

Gehong Wei

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/426422/publications.pdf>

Version: 2024-02-01

122
papers

5,712
citations

101543

36
h-index

98798

67
g-index

123
all docs

123
docs citations

123
times ranked

5945
citing authors

#	ARTICLE	IF	CITATIONS
1	Composition and divergence of coronavirus spike proteins and host ACE2 receptors predict potential intermediate hosts of SARS-CoV-2. <i>Journal of Medical Virology</i> , 2020, 92, 595-601.	5.0	546
2	Soil microbiomes with distinct assemblies through vertical soil profiles drive the cycling of multiple nutrients in reforested ecosystems. <i>Microbiome</i> , 2018, 6, 146.	11.1	368
3	Bacterial communities in oil contaminated soils: Biogeography and co-occurrence patterns. <i>Soil Biology and Biochemistry</i> , 2016, 98, 64-73.	8.8	366
4	A <i>Pseudomonas</i> T6SS effector recruits PQS-containing outer membrane vesicles for iron acquisition. <i>Nature Communications</i> , 2017, 8, 14888.	12.8	236
5	Biogeography and ecological diversity patterns of rare and abundant bacteria in oil-contaminated soils. <i>Molecular Ecology</i> , 2017, 26, 5305-5317.	3.9	220
6	Type VI Secretion System Transports Zn ²⁺ to Combat Multiple Stresses and Host Immunity. <i>PLoS Pathogens</i> , 2015, 11, e1005020.	4.7	169
7	Two cultivated legume plants reveal the enrichment process of the microbiome in the rhizocompartments. <i>Molecular Ecology</i> , 2017, 26, 1641-1651.	3.9	134
8	Beneficial bacteria activate nutrients and promote wheat growth under conditions of reduced fertilizer application. <i>BMC Microbiology</i> , 2020, 20, 38.	3.3	122
9	Soil multitrophic network complexity enhances the link between biodiversity and multifunctionality in agricultural systems. <i>Global Change Biology</i> , 2022, 28, 140-153.	9.5	122
10	Dominant role of abundant rather than rare bacterial taxa in maintaining agro-soil microbiomes under environmental disturbances. <i>Chemosphere</i> , 2019, 235, 248-259.	8.2	115
11	Distinct large-scale biogeographic patterns of fungal communities in bulk soil and soybean rhizosphere in China. <i>Science of the Total Environment</i> , 2018, 644, 791-800.	8.0	103
12	Soil microbial diversity during 30 years of grassland restoration on the Loess Plateau, China: Tight linkages with plant diversity. <i>Land Degradation and Development</i> , 2019, 30, 1172-1182.	3.9	94
13	Natural revegetation of a semiarid habitat alters taxonomic and functional diversity of soil microbial communities. <i>Science of the Total Environment</i> , 2018, 635, 598-606.	8.0	89
14	Microbial succession in response to pollutants in batch-enrichment culture. <i>Scientific Reports</i> , 2016, 6, 21791.	3.3	87
15	Isolation, characterization, and selection of heavy metal-resistant and plant growth-promoting endophytic bacteria from root nodules of <i>Robinia pseudoacacia</i> in a Pb/Zn mining area. <i>Microbiological Research</i> , 2018, 217, 51-59.	5.3	85
16	Linking Bacterial-Fungal Relationships to Microbial Diversity and Soil Nutrient Cycling. <i>MSystems</i> , 2021, 6, .	3.8	81
17	A simplified synthetic community rescues <i>Astragalus mongholicus</i> from root rot disease by activating plant-induced systemic resistance. <i>Microbiome</i> , 2021, 9, 217.	11.1	78
18	Distinct succession patterns of abundant and rare bacteria in temporal microcosms with pollutants. <i>Environmental Pollution</i> , 2017, 225, 497-505.	7.5	77

