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Deciphering microbial interactions and detecting keystone species with co-occurrence networks

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254	From Diversity to Complexity: Microbial Networks in Soils.		
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248	Salinity Is a Key Determinant for the Microeukaryotic Community in Lake Ecosystems of the Inner Mongolia Plateau, China <i>Frontiers in Microbiology</i> , 2022 , 13, 841686	5.7	O
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Table 1. PDF. 2017, 243 Table2.PDF. 2017, 242 Data_Sheet_1.PDF. 2020, 241 Table_1.DOCX. **2018**, 240 Table_2.docx. 2018, 239 Table_3.DOCX. 2018, 238 237 Image_1.pdf. **2018**, Table_1.docx. **2018**, 236 Table_2.docx. 2018, 235 Image_1.TIF. 2018, 234 Data_Sheet_1.docx. 2018, 233 Data_Sheet_2.xlsx. 2018, 232 Image_1.TIF. 2018, 231 Image_2.TIF. 2018, 230 Table_1.DOCX. 2018, 229 228 Data_Sheet_1.PDF. **2019**, Presentation_1.pptx. 2019, 227 Table_1.DOCX. **2019**, 226



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202	Image_1.JPEG. 2020 ,		
201	Data_Sheet_1.docx. 2020 ,		
2 00	Image_1.jpg. 2020 ,		
199	DataSheet_1.zip. 2019 ,		
198	Soil Bacterial Communities of Rice is Dependent on Root Compartment Niches But Independent of Growth Stages in Mollisols of Northeast China.		
197	Soil Bacterial Communities of Rice is Dependent on Root Compartment Niches But Independent of Growth Stages in Mollisols of Northeast China.		
196	Gradual Enhancement of the Assemblage Stability of the Reed Rhizosphere Microbiome with Recovery Time. 2022 , 10, 937		O
195	Mechanisms of fungal community assembly in wild stoneflies moderated by host characteristics and local environment 2022 , 8, 31		O
194	Unique Geothermal Chemistry Shapes Microbial Communities on Mt. Erebus, Antarctica <i>Frontiers in Microbiology</i> , 2022 , 13, 836943	5.7	O
193	Agricultural Management Drive Bacterial Community Assembly in Different Compartments of Soybean Soil-Plant Continuum. <i>Frontiers in Microbiology</i> , 2022 , 13,	5.7	
192	Multitrophic diversity and biotic associations influence subalpine forest ecosystem multifunctionality 2022 , e3745		2
191	Long-term patterns of an interconnected core marine microbiota 2022, 17, 22		О
190	Long-term nickel contamination increased soil fungal diversity and altered fungal community structure and co-occurrence patterns in agricultural soils 2022 , 436, 129113		O

189	Dynamics in diversity, co-occurrence pattern, and community assembly of a perennial desert plant root-associated bacteria. 2022 , 22, 100526		0
188	Response of the biological community to the translocation of seaweed attaching substrate. 2022 , 552, 151739		
187	Vertical distribution characteristics and interactions of polycyclic aromatic compounds and bacterial communities in contaminated soil in oil storage tank areas 2022 , 134695		2
186	Conversion of mangrove forests to shrimp ponds in southeastern China destabilizes sediment microbial networks. 2022 , 421, 115907		O
185	Inter-cluster competition and resource partitioning may govern the ecology of Frankia 2022, 204, 326		
184	Ecological modelling approaches for predicting emergent properties in microbial communities 2022 ,		5
183	Distinct strategies of the habitat generalists and specialists in sediment of Tibetan lakes 2022,		Ο
182	Growth phase estimation for abundant bacterial populations sampled longitudinally from human stool metagenomes.		O
181	Multiple metal(loid) contamination reshaped the structure and function of soil archaeal community. 2022 , 436, 129186		Ο
180	Dynamics of Planktonic Microbial Community Associated with Saccharina japonica Seedling. 2022 , 10, 726		
179	Short-chain fatty acids promote the effect of environmental signals on the gut microbiome and metabolome in mice. 2022 , 5,		3
178	Biological Microbial Interactions from Cooccurrence Networks in a High Mountain Lacustrine District.		О
177	Soil microbial network complexity predicts ecosystem function along elevation gradients on the Tibetan Plateau. 2022 , 108766		1
176	Characterizing the Microbial Consortium L1 Capable of Efficiently Degrading Chlorimuron-Ethyl via Metagenome Combining 16S rDNA Sequencing. <i>Frontiers in Microbiology</i> , 13,	5.7	
175	Changes in Soil Organic Carbon Fractions and Fungal Communities, Subsequent to Different Management Practices in Moso Bamboo Plantations. 2022 , 8, 640		О
174	Soil Microbial Network Complexity Varies With pH as a Continuum, Not a Threshold, Across the North China Plain. <i>Frontiers in Microbiology</i> , 13,	5.7	O
173	High stability of autochthonous dissolved organic matter in karst aquatic ecosystems: Evidence from fluorescence. 2022 , 220, 118723		1
172	Temperature mediated the balance between stochastic and deterministic processes and reoccurrence of microbial community during treating aniline wastewater. 2022 , 221, 118741		О

