Structure of the rare archaeal biosphere and seasonal dy surface coastal waters

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Citation Report

#	Article	IF	Citations
1	Spatiotemporal distributions of rare bacterioplankton populations indicate adaptive strategies in the oligotrophic ocean. Aquatic Microbial Ecology, 2013, 71, 1-13.	0.9	90
3	LIMNOLOGY AND THE PERFECT STORM. Limnology and Oceanography Bulletin, 2013, 22, 70-70.	0.2	1
4	Tropical Aquatic Archaea Show Environment-Specific Community Composition. PLoS ONE, 2013, 8, e76321.	1.1	10
6	The Expanded Diversity of Methylophilaceae from Lake Washington through Cultivation and Genomic Sequencing of Novel Ecotypes. PLoS ONE, 2014, 9, e102458.	1.1	62
7	Linking activity and function to ecosystem dynamics in a coastal bacterioplankton community. Frontiers in Microbiology, 2014, 5, 185.	1.5	55
8	Diversity and seasonal dynamics of airborne archaea. Biogeosciences, 2014, 11, 6067-6079.	1.3	36
9	Single bacterial strain capable of significant contribution to carbon cycling in the surface ocean. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7202-7207.	3.3	207
10	<scp>N</scp>itrospinaâ€like bacteria are the main drivers of nitrite oxidation in the seasonal upwelling area of the <scp>E</scp>astern <scp>S</scp>outh <scp>P</scp>acific (<scp>C</scp>entral <scp>C</scp>hile â¼36Â°<scp>S</scp>). Environmental Microbiology Reports, 2014, 6, 565-573.	1.0	54
11	Planktonic Euryarchaeota are a significant source of archaeal tetraether lipids in the ocean. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9858-9863.	3.3	134
12	Winterâ€“Summer Succession of Unicellular Eukaryotes in a Meso-eutrophic Coastal System. Microbial Ecology, 2014, 67, 13-23.	1.4	39
13	Genomic differentiation among two strains of the PS1 clade isolated from geographically separated marine habitats. FEMS Microbiology Ecology, 2014, 89, 181-197.	1.3	22
14	Diversity of rare and abundant bacteria in surface waters of the Southern Adriatic Sea. Marine Genomics, 2014, 17, 9-15.	0.4	24
15	Olivine alteration and H2 production in carbonate-rich, low temperature aqueous environments. Planetary and Space Science, 2014, 96, 51-61.	0.9	51
16	Rare taxa have potential to make metabolic contributions in enhanced biological phosphorus removal ecosystems. Environmental Microbiology, 2015, 17, 4979-4993.	1.8	68
17	Introduction: Mesocosms and Microcosms. Springer Protocols, 2015, , 1-13.	0.1	2
18	Ecosystem productivity is associated with bacterial phylogenetic distance in surface marine waters. Molecular Ecology, 2015, 24, 5785-5795.	2.0	25
19	Marine Group II Archaea, potentially important players in the global ocean carbon cycle. Frontiers in Microbiology, 2015, 6, 1108.	1.5	119
20	Seasonal variations of marine protist community structure based on taxon-specific traits using the eastern English Channel as a model coastal system. FEMS Microbiology Ecology, 2015, 91, .	1.3	53

#	Article	IF	Citations
21	Bacterial communities in sediments of Lake Baikal from areas with oil and gas discharge. Aquatic Microbial Ecology, 2015, 76, 95-109.	0.9	25
22	Marine microbial community dynamics and their ecological interpretation. Nature Reviews Microbiology, 2015, 13, 133-146.	13.6	681
23	The hidden seasonality of the rare biosphere in coastal marine bacterioplankton. Environmental Microbiology, 2015, 17, 3766-3780.	1.8	109
24	Temporal dynamics of active <scp>A</scp>rchaea in oxygenâ€depleted zones of two deep lakes. Environmental Microbiology Reports, 2015, 7, 321-329.	1.0	31
25	Depth shapes Î±â€•and Î²â€diversities of microbial eukaryotes in surficial sediments of coastal ecosystems. Environmental Microbiology, 2015, 17, 3722-3737.	1.8	98
