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DOI: 10.1038/nrmicro1341

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2232	Can landscape ecology untangle the complexity of antibiotic resistance?. <i>Nature Reviews Microbiology</i> , 2006 , 4, 943-52	22.2	117
2231	Winogradsky and modern microbiology. 2006 , 75, 501-511		16

2230	The marine viromes of four oceanic regions. 2006 , 4, e368	726
2229	Nonrandom distribution of <i>Burkholderia pseudomallei</i> clones in relation to geographical location and virulence. 2006 , 44, 2553-7	68
2228	Phylogenetic comparisons of bacterial communities from serpentine and nonserpentine soils. 2006 , 72, 6965-71	47
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2226	Evolutionary history of <i>Salmonella typhi</i> . 2006 , 314, 1301-4	281
2225	Annually reoccurring bacterial communities are predictable from ocean conditions. 2006 , 103, 13104-9	453
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2223	The power of species sorting: local factors drive bacterial community composition over a wide range of spatial scales. 2007 , 104, 20404-9	327
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2221	Diversification of lupine <i>Bradyrhizobium</i> strains: evidence from nodulation gene trees. 2007 , 73, 3254-64	107
2220	Natural merodiploidy of the lux-rib operon of <i>Photobacterium leiognathi</i> from coastal waters of Honshu, Japan. 2007 , 189, 6148-58	18
2219	Phylogeography of the thermophilic cyanobacterium <i>Mastigocladus laminosus</i> . 2007 , 73, 4751-9	65
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2217	Biogeography of bacterioplankton in lakes and streams of an Arctic tundra catchment. 2007 , 88, 1365-78	134
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2210	Phylogenetic ecology of the freshwater Actinobacteria acI lineage. 2007 , 73, 7169-76		157
2209	Measuring species richness based on microbial community fingerprints: the emperor has no clothes. 2007 , 73, 2399-401; author reply 2399-401		91
2208	Environmental controls on the landscape-scale biogeography of stream bacterial communities. 2007 , 88, 2162-73		157
2207	Ecology and spatial pattern of cyanobacterial community island patches in the Atacama Desert, Chile. 2007 , 112, n/a-n/a		24
2206	A comparison of taxon co-occurrence patterns for macro- and microorganisms. 2007 , 88, 1345-53		190
2205	Infectious diseases in wildlife: the community ecology context. 2007 , 5, 533-539		84
2204	Introduction to Molecular Analysis of Ectomycorrhizal Communities. 2007 , 71, 601-610		12
2203	Biodiversity scaling relationships: are microorganisms fundamentally different?. 2007 , 129-149		5
2202	Microbes and metals: interactions in the environment. 2007 , 47, 453-67		260
2201	Microbial landscapes: new paths to biofilm research. <i>Nature Reviews Microbiology</i> , 2007 , 5, 76-81	22.2	239
2200	Erratum: Can landscape ecology untangle the complexity of antibiotic resistance?. <i>Nature Reviews Microbiology</i> , 2007 , 5, 82-82	22.2	4
2199	The nineteenth century roots of 'everything is everywhere'. <i>Nature Reviews Microbiology</i> , 2007 , 5, 647-51	22.2	143
2198	Visualization, modelling and prediction in soil microbiology. <i>Nature Reviews Microbiology</i> , 2007 , 5, 689-99	22.2	122
2197	Improvements of high-throughput culturing yielded novel SAR11 strains and other abundant marine bacteria from the Oregon coast and the Bermuda Atlantic Time Series study site. 2007 , 1, 361-71		127
2196	The biogeographical distribution of closely related freshwater sediment bacteria is determined by environmental selection. 2007 , 1, 596-605		12
2195	The distance decay of similarity in ecological communities. 2007 , 30, 3-12		662

2194	Bacterial community profiles of endodontic abscesses from Brazilian and USA subjects as compared by denaturing gradient gel electrophoresis analysis. 2007 , 22, 14-8	58
2193	Distinct protistan assemblages characterize the euphotic zone and deep sea (2500 m) of the western North Atlantic (Sargasso Sea and Gulf Stream). 2007 , 9, 1219-32	122
2192	Spatial-temporal variability in diazotroph assemblages in Chesapeake Bay using an oligonucleotide nifH microarray. 2007 , 9, 1823-35	43
2191	Variation in gene content among geographically diverse <i>Sulfolobus</i> isolates. 2008 , 10, 137-46	11
2190	Global phylogeography of marine <i>Synechococcus</i> and <i>Prochlorococcus</i> reveals a distinct partitioning of lineages among oceanic biomes. 2008 , 10, 147-61	289
2189	Does size matter for dispersal distance?. 2007 , 16, 415-425	242
2188	Host islands within the California Northern Channel Islands create fine-scale genetic structure in two sympatric species of the symbiotic ectomycorrhizal fungus <i>Rhizopogon</i> . 2007 , 16, 1811-22	55
2187	Vibrios of the spotted rose snapper <i>Lutjanus guttatus</i> Steindachner, 1869 from northwestern Mexico. 2007 , 102, 1518-26	23
2186	Archaeal diversity in naturally occurring and impacted environments from a tropical region. 2007 , 103, 141-51	27
2185	DISTRIBUTION, PHYLOGENY, AND GROWTH OF COLD-ADAPTED PICOPRASINOPHYTES IN ARCTIC SEAS1. 2007 , 43, 78-89	248
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2182	Particle-attached and free-living bacterial communities in a contrasting marine environment: Victoria Harbor, Hong Kong. 2007 , 61, 496-508	87
2181	Multivariate analyses in microbial ecology. 2007 , 62, 142-60	1108
2180	Microorganisms, macroorganisms and ecology. Proceedings of a joint symposium of the Society for General Microbiology, Environmental Microbiology Group, and the British Ecological Society. September 13, 2006. York, United Kingdom. 2007 , 62, 133-232	6
2179	DNA evidence for global dispersal and probable endemism of protozoa. 2007 , 7, 162	96
2178	Accelerated biodegradation of pesticides: An overview of the phenomenon, its basis and possible solutions; and a discussion on the tropical dimension. 2007 , 26, 1733-1746	113
2177	Allopatric divergence, secondary contact, and genetic isolation in wild yeast populations. 2007 , 17, 407-11	100

2176	Biodiversity and ecosystem functioning in coastal lagoons: Does microbial diversity play any role?. 2007 , 75, 4-12	71
2175	An assessment of potential diatom "barcode" genes (cox1, rbcL, 18S and ITS rDNA) and their effectiveness in determining relationships in Sellaphora (Bacillariophyta). 2007 , 158, 349-64	239
2174	Metagenomic and small-subunit rRNA analyses reveal the genetic diversity of bacteria, archaea, fungi, and viruses in soil. 2007 , 73, 7059-66	406
2173	Global isolation by distance despite strong regional phylogeography in a small metazoan. 2007 , 7, 225	62
2172	Quantitative phylogenetic assessment of microbial communities in diverse environments. 2007 , 315, 1126-30	259
2171	Size doesn't matter: towards a more inclusive philosophy of biology. 2007 , 22, 155-191	101
2170	Diversity of 16S rRNA gene, ITS region and aclB gene of the Aquificales. 2007 , 11, 57-64	36
2169	Distribution and diversity of aquatic protists: an evolutionary and ecological perspective. 2008 , 17, 243-259	89
2168	The diversity and distribution of diatoms: from cosmopolitanism to narrow endemism. 2008 , 17, 393-405	168
2167	Relationship of geographic distance, depth, temperature, and viruses with prokaryotic communities in the eastern tropical Atlantic Ocean. 2008 , 56, 383-9	24
2166	Novel archaea and bacteria dominate stable microbial communities in North America's Largest Hot Spring. 2008 , 56, 292-305	24
2165	Thermophilic bacteria in cool temperate soils: are they metabolically active or continually added by global atmospheric transport?. 2008 , 78, 841-52	48
2164	Microbial communities and immigration in volcanic environments of Canary Islands (Spain). 2008 , 95, 307-15	20
2163	The spatial and temporal distribution of microalgae in the South China Sea: evidence from GIS-based analysis of 18S rDNA sequences. 2008 , 51, 1121-8	5
2162	Vertical distribution of bacterial and archaeal communities along discrete layers of a deep-sea cold sediment sample at the East Pacific Rise (approximately 13 degrees N). 2008 , 12, 573-85	19
2161	Genetic and phenotypic evidence for Streptomyces griseus ecovars isolated from a beach and dune sand system. 2008 , 94, 63-74	40
2160	Aquatic Microbial Ecology: Water Desert, Microcosm, Ecosystem. What's Next?. 2008 , 93, 606-623	14
2159	Protistan Grazing on Marine Bacterioplankton. 383-441	77

2158	Bacterial and Archaeal Community Structure and its Patterns. 45-90		46
2157	Microbial biogeography: from taxonomy to traits. 2008 , 320, 1039-43		414
2156	A planet of bacteria. 2008 , 78, 144-151		7
2155	Potential for atmospheric deposition of bacteria to influence bacterioplankton communities. 2008 , 64, 388-94		32
2154	Chickpea rhizobia symbiosis genes are highly conserved across multiple Mesorhizobium species. 2008 , 66, 391-400		63
2153	Metabolic evidence for biogeographic isolation of the extremophilic bacterium <i>Salinibacter ruber</i> . 2008 , 2, 242-53		83
2152	Differences in soil bacterial diversity: driven by contemporary disturbances or historical contingencies?. 2008 , 2, 254-64		136
2151	Distantly sampled soils carry few species in common. 2008 , 2, 901-10		128
2150	Microbial endemism: does phosphorus limitation enhance speciation?. <i>Nature Reviews Microbiology</i> , 2008 , 6, 559-64	22.2	74
2149	Molecular eco-systems biology: towards an understanding of community function. <i>Nature Reviews Microbiology</i> , 2008 , 6, 693-9	22.2	284
2148	Worlds within worlds: evolution of the vertebrate gut microbiota. <i>Nature Reviews Microbiology</i> , 2008 , 6, 776-88	22.2	1042
2147	CILIATE-SYMBIONT SPECIFICITY OF FRESHWATER ENDOSYMBIOTIC CHLORELLA (TREBOUXIOPHYCEAE, CHLOROPHYTA)(1). 2008 , 44, 77-84		53
2146	Recent evolutionary diversification of a protist lineage. 2008 , 10, 1231-43		25
2145	Volcanic calderas delineate biogeographic provinces among Yellowstone thermophiles. 2008 , 10, 1681-9		56
2144	Microbial community composition in soils of Northern Victoria Land, Antarctica. 2008 , 10, 1713-24		120
2143	High beta diversity of bacteria in the shallow terrestrial subsurface. 2008 , 10, 2537-49		33
2142	Diversification of unicellular eukaryotes: cryptomonad colonizations of marine and fresh waters inferred from revised 18S rRNA phylogeny. 2008 , 10, 2635-44		50
2141	Environmental distribution and population biology of <i>Candidatus Accumulibacter</i> , a primary agent of biological phosphorus removal. 2008 , 10, 2692-703		87

