

Integrated biogeography of planktonic and sedimentary Yangtze River

Microbiome

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Organophosphorus-degrading bacterial community during composting from different sources and their roles in phosphorus transformation. <i>Bioresource Technology</i> , 2018, 264, 277-284.	4.8	31
2	Long-term effects of multi-walled carbon nanotubes on the performance and microbial community structures of an anaerobic granular sludge system. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 9351-9361.	1.7	10
3	Homogeneous selection dominates the microbial community assembly in the sediment of the Three Gorges Reservoir. <i>Science of the Total Environment</i> , 2019, 690, 50-60.	3.9	108
4	Exploration of the antibiotic resistome in a wastewater treatment plant by a nine-year longitudinal metagenomic study. <i>Environment International</i> , 2019, 133, 105270.	4.8	85
5	Quantifying the contribution of microbial immigration in engineered water systems. <i>Microbiome</i> , 2019, 7, 144.	4.9	41
6	Spatial-Temporal Variation of Bacterial Communities in Sediments in Lake Chaohu, a Large, Shallow Eutrophic Lake in China. <i>International Journal of Environmental Research and Public Health</i> , 2019, 16, 3966.	1.2	17
7	Stochastic processes shape microeukaryotic community assembly in a subtropical river across wet and dry seasons. <i>Microbiome</i> , 2019, 7, 138.	4.9	313
8	Biogeography and Diversity of Freshwater Bacteria on a River Catchment Scale. <i>Microbial Ecology</i> , 2019, 78, 324-335.	1.4	7
9	Patterns and assembly processes of planktonic and sedimentary bacterial community differ along a trophic gradient in freshwater lakes. <i>Ecological Indicators</i> , 2019, 106, 105491.	2.6	78
10	Community Assembly Mechanisms Underlying the Core and Random Bacterioplankton and Microeukaryotes in a River Reservoir System. <i>Water (Switzerland)</i> , 2019, 11, 1127.	1.2	29
11	Determination of vertical and horizontal assemblage drivers of bacterial community in a heavily polluted urban river. <i>Water Research</i> , 2019, 161, 98-107.	5.3	85
12	Distinct responses of planktonic and sedimentary bacterial communities to anthropogenic activities: Case study of a tributary of the Three Gorges Reservoir, China. <i>Science of the Total Environment</i> , 2019, 682, 324-332.	3.9	28
13	Bacterial community composition and diversity in Koshi River, the largest river of Nepal. <i>Ecological Indicators</i> , 2019, 104, 501-511.	2.6	32
14	Epiphytic bacterial community composition on the surface of the submerged macrophyte <i>Myriophyllum spicatum</i> in a low-salinity sea area of Hangzhou Bay. <i>Oceanological and Hydrobiological Studies</i> , 2019, 48, 43-55.	0.3	5
15	Coupling growth kinetics modeling with machine learning reveals microbial immigration impacts and identifies key environmental parameters in a biological wastewater treatment process. <i>Microbiome</i> , 2019, 7, 65.	4.9	27
16	Does artificial light at night change the impact of silver nanoparticles on microbial decomposers and leaf litter decomposition in streams?. <i>Environmental Science: Nano</i> , 2019, 6, 1728-1739.	2.2	15
17	Microbial activity and biodiversity responding to contamination of metal(loid) in heterogeneous nonferrous mining and smelting areas. <i>Chemosphere</i> , 2019, 226, 659-667.	4.2	30
18	Antibiotic resistome profile based on metagenomics in raw surface drinking water source and the influence of environmental factor: A case study in Huaihe River Basin, China. <i>Environmental Pollution</i> , 2019, 248, 438-447.	3.7	59

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19	Anammox response to natural and anthropogenic impacts over the Yangtze River. <i>Science of the Total Environment</i> , 2019, 665, 171-180.	3.9	34
20	Small-Scale Heterogeneity in Drinking Water Biofilms. <i>Frontiers in Microbiology</i> , 2019, 10, 2446.	1.5	27
21	Molecular biogeography of planktonic and benthic diatoms in the Yangtze River. <i>Microbiome</i> , 2019, 7, 153.	4.9	50