26	Disentangling seasonal bacterioplankton population dynamics by highâ€frequency sampling. Environmental Microbiology, 2015, 17, 2459-2476.	1.8	142
27	Seasonal dynamics of active SAR11 ecotypes in the oligotrophic Northwest Mediterranean Sea. ISME Journal, 2015, 9, 347-360.	4.4	93
28	Is Planktonic Diversity Well Recorded in Sedimentary DNA? Toward the Reconstruction of Past Protistan Diversity. Microbial Ecology, 2015, 70, 865-875.	1.4	55
29	Ecophysiology of uncultivated marine euryarchaea is linked to particulate organic matter. ISME Journal, 2015, 9, 1747-1763.	4.4	94
30	Capturing prokaryotic dark matter genomes. Research in Microbiology, 2015, 166, 814-830.	1.0	16
31	Resuscitation of the rare biosphere contributes to pulses of ecosystem activity. Frontiers in Microbiology, 2015, 6, 24.	1.5	174
32	Temporal Dynamics of Active Prokaryotic Nitrifiers and Archaeal Communities from River to Sea. Microbial Ecology, 2015, 70, 473-483.	1.4	26
33	Diversity of marine microbes in a changing Mediterranean Sea. Rendiconti Lincei, 2015, 26, 49-58.	1.0	15
34	Next-generation sequencing propels environmental genomics to the front line of research. Heredity, 2015, 114, 429-430.	1.2	14
35	Global dispersion and local diversification of the methane seep microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4015-4020.	3.3	248
36	Unusually low TEX86 values in the transitional zone between Pearl River estuary and coastal South China Sea: Impact of changing archaeal community composition. Chemical Geology, 2015, 402, 18-29.	1.4	42
37	Evidence for an active rare biosphere within freshwater protists community. Molecular Ecology, 2015, 24, 1236-1247.	2.0	85
38	Ecology and exploration of the rare biosphere. Nature Reviews Microbiology, 2015, 13, 217-229.	13.6	926

#	Article	IF	Citations
39	Primers: Functional Genes and 16S rRNA Genes for Methanogens. Springer Protocols, 2015, , 79-139.	0.1	3
40	Rarity in aquatic microbes: placing protists on the map. Research in Microbiology, 2015, 166, 831-841.	1.0	69
41	Metabolic characterization of a model heterotrophic bacterium capable of significant chemical alteration of marine dissolved organic matter. Marine Chemistry, 2015, 177, 357-365.	0.9	18
42	A new class of marine Euryarchaeota group II from the mediterranean deep chlorophyll maximum. ISME Journal, 2015, 9, 1619-1634.	4.4	95
43	Community Composition of Known and Uncultured Archaeal Lineages in Anaerobic or Anoxic Wastewater Treatment Sludge. Microbial Ecology, 2015, 69, 586-596.	1.4	59
44	High Diversity of Anaerobic Alkane-Degrading Microbial Communities in Marine Seep Sediments Based on (1-methylalkyl)succinate Synthase Genes. Frontiers in Microbiology, 2015, 6, 1511.	1.5	47
45	Diversity and Dynamics of Active Small Microbial Eukaryotes in the Anoxic Zone of a Freshwater Meromictic Lake (Pavin, France). Frontiers in Microbiology, 2016, 7, 130.	1.5	41
46	Molecular Evidence for Metabolically Active Bacteria in the Atmosphere. Frontiers in Microbiology, 2016, 7, 772.	1.5	82
47	Bacterial Dormancy Is More Prevalent in Freshwater than Hypersaline Lakes. Frontiers in Microbiology, 2016, 7, 853.	1.5	39
48	Response of Core Microbial Consortia to Chronic Hydrocarbon Contaminations in Coastal Sediment Habitats. Frontiers in Microbiology, 2016, 7, 1637.	1.5	76
49	Variable but persistent coexistence of Prochlorococcus ecotypes along temperature gradients in the ocean's surface mixed layer. Environmental Microbiology Reports, 2016, 8, 272-284.	1.0	24
50	Depth-dependent and seasonal variability in archaeal community structure in the subarctic and subtropical western North Pacific. Journal of Oceanography, 2016, 72, 427-438.	0.7	8
