Haiyan Chu

List of Publications by Year
in descending order

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102	11,115	57631	32761
papers	citations	44	100
		h-index	g-index

103	103	103	12002
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Taxonomic structure and functional association of foxtail millet root microbiome. GigaScience, 2017, 6, 1-12.	3.3	1,228
2	Soil pH drives the spatial distribution of bacterial communities along elevation on Changbai Mountain. Soil Biology and Biochemistry, 2013, 57, 204-211.	4.2	792
3	Bacterial diversity in soils subjected to long-term chemical fertilization can be more stably maintained with the addition of livestock manure than wheat straw. Soil Biology and Biochemistry, 2015, 88, 9-18.	4.2	560
4	Soil bacterial diversity in the Arctic is not fundamentally different from that found in other biomes. Environmental Microbiology, 2010, 12, 2998-3006.	1.8	551
5	Nitrogen fertilization directly affects soil bacterial diversity and indirectly affects bacterial community composition. Soil Biology and Biochemistry, 2016, 92, 41-49.	4.2	484
6	The links between ecosystem multifunctionality and above- and belowground biodiversity are mediated by climate. Nature Communications, 2015, 6, 8159.	5.8	471
7	High throughput sequencing analysis of biogeographical distribution of bacterial communities in the black soils of northeast China. Soil Biology and Biochemistry, 2014, 70, 113-122.	4.2	450
8	Spatial scale affects the relative role of stochasticity versus determinism in soil bacterial communities in wheat fields across the North China Plain. Microbiome, 2018, 6, 27.	4.9	286
9	Soil carbon content drives the biogeographical distribution of fungal communities in the black soil zone of northeast China. Soil Biology and Biochemistry, 2015, 83, 29-39.	4.2	272
10	Soil pH correlates with the co-occurrence and assemblage process of diazotrophic communities in rhizosphere and bulk soils of wheat fields. Soil Biology and Biochemistry, 2018, 121, 185-192.	4.2	259
11	Wheat rhizosphere harbors a less complex and more stable microbial co-occurrence pattern than bulk soil. Soil Biology and Biochemistry, 2018, 125, 251-260.	4.2	253
12	Soil fungal diversity in natural grasslands of the Tibetan Plateau: associations with plant diversity and productivity. New Phytologist, 2017, 215, 756-765.	3.5	248
13	Salinity Is a Key Determinant for Soil Microbial Communities in a Desert Ecosystem. MSystems, 2019, 4, .	1.7	238
14	Rhizosphere-associated bacterial network structure and spatial distribution differ significantly from bulk soil in wheat crop fields. Soil Biology and Biochemistry, 2017, 113, 275-284.	4.2	210
15	Fungal community composition in soils subjected to longâ€term chemical fertilization is most influenced by the type of organic matter. Environmental Microbiology, 2016, 18, 5137-5150.	1.8	209
16	Biodiversity of key-stone phylotypes determines crop production in a 4-decade fertilization experiment. ISME Journal, 2021, 15, 550-561.	4.4	208
17	Suppressed N fixation and diazotrophs after four decades of fertilization. Microbiome, 2019, 7, 143.	4.9	205
18	Contrasting elevational diversity patterns between eukaryotic soil microbes and plants. Ecology, 2014, 95, 3190-3202.	1.5	174

