	8.2	56
62	Lsi1 modulates the antioxidant capacity of rice and protects against ultraviolet-B radiation. <i>Plant Science</i> , 2019, 278, 96-106.	3.6	14
63	Proteomic analysis of positive influence of alternate wetting and moderate soil drying on the process of rice grain filling. <i>Plant Growth Regulation</i> , 2018, 84, 533-548.	3.4	14
64	Differential proteomic analysis of rice seedlings reveals the advantage of dry-raising nursery practices. <i>Plant Growth Regulation</i> , 2018, 84, 359-371.	3.4	3
65	Proteomic Analysis of Alterations in <i>Aeromonas hydrophila</i> Outer Membrane Proteins in Response to Oxytetracycline Stress. <i>Microbial Drug Resistance</i> , 2018, 24, 1067-1074.	2.0	9
66	Reprint of: Quantitative proteomic analysis reveals that chemotaxis is involved in chlortetracycline resistance of <i>Aeromonas hydrophila</i> . <i>Journal of Proteomics</i> , 2018, 180, 138-146.	2.4	12
67	DELLA proteins negatively regulate dark-induced senescence and chlorophyll degradation in Arabidopsis through interaction with the transcription factor WRKY6. <i>Plant Cell Reports</i> , 2018, 37, 981-992.	5.6	66
68	Systematically integrated metabonomic-proteomic studies of <i>Escherichia coli</i> under ciprofloxacin stress. <i>Journal of Proteomics</i> , 2018, 179, 61-70.	2.4	34
69	Alleviatory effect of spent <i>Pleurotus eryngii</i> substrate on replant problem of <i>Rehmannia glutinosa</i> Libosch. <i>International Journal of Phytoremediation</i> , 2018, 20, 61-67.	3.1	3
70	Quantitative proteomic analysis reveals that chemotaxis is involved in chlortetracycline resistance of <i>Aeromonas hydrophila</i> . <i>Journal of Proteomics</i> , 2018, 172, 143-151.	2.4	27
71	GANT61 and GDC449 induce apoptosis of prostate cancer stem cells through a GLI-dependent mechanism. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 3641-3652.	2.6	32
72	Quantitative Proteomics Reveals Antibiotics Resistance Function of Outer Membrane Proteins in <i>Aeromonas hydrophila</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 390.	3.9	21

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73	Gene mutation associated with <i>esl</i> mediates shifts on fungal community composition in rhizosphere soil of rice at grain-filling stage. <i>Scientific Reports</i> , 2018, 8, 17521.	3.3	2
74	Protein Phosphatase (PP2C9) Induces Protein Expression Differentially to Mediate Nitrogen Utilization Efficiency in Rice under Nitrogen-Deficient Condition. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2827.	4.1	18
75	In-Silico Prediction and Modeling of the Quorum Sensing LuxS Protein and Inhibition of AI-2 Biosynthesis in <i>Aeromonas hydrophila</i> . <i>Molecules</i> , 2018, 23, 2627.	3.8	18
76	A positive response of rice rhizosphere to alternate moderate wetting and drying irrigation at grain filling stage. <i>Agricultural Water Management</i> , 2018, 207, 26-36.	5.6	48
77	<i>Lsi1</i> -regulated Cd uptake and phytohormones accumulation in rice seedlings in presence of Si. <i>Plant Growth Regulation</i> , 2018, 86, 149-157.	3.4	7
78	Asymmetric Evolution and Expansion of the NAC Transcription Factor in Polyploidized Cotton. <i>Frontiers in Plant Science</i> , 2018, 9, 47.	3.6	24
79	Rhizosphere Fungal Community Dynamics Associated with <i>Rehmannia glutinosa</i> Replant Disease in a Consecutive Monoculture Regime. <i>Phytopathology</i> , 2018, 108, 1493-1500.	2.2	29
80	Belowground Interactions Impact the Soil Bacterial Community, Soil Fertility, and Crop Yield in Maize/Peanut Intercropping Systems. <i>International Journal of Molecular Sciences</i> , 2018, 19, 622.	4.1	68
81	Barcoded Pyrosequencing Reveals a Shift in the Bacterial Community in the Rhizosphere and Rhizoplane of <i>Rehmannia glutinosa</i> under Consecutive Monoculture. <i>International Journal of Molecular Sciences</i> , 2018, 19, 850.	4.1	47
82	Comparative Metagenomic Analysis of Rhizosphere Microbial Community Composition and Functional Potentials under <i>Rehmannia glutinosa</i> Consecutive Monoculture. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2394.	4.1	37
83	Effect of Sugarcane Straw and Goat Manure on Soil Nutrient Transformation and Bacterial Communities. <i>Sustainability</i> , 2018, 10, 2361.	3.2	35
84	The protective efficacy of four iron-related recombinant proteins and their single-walled carbon nanotube encapsulated counterparts against <i>Aeromonas hydrophila</i> infection in zebrafish. <i>Fish and Shellfish Immunology</i> , 2018, 82, 50-59.	3.6	27