22	Bacterial community composition shaped by water chemistry and geographic distance in an anthropogenically disturbed river. <i>Science of the Total Environment</i> , 2019, 655, 61-69.	3.9	31
23	Environment-driven geographical distribution of bacterial communities and identification of indicator taxa in Songhua River. <i>Ecological Indicators</i> , 2019, 101, 62-70.	2.6	37
24	Fungal community demonstrates stronger dispersal limitation and less network connectivity than bacterial community in sediments along a large river. <i>Environmental Microbiology</i> , 2020, 22, 832-849.	1.8	115
25	Patterns and processes of free-living and particle-associated bacterioplankton and archaeoplankton communities in a subtropical river-bay system in South China. <i>Limnology and Oceanography</i> , 2020, 65, S161.	1.6	48
26	Implications of water-sediment co-varying trends in large rivers. <i>Science Bulletin</i> , 2020, 65, 4-6.	4.3	6
27	Identifying ecological processes driving vertical and horizontal archaeal community assemblages in a contaminated urban river. <i>Chemosphere</i> , 2020, 245, 125615.	4.2	18
28	Large-sized planktonic bioaggregates possess high biofilm formation potentials: Bacterial succession and assembly in the biofilm metacommunity. <i>Water Research</i> , 2020, 170, 115307.	5.3	31
29	Shifts of bacterial community and molecular ecological network at the presence of fluoroquinolones in a constructed wetland system. <i>Science of the Total Environment</i> , 2020, 708, 135156.	3.9	39
30	Biogeographic pattern of bacterioplanktonic community and potential function in the Yangtze River: Roles of abundant and rare taxa. <i>Science of the Total Environment</i> , 2020, 747, 141335.	3.9	46
31	Bacterial community structure upstream and downstream of cascade dams along the Lancang River in southwestern China. <i>Environmental Science and Pollution Research</i> , 2020, 27, 42933-42947.	2.7	19
32	Seasonal variations of soil bacterial communities in Suaeda wetland of Shuangtaizi River estuary, Northeast China. <i>Journal of Environmental Sciences</i> , 2020, 97, 45-53.	3.2	24
33	Biogeography of eukaryotic plankton communities along the upper Yangtze River: The potential impact of cascade dams and reservoirs. <i>Journal of Hydrology</i> , 2020, 590, 125495.	2.3	25
34	The Behavior of Amphibians Shapes Their Symbiotic Microbiomes. <i>MSystems</i> , 2020, 5, .	1.7	19
35	The shape and speciation of Ag nanoparticles drive their impacts on organisms in a lotic ecosystem. <i>Environmental Science: Nano</i> , 2020, 7, 3167-3177.	2.2	9
36	Structural Characteristics and Driving Factors of the Planktonic Eukaryotic Community in the Danjiangkou Reservoir, China. <i>Water (Switzerland)</i> , 2020, 12, 3499.	1.2	10

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37	Contrast diversity patterns and processes of microbial community assembly in a river-lake continuum across a catchment scale in northwestern China. <i>Environmental Microbiomes</i> , 2020, 15, 10.	2.2	34
38	Characteristics of spatial and seasonal bacterial community structures in a river under anthropogenic disturbances. <i>Environmental Pollution</i> , 2020, 264, 114818.	3.7	51
39	Comammox <i>Nitrospira</i> within the Yangtze River continuum: community, biogeography, and ecological drivers. <i>ISME Journal</i> , 2020, 14, 2488-2504.	4.4	106
40	Microplastics provide new microbial niches in aquatic environments. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 6501-6511.	1.7	217
41	Distinct Assembly Mechanisms Underlie Similar Biogeographic Patterns of Rare and Abundant Bacterioplankton in Cascade Reservoirs of a Large River. <i>Frontiers in Microbiology</i> , 2020, 11, 158.	1.5	37
42	Seasonal effects of river flow on microbial community coalescence and diversity in a riverine network. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	33
43	Variability of Gut Microbiota Across the Life Cycle of <i>Grapholita molesta</i> (Lepidoptera: Tortricidae). <i>Frontiers in Microbiology</i> , 2020, 11, 1366.	1.5	38