2140	ORIGINAL ARTICLE: Origins of Bradyrhizobium nodule symbionts from two legume trees in the Philippines. 2008 , 35, 1030-1039	15
2139	Isolation by distance in the spore-forming soil bacterium Myxococcus xanthus. 2008 , 18, 386-91	72
2138	Biodiversity, chemical diversity and drug discovery. 2008 , 65, 141, 143-74	21
2137	Evidence of biogeography in surface ocean bacterioplankton assemblages. 2008 , 1, 55-61	7
2136	A biophysical perspective on dispersal and the geography of evolution in marine and terrestrial systems. 2008 , 5, 135-50	53
2135	Resource partitioning and sympatric differentiation among closely related bacterioplankton. 2008 , 320, 1081-5	389
2134	Microbiology of Extreme Soils. 2008 ,	15
2133	Actinomycetes from Sediments in the Trondheim Fjord, Norway: Diversity and Biological Activity. 2008 , 6, 12-24	106
2132	Profiling of root canal bacterial communities associated with chronic apical periodontitis from Brazilian and Norwegian subjects. 2008 , 34, 1457-61	40
2131	Genetic diversity of Metarhizium anisopliae var. anisopliae in southwestern British Columbia. 2008 , 98, 101-13	42
2130	Unveiling new microbial eukaryotes in the surface ocean. 2008 , 11, 213-8	137
2129	'Everything is everywhere: but the environment selects': ubiquitous distribution and ecological determinism in microbial biogeography. 2008 , 39, 314-25	129
2128	The Ediacaran microbiota and the survival of Snowball Earth conditions. 2008 , 167, 1-15	68
2127	Biodiversity: Extracting Lessons from Extreme Soils. 2008 , 71-84	2
2126	Comparative molecular analysis of endoevaporitic microbial communities. 2008 , 74, 6444-6	38
2125	. 2008 , 47, 437-450	53
2124	Biogeography of Bacterioplankton in Inland Waters. 2008 , 1, 99-114	71
2123	Progress in the Ecological Genetics and Biodiversity of Freshwater Bacteria. 2008 , 58, 103-113	26

2122	Diversity predicts stability and resource use efficiency in natural phytoplankton communities. 2008 , 105, 5134-8	334
2121	Multilocus sequence analysis for assessment of the biogeography and evolutionary genetics of four <i>Bradyrhizobium</i> species that nodulate soybeans on the asiatic continent. 2008 , 74, 6987-96	155
2120	Community Structure of the Mediterranean Fruit Fly Microbiota: Seasonal and Spatial Sources of Variation. 2008 , 54, 181-191	34
2119	Changes in microbial community structure in the wake of Hurricanes Katrina and Rita. 2008 , 42, 9072-8	33
2118	Spatial scaling of functional gene diversity across various microbial taxa. 2008 , 105, 7768-73	223
2117	A latitudinal diversity gradient in planktonic marine bacteria. 2008 , 105, 7774-8	473
2116	Bacterial community composition in Central European running waters examined by temperature gradient gel electrophoresis and sequence analysis of 16S rRNA genes. 2008 , 74, 188-99	61
2115	Macroecology of Microbes [Biogeography of the Glomeromycota. 2008 , 529-563	29
2114	Biome-level biogeography of streambed microbiota. 2008 , 74, 3014-21	28
2113	Biogeographic and phylogenetic diversity of thermoacidophilic cyanidiales in Yellowstone National Park, Japan, and New Zealand. 2008 , 74, 2822-33	90
2112	Islands shaping thought in microbial ecology. 2008 , 64, 167-82	10
2111	Water masses and biogeography of picoeukaryote assemblages in a cold hydrographically complex system. 2008 , 53, 922-935	70
2110	Microbial Ecology. 2008 , 2357-2368	2
2109	IV.9 Seascape Microbial Ecology: Habitat Structure, Biodiversity, and Ecosystem Function. 2009 , 488-500	3
2108	Air-dispersed phytoplankton in a Mediterranean River-Reservoir System (Aliakmon-Polyphytos, Greece). 2009 , 31, 877-884	42
2107	Bacterial community composition of stream biofilms in spatially variable-flow environments. 2009 , 75, 7189-95	90
2106	Bar-coded pyrosequencing reveals shared bacterial community properties along the temperature gradients of two alkaline hot springs in Yellowstone National Park. 2009 , 75, 4565-72	150
2105	Ecology. Seeing the big picture on microbe distribution. 2009 , 325, 1506-7	19

2104	Controls on diatom biogeography in the ocean. 2009 , 325, 1539-41	112
2103	Social interactions and distribution of <i>Bacillus subtilis</i> pherotypes at microscale. 2009 , 191, 1756-64	69
2102	Hidden levels of phylodiversity in Antarctic green algae: further evidence for the existence of glacial refugia. 2009 , 276, 3591-9	120
2101	GenGIS: A geospatial information system for genomic data. 2009 , 19, 1896-904	91
2100	Quantitative community fingerprinting methods for estimating the abundance of operational taxonomic units in natural microbial communities. 2009 , 75, 2495-505	196
2099	Diversity and distribution of anaeromyxobacter strains in a uranium-contaminated subsurface environment with a nonuniform groundwater flow. 2009 , 75, 3679-87	40
2098	Genetic diversity patterns in five protist species occurring in lakes. 2009 , 160, 301-17	39
2097	Three different phototrophic microbial communities colonizing a single natural shelter containing prehistoric paintings. 2009 , 407, 4876-81	19
2096	Influence of hydrological fluxes on the structure of nitrate-reducing bacteria communities in a peatland. 2009 , 41, 1289-1300	8
2095	Environmental and spatial characterisation of bacterial community composition in soil to inform sampling strategies. 2009 , 41, 2292-2298	103
2094	Bacterial community composition in thermophilic microbial mats from five hot springs in central Tibet. 2009 , 13, 139-49	103
2093	May Rapoport's rule apply to human associated pathogens?. 2009 , 6, 509-21	13
2092	Enrichment and identification of polycyclic aromatic compound-degrading bacteria enriched from sediment samples. 2009 , 20, 521-31	7
2091	Site identity and moss species as determinants of soil microbial community structure in Norway spruce forests across three vegetation zones. 2009 , 318, 81-91	8
2090	Unique community structure and biogeography of soybean rhizobia in the saline-alkaline soils of Xinjiang, China. 2009 , 324, 291-305	83
2089	Novel associations between rhizobial populations and legume species within the genera <i>Lathyrus</i> and <i>Oxytropis</i> grown in the temperate region of China. 2009 , 52, 182-92	10
2088	Population structure of <i>Symbiodinium</i> sp. associated with the common sea fan, <i>Gorgonia ventalina</i> , in the Florida Keys across distance, depth, and time. 2009 , 156, 1609-1623	43
2087	The biogeography of ammonia-oxidizing bacterial communities in soil. 2009 , 58, 435-45	110

2086	Fungal-fungal associations affect the assembly of endophyte communities in maize (<i>Zea mays</i>). 2009 , 58, 668-78	49
2085	Microbial community response to seawater amendment in low-salinity tidal sediments. 2009 , 58, 558-68	53
2084	Massively parallel tag sequencing reveals the complexity of anaerobic marine protistan communities. 2009 , 7, 72	168
2083	Phylogeographic reconstruction of a bacterial species with high levels of lateral gene transfer. 2009 , 7, 78	129
2082	Soil biodiversity monitoring in Europe: ongoing activities and challenges. 2009 , 60, 807-819	85
2081	Bacterial community structure of glacier forefields on siliceous and calcareous bedrock. 2009 , 60, 860-870	52
2080	Bacterial 'cosmopolitanism' and importance of local environmental factors for community composition in remote high-altitude lakes. 2009 , 55, 994-1005	57
2079	Litter quality is in the eye of the beholder: initial decomposition rates as a function of inoculum characteristics. 2009 , 23, 627-636	219
2078	Local-regional diversity relationship varies with spatial scale in lotic diatoms. 2009 , 36, 720-727	23
2077	Discovery of a large clonal patch of a social amoeba: implications for social evolution. 2009 , 18, 1273-81	21
2076	Microbial biodiversity in groundwater ecosystems. 2009 , 54, 649-677	346
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2074	Biogeography of two cold-adapted genera: <i>Psychrobacter</i> and <i>Exiguobacterium</i> . 2009 , 3, 658-65	69
2073	Time- and sediment depth-related variations in bacterial diversity and community structure in subtidal sands. 2009 , 3, 780-91	123
2072	Salt marsh sediment bacteria: their distribution and response to external nutrient inputs. 2009 , 3, 924-34	51
2071	Biodiversity of benthic microbial communities in bioturbated coastal sediments is controlled by geochemical microniches. 2009 , 3, 1269-85	130
2070	Microbial community structure and its functional implications. 2009 , 459, 193-9	742
2069	The importance of dispersal related and local factors in shaping the taxonomic structure of diatom metacommunities. 2009 , 118, 1239-1249	148