85	GA-DELLA pathway is involved in regulation of nitrogen deficiency-induced anthocyanin accumulation. <i>Plant Cell Reports</i> , 2017, 36, 557-569.	5.6	67
86	Global protein expression profile response of planktonic <i>Aeromonas hydrophila</i> exposed to chlortetracycline. <i>World Journal of Microbiology and Biotechnology</i> , 2017, 33, 68.	3.6	36
87	The important functionality of 14-3-3 isoforms in rice roots revealed by affinity chromatography. <i>Journal of Proteomics</i> , 2017, 158, 20-30.	2.4	12
88	Proteomic Analysis of the Effect of DHA-Phospholipids from Large Yellow Croaker Roe on Hyperlipidemic Mice. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 5107-5113.	5.2	16
89	The role of organic acids on microbial deterioration in the <i>Radix pseudostellariae</i> rhizosphere under continuous monoculture regimes. <i>Scientific Reports</i> , 2017, 7, 3497.	3.3	29
90	Overexpression of <i>Lsi1</i> in cold-sensitive rice mediates transcriptional regulatory networks and enhances resistance to chilling stress. <i>Plant Science</i> , 2017, 262, 115-126.	3.6	41

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91	Soil microbial community structure and catabolic activity are significantly degenerated in successive rotations of Chinese fir plantations. <i>Scientific Reports</i> , 2017, 7, 6691.	3.3	28
92	Characterizing rhizosphere microbial communities in long-term monoculture tea orchards by fatty acid profiles and substrate utilization. <i>European Journal of Soil Biology</i> , 2017, 81, 48-54.	3.2	30
93	Quantitative proteomic analysis of iron-regulated outer membrane proteins in <i>Aeromonas hydrophila</i> as potential vaccine candidates. <i>Fish and Shellfish Immunology</i> , 2017, 68, 1-9.	3.6	24
94	Cadmium-stress mitigation through gene expression of rice and silicon addition. <i>Plant Growth Regulation</i> , 2017, 81, 91-101.	3.4	32
95	Quantitative proteomic analysis of <i>Edwardsiella tarda</i> in response to oxytetracycline stress in biofilm. <i>Journal of Proteomics</i> , 2017, 150, 141-148.	2.4	37
96	Differential proteomic analysis of replanted <i>Rehmannia glutinosa</i> roots by iTRAQ reveals molecular mechanisms for formation of replant disease. <i>BMC Plant Biology</i> , 2017, 17, 116.	3.6	28
97	Insights into the Mechanism of Proliferation on the Special Microbes Mediated by Phenolic Acids in the <i>Radix pseudostellariae</i> Rhizosphere under Continuous Monoculture Regimes. <i>Frontiers in Plant Science</i> , 2017, 8, 659.	3.6	29
98	Spatial Distribution Patterns of Root-Associated Bacterial Communities Mediated by Root Exudates in Different Aged Ratooning Tea Monoculture Systems. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1727.	4.1	64
99	Assessment of the Diversity of <i>Pseudomonas</i> spp. and <i>Fusarium</i> spp. in <i>Radix pseudostellariae</i> Rhizosphere under Monoculture by Combining DGGE and Quantitative PCR. <i>Frontiers in Microbiology</i> , 2017, 8, 1748.	3.5	33
100	Transcriptome analysis of <i>Pseudostellaria heterophylla</i> in response to the infection of pathogenic <i>Fusarium oxysporum</i> . <i>BMC Plant Biology</i> , 2017, 17, 155.	3.6	12
101	Mixed Phenolic Acids Mediated Proliferation of Pathogens <i>Talaromyces helicus</i> and <i>Kosakonia sacchari</i> in Continuously Monocultured <i>Radix pseudostellariae</i> Rhizosphere Soil. <i>Frontiers in Microbiology</i> , 2016, 7, 335.	3.5	66
102	Insights into the Regulation of Rhizosphere Bacterial Communities by Application of Bio-organic Fertilizer in <i>Pseudostellaria heterophylla</i> Monoculture Regime. <i>Frontiers in Microbiology</i> , 2016, 7, 1788.	3.5	31
103	Effect of silicon on grain yield of rice under cadmium-stress. <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	2.1	18
104	Proteomic Analysis Reveals That Metabolic Flows Affect the Susceptibility of <i>Aeromonas hydrophila</i> to Antibiotics. <i>Scientific Reports</i> , 2016, 6, 39413.	3.3	44
105	Insight into structure dynamics of soil microbiota mediated by the richness of replanted <i>Pseudostellaria heterophylla</i> . <i>Scientific Reports</i> , 2016, 6, 26175.	3.3	47
106	Quantitative proteomic analysis of cell envelope preparations under iron starvation stress in <i>Aeromonas hydrophila</i> . <i>BMC Microbiology</i> , 2016, 16, 161.	3.3	13
107	Methyl-CpG binding domain protein acts to regulate the repair of cyclobutane pyrimidine dimers on rice DNA. <i>Scientific Reports</i> , 2016, 6, 34569.	3.3	8