171	Microbiome and -omics application in food industry. 2022, 377, 109781		1
170	Interlinkages between soil properties and keystone taxa under different tillage practices on the North China Plain. 2022 , 178, 104551		3
169	Land-use type strongly affects soil microbial community assembly process and inter-kingdom co-occurrence pattern in a floodplain ecosystem. 2022 , 179, 104574		0
168	Soil Ph Regulates the Network Patterns and Assembly Processes of Freshwater Wetland Soil Bacteria in Eastern China: A Parallel with Well-Drained Soils.		
167	The Maximum Entropy Principle For Compositional Data.		
166	The Characterization of Microbiome and Interactions on Weathered Rocks in a Subsurface Karst Cave, Central China. <i>Frontiers in Microbiology</i> , 13,	5.7	O
165	Fusarium oxysporum Disrupts Microbiome-Metabolome Networks in Arabidopsis thaliana Roots.		O
164	Primary Succession Changes the Composition and Functioning of the Protist Community on Mine Tailings, Especially Phototrophic Protists.		1
163	Characteristics and diversity of endophytic bacteria in Panax notoginseng under high temperature analysed using full-length 16S rRNA sequencing. 2022 , 204,		O
162	Ecological clusters of soil taxa within bipartite networks are highly sensitive to climatic conditions in global drylands. 2022 , 377,		O
161	Over-optimism in unsupervised microbiome analysis: Insights from network learning and clustering.		0
160	Comparison of the co-occurrence patterns of the gut microbial community between Bt-susceptible and Bt-resistant strains of the rice stem borer, Chilo suppressalis.		O
159	Co-occurrence networks reveal more complexity than community composition in resistance and resilience of microbial communities. 2022 , 13,		O
158	Wheat Rhizosphere Microbiota Respond to Changes in Plant Genotype, Chemical Inputs, and Plant Phenotypic Plasticity. 10,		O
157	Land use alters diazotroph community structure by regulating bacterivores in Mollisols in Northeast China. <i>Frontiers in Microbiology</i> , 13,	5.7	
156	The Responses of Ammonia-Oxidizing Microorganisms to Different Environmental Factors Determine Their Elevational Distribution and Assembly Patterns.		
155	Dysbiosis and Predicted Functions of the Dental Biofilm of Dairy Goats with Periodontitis.		1
154	Identification of key steps and associated microbial populations for efficient anaerobic digestion under high ammonium or salinity conditions. 2022 , 360, 127571		O