51	Insensitivity of Diverse and Temporally Variable Particle-Associated Microbial Communities to Bulk Seawater Environmental Parameters. Applied and Environmental Microbiology, 2016, 82, 3431-3437.	1.4	70
52	Variability of nitrifying communities in surface coastal waters of the Eastern South Pacific (â^¼36Â° S). Environmental Microbiology Reports, 2016, 8, 851-864.	1.0	26
53	Anaerobic digester bioaugmentation influences quasi steady state performance and microbial community. Water Research, 2016, 104, 128-136.	5.3	54
54	Dense water plumes modulate richness and productivity of deep sea microbes. Environmental Microbiology, 2016, 18, 4537-4548.	1.8	17
55	Study of Prokaryotes and Viruses in Aquatic Ecosystems by Metagenetic and Metagenomic Approaches. , 2016, , 245-254.		2
56	Diversity and Biogeography of Picoeukaryotes: New Insights into the Rare Biosphere. , 2016, , 315-328.		1

#	Article	IF	Citations
57	Microorganism-regulated mechanisms of temperature effects on the performance of anaerobic digestion. Microbial Cell Factories, 2016, 15, 96.	1.9	45
58	Diversity at low abundance: The phenomenon of the rare bacterial biosphere. Microbiology, 2016, 85, 272-282.	0.5	18
59	Consortia of low-abundance bacteria drive sulfate reduction-dependent degradation of fermentation products in peat soil microcosms. ISME Journal, 2016, 10, 2365-2375.	4.4	159
60	A novel conceptual approach to read-filtering in high-throughput amplicon sequencing studies. Nucleic Acids Research, 2016, 44, e40-e40.	6.5	35
61	Temperature affects microbial abundance, activity and interactions in anaerobic digestion. Bioresource Technology, 2016, 209, 228-236.	4.8	84
62	Marine microbial community structure assessed from combined metagenomic analysis and ribosomal amplicon deep-sequencing. Marine Biology Research, 2016, 12, 30-42.	0.3	3
63	Competitive strategies differentiate closely related species of marine actinobacteria. ISME Journal, 2016, 10, 478-490.	4.4	44
64	Growth Rates of Microbes in the Oceans. Annual Review of Marine Science, 2016, 8, 285-309.	5.1	218
65	Marine Bacterioplankton Seasonal Succession Dynamics. Trends in Microbiology, 2017, 25, 494-505.	3.5	210
66	Temporal and spatial variations in the composition of freshwater photosynthetic picoeukaryotes revealed by MiSeq sequencing from flow cytometry sorted samples. Environmental Microbiology, 2017, 19, 2286-2300.	1.8	25
67	Tropical Meromictic Lakes: Specifics of Meromixis and Case Studies of Lakes Tanganyika, Malawi, and Matano. Ecological Studies, 2017, , 277-323.	0.4	12
68	The response of archaeal species to seasonal variables in a subtropical aerated soil: insight into the low abundant methanogens. Applied Microbiology and Biotechnology, 2017, 101, 6505-6515.	1.7	7
69	Distinct succession patterns of abundant and rare bacteria in temporal microcosms with pollutants. Environmental Pollution, 2017, 225, 497-505.	3.7	77
70	Marked seasonality and high spatial variation in estuarine ciliates are driven by exchanges between the â€˜abundantâ€™ and â€˜intermediateâ€™ biospheres. Scientific Reports, 2017, 7, 9494.	1.6	27
71	Searching for signatures across microbial communities: Metagenomic analysis of soil samples from mangrove and other ecosystems. Scientific Reports, 2017, 7, 8859.	1.6	50
72	Marine archaeal dynamics and interactions with the microbial community over 5 years from surface to seafloor. ISME Journal, 2017, 11, 2510-2525.	4.4	80
73	Investigation and manipulation of metabolically active methanogen community composition during rumen development in black goats. Scientific Reports, 2017, 7, 422.	1.6	51