2068	Response of bacterioplankton community structures to hydrological conditions and anthropogenic pollution in contrasting subtropical environments. 2009 , 69, 449-60	22
2067	Taxonomic resolution, ecotypes and the biogeography of <i>Prochlorococcus</i> . 2009 , 11, 823-32	155
2066	Species-sorting may explain an apparent minimal effect of immigration on freshwater bacterial community dynamics. 2009 , 11, 905-13	72
2065	Comparison of the microbial diversity at different depths of the GISP2 Greenland ice core in relationship to deposition climates. 2009 , 11, 640-56	76
2064	An interlaboratory comparison of 16S rRNA gene-based terminal restriction fragment length polymorphism and sequencing methods for assessing microbial diversity of seafloor basalts. 2009 , 11, 1728-35	29
2063	Comparison of the structure and composition of bacterial communities from temperate and tropical freshwater ecosystems. 2009 , 11, 2339-50	81
2062	Influences of space, soil, nematodes and plants on microbial community composition of chalk grassland soils. 2010 , 12, 2096-106	37
2061	Biogeography of wetland rice methanotrophs. 2010 , 12, 862-72	82
2060	Impact of space, time and complex environments on microbial communities. 2009 , 15 Suppl 1, 60-2	2
2059	Bacterial and Archaeal Diversity in Permafrost. 2009 , 59-72	24
2058	Pyrosequencing-based assessment of soil pH as a predictor of soil bacterial community structure at the continental scale. 2009 , 75, 5111-20	2437
2057	The rare species <i>Synura lapponica</i> (Synurophyceae) new to the Czech Republic, local vs. global diversity in colonial synurophytes. 2009 , 64, 1070-1075	4
2056	Biogeographic patterns in genomic diversity among a large collection of <i>Vibrio cholerae</i> isolates. 2009 , 75, 1658-66	27
2055	Environmental proteomics: a paradigm shift in characterizing microbial activities at the molecular level. 2009 , 73, 62-70	103
2054	Afforestation alters the composition of functional genes in soil and biogeochemical processes in South American grasslands. 2009 , 75, 6240-8	52
2053	Soil microbial community response to nitrogen enrichment in two scrub oak forests. 2009 , 258, 1383-1390	20
2052	Infrequent marine-freshwater transitions in the microbial world. 2009 , 17, 414-22	230
2051	Current insights into phage biodiversity and biogeography. 2009 , 12, 582-7	66

2050	Testing the functional significance of microbial community composition. 2009 , 90, 441-51	505
2049	Microbial biogeography of six salt lakes in Inner Mongolia, China, and a salt lake in Argentina. 2009 , 75, 5750-60	91
2048	Bacterial community variation in human body habitats across space and time. 2009 , 326, 1694-7	2168
2047	Mycorrhizal Symbioses and Plant Invasions. 2009 , 40, 699-715	308
2046	Evolutionary Biology of Drug Resistance. 2009 , 9-32	4
2045	Local biodiversity patterns in micrometazoans: Are tardigrades everywhere?. 2009 , 7, 259-268	29
2044	Bacteria, Distribution and Community Structure. 2009 , 201-210	3
2043	Ecology of the rare microbial biosphere of the Arctic Ocean. 2009 , 106, 22427-32	411
2042	Sociobiology of the myxobacteria. 2009 , 63, 599-623	167
2041	Spatial and temporal diversity of methanotrophs in a landfill cover soil are differentially related to soil abiotic factors. 2009 , 1, 398-407	30
2040	Picoeukaryotes. 2009 , 674-688	2
2039	Microbial Community Profiling for the Characterisation of Soil Evidence: Forensic Considerations. 2009 , 49-60	15
2038	Marine Habitats. 2009 , 258-277	2
2037	Microbial biodiversity and ecosystem functioning under controlled conditions and in the wild. 2009 , 121-133	21
2036	Contrasting the influences of stream inputs and landscape position on bacterioplankton community structure and dissolved organic matter composition in high-elevation lake chains. 2009 , 54, 1292-1305	36
2035	Effect of Saharan dust inputs on bacterial activity and community composition in Mediterranean lakes and reservoirs. 2009 , 54, 869-879	95
2034	A functional guide to functional diversity measures. 2009 , 49-59	22
2033	Introduction: the ecological and social implications of changing biodiversity. An overview of a decade of biodiversity and ecosystem functioning research. 2009 , 3-13	6

2032	Bacteria in the global atmosphere [Part 1: Review and synthesis of literature data for different ecosystems. 2009 , 9, 9263-9280	358
2031	Biogeography of terrestrial cyanobacteria from Antarctic ice-free areas. 2010 , 51, 171-177	40
2030	Soil microbial community structure in an Asian dust source region (Loess plateau). 2010 , 25, 53-7	10
2029	Effect of ocean acidification on microbial diversity and on microbe-driven biogeochemistry and ecosystem functioning. 2010 , 61, 291-305	130
2028	The spatial factor, rather than elevated CO ₂ controls the soil bacterial community in a temperate Forest Ecosystem. 2010 , 76, 7429-36	28
2027	Associations among rhizobial chromosomal background, nod genes, and host plants based on the analysis of symbiosis of indigenous rhizobia and wild legumes native to Xinjiang. 2010 , 59, 311-23	13
2026	Is there a size limit for cosmopolitan distribution in free-living microorganisms? A biogeographical analysis of testate amoebae from polar areas. 2010 , 59, 635-45	47
2025	Bacterial community composition in an Arctic phytoplankton mesocosm bloom: the impact of silicate and glucose. 2010 , 33, 1557-1565	18
2024	Microbial community shifts influence patterns in tropical forest nitrogen fixation. 2010 , 164, 521-31	97
2023	Differential aerosolization of algal and cyanobacterial particles in the atmosphere. 2010 , 50, 468-73	33
2022	Community analysis of ammonia-oxidizing bacteria in activated sludge of eight wastewater treatment systems. 2010 , 22, 627-34	46
2021	Patterns of genetic diversity in the marine heterotrophic flagellate <i>Oxyrrhis marina</i> (Alveolata: Dinophyceae). 2010 , 161, 212-21	31
2020	Microbial communities and their relevance for ecosystem models: Decomposition as a case study. 2010 , 42, 529-535	259
2019	Plot-scale manipulations of organic matter inputs to soils correlate with shifts in microbial community composition in a lowland tropical rain forest. 2010 , 42, 2153-2160	169
2018	EnvMine: a text-mining system for the automatic extraction of contextual information. 2010 , 11, 294	14
2017	Phylogeography and sexual macrocyst formation in the social amoeba <i>Dictyostelium giganteum</i> . 2010 , 10, 17	11
2016	Environmental distribution of prokaryotic taxa. 2010 , 10, 85	141
2015	The little bacteria that can - diversity, genomics and ecophysiology of 'Dehalococcoides' spp. in contaminated environments. 2010 , 3, 389-402	93

2014	Masters of miniaturization: convergent evolution among interstitial eukaryotes. 2010 , 32, 430-7	43
2013	Statistical methods for estimating complexity from competition experiments between two populations. 2010 , 264, 1043-6	4
2012	Ecological assessment of groundwater ecosystems [Vision or illusion?]. 2010 , 36, 1174-1190	75
2011	The online database MaarjAM reveals global and ecosystemic distribution patterns in arbuscular mycorrhizal fungi (Glomeromycota). 2010 , 188, 223-41	623
2010	Geographical patterns of micro-organismal community structure: are diatoms ubiquitously distributed across boreal streams?. 2010 , 119, 129-137	126
2009	Patterns of <i>Fusarium</i> community structure and abundance in relation to spatial, abiotic and biotic factors in soil. 2010 , 71, 34-42	17
2008	Drivers of bacterial colonization patterns in stream biofilms. 2010 , 72, 47-57	33
2007	Biogeography of thermophilic cyanobacteria: insights from the Zerka Ma'in hot springs (Jordan). 2010 , 72, 103-13	31
2006	Spatio-temporal variations in protistan communities along an O/HS gradient in the anoxic Framvaren Fjord (Norway). 2010 , 72, 89-102	57
2005	The relative importance of local conditions and regional processes in structuring aquatic plant communities. 2010 , 55, 952-966	103
2004	Local factors control the community composition of cyanobacteria in lakes while heterotrophic bacteria follow a neutral model. 2010 , 55, 2447-2457	32
2003	Multiple marker parallel tag environmental DNA sequencing reveals a highly complex eukaryotic community in marine anoxic water. 2010 , 19 Suppl 1, 21-31	706
2002	Life history determines biogeographical patterns of soil bacterial communities over multiple spatial scales. 2010 , 19, 4315-27	104
2001	Complex phylogeographic patterns in the freshwater alga <i>Synura</i> provide new insights into ubiquity vs. endemism in microbial eukaryotes. 2010 , 19, 4328-38	65
2000	Biogeographical patterns of freshwater micro- and macroorganisms: a comparison between phytoplankton, zooplankton and fish in the eastern Mediterranean. 2010 , 37, 1341-1351	45
1999	Bacterial diversity and biogeography in deep-sea surface sediments of the South Atlantic Ocean. 2010 , 4, 159-70	170
1998	Evolutionary divergence and biogeography of sympatric niche-differentiated bacterial populations. 2010 , 4, 488-97	52
1997	Species sorting affects bacterioplankton community composition as determined by 16S rDNA and 16S rRNA fingerprints. 2010 , 4, 729-38	76

1996	[FeFe]-hydrogenase in Yellowstone National Park: evidence for dispersal limitation and phylogenetic niche conservatism. 2010 , 4, 1485-95	56
1995	Experimental tests of the bacterial distance-decay relationship. 2010 , 4, 1357-65	155
1994	Phylogeographic separation of marine and soil myxobacteria at high levels of classification. 2010 , 4, 1520-30	28
1993	Site and plant species are important determinants of the Methylobacterium community composition in the plant phyllosphere. 2010 , 4, 719-28	217
1992	Community structures of ammonia-oxidising archaea and bacteria in high-altitude lakes on the Tibetan Plateau. 2010 , 55, 2375-2390	46
1991	Regional invariance among microbial communities. 2010 , 13, 118-27	100
1990	Invisible invaders: non-pathogenic invasive microbes in aquatic and terrestrial ecosystems. 2010 , 13, 1560-72	169
1989	Soil bacterial diversity in the Arctic is not fundamentally different from that found in other biomes. 2010 , 12, 2998-3006	432
1988	Land use and climatic factors structure regional patterns in soil microbial communities. 2010 , 19, 27-39	203
1987	Broad-scale environmental response and niche conservatism in lacustrine diatom communities. 2010 , 19, no-no	13
1986	. 2010 ,	20
1985	454-pyrosequencing: a molecular battiscope for freshwater viral ecology. 2010 , 1, 210-26	11
1984	Hutchinson Reversed, or Why There Need to Be So Many Species. 2010 , 1-43	43
1983	When Microscopic Organisms Inform General Ecological Theory. 2010 , 43, 45-85	16
1982	Linkage, Selection, and the Clonal Complex. 2010 , 19-35	7
1981	Biodiversity and biogeography of the atmosphere. 2010 , 365, 3645-53	218
1980	Biogeography and biodiversity in sulfide structures of active and inactive vents at deep-sea hydrothermal fields of the Southern Mariana Trough. 2010 , 76, 2968-79	65
1979	Determination of the diversity of Rhodopirellula isolates from European seas by multilocus sequence analysis. 2010 , 76, 776-85	29