153	Nanoscale zero-valent iron changes microbial co-occurrence pattern in pentachlorophenol-contaminated soil. 2022 , 438, 129482		О
152	Microbial co-occurrence networks driven by low-abundance microbial taxa during composting dominate lignocellulose degradation. 2022 , 845, 157197		O
151	Heterogeneity and its drivers of microbial communities and diversity in six typical soils under two different land uses in tropical and subtropical southern China. 2022 , 179, 104555		О
150	Cross-kingdom co-occurrence networks in the plant microbiome: Importance and ecological interpretations. <i>Frontiers in Microbiology</i> , 13,	5.7	1
149	The impact of the rice production system (irrigated vs lowland) on root-associated microbiome from farmer's fields in western Burkina Faso.		O
148	Increased Soil Fertility in Tea Gardens Leads to Declines in Fungal Diversity and Complexity in Subsoils. 2022 , 12, 1751		2
147	Role of jellyfish in mesozooplankton community stability in a subtropical bay under the long-term impacts of temperature changes. 2022 , 157627		0
146	Deterministic assembly process dominates bacterial antibiotic resistome in wastewater effluents receiving river.		O
145	Effects of biodegradable and polyethylene film mulches and their residues on soil bacterial communities.		
144	Soil and Soilless Tomato Cultivation Promote Different Microbial Communities That Provide New Models for Future Crop Interventions. 2022 , 23, 8820		2
143	Diverse and distinct bacterial community involved in a full-scale A/O1/H/O2 combination of bioreactors with simultaneous decarbonation and denitrogenation of coking wastewater.		
142	Shared and contrasting associations in the dynamic nano- and picoplankton communities of two close but contrasting sites from the Bay of Biscay.		
141	Toward FAIR Representations of Microbial Interactions.		1
140	Bacterial species metabolic interaction network for deciphering the lignocellulolytic system in fungal cultivating termite gut microbiota. 2022 , 104763		О
139	Graphical Analysis of A Marine Plankton Community Reveals Spatial, Temporal, and Niche Structure of Sub-Communities. 9,		
138	Impact of soil amendments on nitrous oxide emissions and the associated denitrifying communities in a semi-arid environment. 13,		
137	When does a Lotka-Volterra model represent microbial interactions? Insights from in-vitro nasal bacterial communities.		
136	Host or pathogen primed bacterial consortia alters microbial community structures in Arabidopsis roots and suppresses Fusarium oxysporum.		

135	Precise portrayal of microscopic processes of wastewater biofilm formation: Taking SiO2 as the model carrier. 2022 , 849, 157776	
134	Biochar and lime amendments promote soil nitrification and nitrogen use efficiency by differentially mediating ammonia-oxidizer community in an acidic soil. 2022 , 180, 104619	1
133	Vegetation restoration increases the diversity of bacterial communities in deep soils. 2022, 180, 104631	O
132	Species abundance correlations carry limited information about microbial network interactions. 2022 , 18, e1010491	O
131	Hydrological connectivity promotes coalescence of bacterial communities in a floodplain. 13,	O
130	The network perspective: Vertical connections linking organizational levels. 2022 , 473, 110112	O
129	Co-occurrence patterns and community assembly mechanisms of benthic foraminiferal communities in South Chinese bays. 2022 , 144, 109489	O
128	Effect of water chemistry on nitrogen transformation, dissolved organic matter composition and microbial community structure in hyporheic zone sediment columns. 2022 , 215, 114246	O
127	The role of microbial communities on primary producers in aquatic ecosystems: Implications in turbidity stress resistance. 2022 , 215, 114353	O
126	Compartment niche and bamboo variety influence the diversity, composition, network and potential keystone taxa functions of rhizobacterial communities. 2022 , 24, 100593	O
125	The fecal arsenic excretion, tissue arsenic accumulation, and metabolomics analysis in sub-chronic arsenic-exposed mice after in situ arsenic-induced fecal microbiota transplantation. 2023 , 854, 158583	O
124	The plastisphere of biodegradable and conventional microplastics from residues exhibit distinct microbial structure, network and function in plastic-mulching farmland. 2023 , 442, 130011	2
123	Network analysis reveals significant joint effects of microplastics and tetracycline on the gut than the gill microbiome of marine medaka. 2023 , 442, 129996	O
122	Microbial Ecology of Hot Desert Soils. 2022 , 89-110	O
121	Root exudates and rhizosphere soil bacterial relationships of Nitraria tangutorum are linked to k-strategists bacterial community under salt stress. 13,	O
120	Microplastic pollution and enrichment of distinct microbiota in sediment of mangrove in Zhujiang River estuary, China.	O
119	Rhizosphere-induced shift in the composition of bacterial community favors mineralization of crop residue nitrogen.	O
118	Comparison and interpretation of freshwater bacterial structure and interactions with organic to nutrient imbalances in restored wetlands. 13,	O