74	Identifying the core seed bank of a complex boreal bacterial metacommunity. ISME Journal, 2017, 11, 2012-2021.	4.4	18

#	Article	IF	Citations
75	Biogeography and ecological diversity patterns of rare and abundant bacteria in oilâ€contaminated soils. Molecular Ecology, 2017, 26, 5305-5317.	2.0	220
76	Abundant and rare picoeukaryotic subâ€communities present contrasting patterns in the epipelagic waters of marginal seas in the northwestern <scp>P</scp>acific <scp>O</scp>cean. Environmental Microbiology, 2017, 19, 287-300.	1.8	183
77	Low abundant soil bacteria can be metabolically versatile and fast growing. Ecology, 2017, 98, 555-564.	1.5	83
78	Arsenic Contamination in Agricultural Soil Reduces Metabolic Activity of Total and Free-Living Nitrogen-Fixing Bacteria as Revealed by Real-Time qPCR. Soil and Sediment Contamination, 2017, 26, 736-748.	1.1	7
79	Community structure of rare methanogenic archaea: insight from a single functional group. FEMS Microbiology Ecology, 2017, 93, .	1.3	16
80	Overview of freshwater microbial eukaryotes diversity: a first analysis of publicly available metabarcoding data. FEMS Microbiology Ecology, 2017, 93, .	1.3	132
81	Parasitic Eukaryotes in a Meso-Eutrophic Coastal System with Marked Phaeocystis globosa Blooms. Frontiers in Marine Science, 2017, 4, .	1.2	18
82	Changes in Metabolically Active Bacterial Community during Rumen Development, and Their Alteration by Rhubarb Root Powder Revealed by 16S rRNA Amplicon Sequencing. Frontiers in Microbiology, 2017, 8, 159.	1.5	34
83	Exploring the Ecological Coherence between the Spatial and Temporal Patterns of Bacterioplankton in Boreal Lakes. Frontiers in Microbiology, 2017, 8, 636.	1.5	13
84	Sustaining Rare Marine Microorganisms: Macroorganisms As Repositories and Dispersal Agents of Microbial Diversity. Frontiers in Microbiology, 2017, 8, 947.	1.5	66
85	Variation of Oxygenation Conditions on a Hydrocarbonoclastic Microbial Community Reveals Alcanivorax and Cycloclasticus Ecotypes. Frontiers in Microbiology, 2017, 8, 1549.	1.5	21
86	Bacterial, Archaeal, and Eukaryotic Diversity across Distinct Microhabitats in an Acid Mine Drainage. Frontiers in Microbiology, 2017, 8, 1756.	1.5	88
87	Patterns and Processes in Marine Microeukaryotic Community Biogeography from Xiamen Coastal Waters and Intertidal Sediments, Southeast China. Frontiers in Microbiology, 2017, 8, 1912.	1.5	108
88	Basin Scale Variation on the Composition and Diversity of Archaea in the Pacific Ocean. Frontiers in Microbiology, 2017, 8, 2057.	1.5	21
89	Evaluating Production of Cyclopentyl Tetraethers by Marine Group II Euryarchaeota in the Pearl River Estuary and Coastal South China Sea: Potential Impact on the TEX86 Paleothermometer. Frontiers in Microbiology, 2017, 8, 2077.	1.5	13
90	Changes in Microbial (Bacteria and Archaea) Plankton Community Structure after Artificial Dispersal in Grazer-Free Microcosms. Microorganisms, 2017, 5, 31.	1.6	3
91	Ultrarare marine microbes contribute to key sulphurâ€related ecosystem functions. Molecular Ecology, 2018, 27, 1494-1504.	2.0	14
92	Seasonal and depth-wise variations in bacterial and archaeal groups in the Arabian Sea oxygen minimum zone. Deep-Sea Research Part II: Topical Studies in Oceanography, 2018, 156, 4-18.	0.6	20

#	Article	IF	Citations
93	Integrating Dispersants in Oil Spill Response in Arctic and Other Icy Environments. Environmental Science & Technology, 2018, 52, 6098-6112.	4.6	43
94	The diversity and biogeography of abundant and rare intertidal marine microeukaryotes explained by environment and dispersal limitation. Environmental Microbiology, 2018, 20, 462-476.	1.8	112