44	Changes in the community structure of the symbiotic microbes of wild amphibians from the eastern edge of the Tibetan Plateau. <i>MicrobiologyOpen</i> , 2020, 9, e1004.	1.2	21
45	Metagenomic insights into the profile of antibiotic resistomes in a large drinking water reservoir. <i>Environment International</i> , 2020, 136, 105449.	4.8	65
46	Different response of bacterial community to the changes of nutrients and pollutants in sediments from an urban river network. <i>Frontiers of Environmental Science and Engineering</i> , 2020, 14, 1.	3.3	32
47	Characterization of the normal equine conjunctival bacterial community using culture-independent methods. <i>Veterinary Ophthalmology</i> , 2020, 23, 480-488.	0.6	9
48	Dispersal limitation drives biogeographical patterns of anammox bacterial communities across the Yangtze River. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 5535-5546.	1.7	16
49	Long-term agricultural contamination shaped diversity response of sediment microbiome. <i>Journal of Environmental Sciences</i> , 2021, 99, 90-99.	3.2	13
50	Differential response of microbial diversity and abundance to hydrological residual time and age in cascade reservoirs. <i>Journal of Soils and Sediments</i> , 2021, 21, 1290-1301.	1.5	11
51	Dissolved and emitted methane in the Poyang Lake. <i>Science China Technological Sciences</i> , 2021, 64, 203-212.	2.0	7
52	Microbial diversity accumulates in a downstream direction in the Three Gorges Reservoir. <i>Journal of Environmental Sciences</i> , 2021, 101, 156-167.	3.2	20
53	Determinants of bacterioplankton structures in the typically turbid Weihe River and its clear tributaries from the northern foot of the Qinling Mountains. <i>Ecological Indicators</i> , 2021, 121, 107168.	2.6	10
54	Developing a statistical-weighted index of biotic integrity for large-river ecological evaluations. <i>Journal of Environmental Management</i> , 2021, 277, 111382.	3.8	8

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55	Nitrous oxide (N ₂ O) emissions from a pilot-scale oxidation ditch under different COD/N ratios, aeration rates and two shock-load conditions. <i>Journal of Environmental Management</i> , 2021, 280, 111657.	3.8	16
56	Community structure of bacterioplankton and its relationship with environmental factors in the upper reaches of the Heihe River in Qinghai Plateau. <i>Environmental Microbiology</i> , 2021, 23, 1210-1221.	1.8	25
57	Contrasting community assembly processes structure lotic bacteria metacommunities along the river continuum. <i>Environmental Microbiology</i> , 2021, 23, 484-498.	1.8	50
58	Dams shift microbial community assembly and imprint nitrogen transformation along the Yangtze River. <i>Water Research</i> , 2021, 189, 116579.	5.3	63
59	A study of the gasâ€“water characteristics and their implications for the coalbed methane accumulation modes in the Southern Junggar Basin, China. <i>AAPG Bulletin</i> , 2021, 105, 189-221.	0.7	24
60	Changes in planktonic and sediment bacterial communities under the highly regulated dam in the mid-part of the Three Gorges Reservoir. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 839-852.	1.7	13
61	Diversity and structure of soil bacterial community in intertidal zone of Daliao River estuary, Northeast China. <i>Marine Pollution Bulletin</i> , 2021, 163, 111965.	2.3	9
62	Characteristics of planktonic and sediment bacterial communities in a heavily polluted urban river. <i>PeerJ</i> , 2021, 9, e10866.	0.9	5
63	Biogeographic Pattern of Methanogenic Community in Surface Water along the Yangtze River. <i>Geomicrobiology Journal</i> , 2021, 38, 588-597.	1.0	5
64	Is core bacterial community more vulnerable to environmental changes in dammed river?. <i>IOP Conference Series: Earth and Environmental Science</i> , 2021, 742, 012022.	0.2	1
65	Influence of fish predation on the dynamic of zooplankton and macroinvertebrates in floodplain lakes under different turbidity conditions: an experimental study. <i>Aquatic Sciences</i> , 2021, 83, 1.	0.6	8