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19	Long-term fertilization influences community assembly processes of soil diazotrophs. Soil Biology and Biochemistry, 2018, 126, 151-158.	4.2	172
20	Bacterial community dissimilarity between the surface and subsurface soils equals horizontal differences over several kilometers in the western Tibetan Plateau. Environmental Microbiology, 2016, 18, 1523-1533.	1.8	171
21	Abundance of kinless hubs within soil microbial networks are associated with high functional potential in agricultural ecosystems. Environment International, 2020, 142, 105869.	4.8	158
22	Distinct soil bacterial communities along a small-scale elevational gradient in alpine tundra. Frontiers in Microbiology, 2015, 6, 582.	1.5	137
23	Soil microbial biomass, nutrient availability and nitrogen mineralization potential among vegetation-types in a low arctic tundra landscape. Plant and Soil, 2010, 329, 411-420.	1.8	132
24	Prevalence of antibiotic resistance genes in soils after continually applied with different manure for 30 years. Journal of Hazardous Materials, 2017, 340, 16-25.	6.5	132
25	Rapid recovery of soil bacterial communities after wildfire in a Chinese boreal forest. Scientific Reports, 2014, 4, 3829.	1.6	121
26	Composition of the soil fungal community is more sensitive to phosphorus than nitrogen addition in the alpine meadow on the Qinghai-Tibetan Plateau. Biology and Fertility of Soils, 2016, 52, 1059-1072.	2.3	121
27	Characterizing changes in soil bacterial community structure in response to short-term warming. FEMS Microbiology Ecology, 2014, 89, 281-292.	1.3	107
28	The Influence of Vegetation Type on the Dominant Soil Bacteria, Archaea, and Fungi in a Low Arctic Tundra Landscape. Soil Science Society of America Journal, 2011, 75, 1756-1765.	1.2	105
29	Nitrogen and phosphorus enrichment accelerates soil organic carbon loss in alpine grassland on the Qinghai-Tibetan Plateau. Science of the Total Environment, 2019, 650, 303-312.	3.9	94
30	Vegetation-Associated Impacts on Arctic Tundra Bacterial and Microeukaryotic Communities. Applied and Environmental Microbiology, 2015, 81, 492-501.	1.4	91
31	Soil Microbial Biogeography in a Changing World: Recent Advances and Future Perspectives. MSystems, 2020, 5, .	1.7	84
32	Soil pH dominates elevational diversity pattern for bacteria in high elevation alkaline soils on the Tibetan Plateau. FEMS Microbiology Ecology, 2019, 95, .	1.3	83
33	Fungal Communities Along a Small-Scale Elevational Gradient in an Alpine Tundra Are Determined by Soil Carbon Nitrogen Ratios. Frontiers in Microbiology, 2018, 9, 1815.	1.5	81
34	Co-existing water and sediment bacteria are driven by contrasting environmental factors across glacier-fed aquatic systems. Water Research, 2021, 198, 117139.	5.3	81
35	Environment and geographic distance differ in relative importance for determining fungal community of rhizosphere and bulk soil. Environmental Microbiology, 2017, 19, 3649-3659.	1.8	78
36	Phylogenetic imprint of woody plants on the soil mycobiome in natural mountain forests of eastern China. ISME Journal, 2019, 13, 686-697.	4.4	76

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37	Linking soil fungi to bacterial community assembly in arid ecosystems. , 2022, 1, .		76
38	Salinity drives archaeal distribution patterns in high altitude lake sediments on the Tibetan Plateau. FEMS Microbiology Ecology, 2016, 92, .	1.3	73
39	Space Is More Important than Season when Shaping Soil Microbial Communities at a Large Spatial Scale. MSystems, 2020, 5, .	1.7	71
40	Verrucomicrobial elevational distribution was strongly influenced by soil pH and carbon/nitrogen ratio. Journal of Soils and Sediments, 2017, 17, 2449-2456.	1.5	69
41	Interannual climate variability and altered precipitation influence the soil microbial community structure in a Tibetan Plateau grassland. Science of the Total Environment, 2020, 714, 136794.	3.9	69
42	The biogeography of soil archaeal communities on the eastern Tibetan Plateau. Scientific Reports, 2016, 6, 38893.	1.6	66
43	Distinct methanotrophic communities exist in habitats with different soil water contents. Soil Biology and Biochemistry, 2019, 132, 143-152.	4.2	65
44	Microbial resistance promotes plant production in a four-decade nutrient fertilization experiment. Soil Biology and Biochemistry, 2020, 141, 107679.	4.2	59
45	Soil fungal community development in a high Arctic glacier foreland follows a directional replacement model, with a mid-successional diversity maximum. Scientific Reports, 2016, 6, 26360.	1.6	55
46	Ammonia-Oxidizing Archaea Show More Distinct Biogeographic Distribution Patterns than Ammonia-Oxidizing Bacteria across the Black Soil Zone of Northeast China. Frontiers in Microbiology, 2018, 9, 171.	1.5	51
47	Long-Term Phytoremediation of Coastal Saline Soil Reveals Plant Species-Specific Patterns of Microbial Community Recruitment. MSystems, 2020, 5, .	1.7	49
48	Distinct Community Assembly Processes of Abundant and Rare Soil Bacteria in Coastal Wetlands along an Inundation Gradient. MSystems, 2020, 5, .	1.7	48
49	Soil pH determines bacterial distribution and assembly processes in natural mountain forests of eastern China. Global Ecology and Biogeography, 2021, 30, 2164-2177.	2.7	48
50	AOA and AOB communities respond differently to changes of soil pH under long-term fertilization. Soil Ecology Letters, 2019, 1, 126-135.	2.4	47
51	Fungal community assemblages in a high elevation desert environment: Absence of dispersal limitation and edaphic effects in surface soil. Soil Biology and Biochemistry, 2017, 115, 393-402.	4.2	42
52	Interpreting distanceâ€decay pattern of soil bacteria via quantifying the assembly processes at multiple spatial scales. MicrobiologyOpen, 2019, 8, e00851.	1.2	42
53	The spatial scale dependence of diazotrophic and bacterial community assembly in paddy soil. Global Ecology and Biogeography, 2019, 28, 1093-1105.	2.7	42
54	Organic amendments enhance soil microbial diversity, microbial functionality and crop yields: A meta-analysis. Science of the Total Environment, 2022, 829, 154627.	3.9	42

