

Kai Xue

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

3,439
citations

218381

26
h-index

168136

53
g-index

56
all docs

56
docs citations

56
times ranked

4295
citing authors

#	ARTICLE	IF	CITATIONS
1	Tree mycorrhizal type and tree diversity shape the forest soil microbiota. <i>Environmental Microbiology</i> , 2022, 24, 4236-4255.	1.8	22
2	Long-Term Effects of Soil Remediation with Willow Short Rotation Coppice on Biogeographic Pattern of Microbial Functional Genes. <i>Microorganisms</i> , 2022, 10, 140.	1.6	1
3	Environmental selection overturns the decay relationship of soil prokaryotic community over geographic distance across grassland biotas. <i>ELife</i> , 2022, 11, .	2.8	5
4	Polar soils exhibit distinct patterns in microbial diversity and dominant phylotypes. <i>Soil Biology and Biochemistry</i> , 2022, 166, 108550.	4.2	19
5	Anaerobic methane oxidation linked to Fe(III) reduction in a <i>Candidatus Methanoperedens</i> -enriched consortium from the cold Zoige wetland at Tibetan Plateau. <i>Environmental Microbiology</i> , 2022, 24, 614-625.	1.8	18
6	Soil microbial distribution and assembly are related to vegetation biomass in the alpine permafrost regions of the Qinghai-Tibet Plateau. <i>Science of the Total Environment</i> , 2022, 834, 155259.	3.9	24
7	Altered microbial structure and function after thermokarst formation. <i>Global Change Biology</i> , 2021, 27, 823-835.	4.2	33
8	Linkage between microbial shift and ecosystem functionality. <i>Global Change Biology</i> , 2021, 27, 3197-3199.	4.2	2
9	Reduced microbial stability in the active layer is associated with carbon loss under alpine permafrost degradation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	138
10	Tree diversity and soil chemical properties drive the linkages between soil microbial community and ecosystem functioning. <i>ISME Communications</i> , 2021, 1, .	1.7	28
11	Spatial patterns of microbial nitrogen-cycling gene abundances along a precipitation gradient in various temperate grasslands at a regional scale. <i>Geoderma</i> , 2021, 404, 115236.	2.3	16
12	Promoting resilience of large international collaborative research programs in times of global crisis. <i>Ecology and Evolution</i> , 2020, 10, 12549-12554.	0.8	2
13	Microbial functional genes commonly respond to elevated carbon dioxide. <i>Environment International</i> , 2020, 144, 106068.	4.8	20
14	Phytomanagement Reduces Metal Availability and Microbial Metal Resistance in a Metal Contaminated Soil. <i>Frontiers in Microbiology</i> , 2020, 11, 1899.	1.5	7
15	Soil thermal regime alteration under experimental warming in permafrost regions of the central Tibetan Plateau. <i>Geoderma</i> , 2020, 372, 114397.	2.3	16
16	Functional structures of soil microbial community relate to contrasting N ₂ O emission patterns from a highly acidified forest. <i>Science of the Total Environment</i> , 2020, 725, 138504.	3.9	10
17	Stimulation of soil respiration by elevated CO ₂ is enhanced under nitrogen limitation in a decade-long grassland study. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 33317-33324.	3.3	34
18	Microbial community responses reduce soil carbon loss in Tibetan alpine grasslands under short-term warming. <i>Global Change Biology</i> , 2019, 25, 3438-3449.	4.2	24

