Kai Feng

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Relationships Between Soil Microbial Diversities Across an Aridity Gradient in Temperate Grasslands. Microbial Ecology, 2023, 85, 1013-1027.	2.8	7
2	Assessment of microbial α-diversity in one meter squared topsoil. Soil Ecology Letters, 2022, 4, 224-236.	4.5	10
3	Effect of dietary protein levels on the growth, enzyme activity, and immunological status of Culter mongolicus fingerlings. PLoS ONE, 2022, 17, e0263507.	2.5	4
4	Homogeneous Selection and Dispersal Limitation Dominate the Effect of Soil Strata Under Warming Condition. Frontiers in Microbiology, 2022, 13, 801083.	3.5	4
5	iNAP: An integrated network analysis pipeline for microbiome studies. , 2022, 1, .		126
6	The large-scale spatial patterns of ecological networks between phytoplankton and zooplankton in coastal marine ecosystems. Science of the Total Environment, 2022, 827, 154285.	8.0	8
7	Fungal dynamics and potential functions during anaerobic digestion of food waste. Environmental Research, 2022, 212, 113298.	7.5	6
8	Organic fertilizer potentiates the transfer of typical antibiotic resistance gene among special bacterial species. Journal of Hazardous Materials, 2022, 435, 128985.	12.4	15
9	<scp>ddPCR</scp> surpasses classical <scp>qPCR</scp> technology in quantitating bacteria and fungi in the environment. Molecular Ecology Resources, 2022, 22, 2587-2598.	4.8	9
10	Network analysis reveals the root endophytic fungi associated with Fusarium root rot invasion. Applied Soil Ecology, 2022, 178, 104567.	4.3	10
11	Steeper spatial scaling patterns of subsoil microbiota are shaped by deterministic assembly process. Molecular Ecology, 2021, 30, 1072-1085.	3.9	43
12	Assembly Patterns of the Rhizosphere Microbiome Along the Longitudinal Root Axis of Maize (Zea mays) Tj ETQqC	9.9 rgBT	/Qyerlock 1
13	A Parasite's Paradise: Biotrophic Species Prevail Oomycete Community Composition in Tree Canopies. Frontiers in Forests and Global Change, 2021, 4, .	2.3	2
14	Sampling cores and sequencing depths affected the measurement of microbial diversity in soil quadrats. Science of the Total Environment, 2021, 767, 144966.	8.0	14
15	On the phenology of protists: recurrent patterns reveal seasonal variation of protistan (Rhizaria:) Tj ETQq1 1 0.784	4314 rgBT 2.7	loverlock
16	Temperature and microbial interactions drive the deterministic assembly processes in sediments of hot springs. Science of the Total Environment, 2021, 772, 145465.	8.0	85
17	Interkingdom plant-microbial ecological networks under selective and clear cutting of tropical rainforest. Forest Ecology and Management, 2021, 491, 119182.	3.2	9
18	High-Throughput Single-Cell Technology Reveals the Contribution of Horizontal Gene Transfer to Typical Antibiotic Resistance Gene Dissemination in Wastewater Treatment Plants. Environmental Science & Technology, 2021, 55, 11824-11834.	10.0	33

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19	Fungi-Bacteria Associations in Wilt Diseased Rhizosphere and Endosphere by Interdomain Ecological Network Analysis. Frontiers in Microbiology, 2021, 12, 722626.	3.5	21
20	Warming reshaped the microbial hierarchical interactions. Global Change Biology, 2021, 27, 6331-6347.	9.5	81
21	The Succession of Bacterial Community Attached on Biodegradable Plastic Mulches During the Degradation in Soil. Frontiers in Microbiology, 2021, 12, 785737.	3.5	25
22	The Coexistence Relationship Between Plants and Soil Bacteria Based on Interdomain Ecological Network Analysis. Frontiers in Microbiology, 2021, 12, 745582.	3.5	6
23	Modeling trophic interactions and impacts of introduced icefish (Neosalanx taihuensis Chen) in three large reservoirs in the Yangtze River basin, China. Hydrobiologia, 2020, 847, 3637-3657.	2.0	2
24	ARDEP, a Rapid Degenerate Primer Design Pipeline Based on k-mers for Amplicon Microbiome Studies. International Journal of Environmental Research and Public Health, 2020, 17, 5958.	2.6	4
25	Nitrogen and water addition regulate soil fungal diversity and co-occurrence networks. Journal of Soils and Sediments, 2020, 20, 3192-3203.	3.0	18
26	Network analysis infers the wilt pathogen invasion associated with non-detrimental bacteria. Npj Biofilms and Microbiomes, 2020, 6, 8.	6.4	68
27	Florfenicol restructured the microbial interaction network for wastewater treatment by microbial electrolysis cells. Environmental Research, 2020, 183, 109145.	7.5	14
28	Niche width of above―and belowâ€ground organisms varied in predicting biodiversity profiling along a latitudinal gradient. Molecular Ecology, 2020, 29, 1890-1902.	3.9	16
29	Soil microbiome mediated nutrients decline during forest degradation process. Soil Ecology Letters, 2019, 1, 59-71.	4.5	29
30	Interdomain ecological networks between plants and microbes. Molecular Ecology Resources, 2019, 19, 1565-1577.	4.8	64
31	Electro-driven methanogenic microbial community diversity and variability in the electron abundant niche. Science of the Total Environment, 2019, 661, 178-186.	8.0	26
32	Enhanced nitrate removal in an Fe ⁰ -driven autotrophic denitrification system using hydrogen-rich water. Environmental Science: Water Research and Technology, 2019, 5, 1380-1388.	2.4	11
33	ARGA, a pipeline for primer evaluation on antibiotic resistance genes. Environment International, 2019, 128, 137-145.	10.0	14
34	Unraveling the diversity of sedimentary sulfate-reducing prokaryotes (SRP) across Tibetan saline lakes using epicPCR. Microbiome, 2019, 7, 71.	11.1	16
35	Deterministic Assembly and Diversity Gradient Altered the Biofilm Community Performances of Bioreactors. Environmental Science & amp; Technology, 2019, 53, 1315-1324.	10.0	109
36	Temperature determines the diversity and structure of N ₂ Oâ€reducing microbial assemblages. Functional Ecology, 2018, 32, 1867-1878.	3.6	19

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37	The divergence between fungal and bacterial communities in seasonal and spatial variations of wastewater treatment plants. Science of the Total Environment, 2018, 628-629, 969-978.	8.0	79
38	mcrA sequencing reveals the role of basophilic methanogens in a cathodic methanogenic community. Water Research, 2018, 136, 192-199.	11.3	77
39	Exploring abundance, diversity and variation of a widespread antibiotic resistance gene in wastewater treatment plants. Environment International, 2018, 117, 186-195.	10.0	40
40	The responses and adaptations of microbial communities to salinity in farmland soils: A molecular ecological network analysis. Applied Soil Ecology, 2017, 120, 239-246.	4.3	76
41	Biodiversity and species competition regulate the resilience of microbial biofilm community. Molecular Ecology, 2017, 26, 6170-6182.	3.9	299
42	Soil bacterial quantification approaches coupling with relative abundances reflecting the changes of taxa. Scientific Reports, 2017, 7, 4837.	3.3	131
43	Microbial Community and Functional Structure Significantly Varied among Distinct Types of Paddy Soils But Responded Differently along Gradients of Soil Depth Layers. Frontiers in Microbiology, 2017, 8 945	3.5	76