108	Enhancement of trichothecene mycotoxins of <i>Fusarium oxysporum</i> by ferulic acid aggravates oxidative damage in <i>Rehmannia glutinosa</i> Libosch. <i>Scientific Reports</i> , 2016, 6, 33962.	3.3	21

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109	Effects of consecutive monoculture of <i>Pseudostellaria heterophylla</i> on soil fungal community as determined by pyrosequencing. <i>Scientific Reports</i> , 2016, 6, 26601.	3.3	62
110	Promising Role of Moderate Soil Drying and Subsequent Recovery Through Moderate Wetting at Grain-Filling Stage for Rice Yield Enhancement. <i>Journal of Plant Growth Regulation</i> , 2016, 35, 838-850.	5.1	16
111	Microbial community structure and its temporal changes in <i>Rehmannia glutinosa</i> rhizospheric soils monocultured for different years. <i>European Journal of Soil Biology</i> , 2016, 72, 1-5.	3.2	25
112	Role of allene oxide cyclase in the regulation of rice phenolic acids synthesis and allelopathic inhibition on barnyardgrass. <i>Plant Growth Regulation</i> , 2016, 79, 265-273.	3.4	5
113	Quantitative proteomics study on Lsi1 in regulation of rice (<i>Oryza sativa</i> L.) cold resistance. <i>Plant Growth Regulation</i> , 2016, 78, 307-323.	3.4	31
114	Interaction of <i>Pseudostellaria heterophylla</i> with Quorum Sensing and Quorum Quenching Bacteria Mediated by Root Exudates in a Consecutive Monoculture System. <i>Journal of Microbiology and Biotechnology</i> , 2016, 26, 2159-2170.	2.1	18
115	Plant-microbe rhizosphere interactions mediated by <i>Rehmannia glutinosa</i> root exudates under consecutive monoculture. <i>Scientific Reports</i> , 2015, 5, 15871.	3.3	115
116	Soil Microbial Community Structure and Metabolic Activity of <i>Pinus elliotii</i> Plantations across Different Stand Ages in a Subtropical Area. <i>PLoS ONE</i> , 2015, 10, e0135354.	2.5	41
117	Interaction of <i>Pseudostellaria heterophylla</i> with <i>Fusarium oxysporum</i> f.sp. <i>heterophylla</i> mediated by its root exudates in a consecutive monoculture system. <i>Scientific Reports</i> , 2015, 5, 8197.	3.3	57
118	Analysis of integrated multiple omics™ datasets reveals the mechanisms of initiation and determination in the formation of tuberous roots in <i>Rehmannia glutinosa</i> . <i>Journal of Experimental Botany</i> , 2015, 66, 5837-5851.	4.8	24
119	Identification and comparative analysis of microRNAs in barnyardgrass (<i>Echinochloa crus-galli</i>) in response to rice allelopathy. <i>Plant, Cell and Environment</i> , 2015, 38, 1368-1381.	5.7	30
120	Determination of Phenolic Acids in Root Exudates of Allelopathic Rice by Solid Phase Extraction-Ion Chromatography with Conductivity Detection. <i>Analytical Letters</i> , 2014, 47, 2156-2164.	1.8	3
121	Proteomic analysis of silicon-mediated resistance to <i>Magnaporthe oryzae</i> in rice (<i>Oryza sativa</i> L.). <i>European Journal of Plant Pathology</i> , 2014, 139, 579-592.	1.7	20
122	A Proteomic Study on Molecular Mechanism of Poor Grain-Filling of Rice (<i>Oryza sativa</i> L.) Inferior Spikelets. <i>PLoS ONE</i> , 2014, 9, e89140.	2.5	51
123	Assessment of shifts in microbial community structure and catabolic diversity in response to <i>Rehmannia glutinosa</i> monoculture. <i>Applied Soil Ecology</i> , 2013, 67, 1-9.	4.3	83
124	Changes in Rice Allelopathy and Rhizosphere Microflora by Inhibiting Rice Phenylalanine Ammonia-lyase Gene Expression. <i>Journal of Chemical Ecology</i> , 2013, 39, 204-212.	1.8	77
125	Metaproteomic analysis of ratoon sugarcane rhizospheric soil. <i>BMC Microbiology</i> , 2013, 13, 135.	3.3	78
126	Barnyard grass stress up regulates the biosynthesis of phenolic compounds in allelopathic rice. <i>Journal of Plant Physiology</i> , 2012, 169, 1747-1753.	3.5	46

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127	Electrochemical sensor of 4-aminobutyric acid based on molecularly imprinted electropolymer. <i>Analytical Methods</i> , 2012, 4, 482.	2.7	17
128	Comparative Metaproteomic Analysis on Consecutively <i>Rehmannia glutinosa</i> -Monocultured Rhizosphere Soil. <i>PLoS ONE</i> , 2011, 6, e20611.	2.5	100
129	Rice allelopathy and its properties of molecular ecology. <i>Frontiers in Biology</i> , 2010, 5, 255-262.	0.7	7
130	Allelopathic Enhancement and Differential Gene Expression in Rice under Low Nitrogen Treatment. <i>Journal of Chemical Ecology</i> , 2008, 34, 688-695.	1.8	41