66	Disturbances consistently restrain the role of random migration in grassland soil microbial community assembly. <i>Global Ecology and Conservation</i> , 2021, 26, e01452.	1.0	0
67	Effect of Water Chemistry, Land Use Patterns, and Geographic Distances on the Spatial Distribution of Bacterioplankton Communities in an Anthropogenically Disturbed Riverine Ecosystem. <i>Frontiers in Microbiology</i> , 2021, 12, 633993.	1.5	6
68	The Lifestyle-Dependent Microbial Interactions Vary Between Upstream and Downstream of the Three Gorges Dam. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	2
69	Habitats and seasons differentiate the assembly of bacterial communities along a trophic gradient of freshwater lakes. <i>Freshwater Biology</i> , 2021, 66, 1515-1529.	1.2	16
70	Characterization of the bacterioplankton community and the influencing factors in the upper reaches of the Han River basin. <i>Environmental Science and Pollution Research</i> , 2021, 28, 61748-61759.	2.7	2
71	Co-existing water and sediment bacteria are driven by contrasting environmental factors across glacier-fed aquatic systems. <i>Water Research</i> , 2021, 198, 117139.	5.3	81
72	Vertical and horizontal distributions of clinical antibiotic resistance genes and bacterial communities in Danjiangkou Reservoir, China. <i>Environmental Science and Pollution Research</i> , 2021, 28, 61163-61175.	2.7	4

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73	Spatial and Temporal Distribution of Bacterioplankton Molecular Ecological Networks in the Yuan River under Different Human Activity Intensity. <i>Microorganisms</i> , 2021, 9, 1532.	1.6	7
75	Assembly processes and co-occurrence relationships in the bacterioplankton communities of a large river system. <i>Ecological Indicators</i> , 2021, 126, 107643.	2.6	21
76	Microbial abundance and diversity investigations along rivers: Current knowledge and future directions. <i>Wiley Interdisciplinary Reviews: Water</i> , 2021, 8, e1547.	2.8	19
77	Unraveling the bacterial community composition across aquatic sediments in the Southwestern coast of India by employing high-throughput 16S rRNA gene sequencing. <i>Regional Studies in Marine Science</i> , 2021, 46, 101890.	0.4	4
78	Changes in protist communities in drainages across the Pearl River Delta under anthropogenic influence. <i>Water Research</i> , 2021, 200, 117294.	5.3	35
79	Microbiome of permeable sandy substrate in headwater river is shaped by water chemistry rather than grain size and heterogeneity. <i>Science of the Total Environment</i> , 2021, 780, 146552.	3.9	8
80	Characteristics of spatial distribution for microbial ecology inside and outside source water reservoir. <i>Journal of Cleaner Production</i> , 2021, 311, 127697.	4.6	12
81	Estimating aquatic plant diversity and distribution in rivers from Jingjinji region, China, using environmental DNA metabarcoding and a traditional survey method. <i>Environmental Research</i> , 2021, 199, 111348.	3.7	10
82	Exploring the Microbial Ecological Functions in Response to Vertical Gradients in a Polluted Urban River. <i>Clean - Soil, Air, Water</i> , 2021, 49, 2100004.	0.7	5
83	How environmental stress leads to alternative microbiota states in a river ecosystem: A new insight into river restoration. <i>Water Research</i> , 2021, 203, 117538.	5.3	21
84	Distinct profile of bacterial community and antibiotic resistance genes on microplastics in Ganjiang River at the watershed level. <i>Environmental Research</i> , 2021, 200, 111363.	3.7	48
85	Marked Seasonal Variation in Structure and Function of Gut Microbiota in Forest and Alpine Musk Deer. <i>Frontiers in Microbiology</i> , 2021, 12, 699797.	1.5	44
86	Microbial river-to-sea continuum: gradients in benthic and planktonic diversity, osmoregulation and nutrient cycling. <i>Microbiome</i> , 2021, 9, 190.	4.9	29
87	Microbial community coalescence: does it matter in the Three Gorges Reservoir?. <i>Water Research</i> , 2021, 205, 117638.	5.3	34