95	Analysis of airborne microbial communities using 16S ribosomal RNA: Potential bias due to air sampling stress. Science of the Total Environment, 2018, 621, 939-947.	3.9	18
96	Localized high abundance of Marine Group II archaea in the subtropical Pearl River Estuary: implications for their niche adaptation. Environmental Microbiology, 2018, 20, 734-754.	1.8	53
97	Deep ocean prokaryotic communities are remarkably malleable when facing longâ€term starvation. Environmental Microbiology, 2018, 20, 713-723.	1.8	35
98	First evidence of the presence and activity of archaeal C3 group members in an Atlantic intertidal mudflat. Scientific Reports, 2018, 8, 11790.	1.6	5
99	GLOSSary: the GLobal Ocean 16S subunit web accessible resource. BMC Bioinformatics, 2018, 19, 443.	1.2	4
100	Abundant and Rare Microbial Biospheres Respond Differently to Environmental and Spatial Factors in Tibetan Hot Springs. Frontiers in Microbiology, 2018, 9, 2096.	1.5	45
101	Toward an Intensive Longitudinal Understanding of Activated Sludge Bacterial Assembly and Dynamics. Environmental Science & Technology, 2018, 52, 8224-8232.	4.6	32
102	Diversity of Rare and Abundant Prokaryotic Phylotypes in the Prony Hydrothermal Field and Comparison with Other Serpentinite-Hosted Ecosystems. Frontiers in Microbiology, 2018, 9, 102.	1.5	23
103	Conditionally Rare Taxa Contribute but Do Not Account for Changes in Soil Prokaryotic Community Structure. Frontiers in Microbiology, 2018, 9, 809.	1.5	12
104	Diversity and potential activity patterns of planktonic eukaryotic microbes in a mesoeutrophic coastal area (eastern English Channel). PLoS ONE, 2018, 13, e0196987.	1.1	13
105	Fine metagenomic profile of the Mediterranean stratified and mixed water columns revealed by assembly and recruitment. Microbiome, 2018, 6, 128.	4.9	95
106	Diversity and distribution of Archaea in global estuarine ecosystems. Science of the Total Environment, 2018, 637-638, 349-358.	3.9	62
107	Ammonia oxidizers in the sea-surface microlayer of a coastal marine inlet. PLoS ONE, 2018, 13, e0202636.	1.1	7
108	A strong link between marine microbial community composition and function challenges the idea of functional redundancy. ISME Journal, 2018, 12, 2470-2478.	4.4	180
109	High contribution of ammonia-oxidizing archaea (AOA) to ammonia oxidation related to a potential active AOA species in various arable land soils. Journal of Soils and Sediments, 2019, 19, 1077-1087.	1.5	23
110	Genomic ecology of Marine Group II, the most common marine planktonic Archaea across the surface ocean. MicrobiologyOpen, 2019, 8, e00852.	1.2	27

#	Article	IF	Citations
111	Microbial assembly, interaction, functioning, activity and diversification: a review derived from community compositional data. Marine Life Science and Technology, 2019, 1, 112-128.	1.8	104
112	Diversity and geochemical community assembly processes of the living rare biosphere in a sand-and-gravel aquifer ecosystem in the Midwestern United States. Scientific Reports, 2019, 9, 13484.	1.6	14
113	Metagenomic Characterization Reveals Pronounced Seasonality in the Diversity and Structure of the Phyllosphere Bacterial Community in a Mediterranean Ecosystem. Microorganisms, 2019, 7, 518.	1.6	13
114	Niche differentiation among annually recurrent coastal Marine Group II Euryarchaeota. ISME Journal, 2019, 13, 3024-3036.	4.4	41
115	Comparative evaluation of three archaeal primer pairs for exploring archaeal communities in deep-sea sediments and permafrost soils. Extremophiles, 2019, 23, 747-757.	0.9	12
116	Metabolic diversity within the globally abundant Marine Group II Euryarchaea offers insight into ecological patterns. Nature Communications, 2019, 10, 271.	5.8	66