1978	Community structure of subsurface biofilms in the thermal sulfidic caves of Acquasanta Terme, Italy. 2010 , 76, 5902-10	46
1977	Impacts of inter- and intralaboratory variations on the reproducibility of microbial community analyses. 2010 , 76, 7451-8	29
1976	Polyphasic evaluation of <i>Aphanizomenon issatschenkoi</i> and <i>Raphidiopsis mediterranea</i> in a Mediterranean lake. 2010 , 32, 927-936	25
1975	Eukaryotic Microorganisms and Stone Biodeterioration. 2010 , 27, 630-646	53
1974	Latitudinal patterns in the abundance of major marine bacterioplankton groups. 2010 , 61, 179-189	84
1973	Scaling community structure: how bacteria, fungi, and ant taxocenes differentiate along a tropical forest floor. 2010 , 91, 2221-6	16
1972	Multi-element fingerprinting and high throughput sequencing identify multiple elements that affect fungal communities in <i>Quercus macrocarpa</i> foliage. 2010 , 5, 1157-61	4
1971	Metagenomics and the Units of Biological Organization. 2010 , 60, 102-112	39
1970	Marine isolates of <i>Aspergillus flavus</i> : denizens of the deep or lost at sea?. 2010 , 3, 386-391	13
1969	Phytoplankton biogeography and community stability in the ocean. 2010 , 5, e10037	38
1968	Biogeography and habitat modelling of high-alpine bacteria. 2010 , 1, 53	113
1967	Multilevel analysis of the bacterial diversity along the environmental gradient R� de la Plata South Atlantic Ocean. 2010 , 61, 57-72	20
1966	Indoor fungal composition is geographically patterned and more diverse in temperate zones than in the tropics. 2010 , 107, 13748-53	282
1965	A global network of coexisting microbes from environmental and whole-genome sequence data. 2010 , 20, 947-59	305
1964	Bacterial communities from soil sediments of a mountain oasis in northern Oman. 2010 , 82, 102-111	2
1963	Changes through time: integrating microorganisms into the study of succession. 2010 , 161, 635-42	232
1962	The ecology of the phyllosphere: geographic and phylogenetic variability in the distribution of bacteria on tree leaves. 2010 , 12, 2885-93	414
1961	Advancing the understanding of biogeography-diversity relationships of benthic microorganisms in the North Sea. 2010 , 74, 410-29	23

1960	From structure to function: the ecology of host-associated microbial communities. 2010 , 74, 453-76	251
1959	Regional species pools control community saturation in lake phytoplankton. 2010 , 277, 3755-64	62
1958	Patterns of diversity in marine phytoplankton. 2010 , 327, 1509-11	239
1957	Soil Biology and Agriculture in the Tropics. 2010 ,	3
1956	The Genus Geobacillus and Hydrocarbon Utilization. 2010 , 1887-1896	6
1955	Microbial Degradation of Pesticides in Tropical Soils. 2010 , 251-274	7
1954	An experimental test of Darwin's naturalization hypothesis. 2010 , 175, 415-23	76
1953	Dormancy contributes to the maintenance of microbial diversity. 2010 , 107, 5881-6	577
1952	A Multi-scale Agent-Based Distributed Simulation Framework for Groundwater Pollution Management. 2011 ,	
1951	Phages in nature. 2011 , 1, 31-45	507
1950	Drivers of bacterial beta-diversity depend on spatial scale. 2011 , 108, 7850-4	491
1949	Complex function by design using spatially pre-structured synthetic microbial communities: degradation of pentachlorophenol in the presence of Hg(ii). 2011 , 3, 126-33	37
1948	Large-scale biodiversity patterns in freshwater phytoplankton. 2011 , 92, 2096-107	141
1947	Biodiversity and biogeography of microalgae: progress and pitfalls. 2011 , 19, 1-15	24
1946	Importance of dispersal and thermal environment for mycorrhizal communities: lessons from Yellowstone National Park. 2011 , 92, 1292-302	72
1945	Metagenomic Insights into Bacterial Species. 2011 , 89-98	2
1944	Approaches to Understanding Population Level Functional Diversity in a Microbial Community. 2011 , 341-354	
1943	Microbial evolution of sulphate reduction when lateral gene transfer is geographically restricted. 2011 , 61, 1725-1735	6

1942	Animal leptospirosis in small tropical areas. 2011 , 139, 167-88	57
1941	Disentangling the spatial patterns in community composition of prokaryotic and eukaryotic lake plankton. 2011 , 56, 508-520	99
1940	Population genetics of ectomycorrhizal fungi: from current knowledge to emerging directions. 2011 , 115, 569-97	111
1939	Influence of geographical location, crop type and crop residue cover on bacterial and fungal community structures. 2011 , 160, 271-280	7
1938	Response of soil microbial communities to different management practices in surface soils of a soybean agroecosystem in Argentina. 2011 , 47, 55-60	60
1937	Geographical structure of soil microbial communities in northern Japan: Effects of distance, land use type and soil properties. 2011 , 47, 88-94	29
1936	The generation and maintenance of diversity in microbial communities. 2011 , 98, 439-48	160
1935	The assembly of ecological communities inferred from taxonomic and functional composition. 2011 , 177, 630-44	19
1934	Ancient origins determine global biogeography of hot and cold desert cyanobacteria. 2011 , 2, 163	151
1933	Rethinking microbial diversity analysis in the high throughput sequencing era. 2011 , 86, 42-51	195
1932	Prevalence and dispersal of a facultative bacterial symbiont associated with an endemic metazoan host. 2011 , 54, 153-157	10
1931	Diversity and ecology of psychrophilic microorganisms. 2011 , 162, 346-61	320
1930	Empirical approaches to metacommunities: a review and comparison with theory. 2011 , 26, 482-91	490
1929	Current approaches to exploit actinomycetes as a source of novel natural products. 2011 , 38, 375-89	132
1928	Structure of Diversity in Dark Septate Endophytes: From Species to Genes. 2011 , 3-30	27
1927	The effect of resource history on the functioning of soil microbial communities is maintained across time. 2011 , 8, 1477-1486	80
1926	Non-random assembly of bacterioplankton communities in the subtropical north pacific ocean. 2011 , 2, 140	29
1925	Everything is everywhere: a twenty-first century de-/reconstruction with respect to protists. 88-110	19

1924	Global diversity of aloricate Oligotrichea (Protista, Ciliophora, Spirotricha) in marine and brackish sea water. 2011 , 6, e22466	65
1923	Contrasting diversity patterns of crenarchaeal, bacterial and fungal soil communities in an alpine landscape. 2011 , 6, e19950	86
1922	Global distribution of Polaromonas phylotypes--evidence for a highly successful dispersal capacity. 2011 , 6, e23742	90
1921	Global patterns of bacterial beta-diversity in seafloor and seawater ecosystems. 2011 , 6, e24570	398
1920	Latitudinal gradients in degradation of marine dissolved organic carbon. 2011 , 6, e28900	62
1919	Regulatory Research on Antimicrobial Resistance in the Environment. 2011 , 549-567	
1918	Environmental Antibiotic Resistome: New Insights from Culture-Independent Approaches. 2011 , 123-148	2
1917	Geographic variation in the diversity of microbial communities: research directions and prospects for experimental biogeography. 335-357	8
1916	Toward molecular trait-based ecology through integration of biogeochemical, geographical and metagenomic data. 2011 , 7, 473	129
1915	Global patterns in the biogeography of bacterial taxa. 2011 , 13, 135-144	279
1914	Spatial scaling of arbuscular mycorrhizal fungal diversity is affected by farming practice. 2011 , 13, 241-249	80
1913	The bacterial biogeography of British soils. 2011 , 13, 1642-54	564
1912	Genetic differentiation, recombination and clonal expansion in environmental populations of <i>Cryptococcus gattii</i> in India. 2011 , 13, 1875-88	28
1911	No biogeographical pattern for a root-associated fungal species complex. 2011 , 20, 160-169	69
1910	Assessing microbial diversity using recent lake sediments and estimations of spatio-temporal diversity. 2011 , 38, 2033-2040	10
1909	The control of community composition by distance, environment and history: a regional-scale study of the mountain grasslands of southern New Zealand. 2011 , 38, 2384-2396	14
1908	A macroecological perspective of diversity patterns in the freshwater realm. 2011 , 56, 1703-1722	221
1907	Water mass-specificity of bacterial communities in the North Atlantic revealed by massively parallel sequencing. 2011 , 20, 258-74	164

1906	Speciation despite globally overlapping distributions in <i>Penicillium chrysogenum</i> : the population genetics of Alexander Fleming's lucky fungus. 2011 , 20, 4288-301	45
1905	THE POTENTIAL INDICATOR VALUE OF RARE TAXA RICHNESS IN DIATOM-BASED STREAM BIOASSESSMENT. 2011 , 47, 471-482	9
1904	Soil microbial communities adapt to genetic variation in leaf litter inputs. 2011 , 120, 1696-1704	51
1903	Low cyanobacterial diversity in biotopes of the Transantarctic Mountains and Shackleton Range (80-82°S), Antarctica. 2011 , 77, 503-17	26
1902	Comparison of 16S rRNA and protein-coding genes as molecular markers for assessing microbial diversity (Bacteria and Archaea) in ecosystems. 2011 , 78, 617-28	43
1901	Microbial seed banks: the ecological and evolutionary implications of dormancy. <i>Nature Reviews Microbiology</i> , 2011 , 9, 119-30	22.2 972
1900	Determinants of the distribution of nitrogen-cycling microbial communities at the landscape scale. 2011 , 5, 532-42	279
1899	Pyrosequencing reveals highly diverse and species-specific microbial communities in sponges from the Red Sea. 2011 , 5, 650-64	213
1898	Quantitative proteomic analyses of the response of acidophilic microbial communities to different pH conditions. 2011 , 5, 1152-61	46
1897	Protistan microbial observatory in the Cariaco Basin, Caribbean. II. Habitat specialization. 2011 , 5, 1357-73	72
1896	Bacterial community structure in a latitudinal gradient of lakes: the roles of spatial versus environmental factors. 2011 , 56, 1973-1991	50
1895	Microbial biogeography at the soil pore scale. 2011 , 43, 280-286	132
1894	Global diversity and distribution of arbuscular mycorrhizal fungi. 2011 , 43, 2294-2303	286
1893	Population genetics: the next stop for microbial ecologists?. 2011 , 6, 887-892	1
1892	Microbial metagenomics: beyond the genome. 2011 , 3, 347-71	258
1891	Microbial extracellular enzymes and the marine carbon cycle. 2011 , 3, 401-25	292
1890	Microbial response to drying and rewetting: osmotic and matric effects. 2011 , 348, 99-102	13
1889	Determination of genetic variability among the isolates of <i>Metarhizium anisopliae</i> var. <i>anisopliae</i> from different geographical origins. 2011 , 27, 359-370	18