#	ARTICLE	IF	CITATIONS
19	Interactions of plant growth-promoting rhizobacteria and soil factors in two leguminous plants. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 8485-8497.	3.6	76
20	Linking soil fungi to bacterial community assembly in arid ecosystems. , 2022, 1, .		76
21	Microbial communities in riparian soils of a settling pond for mine drainage treatment. <i>Water Research</i> , 2016, 96, 198-207.	11.3	69
22	Temporal dynamics of microbial communities in microcosms in response to pollutants. <i>Molecular Ecology</i> , 2017, 26, 923-936.	3.9	69
23	Comprehensive expression analysis of Arabidopsis GA2-oxidase genes and their functional insights. <i>Plant Science</i> , 2019, 285, 1-13.	3.6	68
24	Effects of 1-aminocyclopropane-1-carboxylate (ACC) deaminase-overproducing <i>Sinorhizobium meliloti</i> on plant growth and copper tolerance of <i>Medicago lupulina</i> . <i>Plant and Soil</i> , 2015, 391, 383-398.	3.7	66
25	Genome Sequence and Mutational Analysis of Plant-Growth-Promoting Bacterium <i>Agrobacterium tumefaciens</i> CCNWGS0286 Isolated from a Zinc-Lead Mine Tailing. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5384-5394.	3.1	64
26	Enhanced phytoremediation of <i>Robinia pseudoacacia</i> in heavy metal-contaminated soils with rhizobia and the associated bacterial community structure and function. <i>Chemosphere</i> , 2018, 197, 729-740.	8.2	64
27	Core microbiota drive functional stability of soil microbiome in reforestation ecosystems. <i>Global Change Biology</i> , 2022, 28, 1038-1047.	9.5	58
28	Copper Tolerance Mechanisms of <i>Mesorhizobium amorphae</i> and Its Role in Aiding Phytostabilization by <i>Robinia pseudoacacia</i> in Copper Contaminated Soil. <i>Environmental Science & Technology</i> , 2015, 49, 2328-2340.	10.0	56
29	Kinetics of soil dehydrogenase in response to exogenous Cd toxicity. <i>Journal of Hazardous Materials</i> , 2017, 329, 299-309.	12.4	55
30	Biogeography and ecological processes affecting root-associated bacterial communities in soybean fields across China. <i>Science of the Total Environment</i> , 2018, 627, 20-27.	8.0	53
31	Linking phylogenetic niche conservatism to soil archaeal biogeography, community assembly and species coexistence. <i>Global Ecology and Biogeography</i> , 2021, 30, 1488-1501.	5.8	48
32	Rare prokaryotic sub-communities dominate the complexity of ecological networks and soil multinutrient cycling during long-term secondary succession in China's Loess Plateau. <i>Science of the Total Environment</i> , 2021, 774, 145737.	8.0	47
33	Resilience and Assemblage of Soil Microbiome in Response to Chemical Contamination Combined with Plant Growth. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	46
34	Stochastic community assembly decreases soil fungal richness in arid ecosystems. <i>Molecular Ecology</i> , 2021, 30, 4338-4348.	3.9	45
35	Genomic insight into the taxonomy of <i>Rhizobium</i> genospecies that nodulate <i>Phaseolus vulgaris</i> . <i>Systematic and Applied Microbiology</i> , 2018, 41, 300-310.	2.8	44
36	T6SS secretes an LPS-binding effector to recruit OMVs for exploitative competition and horizontal gene transfer. <i>ISME Journal</i> , 2022, 16, 500-510.	9.8	44