117	Climate warming restructures seasonal dynamics of grassland soil microbial communities. 2022 , 1, 245-256	O
116	Small molecule modulation of microbiota: a systems pharmacology perspective. 2022 , 23,	О
115	Microbial co-occurrence network in the rhizosphere microbiome: its association with physicochemical properties and soybean yield at a regional scale. 2022 , 60, 986-997	О
114	Impact of Elexacaftor/Tezacaftor/Ivacaftor Therapy on the Cystic Fibrosis Airway Microbial Metagenome.	O
113	Keystone taxa: an emerging area of microbiome research for future disease diagnosis and health safety in human. 2022 , 127203	O
112	Assessment of the Pollution of Soil Heavy Metal(loid)s and Its Relation with Soil Microorganisms in Wetland Soils. 2022 , 14, 12164	O
111	Comparison of assembly process and co-occurrence pattern between planktonic and benthic microbial communities in the Bohai Sea. 13,	О
110	Effective data filtering is prerequisite for robust microbial association network construction. 13,	O
109	Absence of oxygen effect on microbial structure and methane production during drying and rewetting events. 2022 , 12,	O
108	Co-occurrences enhance our understanding of aquatic fungal metacommunity assembly and reveal potential hostparasite interactions.	O
107	Soil microbial community assembly and stability are associated with potato (Solanum tuberosum L.) fitness under continuous cropping regime. 13,	1
106	Functional Guilds, Community Assembly, and Co-occurrence Patterns of Fungi in Metalliferous Mine Tailings Ponds in Mainland China.	O
105	Similar assembly mechanisms but distinct co-occurrence patterns of free-living vs. particle-attached bacterial communities across different habitats and seasons in shallow, eutrophic Lake Taihu. 2022 , 314, 120305	1
104	Effects of wind-wave disturbance and nutrient addition on aquatic bacterial diversity, community composition, and co-occurrence patterns: A mesocosm study. 2022 , 3, 100168	O
103	Subgingival host-microbiome metatranscriptomic changes following scaling and root planning in Grade II / III Periodontitis.	O
102	A comparison of microbial composition under three tree ecosystems using the stochastic process and network complexity approaches. 13,	O
101	Contrasting sea ice conditions shape microbial food webs in Hudson Bay (Canadian Arctic). 2022, 2,	О
100	PANOMICS at the interface of rootBoil microbiome and BNI. 2022 ,	O

99	The maximum entropy principle for compositional data. 2022 , 23,	O
98	Differential Response of Soil Microbial Community Structure in Coal Mining Areas during Different Ecological Restoration Processes. 2022 , 10, 2013	O
97	Plant types shape soil microbial composition, diversity, function, and co-occurrence patterns in the cultivated land of a karst area.	О
96	Soil bacterial community response to cover crop introduction in a wheat-based dryland cropping system. 6,	O
95	synDNAE Synthetic DNA Spike-in Method for Absolute Quantification of Shotgun Metagenomic Sequencing.	O
94	Effects of Microbial Transfer during Food-Gut-Feces Circulation on the Health of Bombyx mori.	1
93	Microbial community structures and important taxa across oxygen gradients in the Andaman Sea and eastern Bay of Bengal epipelagic waters. 13,	O
92	Diversity, community structure and potential functions of root-associated bacterial communities of different wheat (Triticum aestivum) cultivars under field conditions.	O
91	Adaptation of rhizosphere and endosphere microbiome to heavy metal pollution in castor bean. 2022 , 24, 100618	O
90	Oyster culture changed the phosphorus speciation in sediments through biodeposition. 2023 , 216, 114586	O
89	Long-term N addition accelerated organic carbon mineralization in aggregates by shifting microbial community composition. 2023 , 342, 108249	0
88	Targeting keystone species helps restore the dysbiosis of butyrate-producing bacteria in nonalcoholic fatty liver disease.	O
87	Review: Current understanding on biological filtration for the removal of microcystins. 2022, 137160	O
86	Hydrodynamic and anthropogenic disturbances co-shape microbiota rhythmicity and community assembly within intertidal groundwater-surface water continuum.	O
85	Seasonal characterization of the prokaryotic microbiota of full-scale anaerobic UASB reactors treating domestic sewage in southern Brazil.	0
	treating domestic sewage in southern bruzit.	
84	Presence and distribution of triazine herbicides and their effects on microbial communities in the Laizhou Bay, Northern China. 2023 , 186, 114460	O
83	Presence and distribution of triazine herbicides and their effects on microbial communities in the	0