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55	Existing Climate Change Will Lead to Pronounced Shifts in the Diversity of Soil Prokaryotes. MSystems, 2018, 3, .	1.7	41
56	Distinct fungal successional trajectories following wildfire between soil horizons in a coldâ€temperate forest. New Phytologist, 2020, 227, 572-587.	3.5	41
57	Aboveâ€•and belowground biodiversity jointly drive ecosystem stability in natural alpine grasslands on the Tibetan Plateau. Global Ecology and Biogeography, 2021, 30, 1418-1429.	2.7	40
58	Dramatic Increases of Soil Microbial Functional Gene Diversity at the Treeline Ecotone of Changbai Mountain. Frontiers in Microbiology, 2016, 7, 1184.	1.5	38
59	Distinct Soil Microbial Communities in habitats of differing soil water balance on the Tibetan Plateau. Scientific Reports, 2017, 7, 46407.	1.6	38
60	The Effect of Freeze-Thaw Conditions on Arctic Soil Bacterial Communities. Biology, 2013, 2, 356-377.	1.3	37
61	Archaea Enhance the Robustness of Microbial Coâ€occurrence Networks in Tibetan Plateau Soils. Soil Science Society of America Journal, 2019, 83, 1093-1099.	1.2	37
62	Carbon constrains fungal endophyte assemblages along the timberline. Environmental Microbiology, 2016, 18, 2455-2469.	1.8	35
63	Arbuscular mycorrhizal fungal communities show low resistance and high resilience to wildfire disturbance. Plant and Soil, 2015, 397, 347-356.	1.8	33
64	Environmental filtering of bacterial functional diversity along an aridity gradient. Scientific Reports, 2019, 9, 866.	1.6	33
65	Fungal Assemblages in Different Habitats in an Ermanâ€™s Birch Forest. Frontiers in Microbiology, 2016, 7, 1368.	1.5	30
66	Shrub encroachment is associated with changes in soil bacterial community composition in a temperate grassland ecosystem. Plant and Soil, 2018, 425, 539-551.	1.8	30
67	Microbes changed their carbon use strategy to regulate the priming effect in an 11-year nitrogen addition experiment in grassland. Science of the Total Environment, 2020, 727, 138645.	3.9	29
68	Rapid response of arbuscular mycorrhizal fungal communities to short-term fertilization in an alpine grassland on the Qinghai-Tibet Plateau. PeerJ, 2016, 4, e2226.	0.9	29
69	Biogeographic Distribution Patterns of the Archaeal Communities Across the Black Soil Zone of Northeast China. Frontiers in Microbiology, 2019, 10, 23.	1.5	27
70	The response of methanotrophs to additions of either ammonium, nitrate or urea in alpine swamp meadow soil as revealed by stable isotope probing. FEMS Microbiology Ecology, 2019, 95, .	1.3	26
71	Soil fungal community assembly processes under longâ€term fertilization. European Journal of Soil Science, 2020, 71, 716-726.	1.8	26
72	Bacterial diversity is strongly associated with historical penguin activity in an Antarctic lake sediment profile. Scientific Reports, 2015, 5, 17231.	1.6	23