88	Untangling Microbiota Diversity and Assembly Patterns in the World's Largest Water Diversion Canal. <i>Water Research</i> , 2021, 204, 117617.	5.3	57
89	Response of sediment and water microbial communities to submerged vegetations restoration in a shallow eutrophic lake. <i>Science of the Total Environment</i> , 2021, 801, 149701.	3.9	36
90	Shift of lakeshore cropland to buffer zones greatly reduced nitrogen loss from the soil profile caused by the interaction of lake water and shallow groundwater. <i>Science of the Total Environment</i> , 2022, 803, 150093.	3.9	6
91	Sedimentary microeukaryotes reveal more dispersal limitation and form networks with less connectivity than planktonic microeukaryotes in a highly regulated river. <i>Freshwater Biology</i> , 2021, 66, 826-841.	1.2	13

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92	Benthic microbial biogeography along the continental shelf shaped by substrates from the Changjiang River plume. <i>Acta Oceanologica Sinica</i> , 2022, 41, 118-131.	0.4	7
93	Coupled effects of landscape structures and water chemistry on bacterioplankton communities at multi-spatial scales. <i>Science of the Total Environment</i> , 2022, 811, 151350.	3.9	8
94	Bacterial communities in cascade reservoirs along a large river. <i>Limnology and Oceanography</i> , 2021, 66, 4363-4374.	1.6	17
95	Composition and Functional Characteristics and Influencing Factors of Bacterioplankton Community in the Huangshui River, China. <i>Microorganisms</i> , 2021, 9, 2260.	1.6	4
96	Distinct Composition and Assembly Processes of Bacterial Communities in a River from the Arid Area: Ecotypes or Habitat Types?. <i>Microbial Ecology</i> , 2022, 84, 769-779.	1.4	2
98	Distinct community assembly processes underlie significant spatiotemporal dynamics of abundant and rare bacterioplankton in the Yangtze River. <i>Frontiers of Environmental Science and Engineering</i> , 2022, 16, 1.	3.3	14
99	Genome-centric metagenomics provides new insights into the microbial community and metabolic potential of landfill leachate microbiota. <i>Science of the Total Environment</i> , 2022, 816, 151635.	3.9	7
100	Estuarine gradients dictate spatiotemporal variations of microbiome networks in the Chesapeake Bay. <i>Environmental Microbiomes</i> , 2021, 16, 22.	2.2	18
101	Effects of Three-Layer Encapsulated Tea Tree Oil on Growth Performance, Antioxidant Capacity, and Intestinal Microbiota of Weaned Pigs. <i>Frontiers in Veterinary Science</i> , 2021, 8, 789225.	0.9	10
102	Seasonal variations and co-occurrence networks of bacterial communities in the water and sediment of artificial habitat in Laoshan Bay, China. <i>PeerJ</i> , 2022, 9, e12705.	0.9	4
103	Unveil the role of dissolved and sedimentary metal(loid)s on bacterial communities and metal resistance genes (MRGs) in an urban river of the Qinghai-Tibet Plateau. <i>Water Research</i> , 2022, 211, 118050.	5.3	22
105	Damming river shapes distinct patterns and processes of planktonic bacterial and microeukaryotic communities. <i>Environmental Microbiology</i> , 2022, 24, 1760-1774.	1.8	17
106	The impact of different rotation regime on the soil bacterial and fungal communities in an intensively managed agricultural region. <i>Archives of Microbiology</i> , 2022, 204, 142.	1.0	5
107	Different spatiotemporal dynamics, ecological drivers and assembly processes of bacterial, archaeal and fungal communities in brackish-saline groundwater. <i>Water Research</i> , 2022, 214, 118193.	5.3	15
108	Different Assembly Patterns of Planktonic and Sedimentary Bacterial Community in a Few Connected Eutrophic Lakes. <i>Water (Switzerland)</i> , 2022, 14, 723.	1.2	6
109	Distinct assembly mechanisms of microbial sub-communities with different rarity along the Nu River. <i>Journal of Soils and Sediments</i> , 2022, 22, 1530-1545.	1.5	30
110	Spatiotemporal Dynamics of Bacterial Taxonomic and Functional Profiles in Estuarine Intertidal Soils of China Coastal Zone. <i>Microbial Ecology</i> , 2023, 85, 383-399.	1.4	15