1888	Linking Microbial and Ecosystem Ecology Using Ecological Stoichiometry: A Synthesis of Conceptual and Empirical Approaches. 2011 , 14, 261-273	66
1887	Placing the effects of leaf litter diversity on saprotrophic microorganisms in the context of leaf type and habitat. 2011 , 61, 399-409	16
1886	Bacterioplankton community variation across river to ocean environmental gradients. 2011 , 62, 374-82	56
1885	Diversity and biogeography of rhizobia isolated from root nodules of <i>Glycine max</i> grown in Hebei Province, China. 2011 , 61, 917-31	67
1884	The microbial Phyllogeography of the carnivorous plant <i>Sarracenia alata</i> . 2011 , 61, 750-8	27
1883	Differential habitat use and niche partitioning by <i>Pseudomonas</i> species in human homes. 2011 , 62, 505-17	39
1882	Microbial diversity on a marble monument: a case study. 2011 , 63, 1701-1711	31
1881	DMTB: A comprehensive online resource of 16S rRNA genes, ecological metadata, oligonucleotides, and magnetic properties of magnetotactic bacteria. 2011 , 56, 476-478	3
1880	16s rDNA based microbial diversity analysis of eleven acid mine drainages obtained from three Chinese copper mines. 2011 , 18, 1930-1939	5
1879	Where the bugs are: analyzing distributions of bacterial phyla by descriptor keyword search in the nucleotide database. 2011 , 1, 7	1
1878	Worldwide distribution of major clones of <i>Listeria monocytogenes</i> . 2011 , 17, 1110-2	87
1877	Phylogeography of microbial phototrophs in the dry valleys of the high Himalayas and Antarctica. 2011 , 278, 702-8	63
1876	Biodiversity and emerging biogeography of the neutrophilic iron-oxidizing Zetaproteobacteria. 2011 , 77, 5445-57	84
1875	Microbial eukaryotic distribution in a dynamic Beaufort Sea and the Arctic Ocean. 2011 , 33, 431-444	69
1874	Niche partitioning of marine group I Crenarchaeota in the euphotic and upper mesopelagic zones of the East China Sea. 2011 , 77, 7469-78	42
1873	Analysis of the bacterial communities present in lungs of patients with cystic fibrosis from American and British centers. 2011 , 49, 281-91	54
1872	Metacommunity organization of soil microorganisms depends on habitat defined by presence of <i>Lobelia siphilitica</i> plants. 2011 , 92, 57-65	30
1871	Microorganisms with novel dissimilatory (bi)sulfite reductase genes are widespread and part of the core microbiota in low-sulfate peatlands. 2011 , 77, 1231-42	35

1870	The sulfate-rich and extreme saline sediment of the ephemeral tirez lagoon: a biotope for acetoclastic sulfate-reducing bacteria and hydrogenotrophic methanogenic archaea. 2011 , 2011, 753758	13
1869	Field-scale transplantation experiment to investigate structures of soil bacterial communities at pioneering sites. 2011 , 77, 8241-8	30
1868	Soil rotifer communities are extremely diverse globally but spatially autocorrelated locally. 2011 , 108, 4406-10	72
1867	Cost of movement in the multicellular stage of the social amoebae <i>Dictyostelium discoideum</i> and <i>D. purpureum</i> . 2011 , 23, 358-367	2
1866	Geographical location determines the population structure in phyllosphere microbial communities of a salt-excreting desert tree. 2011 , 77, 7647-55	126
1865	PhyLOTU: a high-throughput procedure quantifies microbial community diversity and resolves novel taxa from metagenomic data. 2011 , 7, e1001061	62
1864	Collection, isolation and culturing strategies for <i>Oxyrrhis marina</i> . 2011 , 33, 569-578	27
1863	Diversity of Bacterial Communities in Contrasting Aquatic Environments: Lake Timsah, Egypt. 2011 , 4, MBI.S6948	1
1862	Phytoplankton responses to human impacts at different scales. 2012 ,	1
1861	A 'universal' type II chaperonin PCR detection system for the investigation of Archaea in complex microbial communities. 2012 , 6, 430-9	21
1860	Analysis of the community structure of abyssal kinetoplastids revealed similar communities at larger spatial scales. 2012 , 6, 713-23	21
1859	Constrained ordination analysis in the presence of zero inflation. 2012 , 12, 463-485	7
1858	Comparison of microbial community structures in four Black soils along a climatic gradient in northeast China. 2012 , 92, 543-549	11
1857	Natural product biosynthetic gene diversity in geographically distinct soil microbiomes. 2012 , 78, 3744-52	70
1856	Distance-decay relationships partially determine diversity patterns of phyllosphere bacteria on <i>Tamarix</i> trees across the Sonoran Desert [corrected]. 2012 , 78, 6187-93	70
1855	Rodent models to study the relationships between mammals and their bacterial inhabitants. 2012 , 3, 536-43	12
1854	Population genetic structure and connectivity of the harmful dinoflagellate <i>Alexandrium minutum</i> in the Mediterranean Sea. 2012 , 279, 129-38	45
1853	Marine planktonic microbes survived climatic instabilities in the past. 2012 , 279, 474-9	5

1852	A biogeographic distribution of magnetotactic bacteria influenced by salinity. 2012 , 6, 475-9	38
1851	Architectural design influences the diversity and structure of the built environment microbiome. 2012 , 6, 1469-79	302
1850	Fungal endophyte communities reflect environmental structuring across a Hawaiian landscape. 2012 , 109, 13022-7	227
1849	Insights into the Global Microbial Community Structure Associated with Iron Oxyhydroxide Minerals Deposited in the Aerobic Biogeosphere. 2012 , 29, 587-610	24
1848	Dissolved organic carbon influences microbial community composition and diversity in managed aquifer recharge systems. 2012 , 78, 6819-28	92
1847	Combined analyses of bacterial, fungal and nematode communities in andosolic agricultural soils in Japan. 2012 , 27, 72-9	20
1846	Diversification of bacterial community composition along a temperature gradient at a thermal spring. 2012 , 27, 374-81	55
1845	FOREL'S LIMNOLOGY [FROM LAKE PHYSICS TO ECOSYSTEM SERVICES. 2012 , 21, 70-77	2
1844	Taxonomy, Phylogeny and Evolution. 2012 , 1-75	
1843	A legacy of contrasting spatial genetic structure on either side of the Atlantic-Mediterranean transition zone in a marine protist. 2012 , 109, 20998-1003	19
1842	Geographic delineations of yeast communities and populations associated with vines and wines in New Zealand. 2012 , 6, 1281-90	90
1841	Is catchment productivity a useful predictor of taxa richness in lake plankton communities?. 2012 , 22, 624-33	29
1840	Comparison of soil bacterial communities between coastal and inland forests in a subtropical area. 2012 , 60, 49-55	13
1839	Water-sediment niche differentiation in ancient marine lineages of <i>Exiguobacterium</i> endemic to the Cuatro Ciénegas Basin. 2012 , 14, 2323-33	29
1838	Changes in soil bacterial community triggered by drought-induced gap succession preceded changes in soil C stocks and quality. 2012 , 2, 3016-31	31
1837	Watershed land use types as drivers of freshwater phytoplankton structure. 2012 , 698, 121-131	42
1836	The effects of sand dust storms on greenhouse gases. 2012 , 33, 6838-6853	8
1835	Biogeographical diversity of leaf-associated microbial communities from salt-secreting <i>Tamarix</i> trees of the Dead Sea region. 2012 , 163, 142-50	20

1834	Arbuscular mycorrhizal fungal diversity along a Tibetan elevation gradient. 2012 , 55, 145-151	79
1833	Distinct Bradyrhizobium [corrected] communities nodulate legumes native to temperate and tropical monsoon Australia. 2012 , 63, 265-77	41
1832	Long-distance dispersal: a framework for hypothesis testing. 2012 , 27, 47-56	360
1831	Glaciers and ice sheets as a biome. 2012 , 27, 219-25	205
1830	Genomic evidence of rapid, global-scale gene flow in a Sulfolobus species. 2012 , 6, 1613-6	17
1829	Linking symbiont community structures in a model arbuscular mycorrhizal system. 2012 , 194, 800-809	22
1828	Dynamics of bacterial communities in relation to soil aggregate formation during the decomposition of ¹³ C-labelled rice straw. 2012 , 53, 1-9	63
1827	Determining a minimum detection threshold in terminal restriction fragment length polymorphism analysis. 2012 , 88, 14-8	11
1826	Phylogeography of the cosmopolitan fungus Aspergillus flavus: is everything everywhere?. 2012 , 116, 452-63	38
1825	Symbiotic Frankia bacteria in Alnus forests in Mexico and the United States of America: is geographic location a good predictor of assemblage structure?. 2012 , 90, 423-431	10
1824	Selectivity by host plants affects the distribution of arbuscular mycorrhizal fungi: evidence from ITS rDNA sequence metadata. 2012 , 12, 50	49
1823	Patterns of diversity for fungal assemblages of biological soil crusts from the southwestern United States. 2012 , 104, 353-61	66
1822	Environmental and Evolutionary Genomics of Microbial Algae: Power and Challenges of Metagenomics. 2012 , 64, 383-427	10
1821	Bacterial community dynamics in full-scale activated sludge bioreactors: operational and ecological factors driving community assembly and performance. 2012 , 7, e42524	75
1820	Importance of space and the local environment for linking local and regional abundances of microbes. 2012 , 67, 35-45	5
1819	Meta-analyses of environmental sequence data identify anoxia and salinity as parameters shaping ciliate communities. 2012 , 10, 277-288	28
1818	Modelling the global distribution of fungal species: new insights into microbial cosmopolitanism. 2012 , 21, 5599-612	51
1817	Travel, sex, and food: what's speciation got to do with it?. 2012 , 12, 634-40	17