#	ARTICLE	IF	CITATIONS
37	Diversity of endophytic bacteria associated with nodules of two indigenous legumes at different altitudes of the Qilian Mountains in China. <i>Systematic and Applied Microbiology</i> , 2014, 37, 457-465.	2.8	42
38	Distribution and diversity of rhizobia associated with wild soybean (<i>Glycine soja</i> Sieb. & Zucc.) in Northwest China. <i>Systematic and Applied Microbiology</i> , 2014, 37, 449-456.	2.8	40
39	Above- and belowground biodiversity drives soil multifunctionality along a long-term grassland restoration chronosequence. <i>Science of the Total Environment</i> , 2021, 772, 145010.	8.0	40
40	Distinct biogeographic patterns of rhizobia and non-rhizobial endophytes associated with soybean nodules across China. <i>Science of the Total Environment</i> , 2018, 643, 569-578.	8.0	39
41	Temporal and spatial succession and dynamics of soil fungal communities in restored grassland on the Loess Plateau in China. <i>Land Degradation and Development</i> , 2019, 30, 1273-1287.	3.9	39
42	Insight into the assembly of root-associated microbiome in the medicinal plant <i>Polygonum cuspidatum</i> . <i>Industrial Crops and Products</i> , 2020, 145, 112163.	5.2	38
43	Genomic analyses of metal resistance genes in three plant growth promoting bacteria of legume plants in Northwest mine tailings, China. <i>Journal of Environmental Sciences</i> , 2015, 27, 179-187.	6.1	37
44	Microbial traits determine soil C emission in response to fresh carbon inputs in forests across biomes. <i>Global Change Biology</i> , 2022, 28, 1516-1528.	9.5	37
45	Draft Genome Sequence of Plant Growth-Promoting Rhizobium <i>Mesorhizobium amorphae</i> , Isolated from Zinc-Lead Mine Tailings. <i>Journal of Bacteriology</i> , 2012, 194, 736-737.	2.2	36
46	A Novel Strategy for Detecting Recent Horizontal Gene Transfer and Its Application to Rhizobium Strains. <i>Frontiers in Microbiology</i> , 2018, 9, 973.	3.5	36
47	Assembly and Annotation of a Draft Genome of the Medicinal Plant <i>Polygonum cuspidatum</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1274.	3.6	36
48	Prevalence of mental health problems in frontline healthcare workers after the first outbreak of COVID-19 in China: a cross-sectional study. <i>Health and Quality of Life Outcomes</i> , 2021, 19, 103.	2.4	36
49	Rare Species-Driven Diversityâ€™Ecosystem Multifunctionality Relationships are Promoted by Stochastic Community Assembly. <i>MBio</i> , 2022, 13, e0044922.	4.1	36
50	A new computational strategy for predicting essential genes. <i>BMC Genomics</i> , 2013, 14, 910.	2.8	34
51	Soil potassium is correlated with root secondary metabolites and root-associated core bacteria in licorice of different ages. <i>Plant and Soil</i> , 2020, 456, 61-79.	3.7	33
52	HY5 Contributes to Light-Regulated Root System Architecture Under a Root-Covered Culture System. <i>Frontiers in Plant Science</i> , 2019, 10, 1490.	3.6	32
53	Graded Response of the Multifunctional 2-Cysteine Peroxiredoxin, CgPrx, to Increasing Levels of Hydrogen Peroxide in <i>Corynebacterium glutamicum</i> . <i>Antioxidants and Redox Signaling</i> , 2017, 26, 1-14.	5.4	28
54	Divergent assemblage patterns of abundant and rare microbial sub-communities in response to inorganic carbon stresses in a simultaneous anammox and denitrification (SAD) system. <i>Bioresource Technology</i> , 2018, 257, 249-259.	9.6	28

#	ARTICLE	IF	CITATIONS
55	Responses of soil bacteria and fungal communities to pristine and sulfidized zinc oxide nanoparticles relative to Zn ions. <i>Journal of Hazardous Materials</i> , 2021, 405, 124258.	12.4	28
56	Ohr Protects <i>Corynebacterium glutamicum</i> against Organic Hydroperoxide Induced Oxidative Stress. <i>PLoS ONE</i> , 2015, 10, e0131634.	2.5	28
57	Halophytes increase rhizosphere microbial diversity, network complexity and function in inland saline ecosystem. <i>Science of the Total Environment</i> , 2022, 831, 154944.	8.0	28
58	Transcriptome Response to Heavy Metals in <i>Sinorhizobium meliloti</i> CCNWSX0020 Reveals New Metal Resistance Determinants That Also Promote Bioremediation by <i>Medicago lupulina</i> in Metal-Contaminated Soil. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	26
59	Topography affects the soil conditions and bacterial communities along a restoration gradient on Loess-Plateau. <i>Applied Soil Ecology</i> , 2020, 150, 103471.	4.3	26
60	Global transcriptome analysis of <i>Mesorhizobium alhagi</i> CCNWXJ12-2 under salt stress. <i>BMC Microbiology</i> , 2014, 14, 1.	3.3	25
61	Stochastic processes shape the biogeographic variations in core bacterial communities between aerial and belowground compartments of common bean. <i>Environmental Microbiology</i> , 2021, 23, 949-964.	3.8	25
62	The dual transcriptional regulator <i>RovM</i> regulates the expression of <i>AR3</i> and <i>T6SS4</i> -dependent acid survival systems in response to nutritional status in <i>Yersinia pseudotuberculosis</i> . <i>Environmental Microbiology</i> , 2015, 17, 4631-4645.	3.8	24
63	Genomic insight into the origins and evolution of symbiosis genes in <i>Phaseolus vulgaris</i> microsymbionts. <i>BMC Genomics</i> , 2020, 21, 186.	2.8	24
64	rDNA- and rRNA-derived communities present divergent assemblage patterns and functional traits throughout full-scale landfill leachate treatment process trains. <i>Science of the Total Environment</i> , 2019, 646, 1069-1079.	8.0	23
65	<i>Flavitalea gansuensis</i> sp. nov., isolated from soil from an arid area, and emended descriptions of the genus <i>Flavitalea</i> and <i>Flavitalea populi</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 490-495.	1.7	21
66	Role of exopolysaccharide in salt stress resistance and cell motility of <i>Mesorhizobium alhagi</i> CCNWXJ12-2. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 2967-2978.	3.6	21
67	Epidemiological and Clinical Characteristics of Patients With Coronavirus Disease-2019 in Shiyuan City, China. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 284.	3.9	21
68	Abundant and rare microbial sub-communities in anammox granules present contrasting assemblage patterns and metabolic functions in response to inorganic carbon stresses. <i>Bioresource Technology</i> , 2018, 265, 299-309.	9.6	20
69	Complexity of bacterial communities within the rhizospheres of legumes drives phenanthrene degradation. <i>Geoderma</i> , 2019, 353, 1-10.	5.1	20
70	Rhizosphere bacterial and fungal spatial distribution and network pattern of <i>Astragalus mongholicus</i> in representative planting sites differ the bulk soil. <i>Applied Soil Ecology</i> , 2021, 168, 104114.	4.3	20
71	Regulation of soil micro-foodwebs to root secondary metabolites in cultivated and wild licorice plants. <i>Science of the Total Environment</i> , 2022, 828, 154302.	8.0	20
72	Comparative analysis of rhizobial chromosomes and plasmids to estimate their evolutionary relationships. <i>Plasmid</i> , 2018, 96-97, 13-24.	1.4	19