111	Unique bacterial communities associated with components of an artificial aquarium ecosystem and their possible contributions to nutrient cycling in this microecosystem. <i>World Journal of Microbiology and Biotechnology</i> , 2022, 38, 72.	1.7	2

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112	Spatial and Seasonal Patterns of Sediment Bacterial Communities in Large River Cascade Reservoirs: Drivers, Assembly Processes, and Co-occurrence Relationship. <i>Microbial Ecology</i> , 2023, 85, 586-603.	1.4	7
113	Community Structure of Eukaryotic Phytoplankton in Wetland of Golmud River and Its Lower Reaches and Relative Environmental Factors. <i>Diversity</i> , 2022, 14, 269.	0.7	0
114	Nationwide biogeography and health implications of bacterial communities in household drinking water. <i>Water Research</i> , 2022, 215, 118238.	5.3	7
115	Rare biosphere regulates the planktonic and sedimentary bacteria by disparate ecological processes in a large source water reservoir. <i>Water Research</i> , 2022, 216, 118296.	5.3	25
116	Distribution and Assembly Processes of Soil Fungal Communities along an Altitudinal Gradient in Tibetan Plateau. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 1082.	1.5	11
117	Diversity and functions of microbes in surface sediments under heavy metal pollution of western Chaohu Lake. <i>Letters in Applied Microbiology</i> , 2022, 75, 1093-1102.	1.0	2
118	Skin microbiome reconstruction and lipid metabolism profile alteration reveal the treatment mechanism of Cryptotanshinone in the acne rat. <i>Phytomedicine</i> , 2022, 101, 154101.	2.3	5
119	Local-Scale Damming Impact on the Planktonic Bacterial and Eukaryotic Assemblages in the upper Yangtze River. <i>Microbial Ecology</i> , 2023, 85, 1323-1337.	1.4	4
127	Anthropogenic Intensity-Determined Assembly and Network Stability of Bacterioplankton Communities in the Leian River. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	2
128	An Analysis of the Colony Structure of Prokaryotes in the Jialing River Waters in Chongqing. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 5525.	1.2	4
129	Occurrence, source apportionment, and pollution assessment of per- and polyfluoroalkyl substances in a river across rural and urban areas. <i>Science of the Total Environment</i> , 2022, 835, 155505.	3.9	12
130	Spatial turnover of core and occasional bacterial taxa in the plastsphere from a plateau river, China. <i>Science of the Total Environment</i> , 2022, 838, 156179.	3.9	5
131	Bacterioplankton community indicators for seasonal variation in a fragmented subtropical river. <i>Environmental Monitoring and Assessment</i> , 2022, 194, .	1.3	4
132	Environmental conditions and mechanisms restricting microbial methanogenesis in the Miquan region of the southern Junggar Basin, NW China. <i>Bulletin of the Geological Society of America</i> , 2023, 135, 420-434.	1.6	7
133	Biogeographic Patterns and Elevational Differentiation of Sedimentary Bacterial Communities across River Systems in China. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	2
134	Geographic Dispersal Limitation Dominated Assembly Processes of Bacterial Communities on Microplastics Compared to Water and Sediment. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	7
135	Contrasting assembly mechanisms explain the biogeographic patterns of benthic bacterial and fungal communities on the Tibetan Plateau. <i>Environmental Research</i> , 2022, 214, 113836.	3.7	5
136	Riverine bacterioplankton and phytoplankton assembly along an environmental gradient induced by urbanization. <i>Limnology and Oceanography</i> , 2022, 67, 1943-1958.	1.6	21

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137	Co-Occurrence Relationship and Stochastic Processes Affect Sedimentary Archaeal and Bacterial Community Assembly in Estuarineâ€Coastal Margins. <i>Microorganisms</i> , 2022, 10, 1339.	1.6	7
138	Supercarriers of antibiotic resistome in a worldâ€™s large river. <i>Microbiome</i> , 2022, 10, .	4.9	20