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73	Depth-Dependent Patterns of Bacterial Communities and Assembly Processes in a Typical Red Soil Critical Zone. Geomicrobiology Journal, 2020, 37, 201-212.	1.0	23
74	DNA stable-isotope probing highlights the effects of temperature on functionally active methanotrophs in natural wetlands. Soil Biology and Biochemistry, 2020, 149, 107954.	4.2	23
75	Dramatic change of bacterial assembly process and co-occurrence pattern in Spartina alterniflora salt marsh along an inundation frequency gradient. Science of the Total Environment, 2021, 755, 142546.	3.9	23
76	Differential Responses of Arbuscular Mycorrhizal Fungal Communities to Long-Term Fertilization in the Wheat Rhizosphere and Root Endosphere. Applied and Environmental Microbiology, 2021, 87, e0034921.	1.4	23
77	Threshold effects of soil pH on microbial co-occurrence structure in acidic and alkaline arable lands. Science of the Total Environment, 2021, 800, 149592.	3.9	23
78	Ex-situ enzyme activity and bacterial community diversity through soil depth profiles in penguin and seal colonies on Vestfold Hills, East Antarctica. Polar Biology, 2013, 36, 1347-1361.	0.5	22
79	Optimization of Laccase-mediated Benzo[a]pyrene Oxidation and the Bioremedial Application in Aged Polycyclic Aromatic Hydrocarbons-contaminated Soil. Journal of Health Science, 2010, 56, 534-540.	0.9	20
80	Protaetia brevitarsis larvae can efficiently convert herbaceous and ligneous plant residues to humic acids. Waste Management, 2019, 83, 79-82.	3.7	20
81	Saprotrophic fungal diversity predicts ectomycorrhizal fungal diversity along the timberline in the framework of island biogeography theory. ISME Communications, 2021, 1, .	1.7	16
82	Increasing Inundation Frequencies Enhance the Stochastic Process and Network Complexity of the Soil Archaeal Community in Coastal Wetlands. Applied and Environmental Microbiology, 2021, 87, .	1.4	15
83	Template Preparation Affects 16S rRNA High-Throughput Sequencing Analysis of Phyllosphere Microbial Communities. Frontiers in Plant Science, 2017, 8, 1623.	1.7	14
84	The spatial variation of soil bacterial community assembly processes affects the accuracy of source tracking in ten major Chinese cities. Science China Life Sciences, 2021, 64, 1546-1559.	2.3	14
85	Identification of the rhizosphere microbes that actively consume plant-derived carbon. Soil Biology and Biochemistry, 2022, 166, 108577.	4.2	14
86	Continentalâ€scale plant invasions reshuffle the soil microbiome of blue carbon ecosystems. Global Change Biology, 2022, 28, 4423-4438.	4.2	14
87	Strong partitioning of soil bacterial community composition and co-occurrence networks along a small-scale elevational gradient on Zijin Mountain. Soil Ecology Letters, 2021, 3, 290-302.	2.4	13
88	On the controls of abundance for soilâ€dwelling organisms on the Tibetan Plateau. Ecosphere, 2017, 8, e01901.	1.0	11
89	The influence of aboveground and belowground species composition on spatial turnover in nutrient pools in alpine grasslands. Global Ecology and Biogeography, 2022, 31, 486-500.	2.7	11
90	Land-use type strongly affects soil microbial community assembly process and inter-kingdom co-occurrence pattern in a floodplain ecosystem. Applied Soil Ecology, 2022, 179, 104574.	2.1	11

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91	A biogeographic map of soil bacterial communities in wheats field of the North China Plain. Soil Ecology Letters, 2019, 1, 50-58.	2.4	10
92	Microbial Functional Responses Explain Alpine Soil Carbon Fluxes under Future Climate Scenarios. MBio, 2021, 12, .	1.8	10
93	Phosphorus and Zinc Are Strongly Associated with Belowground Fungal Communities in Wheat Field under Long-Term Fertilization. Microbiology Spectrum, 2022, 10, e0011022.	1.2	10
94	Effect of long-term fertilization on bacterial communities in wheat endosphere. Pedosphere, 2021, 31, 538-548.	2.1	9
95	Proximate grassland and shrub-encroached sites show dramatic restructuring of soil bacterial communities. PeerJ, 2019, 7, e7304.	0.9	7
96	The Role Transition of Dietary Species Richness in Modulating the Gut Microbial Assembly and Postweaning Performance of a Generalist Herbivore. MSystems, 2021, 6, e0097921.	1.7	6
97	Editorial: Rhizosphere microbiome special issue. Plant and Soil, 2022, 470, 1-3.	1.8	5
98	Developing a method for exploiting soil bacterial communities as evidence in environmental forensic investigations. Environmental Forensics, 2021, 22, 385-392.	1.3	4
99	Root stoichiometry explains wheat endophytes and their link with crop production after four decades of fertilization. Science of the Total Environment, 2022, 846, 157407.	3.9	4
100	Editorial: China Soil Microbiome thematic issue. FEMS Microbiology Ecology, 2019, 95, .	1.3	2
101	Distinct Co-occurrence Relationships and Assembly Processes of Active Methane-Oxidizing Bacterial Communities Between Paddy and Natural Wetlands of Northeast China. Frontiers in Microbiology, 2022, 13, 809074.	1.5	1
102	Special Issue on Soil Microbial Ecology. Soil Ecology Letters, 2021, 3, 289-289.	2.4	1