#	ARTICLE	IF	CITATIONS
73	Soil phosphorus determines the distinct assembly strategies for abundant and rare bacterial communities during successional reforestation. <i>Soil Ecology Letters</i> , 2021, 3, 342-355.	4.5	19
74	Responses of soil bacterial community structure and function to dry-wet cycles more stable in paddy than in dryland agricultural ecosystems. <i>Global Ecology and Biogeography</i> , 2022, 31, 362-377.	5.8	19
75	<i>Sphingobacterium gobiense</i> sp. nov., isolated from soil of the Gobi Desert. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 3931-3935.	1.7	18
76	Zinc Resistance Mechanisms of P1B-type ATPases in <i>Sinorhizobium meliloti</i> CCNWSX0020. <i>Scientific Reports</i> , 2016, 6, 29355.	3.3	18
77	Keystone taxa regulate microbial assemblage patterns and functional traits of different microbial aggregates in simultaneous anammox and denitrification (SAD) systems. <i>Bioresource Technology</i> , 2019, 290, 121778.	9.6	18
78	Effect of Root Diameter on the Selection and Network Interactions of Root-Associated Bacterial Microbiomes in <i>Robinia pseudoacacia</i> L. <i>Microbial Ecology</i> , 2021, 82, 391-402.	2.8	18
79	Plant growth and oil contamination alter the diversity and composition of bacterial communities in agricultural soils across China. <i>Land Degradation and Development</i> , 2018, 29, 1660-1671.	3.9	17
80	A new clade of <i>Mesorhizobium</i> nodulating <i>Alhagi sparsifolia</i> . <i>Systematic and Applied Microbiology</i> , 2009, 32, 8-16.	2.8	16
81	Multifunctionality and microbial communities in agricultural soils regulate the dynamics of a soil-borne pathogen. <i>Plant and Soil</i> , 2021, 461, 309-322.	3.7	16
82	A translationally controlled tumor protein gene <i>Rpf41</i> is required for the nodulation of <i>Robinia pseudoacacia</i> . <i>Plant Molecular Biology</i> , 2016, 90, 389-402.	3.9	15
83	Temporal dynamics of soil bacterial communities and multifunctionality are more sensitive to introduced plants than to microbial additions in a multicontaminated soil. <i>Land Degradation and Development</i> , 2019, 30, 852-865.	3.9	15
84	Aridity Threshold Induces Abrupt Change of Soil Abundant and Rare Bacterial Biogeography in Dryland Ecosystems. <i>MSystems</i> , 2022, 7, e0130921.	3.8	15
85	The global biogeography of soil priming effect intensity. <i>Global Ecology and Biogeography</i> , 2022, 31, 1679-1687.	5.8	15
86	Altered Metabolic Strategies: Elaborate Mechanisms Adopted by <i>Oenococcus oeni</i> in Response to Acid Stress. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 2906-2918.	5.2	14
87	Removal of Zinc from Aqueous Solution by Metal Resistant Symbiotic Bacterium <i>Mesorhizobium amorphae</i> . <i>Separation Science and Technology</i> , 2014, 49, 376-387.	2.5	13
88	Effects of cowpea (<i>Vigna unguiculata</i>) root mucilage on microbial community response and capacity for phenanthrene remediation. <i>Journal of Environmental Sciences</i> , 2015, 33, 45-59.	6.1	12
89	Functional analysis of <i>PrkA</i> - a putative serine protein kinase from <i>Mesorhizobium alhagi</i> CCNWXJ12-2 - in stress resistance. <i>BMC Microbiology</i> , 2016, 16, 227.	3.3	12
90	Functional characterization of a <i>csoR-cueA</i> divergon in <i>Bradyrhizobium liaoningense</i> CCNWSX0360, involved in copper, zinc and cadmium cotolerance. <i>Scientific Reports</i> , 2016, 6, 35155.	3.3	12