1816	Nitrogen deposition alters soil chemical properties and bacterial communities in the Inner Mongolia grassland. 2012 , 24, 1483-91	32
1815	Characterizing microbial communities through space and time. 2012 , 23, 431-6	73
1814	A biogeographical evaluation of high-elevation myxomycete assemblages in the northern Neotropics. 2012 , 5, 99-113	8
1813	Twenty years of research on fungal-plant interactions on Lyman Glacier forefront: Lessons learned and questions yet unanswered. 2012 , 5, 430-442	36
1812	Environmental microbiology through the lens of high-throughput DNA sequencing: synopsis of current platforms and bioinformatics approaches. 2012 , 91, 106-13	90
1811	Diverse Mesorhizobium spp. with unique nodA nodulating the South African legume species of the genus Lessertia. 2012 , 358, 385-401	20
1810	Microbial diversity in arctic freshwaters is structured by inoculation of microbes from soils. 2012 , 6, 1629-39	216
1809	Effects of remediation on the bacterial community of an acid mine drainage impacted stream. 2012 , 58, 1316-26	7
1808	Free tropospheric transport of microorganisms from Asia to North America. 2012 , 64, 973-85	103
1807	Analysis of the global ocean sampling (GOS) project for trends in iron uptake by surface ocean microbes. 2012 , 7, e30931	46
1806	Functional biogeography of ocean microbes revealed through non-negative matrix factorization. 2012 , 7, e43866	32
1805	At limits of life: multidisciplinary insights reveal environmental constraints on biotic diversity in continental Antarctica. 2012 , 7, e44578	43
1804	Distance decay of similarity in neotropical diatom communities. 2012 , 7, e45071	82
1803	Phylogeography of the Microcoleus vaginatus (Cyanobacteria) from three continents--a spatial and temporal characterization. 2012 , 7, e40153	35
1802	Bacterial indicator of agricultural management for soil under no-till crop production. 2012 , 7, e51075	69
1801	Prospects for the study of evolution in the deep biosphere. 2011 , 2, 285	28
1800	Specificity of Salt Marsh Diazotrophs for Vegetation Zones and Plant Hosts: Results from a North American marsh. 2012 , 3, 84	14
1799	Ecology and biogeography of bacterial communities associated with chloroethene-contaminated aquifers. 2012 , 3, 260	17

1798	Spatial and temporal scales of aquatic bacterial beta diversity. 2012 , 3, 318	50
1797	Co-occurrence patterns of plants and soil bacteria in the high-alpine subnival zone track environmental harshness. 2012 , 3, 347	44
1796	Sedimentological imprint on seafloor microbial communities in Western Mediterranean Sea Quaternary sediments. 2012 , 9, 3491-3512	12
1795	Temperature characteristics of bacterial sulfate reduction in continental shelf and slope sediments. 2012 , 9, 3425-3435	29
1794	Biogeography in the air: fungal diversity over land and oceans. 2012 , 9, 1125-1136	124
1793	Bacterial assemblages of the eastern Atlantic Ocean reveal both vertical and latitudinal biogeographic signatures. 2012 , 9, 2177-2193	32
1792	symposium summary: The importance of being small: does size matter in biogeography?. 2012 , 1,	
1791	Freshwater bacterioplankton richness in oligotrophic lakes depends on nutrient availability rather than on species-area relationships. 2012 , 6, 1127-36	78
1790	Patterns in the distribution of soil bacterial 16S rRNA gene sequences from different regions of Antarctica. 2012 , 181-182, 45-55	34
1789	Cyanobacteria in Geothermal Habitats. 2012 , 39-63	40
1788	Beyond biogeographic patterns: processes shaping the microbial landscape. <i>Nature Reviews Microbiology</i> , 2012 , 10, 497-506	22.2 890
1787	Dispersal limitation and the assembly of soil Actinobacteria communities in a long-term chronosequence. 2012 , 2, 538-49	32
1786	Phylogenetic analysis suggests that habitat filtering is structuring marine bacterial communities across the globe. 2012 , 64, 8-17	47
1785	Burning fire-prone Mediterranean shrublands: immediate changes in soil microbial community structure and ecosystem functions. 2012 , 64, 242-55	71
1784	Biogeography of bacterial communities in hot springs: a focus on the actinobacteria. 2012 , 16, 669-79	41
1783	Distance decay of similarity in freshwater communities: do macro- and microorganisms follow the same rules?. 2012 , 21, 365-375	216
1782	Biogeography of pelagic bacterioplankton across an antagonistic temperature-salinity gradient in the Red Sea. 2012 , 21, 388-405	84
1781	Modelling the effect of size on the aerial dispersal of microorganisms. 2012 , 39, 89-97	167

- 1780 Biogeographic patterns in scaled chrysophytes from the east coast of North America. **2012**, 57, 451-466 21
- 1779 Biogeography of symbiotic and other endophytic bacteria isolated from medicinal *Glycyrrhiza* species in China. **2012**, 79, 46-68 83
- 1778 Bacterial taxa associated with the lung lichen *Lobaria pulmonaria* are differentially shaped by geography and habitat. **2012**, 329, 111-5 40
- 1777 Dispersal limitation is stronger in communities of microorganisms than macroorganisms across Central European cities. **2012**, 39, 1101-1111 22
- 1776 What's on your boots: an investigation into the role we play in protist dispersal. **2012**, 39, 998-1003 12
- 1775 Local and regional factors influencing bacterial community assembly. **2012**, 4, 1-9 315
- 1774 Macroecology of unicellular organisms - patterns and processes. **2012**, 4, 10-22 93
- 1773 Which sequencing depth is sufficient to describe patterns in bacterial α and β diversity?. **2012**, 4, 367-72 83
- 1772 Community patterns of soil bacteria and nematodes in relation to geographic distance. **2012**, 45, 1-7 48
- 1771 Appraisal of the crop-rotation effect of rhizobial inoculation on potato cropping systems in relation to soil bacterial communities. **2012**, 54, 1-6 42
- 1770 Geographical variation in cone volatile composition among populations of the African cycad *Encephalartos villosus*. **2012**, 106, 514-527 22
- 1769 Polar lakes may act as ecological islands to aquatic protists. **2012**, 21, 3200-9 23
- 1768 Different biogeographic patterns of prokaryotes and microbial eukaryotes in epilithic biofilms. **2012**, 21, 3852-68 44
- 1767 Body size and dispersal mode as key traits determining metacommunity structure of aquatic organisms. **2012**, 15, 740-7 403
- 1766 Microdiversity and evidence for high dispersal rates in the marine actinomycete '*Salinispora pacifica*'. **2012**, 14, 480-93 36
- 1765 *amoA*-based consensus phylogeny of ammonia-oxidizing archaea and deep sequencing of *amoA* genes from soils of four different geographic regions. **2012**, 14, 525-39 402
- 1764 Geographic distance and pH drive bacterial distribution in alkaline lake sediments across Tibetan Plateau. **2012**, 14, 2457-66 353
- 1763 Patterns of elevational beta diversity in micro- and macroorganisms. **2012**, 21, 743-750 73

1762	Analysis of the structure of microbial community in soils with different degrees of salinization using T-RFLP and real-time PCR techniques. 2012 , 45, 147-156	49
1761	Dust storms loads analyses Iraq. 2012 , 5, 121-131	50
1760	Biogeographic patterns of the myxomycete biota of the Americas using a parsimony analysis of endemism. 2013 , 59, 159-177	18
1759	Microbial communities may modify how litter quality affects potential decomposition rates as tree species migrate. 2013 , 372, 167-176	37
1758	Assessment of the relationship between geologic origin of soil, rhizobacterial community composition and soil receptivity to tobacco black root rot in Savoie region (France). 2013 , 371, 397-408	19
1757	Biogeography and host fidelity of bacterial communities in <i>Ircinia</i> spp. from the Bahamas. 2013 , 66, 437-47	21
1756	Host rules: spatial stability of bacterial communities associated with marine sponges (<i>Ircinia</i> spp.) in the Western Mediterranean Sea. 2013 , 86, 268-76	53
1755	Microbial community responses to anthropogenically induced environmental change: towards a systems approach. 2013 , 16 Suppl 1, 128-39	169
1754	No-till and cover crops shift soil microbial abundance and diversity in Laos tropical grasslands. 2013 , 33, 375-384	70
1753	Evidence for isolated evolution of deep-sea ciliate communities through geological separation and environmental selection. 2013 , 13, 150	35
1752	Microbial diversity and the lower-limit problem of biodiversity. 2013 , 28, 219-239	6
1751	Beyond the genome: community-level analysis of the microbial world. 2013 , 28, 261-282	62
1750	Land-use change and soil type are drivers of fungal and archaeal communities in the Pampa biome. 2013 , 29, 223-33	31
1749	Estimation of hydrocarbon biodegradation rates in marine environments: a critical review of the Q10 approach. 2013 , 89, 83-90	40
1748	Phylogenetic and morphologic complexity of giant sulphur bacteria. 2013 , 104, 169-86	43
1747	The distance decay of similarity in communities of ectomycorrhizal fungi in different ecosystems and scales. 2013 , 101, 1335-1344	91
1746	Environmental effects on biofilm bacterial communities: a comparison of natural and anthropogenic factors in New Zealand streams. 2013 , 58, n/a-n/a	2
1745	Species turnover and geographic distance in an urban river network. 2013 , 19, 1429-1439	62

