

# Binbin Liu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5167729/publications.pdf>

Version: 2024-02-01

30  
papers

2,216  
citations

394421

19  
h-index

454955

30  
g-index

30  
all docs

30  
docs citations

30  
times ranked

2578  
citing authors

#	ARTICLE	IF	CITATIONS
1	Plants are a natural source of nitrous oxide even in field conditions as explained by 15N site preference. <i>Science of the Total Environment</i> , 2022, 805, 150262.	8.0	9
2	Meta-analysis of the priming effect on native soil organic carbon in response to glucose amendment across soil depths. <i>Plant and Soil</i> , 2022, 479, 107-124.	3.7	11
3	An Assessment of the Lactic Acid-Producing Potential of Bacterial Strains Isolated from Food Waste. <i>Microbiology Research</i> , 2022, 13, 278-291.	1.9	6
4	Long-term nitrogen fertilization alters microbial community structure and denitrifier abundance in the deep vadose zone. <i>Journal of Soils and Sediments</i> , 2021, 21, 2394-2403.	3.0	9
5	Metagenomics reveals taxon-specific responses of the nitrogen-cycling microbial community to long-term nitrogen fertilization. <i>Soil Biology and Biochemistry</i> , 2021, 156, 108214.	8.8	53
6	Long-Term Amelioration Practices Reshape the Soil Microbiome in a Coastal Saline Soil and Alter the Richness and Vertical Distribution Differently Among Bacterial, Archaeal, and Fungal Communities. <i>Frontiers in Microbiology</i> , 2021, 12, 768203.	3.5	13
7	Trichoderma Enhances Net Photosynthesis, Water Use Efficiency, and Growth of Wheat ( <i>Triticum</i> ) Tj ETQq1 1 0.784314 rgBT/Overlook	3.6	41
8	Different contribution of species sorting and exogenous species immigration from manure to soil fungal diversity and community assemblage under long-term fertilization. <i>Soil Biology and Biochemistry</i> , 2020, 151, 108049.	8.8	53
9	Cultivation-independent and cultivation-dependent metagenomes reveal genetic and enzymatic potential of microbial community involved in the degradation of a complex microbial polymer. <i>Microbiome</i> , 2020, 8, 76.	11.1	59
10	Nitrogen leaching greatly impacts bacterial community and denitrifiers abundance in subsoil under long-term fertilization. <i>Agriculture, Ecosystems and Environment</i> , 2020, 294, 106885.	5.3	35
11	Fifteen-Year Application of Manure and Chemical Fertilizers Differently Impacts Soil ARGs and Microbial Community Structure. <i>Frontiers in Microbiology</i> , 2020, 11, 62.	3.5	66
12	Long-Term Phytoremediation of Coastal Saline Soil Reveals Plant Species-Specific Patterns of Microbial Community Recruitment. <i>MSystems</i> , 2020, 5, .	3.8	49
13	A comparison of the efficiency of different urease inhibitors and their effects on soil prokaryotic community in a short-term incubation experiment. <i>Geoderma</i> , 2019, 354, 113877.	5.1	17
14	Root-associated microbiomes of wheat under the combined effect of plant development and nitrogen fertilization. <i>Microbiome</i> , 2019, 7, 136.	11.1	270
15	Electrodes Donate Electrons for Nitrate Reduction in a Soil Matrix via DNRA and Denitrification. <i>Environmental Science &amp; Technology</i> , 2019, 53, 2002-2012.	10.0	31
16	Long-term urea fertilization alters the composition and increases the abundance of soil ureolytic bacterial communities in an upland soil. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	32
17	High-Quality Draft Genome Sequence of <i>Pseudomonas songnenensis</i> L103, a Denitrifier Isolated from a 100-Meter-Deep Aquifer in a Heavily Nitrogen-Fertilized Agricultural Area. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
18	Inter-laboratory testing of the effect of DNA blocking reagent G2 on DNA extraction from low-biomass clay samples. <i>Scientific Reports</i> , 2018, 8, 5711.	3.3	9

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19	Organic carbon availability limiting microbial denitrification in the deep vadose zone. <i>Environmental Microbiology</i> , 2018, 20, 980-992.	3.8	81
20	Long-Term Nitrogen Fertilization Elevates the Activity and Abundance of Nitrifying and Denitrifying Microbial Communities in an Upland Soil: Implications for Nitrogen Loss From Intensive Agricultural Systems. <i>Frontiers in Microbiology</i> , 2018, 9, 2424.	3.5	64
21	Response of Nitrifier and Denitrifier Abundance and Microbial Community Structure to Experimental Warming in an Agricultural Ecosystem. <i>Frontiers in Microbiology</i> , 2018, 9, 474.	3.5	35
22	Tillage Changes Vertical Distribution of Soil Bacterial and Fungal Communities. <i>Frontiers in Microbiology</i> , 2018, 9, 699.	3.5	126
23	Rapid Succession of Actively Transcribing Denitrifier Populations in Agricultural Soil During an Anoxic Spell. <i>Frontiers in Microbiology</i> , 2018, 9, 3208.	3.5	12
24	Impaired Reduction of N <sub>2</sub> O to N <sub>2</sub> in Acid Soils Is Due to a Posttranscriptional Interference with the Expression of <i>nosZ</i> . <i>MBio</i> , 2014, 5, e01383-14.	4.1	170
25	Role of <i>norEF</i> in Denitrification, Elucidated by Physiological Experiments with <i>Rhodobacter sphaeroides</i> . <i>Journal of Bacteriology</i> , 2014, 196, 2190-2200.	2.2	10
26	<i>Mesorhizobium shonense</i> sp. nov., <i>Mesorhizobium hawassense</i> sp. nov. and <i>Mesorhizobium abyssinicae</i> sp. nov., isolated from root nodules of different agroforestry legume trees. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 1746-1753.	1.7	58
27	Draft Genome Sequences of Five Strains in the Genus <i>Thauera</i> . <i>Genome Announcements</i> , 2013, 1, .	0.8	16
28	Strains in the genus <i>Thauera</i> exhibit remarkably different denitrification regulatory phenotypes. <i>Environmental Microbiology</i> , 2013, 15, 2816-2828.	3.8	207
29	Regulation of denitrification at the cellular level: a clue to the understanding of N <sub>2</sub> O emissions from soils. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 1226-1234.	4.0	272
30	Denitrification gene pools, transcription and kinetics of $\delta^{15}N$ NO, N <sub>2</sub> O and N <sub>2</sub> production as affected by soil pH. <i>FEMS Microbiology Ecology</i> , 2010, 72, 407-417.	2.7	401