#	ARTICLE	IF	CITATIONS
91	Identification of Phycocyanin Gene Family in Legume Plants and their Involvement in Nodulation of <i>Medicago truncatula</i> . <i>Plant and Cell Physiology</i> , 2019, 60, 900-915.	3.1	12
92	Particular microbial clades rather than total microbial diversity best predict the vertical profile variation in soil multifunctionality in desert ecosystems. <i>Land Degradation and Development</i> , 2021, 32, 2157-2168.	3.9	12
93	Regulation of root secondary metabolites by partial root-associated microbiotas under the shaping of licorice ecotypic differentiation in northwest China. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 2093-2109.	8.5	12
94	The Composition of Root-Associated Bacteria and Fungi of <i>Astragalus mongholicus</i> and Their Relationship With the Bioactive Ingredients. <i>Frontiers in Microbiology</i> , 2021, 12, 642730.	3.5	11
95	Evolution and taxonomy of native mesorhizobia nodulating medicinal <i>Glycyrrhiza</i> species in China. <i>Systematic and Applied Microbiology</i> , 2016, 39, 260-265.	2.8	10
96	The Rpf84 gene, encoding a ribosomal large subunit protein, RPL22, regulates symbiotic nodulation in <i>Robinia pseudoacacia</i> . <i>Planta</i> , 2019, 250, 1897-1910.	3.2	10
97	Comprehensive analysis of phenotype, microstructure and global transcriptional profiling to unravel the effect of excess copper on the symbiosis between nitrogen-fixing bacteria and <i>Medicago lupulina</i> . <i>Science of the Total Environment</i> , 2019, 656, 1346-1357.	8.0	10
98	Identification of <i>Robinia pseudoacacia</i> target proteins responsive to <i>Mesorhizobium amphore</i> CCNWGS0123 effector protein NopT. <i>Journal of Experimental Botany</i> , 2020, 71, 7347-7363.	4.8	10
99	Long-term effects of straw mulching coupled with N application on soil organic carbon sequestration and soil aggregation in a winter wheat monoculture system. <i>Agronomy Journal</i> , 2021, 113, 2118-2131.	1.8	10
100	Nickel and cobalt resistance properties of <i>Sinorhizobium meliloti</i> isolated from <i>Medicago lupulina</i> growing in gold mine tailing. <i>PeerJ</i> , 2018, 6, e5202.	2.0	10
101	Population structure of <i>Rhizobium etli</i> -like strains nodulated with <i>Phaseolus vulgaris</i> in two ecoregions of China. <i>Soil Biology and Biochemistry</i> , 2017, 112, 14-23.	8.8	9
102	Type III secretion systems impact <i>Mesorhizobium amorphae</i> CCNWGS0123 compatibility with <i>Robinia pseudoacacia</i> . <i>Tree Physiology</i> , 2019, 39, 1533-1550.	3.1	9
103	New Insight into the Evolution of Symbiotic Genes in Black Locust-Associated Rhizobia. <i>Genome Biology and Evolution</i> , 2019, 11, 1736-1750.	2.5	9
104	Short-term effects of combined organic amendments on soil organic carbon sequestration in a rain-fed winter wheat system. <i>Agronomy Journal</i> , 2021, 113, 2150-2164.	1.8	9
105	Comparison of Clinical Features and Outcomes of Medically Attended COVID-19 and Influenza Patients in a Defined Population in the 2020 Respiratory Virus Season. <i>Frontiers in Public Health</i> , 2021, 9, 587425.	2.7	8
106	Exploring the evolutionary dynamics of <i>Rhizobium</i> plasmids through bipartite network analysis. <i>Environmental Microbiology</i> , 2020, 22, 934-951.	3.8	7
107	Taxonomic Compositions and Co-occurrence Relationships of Protists in Bulk Soil and Rhizosphere of Soybean Fields in Different Regions of China. <i>Frontiers in Microbiology</i> , 2021, 12, 738129.	3.5	7
108	Molecular characterization of a eukaryotic-like phenol hydroxylase from <i>Corynebacterium glutamicum</i> . <i>Journal of General and Applied Microbiology</i> , 2015, 61, 99-107.	0.7	6