1744	Microbiology. Some like it hot, some not. 2013 , 340, 1533-4	12
1743	Critical assessment of air pollution by ANOVA test and human health effects. 2013 , 71, 84-91	9
1742	Global marine bacterial diversity peaks at high latitudes in winter. 2013 , 7, 1669-77	141
1741	Energy, ecology and the distribution of microbial life. 2013 , 368, 20120383	26
1740	Disentangling the roles of spatial and environmental variables in shaping benthic algal assemblages in rivers of central and northern China. 2013 , 47, 453-466	17
1739	High-flying diatoms: Widespread dispersal of microorganisms in an explosive volcanic eruption. 2013 , 41, 1187-1190	33
1738	Plant-parasitic nematodes as invasive species: characteristics, uncertainty and biosecurity implications. 2013 , 163, n/a-n/a	9
1737	Environmental selection of protistan plankton communities in hypersaline anoxic deep-sea basins, Eastern Mediterranean Sea. 2013 , 2, 54-63	11
1736	Advection shapes Southern Ocean microbial assemblages independent of distance and environment effects. 2013 , 4, 2457	87
1735	Composition, richness and nonrandom assembly of culturable bacterial-microfungal communities in floral nectar of Mediterranean plants. 2013 , 83, 685-99	69
1734	Determining indicator taxa across spatial and seasonal gradients in the Columbia River coastal margin. 2013 , 7, 1899-911	101
1733	Quantifying community assembly processes and identifying features that impose them. 2013 , 7, 2069-79	624
1732	A meta-analysis of changes in bacterial and archaeal communities with time. 2013 , 7, 1493-506	236
1731	Water mass and depth determine the distribution and diversity of Rhodobacterales in an Arctic marine system. 2013 , 84, 564-76	14
1730	Marine cyanophages exhibit local and regional biogeography. 2013 , 15, 1452-63	26
1729	Marine bacteria exhibit a bipolar distribution. 2013 , 110, 2342-7	145
1728	Global biogeography of highly diverse protistan communities in soil. 2013 , 7, 652-9	302
1727	Dispersal of thermophilic <i>Desulfotomaculum</i> endospores into Baltic Sea sediments over thousands of years. 2013 , 7, 72-84	58

1726	Measures of phylogenetic differentiation provide robust and complementary insights into microbial communities. 2013 , 7, 173-83	28
1725	The spatial scaling of saprotrophic fungal beta diversity in decomposing leaves. 2013 , 22, 1171-84	20
1724	Role of oxygen gradients in shaping redox relationships between the human intestine and its microbiota. 2013 , 55, 130-40	223
1723	The role of local environment and geographical distance in determining community composition of arbuscular mycorrhizal fungi at the landscape scale. 2013 , 7, 498-508	189
1722	Biogeographical note on Antarctic microflorae: Endemism and cosmopolitanism. 2013 , 4, 633-646	10
1721	Yeast and bacterial diversity along a transect in an acidic, As-Fe rich environment revealed by cultural approaches. 2013 , 463-464, 823-8	10
1720	Patterns and processes of microbial community assembly. 2013 , 77, 342-56	798
1719	Turnover of soil bacterial diversity driven by wide-scale environmental heterogeneity. 2013 , 4, 1434	150
1718	Ocean currents shape the microbiome of Arctic marine sediments. 2013 , 7, 685-96	108
1717	Temporal dynamics in the free-living bacterial community composition in the coastal North Sea. 2013 , 83, 413-24	25
1716	Geographic distance and ecosystem size determine the distribution of smallest protists in lacustrine ecosystems. 2013 , 85, 85-94	44
1715	Microbial composition affects the functioning of estuarine sediments. 2013 , 7, 868-79	93
1714	Reproducibility of Vibrionaceae population structure in coastal bacterioplankton. 2013 , 7, 509-19	45
1713	Distribution of Genes. 2013 , 127-142	
1712	Shifts in soil bacterial community after eight years of land-use change. 2013 , 36, 137-44	73
1711	Antagonism influences assembly of a Bacillus guild in a local community and is depicted as a food-chain network. 2013 , 7, 487-97	68
1710	Bacterial composition of microbial mats in hot springs in Northern Patagonia: variations with seasons and temperature. 2013 , 17, 123-36	49
1709	Large-scale geographic patterns of diversity and community structure of pelagic crustacean zooplankton in Canadian lakes. 2013 , 22, 784-795	49

1708	Dispersal in microbes: fungi in indoor air are dominated by outdoor air and show dispersal limitation at short distances. 2013 , 7, 1262-73	373
1707	Multi-scale structure and geographic drivers of cross-infection within marine bacteria and phages. 2013 , 7, 520-32	111
1706	The biogeography of fungal communities in wetland sediments along the Changjiang River and other sites in China. 2013 , 7, 1299-309	67
1705	Stochastic species distributions are driven by organism size. 2013 , 94, 660-70	47
1704	Experimentally induced habitat filtering in marine bacterial communities. 2013 , 477, 77-86	11
1703	Microbial community biogeographic patterns in the rhizosphere of two Brazilian semi-arid leguminous trees. 2013 , 29, 1233-41	13
1702	Effects of nitrogen addition on soil microbial diversity and methane cycling capacity depend on drainage conditions in a pine forest soil. 2013 , 62, 119-128	15
1701	Biogeography of the uncultured marine picoeukaryote MAST-4: temperature-driven distribution patterns. 2013 , 7, 1531-43	29
1700	Microbially Mediated Plant Functional Traits. 2013 , 87-102	20
1699	Body-size distribution and biogeographical patterns in non-marine ostracods (Crustacea: Ostracoda). 2013 , 109, 409-423	6
1698	Micro-scale determinants of bacterial diversity in soil. 2013 , 37, 936-54	305
1697	Phylogenetic beta diversity in bacterial assemblages across ecosystems: deterministic versus stochastic processes. 2013 , 7, 1310-21	352
1696	A global analysis of soil microbial biomass carbon, nitrogen and phosphorus in terrestrial ecosystems. 2013 , 22, 737-749	490
1695	Biogeography of bacterioplankton in the tropical seawaters of Singapore. 2013 , 84, 259-69	9
1694	Evidence of variability in the structure and recruitment of rhizospheric and endophytic bacterial communities associated with arable sweet sorghum (<i>Sorghum bicolor</i> (L) Moench). 2013 , 372, 265-278	22
1693	Changes in assembly processes in soil bacterial communities following a wildfire disturbance. 2013 , 7, 1102-11	239
1692	Phylogeographic analysis of filterable bacteria with special reference to Rhizobiales strains that occur in cryospheric habitats. 2013 , 25, 219-228	18
1691	Structure of soil bacterial communities in relation to environmental variables in a semi-arid region of Mongolia. 2013 , 89, 38-44	16

1690	Molecular analysis of the diversity of genus <i>Psychrobacter</i> present within a temperate estuary. 2013 , 84, 451-60	14
1689	Seasonality and disturbance: annual pattern and response of the bacterial and microbial eukaryotic assemblages in a freshwater ecosystem. 2013 , 15, 2557-72	25
1688	Microbial Biogeography. 2013 , 271-279	1
1687	Integrating niche-based process and spatial process in biogeography of magnetotactic bacteria. 2013 , 3, 1643	50
1686	The root microbiota fingerprint in the soil?. 2013 , 370, 671-686	65
1685	The Biodiversity, Ecology, and Biogeography of Ascomycetous Yeasts. 2013 , 355-370	4
1684	Encyclopedia of Metagenomics. 2013 , 1-11	1
1683	Contemporary environmental variation determines microbial diversity patterns in acid mine drainage. 2013 , 7, 1038-50	235
1682	One-dimensional TRFLP-SSCP is an effective DNA fingerprinting strategy for soil Archaea that is able to simultaneously differentiate broad taxonomic clades based on terminal fragment length polymorphisms and closely related sequences based on single stranded conformation polymorphisms. 2013 , 94, 317-24	1
1681	Symbiotic prokaryotic communities from different populations of the giant barrel sponge, <i>Xestospongia muta</i> . 2013 , 2, 938-52	31
1680	Trade-offs, spatial heterogeneity, and the maintenance of microbial diversity. 2013 , 67, 599-608	34
1679	Local and regional influences over soil microbial metacommunities in the Transantarctic Mountains. 2013 , 4, art136	29
1678	454 Pyrosequencing Analysis of Fungal Assemblages from Geographically Distant, Disparate Soils Reveals Spatial Patterning and a Core Mycobiome. 2013 , 5, 73-98	58
1677	The world bacterial biogeography and biodiversity through databases: a case study of NCBI Nucleotide Database and GBIF Database. 2013 , 2013, 240175	5
1676	Headwaters are critical reservoirs of microbial diversity for fluvial networks. 2013 , 280, 20131760	122
1675	Comparative genomic analysis of phylogenetically closely related <i>Hydrogenobaculum</i> sp. isolates from Yellowstone National Park. 2013 , 79, 2932-43	28
1674	Sympatric chimpanzees and gorillas harbor convergent gut microbial communities. 2013 , 23, 1715-20	106
1673	Community composition of ammonia-oxidizing archaea from surface and anoxic depths of oceanic oxygen minimum zones. 2013 , 4, 177	33

1672	Assessing the relative effects of geographic location and soil type on microbial communities associated with straw decomposition. 2013 , 79, 3327-35	54
1671	Quantification of endospore-forming firmicutes by quantitative PCR with the functional gene spo0A. 2013 , 79, 5302-12	32
1670	Influence of hyporheic zone characteristics on the structure and activity of microbial assemblages. 2013 , 58, 2567-2583	27
1669	Spatial patterns of methanotrophic communities along a hydrological gradient in a riparian wetland. 2013 , 86, 59-70	14
1668	Response of bacterioplankton to a glucose gradient in the absence of lysis and grazing. 2013 , 85, 443-51	8
1667	Microbiome of the upper troposphere: species composition and prevalence, effects of tropical storms, and atmospheric implications. 2013 , 110, 2575-80	297
1666	Molecular evidence for an active endogenous microbiome beneath glacial ice. 2013 , 7, 1402-12	91
1665	Effects of environmental variation and spatial distance on bacteria, archaea and viruses in sub-polar and arctic waters. 2013 , 7, 1507-18	62
1664	Temperature drives the continental-scale distribution of key microbes in topsoil communities. 2013 , 340, 1574-7	198
1663	Evidence for a persistent microbial seed bank throughout the global ocean. 2013 , 110, 4651-5	158
1662	Environmental controls over bacterial communities in polar desert soils. 2013 , 4, art127	22
1661	Biogeographical characterization of <i>Saccharomyces cerevisiae</i> wine yeast by molecular methods. 2013 , 4, 166	26
1660	Towards an Ecosystem Approach to Cheese Microbiology. 2013 , 1,	5
1659	Soil bacterial community structure in five tropical forests in Malaysia and one temperate forest in Japan revealed by pyrosequencing analyses of 16S rRNA gene sequence variation. 2013 , 88, 93-103	26
1658	Response of bacterioplankton community structure to an artificial gradient of CO_2 in the Arctic Ocean. 2013 , 10, 3679-3689	19
1657	DNA from lake sediments reveals the long-term dynamics and diversity of <i>Synechococcus</i> assemblages. 2013 , 10, 3817-3838	31
1656	PALEOLIMNOLOGY Contributions of Paleolimnological Research to Biogeography. 2013 , 313-325	
1655	Ecological drivers of biogeographic patterns of soil archaeal community. 2013 , 8, e63375	22