81	Response mechanism of meiofaunal communities to multi-type of artificial reef habitats from the perspective of high-throughput sequencing technology. 2023 , 863, 160927	O
80	Disentangling the impact of straw incorporation on soil microbial communities: Enhanced network complexity and ecological stochasticity. 2023 , 863, 160918	O
79	Clean recovery and recycling of seasonal surplus forage grass by microbial driven anaerobic fermentation: a case study of napiergrass. 2022 , 9,	O
78	Nutritional and host environments determine community ecology and keystone species in a synthetic gut bacterial community.	O
77	Environmental and Anthropogenic Factors Shape the Skin Bacterial Communities of a Semi-Arid Amphibian Species.	O
76	Habitats modulate influencing factors shaping the spatial distribution of bacterial communities along a Tibetan Plateau riverine wetland. 2022 , 160418	O
75	Defining the Benefits of Antibiotic Resistance in Commensals and the Scope for Resistance Optimization.	0
74	Microbial community diversity and function analysis of Aconitum carmichaelii Debeaux in rhizosphere soil of farmlands in Southwest China. 13,	O
73	Inference of dynamic interaction networks: A comparison between Lotka-Volterra and multivariate autoregressive models. 2,	0
7 ²	The helminth holobiont: a multidimensional hostparasitefhicrobiota interaction. 2022,	1
71	Methane supply drives prokaryotic community assembly and networks at cold seeps of the South China Sea.	0
70	Habitats within the plant root differ in bacterial network topology and taxonomic assortativity.	O
69	Dynamic Monitoring of Changes in Fecal Flora of Giant Pandas in Mice: Co-Occurrence Network Reconstruction.	0
68	Combined organic-inorganic fertilization builds higher stability of soil and root microbial networks than exclusive mineral or organic fertilization. 2023 , 5,	O
67	Populus root exudates are associated with rhizosphere microbial communities and symbiotic patterns. 13,	0
66	Decreased precipitation reduced the complexity and stability of bacterial co-occurrence patterns in a semiarid grassland. 13,	O
65	Over-optimism in unsupervised microbiome analysis: Insights from network learning and clustering. 2023 , 19, e1010820	1
64	Biogeographic Pattern and Network of Rhizosphere Fungal and Bacterial Communities in Panicum miliaceum Fields: Roles of Abundant and Rare Taxa. 2023 , 11, 134	O