#	ARTICLE	IF	CITATIONS
109	Phylogenetic Diversity of Ammopiptanthus Rhizobia and Distribution of Rhizobia Associated with Ammopiptanthus mongolicus in Diverse Regions of Northwest China. Microbial Ecology, 2016, 72, 231-239.	2.8	6
110	TRAPPC13 Is a Novel Target of <i>Mesorhizobium amorphae</i> Type III Secretion System Effector NopP. Molecular Plant-Microbe Interactions, 2021, 34, 511-523.	2.6	6
111	Biosorption and Bioaccumulation of Cu ²⁺ from Aqueous Solution Using Living <i>M. amorphae</i> Isolated from Mine Tailings. Mine Water and the Environment, 2012, 31, 312-319.	2.0	5
112	Multiple Metabolic Phenotypes as Screening Criteria Are Correlated With the Plant Growth-Promoting Ability of Rhizobacterial Isolates. Frontiers in Microbiology, 2021, 12, 747982.	3.5	5
113	Local domestication of soybean leads to strong root selection and diverse filtration of root-associated bacterial communities. Plant and Soil, 2022, 480, 439-455.	3.7	5
114	Compositional response of Phaseolus vulgaris rhizomicrobiome to a changing soil environment is regulated by long-distance plant signaling. Plant and Soil, 2019, 442, 257-269.	3.7	4
115	Inter-phylum negative interactions affect soil bacterial community dynamics and functions during soybean development under long-term nitrogen fertilization. Stress Biology, 2021, 1, 1.	3.1	4
116	Coupling Root Diameter With Rooting Depth to Reveal the Heterogeneous Assembly of Root-Associated Bacterial Communities in Soybean. Frontiers in Microbiology, 2021, 12, 783563.	3.5	4
117	A Nod factor- and type III secretion system-dependent manner for <i>Robinia pseudoacacia</i> to establish symbiosis with <i>Mesorhizobium amorphae</i> CCNWGS0123. Tree Physiology, 2021, 41, 817-835.	3.1	3
118	The Role of Gut Microbiota in Duodenal-jejunal Bypass Surgery-Induced Improvement of Hepatic Steatosis in HFD-Fed Rats. Frontiers in Cellular and Infection Microbiology, 2021, 11, 640448.	3.9	3
119	Agricultural Management Drive Bacterial Community Assembly in Different Compartments of Soybean Soil-Plant Continuum. Frontiers in Microbiology, 2022, 13, .	3.5	3
120	Distinct response patterns of bacterial communities in Ag- and ZnO-rGO nanocomposite-amended silt loam soils. Science of the Total Environment, 2021, 810, 151270.	8.0	2
121	Type III secretion systems impact <i>Mesorhizobium amorphae</i> CCNWGS0123 compatibility with <i>Robinia pseudoacacia</i> . Tree Physiology, 2020, 40, 284-284.	3.1	1
122	Rhizobial HmuS _{pSym} as a heme-binding factor is required for optimal symbiosis between <i>Mesorhizobium amorphae</i> CCNWGS0123 and <i>Robinia pseudoacacia</i> . Plant, Cell and Environment, 2022, , .	5.7	0