117	Dynamics of microbial communities across the three domains of life over an annual cycle with emphasis on marine mucilage in the Southern Bay of Biscay resolved by microbial fingerprinting. Continental Shelf Research, 2019, 186, 127-137.	0.9	6
118	Dominant role of abundant rather than rare bacterial taxa in maintaining agro-soil microbiomes under environmental disturbances. Chemosphere, 2019, 235, 248-259.	4.2	115
119	Archaeal biogeography and interactions with microbial community across complex subtropical coastal waters. Molecular Ecology, 2019, 28, 3101-3118.	2.0	23
120	Limits of our knowledge, part 2: Selected frontiers in marine organic biogeochemistry. Marine Chemistry, 2019, 212, 16-46.	0.9	23
121	Archaeal Sources of Intact Membrane Lipid Biomarkers in the Oxygen Deficient Zone of the Eastern Tropical South Pacific. Frontiers in Microbiology, 2019, 10, 765.	1.5	21
122	Long-Term Transcriptional Activity at Zero Growth of a Cosmopolitan Rare Biosphere Member. MBio, 2019, 10, .	1.8	35
123	Elevated level of arsenic negatively influences nifH gene expression of isolated soil bacteria in culture condition as well as soil system. Environmental Geochemistry and Health, 2019, 41, 1953-1966.	1.8	5
124	Scaling of species distribution explains the vast potential marine prokaryote diversity. Scientific Reports, 2019, 9, 18710.	1.6	8
125	Planktonic Marine Archaea. Annual Review of Marine Science, 2019, 11, 131-158.	5.1	129
126	A phylogenomic and ecological analysis of the globally abundant Marine Group II archaea (Ca.) Tj ETQq1 1 0.784314 rgBT /Ove	4.4	158
127	A De Novo Robust Clustering Approach for Amplicon-Based Sequence Data. Journal of Computational Biology, 2019, 26, 618-624.	0.8	2
128	Ecology of Rare Microorganisms. , 2019, , 90-90.		0

#	Article	IF	Citations
129	Rhythmicity of coastal marine picoeukaryotes, bacteria and archaea despite irregular environmental perturbations. ISME Journal, 2019, 13, 388-401.	4.4	105
130	Patterns and processes of freeâ€living and particleâ€associated bacterioplankton and archaeaplankton communities in a subtropical riverâ€bay system in South China. Limnology and Oceanography, 2020, 65, S161.	1.6	48
131	Spatioâ€temporal insights into microbiology of the freshwaterâ€toâ€hypersaline, oxicâ€hypoxicâ€euxinicÂwaters ofÂUrsu Lake. Environmental Microbiology, 2021, 23, 3523-3540.	1.8	25
132	Effect of Clinoptilolite and Halloysite Addition on Biogas Production and Microbial Community Structure during Anaerobic Digestion. Materials, 2020, 13, 4127.	1.3	4
133	Transient Dynamics of Archaea and Bacteria in Sediments and Brine Across a Salinity Gradient in a Solar Saltern of Goa, India. Frontiers in Microbiology, 2020, 11, 1891.	1.5	16
134	Functional Seasonality of Free-Living and Particle-Associated Prokaryotic Communities in the Coastal Adriatic Sea. Frontiers in Microbiology, 2020, 11, 584222.	1.5	9
135	Prokaryotic Diversity and Distribution Along Physical and Nutrient Gradients in the Tunisian Coastal Waters (South Mediterranean Sea). Frontiers in Microbiology, 2020, 11, 593540.	1.5	9
136	Seasonal Niche Partitioning of Surface Temperate Open Ocean Prokaryotic Communities. Frontiers in Microbiology, 2020, 11, 1749.	1.5	14
137	Biogeochemistry and hydrography shape microbial community assembly and activity in the eastern tropical North Pacific Ocean oxygen minimum zone. Environmental Microbiology, 2021, 23, 2765-2781.	1.8	12
138	Mesozooplankton taurine production and prokaryotic uptake in the northern Adriatic Sea. Limnology and Oceanography, 2020, 65, 2730-2747.	1.6	4