63	Preliminary analysis of mucosal and salivary bacterial communities in oral lichen planus.	O
62	Effects of milk replacer feeding level on growth performance, rumen development and the ruminal bacterial community in lambs. 13,	O
61	River water influenced by shale gas wastewater discharge for paddy irrigation has limited effects on soil properties and microbial communities. 2023 , 251, 114552	0
60	Soil bacterial community structure and functions but not assembly processes are affected by the conversion from monospecific Cunninghamia lanceolata plantations to mixed plantations. 2023 , 185, 104775	0
59	Continuous cropping of cut chrysanthemum reduces rhizospheric soil bacterial community diversity and co-occurrence network complexity. 2023 , 185, 104801	0
58	The putative maintaining mechanism of gut bacterial ecosystem in giant pandas and its potential application in conservation. 2023 , 16, 36-47	O
57	Facilitative interaction networks in experimental microbial community dynamics.	0
56	Divergence of epibacterial community assemblage correlates with malformation disease severity in Saccharina japonica seedlings. 10,	Ο
55	Clomazone impact on fungal network complexity and stability. 14,	0
54	Declined symptoms in Myrica rubra: The influence of soil acidification and rhizosphere microbial communities. 2023 , 313, 111892	O
53	Geographic patterns of microbial traits of river basins in China. 2023, 871, 162070	O
52	Deciphering microeukaryoticBacterial co-occurrence networks in coastal aquaculture ponds. 2023 , 5, 44-55	O
51	Elevated CO2 and temperature increase arbuscular mycorrhizal fungal diversity, but decrease root colonization, in maize and wheat. 2023 , 873, 162321	O
50	Contributions of plant litter to soil microbial activity improvement and soil nutrient enhancement along with herb and shrub colonization expansions in an arid sandy land. 2023 , 227, 107098	O
49	Spatial and temporal changes in the assembly mechanism and co-occurrence network of the chromophytic phytoplankton communities in coastal ecosystems under anthropogenic influences. 2023 , 877, 162831	0
48	Metagenomics analysis reveals the effects of norfloxacin on the gut microbiota of juvenile common carp (Cyprinus carpio). 2023 , 325, 138389	Ο
47	RNA outperforms DNA-based metabarcoding in assessing the diversity and response of microeukaryotes to environmental variables in the Arctic Ocean. 2023 , 876, 162608	0
46	Depth and contaminant-shaped bacterial community structure and assembly at an aged chlorinated aliphatic hydrocarbon-contaminated site. 2023 , 452, 131220	O

45	Depth-dependent effects of tree species identity on soil microbial community characteristics and multifunctionality. 2023 , 878, 162972	O
44	Distinct community assembly processes and habitat specialization driving the biogeographic patterns of abundant and rare bacterioplankton in a brackish coastal lagoon. 2023 , 879, 163109	O
43	Response of soil fungal community to chromium contamination in agricultural soils with different physicochemical properties. 2023 , 879, 163244	O
42	Revealing the response of microbial communities to polyethylene micro(nano)plastics exposure in cold seep sediment. 2023 , 881, 163366	O
41	Metagenomics and network analysis decipher profiles and co-occurrence patterns of bacterial taxa in soils amended with biogas slurry. 2023 , 877, 162911	O
40	Community dynamics of microbial eukaryotes in intertidal mudflats in the hypertidal Bay of Fundy. 2023 , 3,	O
39	Soil bacterial communities of paddy are dependent on root compartment niches but independent of growth stages from Mollisols of Northeast China. 14,	O
38	Nitrogen application influences the effect of bacteria on the belowground allocation of photosynthesized carbon under elevated CO2. 2023 , 180, 109021	O
37	Proportional stochastic generalized LotkaWolterra model with an application to learning microbial community structures. 2023 , 448, 127932	O
36	Dynamic network modeling of gut microbiota during Alzheimer disease progression in mice. 2023 , 15,	O
35	The ecology of bacterial communities in groundwater of industrial areas: Diversity, composition, network, and assembly. 2023 , 322, 121207	0
34	Winter mulching practice alters soil bacterial communities and networks in lei bamboo (Phyllostachys praecox) forests.	O
33	Assembly and Network Stability of Planktonic Microorganisms under the Influence of Salinity Gradient: an Arctic Case Study from the Lena River Estuary to the Laptev Sea. 2023 , 11,	O
32	Structure and Functional Properties of Bacterial Communities in Surface Sediments of the Recently Declared Nutrient-Saturated Lake Villarrica in Southern Chile.	O
31	Temporal assessment of N-cycle microbial functions in a tropical agricultural soil using gene co-occurrence networks. 2023 , 18, e0281442	O
30	Unravelling microalgal-bacterial interactions in aquatic ecosystems through 16S rRNA gene-based co-occurrence networks. 2023 , 13,	O
29	Comparative Analysis of the Symbiotic Microbiota in the Chinese Mitten Crab (Eriocheir sinensis): Microbial Structure, Co-Occurrence Patterns, and Predictive Functions. 2023 , 11, 544	1
28	From guest to host: parasite Cistanche deserticola shapes and dominates bacterial and fungal community structure and network complexity. 2023 , 18,	O