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19	Phosphorus mediates soil prokaryote distribution pattern along a small-scale elevation gradient in Noijin Kangsang Peak, Tibetan Plateau. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	17
20	Trait complementarity between fine roots of <i>Stipa purpurea</i> and their associated arbuscular mycorrhizal fungi along a precipitation gradient in Tibetan alpine steppe. <i>Journal of Mountain Science</i> , 2019, 16, 542-547.	0.8	13
21	Warming counteracts grazing effects on the functional structure of the soil microbial community in a Tibetan grassland. <i>Soil Biology and Biochemistry</i> , 2019, 134, 113-121.	4.2	42
22	Soil microbial communities in alpine grasslands on the Tibet Plateau and their influencing factors. <i>Chinese Science Bulletin</i> , 2019, 64, 2915-2927.	0.4	13
23	Microbial functional diversity covaries with permafrost thaw-induced environmental heterogeneity in tundra soil. <i>Global Change Biology</i> , 2018, 24, 297-307.	4.2	22
24	Autotrophic and symbiotic diazotrophs dominate nitrogen-fixing communities in Tibetan grassland soils. <i>Science of the Total Environment</i> , 2018, 639, 997-1006.	3.9	88
25	Functional activity and functional gene diversity of a Cu-contaminated soil remediated by aided phytostabilization using compost, dolomitic limestone and a mixed tree stand. <i>Environmental Pollution</i> , 2018, 242, 229-238.	3.7	24
26	Spatial scaling of forest soil microbial communities across a temperature gradient. <i>Environmental Microbiology</i> , 2018, 20, 3504-3513.	1.8	24
27	Warming enhances old organic carbon decomposition through altering functional microbial communities. <i>ISME Journal</i> , 2017, 11, 1825-1835.	4.4	136
28	Correspondence: Reply to "Analytical flaws in a continental-scale forest soil microbial diversity study". <i>Nature Communications</i> , 2017, 8, 15583.	5.8	4
29	Metagenomic reconstruction of nitrogen cycling pathways in a CO ₂ -enriched grassland ecosystem. <i>Soil Biology and Biochemistry</i> , 2017, 106, 99-108.	4.2	63
30	Evaluation of the reproducibility of amplicon sequencing with Illumina MiSeq platform. <i>PLoS ONE</i> , 2017, 12, e0176716.	1.1	107
31	Warming Alters Expressions of Microbial Functional Genes Important to Ecosystem Functioning. <i>Frontiers in Microbiology</i> , 2016, 7, 668.	1.5	46
32	Annual Removal of Aboveground Plant Biomass Alters Soil Microbial Responses to Warming. <i>MBio</i> , 2016, 7, .	1.8	43
33	Temperature mediates continental-scale diversity of microbes in forest soils. <i>Nature Communications</i> , 2016, 7, 12083.	5.8	419
34	Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. <i>Nature Climate Change</i> , 2016, 6, 595-600.	8.1	260
35	Planting increases the abundance and structure complexity of soil core functional genes relevant to carbon and nitrogen cycling. <i>Scientific Reports</i> , 2015, 5, 14345.	1.6	26
36	Long-term soil transplant simulating climate change with latitude significantly alters microbial temporal turnover. <i>ISME Journal</i> , 2015, 9, 2561-2572.	4.4	134

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37	Fungal Communities Respond to Long-Term CO ₂ Elevation by Community Reassembly. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2445-2454.	1.4	48
38	Over 150 Years of Long-Term Fertilization Alters Spatial Scaling of Microbial Biodiversity. <i>MBio</i> , 2015, 6, .	1.8	57
39	Shifts of tundra bacterial and archaeal communities along a permafrost thaw gradient in Alaska. <i>Molecular Ecology</i> , 2015, 24, 222-234.	2.0	127
40	The interactive effects of soil transplant into colder regions and cropping on soil microbiology and biogeochemistry. <i>Environmental Microbiology</i> , 2015, 17, 566-576.	1.8	47
41	Soil Microbial Community Responses to a Decade of Warming as Revealed by Comparative Metagenomics. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1777-1786.	1.4	131
42	Distinct responses of soil microbial communities to elevated CO ₂ and O ₃ in a soybean agro-ecosystem. <i>ISME Journal</i> , 2014, 8, 714-726.	4.4	80
43	GeoChip 4: a functional gene-based high-throughput environmental technology for microbial community analysis. <i>Molecular Ecology Resources</i> , 2014, 14, 914-928.	2.2	183
44	Microbial mediation of biogeochemical cycles revealed by simulation of global changes with soil transplant and cropping. <i>ISME Journal</i> , 2014, 8, 2045-2055.	4.4	97
45	GeoChip profiling of microbial community in response to global changes simulated by soil transplant and cropping. <i>Genomics Data</i> , 2014, 2, 166-169.	1.3	3
46	Stability of Cry3Bb1 protein in soils and its degradation in transgenic corn residues. <i>Soil Biology and Biochemistry</i> , 2014, 76, 119-126.	4.2	15
47	Effects of Substrate Addition on Soil Respiratory Carbon Release Under Long-Term Warming and Clipping in a Tallgrass Prairie. <i>PLoS ONE</i> , 2014, 9, e114203.	1.1	12
48	Functional Gene Differences in Soil Microbial Communities from Conventional, Low-Input, and Organic Farmlands. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1284-1292.	1.4	90
49	Random Sampling Process Leads to Overestimation of $\hat{\alpha}^2$ -Diversity of Microbial Communities. <i>MBio</i> , 2013, 4, e00324-13.	1.8	96
50	Short-term carbon allocation and root lignin of Cry3Bb Bt and NonBt corn in the presence of corn rootworm. <i>Applied Soil Ecology</i> , 2012, 57, 16-22.	2.1	7
51	Microbial mediation of carbon-cycle feedbacks to climate warming. <i>Nature Climate Change</i> , 2012, 2, 106-110.	8.1	502
52	Decomposition Rates and Residue-Colonizing Microbial Communities of <i>Bacillus thuringiensis</i> Insecticidal Protein Cry3Bb-Expressing (Bt) and Non-Bt Corn Hybrids in the Field. <i>Applied and Environmental Microbiology</i> , 2011, 77, 839-846.	1.4	30
53	Changes in soil microbial community structure associated with two types of genetically engineered plants analyzing by PLFA. <i>Journal of Environmental Sciences</i> , 2005, 17, 130-4.	3.2	14