139	Comparison of environmental microbiomes in an antibiotic resistance-polluted urban river highlights periphyton and fish gut communities as reservoirs of concern. <i>Science of the Total Environment</i> , 2022, 851, 158042.	3.9	4
140	Biodegradation of early thermogenic gas and generation of secondary microbial gas in the Tieliekedong region of the northern Tarim Basin, NW China. <i>International Journal of Coal Geology</i> , 2022, 261, 104075.	1.9	21
141	Microbial community regulation and performance enhancement in gas biofilters by interrupting bacterial communication. <i>Microbiome</i> , 2022, 10, .	4.9	6
142	Hydrological connectivity promotes coalescence of bacterial communities in a floodplain. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
143	Deep-sea cage culture altered microbial community composition in the sediments of the Yellow Sea Cold Water Mass. <i>Marine Pollution Bulletin</i> , 2022, 183, 114081.	2.3	2
144	Metagenomic insights into resistome coalescence in an urban sewage treatment plant-river system. <i>Water Research</i> , 2022, 224, 119061.	5.3	18
145	Co-occurrence patterns and community assembly mechanisms of benthic foraminiferal communities in South Chinese bays. <i>Ecological Indicators</i> , 2022, 144, 109489.	2.6	1
146	Suspended particulates mediate bacterial community coalescence in different habitats of a large sediment-laden river. <i>Ecological Indicators</i> , 2022, 144, 109462.	2.6	3
147	Microbial plankton responses to perfluoroalkyl acids and their alternatives in the aquatic environment. <i>Journal of Hazardous Materials</i> , 2023, 441, 129980.	6.5	5
148	Comparison of assembly process and co-occurrence pattern between planktonic and benthic microbial communities in the Bohai Sea. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
149	Environmental DNA metabarcoding reveals the impacts of anthropogenic pollution on multitrophic aquatic communities across an urban river of western China. <i>Environmental Research</i> , 2023, 216, 114512.	3.7	3
150	Wastewater treatment effectiveness is facilitated by crucial bacterial communities in the wetland ecosystem. <i>Science of the Total Environment</i> , 2023, 857, 159375.	3.9	11
151	Trends and prospects in the Yangtze River Basin research: A bibliometric analysis. <i>River Research and Applications</i> , 2023, 39, 134-148.	0.7	1
152	Differential patterns and assembly processes of bacterial communities from distinct microhabitats in a subtropical estuary. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
153	Longitudinal patterns of dissolved organic matter quality and bacterial community degradation function along the mainstream of Three Gorges Reservoir during impoundment period. <i>Journal of Hydrology</i> , 2023, 617, 128997.	2.3	3
154	Differences in bacterial diversity, composition, and community networks in lake water across three distinct regions on the Qinghai-Tibet Plateau. <i>Frontiers in Environmental Science</i> , 0, 10, .	1.5	2

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155	Geographical distance, host evolutionary history and diet drive gut microbiome diversity of fish across the Yellow River. <i>Molecular Ecology</i> , 2023, 32, 1183-1196.	2.0	6
156	Effects of Dam Building on Niche Differentiation of Comammox Nitrospira in the Main Stream of the Three Gorges Reservoir Area. <i>Water (Switzerland)</i> , 2022, 14, 4014.	1.2	1
157	Differences in bacterial community composition, structure and function between sediments in waterways and non-navigable channels in a plain river network area. <i>Environmental Science and Pollution Research</i> , 2023, 30, 45910-45923.	2.7	1
158	Analysis of bacterial community distribution characteristics in the downstream section of a cross confluence in a polluted urban channel. <i>Environmental Science and Pollution Research</i> , 2023, 30, 43677-43689.	2.7	0
159	More Robust Co-Occurrence Patterns and Stronger Dispersal Limitations of Bacterial Communities in Wet than Dry Seasons of Riparian Wetlands. <i>MSystems</i> , 2023, 8, .	1.7	9
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