139	Seasonal Water Level Fluctuation and Concomitant Change of Nutrients Shift Microeukaryotic Communities in a Shallow Lake. Water (Switzerland), 2020, 12, 2317.	1.2	9
140	Characteristics and implications of isoprenoid and hydroxy tetraether lipids in hadal sediments of Mariana and Yap Trenches. Chemical Geology, 2020, 551, 119742.	1.4	8
141	Distinct assembly mechanisms underlie similar biogeographical patterns of rare and abundant bacteria in Tibetan Plateau grassland soils. Environmental Microbiology, 2020, 22, 2261-2272.	1.8	77
142	The Link Between the Ecology of the Prokaryotic Rare Biosphere and Its Biotechnological Potential. Frontiers in Microbiology, 2020, 11, 231.	1.5	37
143	Biogeographic patterns of abundant and rare bacterial and microeukaryotic subcommunities in connected freshwater lake zones subjected to different levels of nutrient loading. Journal of Applied Microbiology, 2021, 130, 123-132.	1.4	6
144	Differential response of abundant and rare bacterial subcommunities to abiotic and biotic gradients across temperate deserts. Science of the Total Environment, 2021, 763, 142942.	3.9	13
145	The microbial rare biosphere: current concepts, methods and ecological principles. FEMS Microbiology Ecology, 2021, 97, .	1.3	61
146	Seasonality of archaeal proteorhodopsin and associated Marine Group IIb ecotypes (Ca.) Tj ETQq1 1 0.784314 rgBT /Overlock	4.4	9

#	Article	IF	Citations
147	Benchmarking microbial growth rate predictions from metagenomes. ISME Journal, 2021, 15, 183-195.	4.4	52
148	Small-Scale Variability in Bacterial Community Structure in Different Soil Types. Microbial Ecology, 2021, 82, 470-483.	1.4	5
149	Biogeographical Distribution and Community Assembly of Active Protistan Assemblages along an Estuary to a Basin Transect of the Northern South China Sea. Microorganisms, 2021, 9, 351.	1.6	6
150	Marine Group-II archaea dominate particle-attached as well as free-living archaeal assemblages in the surface waters of Kongsfjorden, Svalbard, Arctic Ocean. Antonie Van Leeuwenhoek, 2021, 114, 633-647.	0.7	9
151	Transcriptional activity differentiates families of Marine Group II Euryarchaeota in the coastal ocean. ISME Communications, 2021, 1, .	1.7	2
153	Seasonal marine microorganisms change neighbours under contrasting environmental conditions. Environmental Microbiology, 2021, 23, 2592-2604.	1.8	18
154	Seasonal succession of microbes in different size-fractions and their modular structures determined by both macro- and micro-environmental filtering in dynamic coastal waters. Science of the Total Environment, 2021, 784, 147046.	3.9	18
155	Planktonic Archaeal Ether Lipid Origins in Surface Waters of the North Pacific Subtropical Gyre. Frontiers in Microbiology, 2021, 12, 610675.	1.5	5
156	Distinct patterns of abundant and rare subcommunities in paddy soil during wettingâ€“drying cycles. Science of the Total Environment, 2021, 785, 147298.	3.9	14
157	Reduction in VOC emissions by intermittent aeration in bioreactor landfills with gas-water joint regulation. Environmental Pollution, 2021, 290, 118059.	3.7	10
158	Dynamics and ecological distributions of the Archaea microbiome from inland saline lakes (Monegros) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.3	11
161	Seasonal variation in marine-snow-associated and ambient-water prokaryotic communities in the northern Adriatic Sea. Aquatic Microbial Ecology, 2014, 73, 211-224.	0.9	41
162	Lifestyles of rarity: understanding heterotrophic strategies to inform the ecology of the microbial rare biosphere. Aquatic Microbial Ecology, 2016, 78, 51-63.	0.9	39
164	Response of the rare biosphere to environmental stressors in a highly diverse ecosystem (Zodletone) Tj ETQq1 1 0.784314 rgBT /Over	0.9	40