27	Network analysis of 16S rRNA sequences suggests microbial keystone taxa contribute to marine N2O cycling. 2023 , 6,	О
26	Nitrate has a stronger rhizobacterial-based effect on rice growth and nitrogen use than ammonium in acidic paddy soil.	O
25	Deciphering the microbial community structures and functions of wastewater treatment at high-altitude area. 11,	О
24	Soil Fungal Community Structure and Its Effect on CO2 Emissions in the Yellow River Delta. 2023 , 20, 4190	О
23	Keystone taxa responsible for the microbial community stability and performance of activated sludges.	О
22	Gut microbiota-derived melatonin from Puerariae Lobatae Radix-resistant starch supplementation attenuates ischemic stroke injury via a positive microbial co-occurrence pattern. 2023 , 190, 106714	О
21	Occurrence of OCPs & DCPs and their effects on multitrophic biological communities in riparian groundwater of the Beiluo River, China. 2023 , 253, 114713	О
20	Community differentiation of rhizosphere microorganisms and their responses to environmental factors at different development stages of medicinal plant Glehnia littoralis. 11, e14988	O
19	Community response of soil microorganisms to combined contamination of polycyclic aromatic hydrocarbons and potentially toxic elements in a typical coking plant. 14,	О
18	Rapeseed Domestication Affects the Diversity of Rhizosphere Microbiota. 2023 , 11, 724	O
17	Co-occurrence network of soil bacterial communities in agricultural fields in central Yunnan under different fertilization treatments.	О
16	Sensitive or tolerant functional microorganisms under cadmium stress: suggesting potential specific interaction network characteristics in the rhizosphere system of karst potato. 2023 , 30, 55932-55947	О
15	Contrasting Response of Microeukaryotic and Bacterial Communities to the Interplay of Seasonality and Stochastic Events in Shallow Soda Lakes.	О
14	Identifying keystone species in microbial communities using deep learning.	O
13	The potential to produce tropodithietic acid by Phaeobacter inhibens affects the assembly of microbial biofilm communities in natural seawater. 2023 , 9,	О
12	Exploration of lung mycobiome in the patients with non-small-cell lung cancer. 2023 , 23,	0
11	Changes in the structure and function of rhizosphere soil microbial communities induced by Amaranthus palmeri invasion. 14,	0
10	Niche Modification by Sulfate-Reducing Bacteria Drives Microbial Community Assembly in Anoxic Marine Sediments.	О

9	Short-term responses of plant growth-promoting bacterial community to the herbicides imazethapyr and flumioxazin. 2023 , 328, 138581	Ο
8	Dynamics of Phyllosphere Microbiota and Chemical Parameters at Various Growth Stages and Their Contribution to Anaerobic Fermentation of Pennisetum giganteum.	O
7	Bacterial co-occurrence patterns are more complex but less stable than archaea in enhanced oil recovery applied oil reservoirs. 2023 , 130, 40-49	О
6	Facilitative interaction networks in experimental microbial community dynamics. 14,	Ο
5	Different grazers and grazing practices alter the growth, soil properties, and rhizosphere soil bacterial communities of Medicago ruthenica in the Qinghai-Tibetan Plateau grassland. 2023 , 352, 108522	0
4	Microbial functional genes within soil aggregates drive organic carbon mineralization under contrasting tillage practices.	О
3	Effects of biochar addition on aeolian soil microbial community assembly and structure.	О
2	Gut microbiome responds compositionally and functionally to the seasonal diet variations in wild gibbons. 2023 , 9,	Ο
1	Shifts in composition and co-occurrence patterns of the fish community in the south inshore of Zhejiang, China. 2023 , 44, e02502	0