165	Metabarcoding monitoring analysis: the pros and cons of using co-extracted environmental DNA and RNA data to assess offshore oil production impacts on benthic communities. PeerJ, 2017, 5, e3347.	0.9	101
166	Prokaryotic responses to a warm temperature anomaly in northeast subarctic Pacific waters. Communications Biology, 2021, 4, 1217.	2.0	14
169	â€œDeciphering Archaeal Communitiesâ€•Omics Tools in the Study of Archaeal Communities. Methods in Molecular Biology, 2016, 1399, 1-28.	0.4	0
173	A simplified synthetic community rescues Astragalus mongholicus from root rot disease by activating plant-induced systemic resistance. Microbiome, 2021, 9, 217.	4.9	78

#	Article	IF	Citations
175	The influence of the Doce River mouth on the microbiome of nearby coastal areas three years after the FundÃ£o Dam failure, Brazil. Science of the Total Environment, 2022, 807, 151777.	3.9	7
176	Interactions Between Marine Group II Archaea and Phytoplankton Revealed by Population Correlations in the Northern Coast of South China Sea. Frontiers in Microbiology, 2021, 12, 785532.	1.5	6
177	Metagenomic assemblage genomes analyses reveal the polysaccharides hydrolyzing potential of marine group II euryarchaea. Environmental Research, 2022, 209, 112865.	3.7	6
178	Dynamics of actively dividing prokaryotes in the western Mediterranean Sea. Scientific Reports, 2022, 12, 2064.	1.6	3
180	Biodiversity and Biogeography of Abundant and Rare Microbial Assemblages in the Western Subtropical Pacific Ocean. Frontiers in Microbiology, 2022, 13, 839562.	1.5	6
181	Archaeal diversity in the seawater of Changjiang River estuary reveals its adaptability to bottom seawaters. Journal of Oceanology and Limnology, 2022, 40, 1051-1069.	0.6	1
182	Compositional Changes and Co-Occurrence Patterns of Planktonic Bacteria and Microeukaryotes in a Subtropical Estuarine Ecosystem, the Pearl River Delta. Water (Switzerland), 2022, 14, 1227.	1.2	2
183	Microbial Diversity in a North Western Mediterranean Sea Shallow Coastal Lagoon Under Contrasting Water Temperature Conditions. Frontiers in Marine Science, 2022, 9, .	1.2	4
216	Differentiated Evolutionary Strategies of Genetic Diversification in Atlantic and Pacific Thaumarchaeal Populations. MSystems, 2022, 7, .	1.7	3
217	Seasonal Succession and Temperature Response Pattern of a Microbial Community in the Yellow Sea Cold Water Mass. Applied and Environmental Microbiology, 2022, 88, .	1.4	4
218	Characterization of anaerobic oxidation of methane and microbial community in landfills with aeration. Environmental Research, 2022, 214, 114102.	3.7	5
219	Seasonal microbial dynamics in the ocean inferred from assembled and unassembled data: a view on the unknown biosphere. ISME Communications, 2022, 2, .	1.7	1
220	Characteristic pollutants and microbial community in underlying soils for evaluating landfill leakage. Waste Management, 2023, 155, 269-280.	3.7	6
221	Metabarcoding of the Three Domains of Life in Aquatic Saline Ecosystems. Methods in Molecular Biology, 2023, , 17-35.	0.4	0
222	Water mass age and dissolved organic matter properties drive the diversity of pelagic prokaryotes in the Western Mediterranean Sea. Deep-Sea Research Part I: Oceanographic Research Papers, 2023, 196, 104022.	0.6	0
223	Electric-Inducive Microbial Interactions in a Thermophilic Anaerobic Digester Revealed by High-Throughput Sequencing of Micron-Scale Single Flocs. Environmental Science & Technology, 2023, 57, 4367-4378.	4.6	5
224	Prokaryotic Diversity and Dynamics during Dinoflagellate Bloom Decays in Coastal Tunisian Waters. Diversity, 2023, 15, 273.	0.7	1