1654	Stream hydrological fragmentation drives bacterioplankton community composition. 2013 , 8, e64109	47
1653	Population genetic structure of a microalgal species under expansion. 2013 , 8, e82510	16
1652	Biogeography of <i>Persephonella</i> in deep-sea hydrothermal vents of the Western Pacific. 2013 , 4, 107	23
1651	Biogeochemical implications of the ubiquitous colonization of marine habitats and redox gradients by <i>Marinobacter</i> species. 2013 , 4, 136	53
1650	Multilocus sequence analysis of <i>Thermoanaerobacter</i> isolates reveals recombining, but differentiated, populations from geothermal springs of the Uzon Caldera, Kamchatka, Russia. 2013 , 4, 169	5
1649	Microbial habitat connectivity across spatial scales and hydrothermal temperature gradients at Guaymas Basin. 2013 , 4, 207	21
1648	An horizon scan of biogeography. 2013 , 5,	1
1647	ObStruct: a method to objectively analyse factors driving population structure using Bayesian ancestry profiles. 2014 , 9, e85196	36
1646	Evaluating Darwin's naturalization hypothesis in experimental plant assemblages: phylogenetic relationships do not determine colonization success. 2014 , 9, e105535	11
1645	Dispersal ability determines the role of environmental, spatial and temporal drivers of metacommunity structure. 2014 , 9, e111227	178
1644	Patterns of Microbially Driven Carbon Cycling in the Ocean: Links between Extracellular Enzymes and Microbial Communities. 2014 , 2014, 1-12	24
1643	Perspectives on the use of lakes and ponds as model systems for macroecological research. 2014 , 73,	24
1642	Microbial dispersal in unsaturated porous media: Characteristics of motile bacterial cell motions in unsaturated angular pore networks. 2014 , 50, 7406-7429	61
1641	Bacteria dialog with Santa Rosalia: Are aggregations of cosmopolitan bacteria mainly explained by habitat filtering or by ecological interactions?. 2014 , 14, 284	18
1640	Quantification of historical livestock importation into New Zealand 1860-1979. 2014 , 62, 309-14	9
1639	Evidence of global-scale aeolian dispersal and endemism in isolated geothermal microbial communities of Antarctica. 2014 , 5, 3875	49
1638	Microbial diversity and community-environment relationships in boreal streams. 2014 , 41, 2234-2244	40
1637	Dissolved Organic Matter in Aquatic Systems. 2014 , 125-156	49

- 1636 Diversity and Function of Bacterial Assemblages in Savanna Vegetation Soils. **2014**, 147-165
- 1635 16S rDNA-based analysis reveals cosmopolitan occurrence but limited diversity of two cyanobacterial lineages with contrasted patterns of intracellular carbonate mineralization. **2014**, 5, 331 25
- 1634 Untangling the fungal niche: the trait-based approach. **2014**, 5, 579 150
- 1633 Biogeographic congruency among bacterial communities from terrestrial sulfidic springs. **2014**, 5, 473 17
- 1632 Phylogeny and phylogeography of functional genes shared among seven terrestrial subsurface metagenomes reveal N-cycling and microbial evolutionary relationships. **2014**, 5, 531 46
- 1631 European bats as carriers of viruses with zoonotic potential. **2014**, 6, 3110-28 30
- 1630 A long-term field experiment of soil transplantation demonstrating the role of contemporary geographic separation in shaping soil microbial community structure. **2014**, 4, 1073-87 30
- 1629 Relationships between phyllosphere bacterial communities and plant functional traits in a neotropical forest. **2014**, 111, 13715-20 302
- 1628 Endospores of thermophilic bacteria as tracers of microbial dispersal by ocean currents. **2014**, 8, 1153-65 85
- 1627 Productivity and salinity structuring of the microplankton revealed by comparative freshwater metagenomics. **2014**, 16, 2682-98 60
- 1626 Determinants of root-associated fungal communities within Asteraceae in a semi-arid grassland. **2014**, 102, 425-436 53
- 1625 Pyrosequencing reveals regional differences in fruit-associated fungal communities. **2014**, 16, 2848-58 117
- 1624 Genetic diversity of picocyanobacteria in tibetan lakes: assessing the endemic and universal distributions. **2014**, 80, 7640-50 12
- 1623 Elucidation of bacteria found in car interiors and strategies to reduce the presence of potential pathogens. **2014**, 30, 337-46 17
- 1622 The spatial structure of bacterial communities is influenced by historical environmental conditions. **2014**, 95, 1134-40 49
- 1621 Trait-based approaches for understanding microbial biodiversity and ecosystem functioning. **2014**, 5, 251 212
- 1620 Biogeography of a defensive symbiosis. **2014**, 7, e993265 5
- 1619 The microbial contribution to macroecology. **2014**, 5, 203 84

1618	Similar processes but different environmental filters for soil bacterial and fungal community composition turnover on a broad spatial scale. 2014 , 9, e111667	28
1617	A role for biotic filtering in driving phylogenetic clustering in soil bacterial communities. 2014 , 23, 1346-1355	39
1616	Global biogeography of <i>Alnus</i> -associated <i>Frankia</i> actinobacteria. 2014 , 204, 979-88	34
1615	Ecology in the age of DNA barcoding: the resource, the promise and the challenges ahead. 2014 , 14, 221-32	80
1614	Current developments in groundwater ecology--from biodiversity to ecosystem function and services. 2014 , 27, 159-67	87
1613	Interactions in the microbiome: communities of organisms and communities of genes. 2014 , 38, 90-118	135
1612	Microscale evidence for a high decrease of soil bacterial density and diversity by cropping. 2014 , 34, 831-840	31
1611	Composition and variation of sediment bacterial and nirS-harboring bacterial communities at representative sites of the Bohai Gulf coastal zone, China. 2014 , 30, 1291-300	7
1610	Patterns of rare and abundant marine microbial eukaryotes. 2014 , 24, 813-21	306
1609	Eutrophication decreases distance decay of similarity in diatom communities. 2014 , 59, 1522-1531	35
1608	Spatial variation in the bacterial and denitrifying bacterial community in a biofilter treating subsurface agricultural drainage. 2014 , 67, 265-72	13
1607	Life with compass: diversity and biogeography of magnetotactic bacteria. 2014 , 16, 2646-58	84
1606	Rhizosphere stoichiometry: are C : N : P ratios of plants, soils, and enzymes conserved at the plant species-level?. 2014 , 201, 505-517	131
1605	Bacterial community composition of divergent soil habitats in a polar desert. 2014 , 89, 490-4	32
1604	Global biogeography of <i>Streptomyces</i> antibiotic inhibition, resistance, and resource use. 2014 , 88, 386-97	30
1603	Temporal variation in fungal communities associated with tropical hummingbirds and nectarivorous bats. 2014 , 12, 44-51	21
1602	Endemism and functional convergence across the North American soil mycobiome. 2014 , 111, 6341-6	351
1601	Prevalence and beta diversity in avian malaria communities: host species is a better predictor than geography. 2014 , 83, 1387-97	34

1600	Meta-analysis of deep-sequenced fungal communities indicates limited taxon sharing between studies and the presence of biogeographic patterns. 2014 , 201, 623-635	86
1599	Biogeography of the sediment bacterial community responds to a nitrogen pollution gradient in the East China Sea. 2014 , 80, 1919-25	62
1598	A social-ecological framework for managing microbial services. 2014 , 12, 524-531	11
1597	Multiscale patterns of arbuscular mycorrhizal fungal abundance and diversity in semiarid shrublands. 2014 , 12, 32-43	28
1596	Bacterial profiling of White Plague Disease across corals and oceans indicates a conserved and distinct disease microbiome. 2014 , 23, 965-74	66
1595	Microbial terroir for wine grapes. 2014 , 111, 5-6	155
1594	Distinct patterns of marine bacterial communities in the South and North Pacific Oceans. 2014 , 52, 834-41	8
1593	Soil fungal communities of grasslands are environmentally structured at a regional scale in the Alps. 2014 , 23, 4274-90	85
1592	Can the freshwater bacterial communities shift to the "marine-like" taxa?. 2014 , 54, 1264-72	14
1591	Free-Living and Particle-Associated Bacterioplankton in Large Rivers of the Mississippi River Basin Demonstrate Biogeographic Patterns. 2014 , 80, 7186-95	40
1590	Population structure of root nodulating <i>Rhizobium leguminosarum</i> in <i>Vicia cracca</i> populations at local to regional geographic scales. 2014 , 37, 613-21	29
1589	Microbial biogeography of wine grapes is conditioned by cultivar, vintage, and climate. 2014 , 111, E139-48	557
1588	Biogeographic patterns in below-ground diversity in New York City's Central Park are similar to those observed globally. 2014 , 281,	201
1587	Microbial abundance and community composition influence production performance in a low-temperature petroleum reservoir. 2014 , 48, 5336-44	47
1586	Diversity and distribution of rhizobia nodulated with <i>Phaseolus vulgaris</i> in two ecoregions of China. 2014 , 78, 128-137	55
1585	Bacteria-phage interactions in natural environments. 2014 , 89, 135-83	93
1584	Biogeography of <i>Sinorhizobium meliloti</i> nodulating alfalfa in different Croatian regions. 2014 , 165, 508-16	10
1583	A quantitative analysis of species sorting across organisms and ecosystems. 2014 , 95, 3284-3292	102

1582	Global biogeography of the ectomycorrhizal /sebacina lineage (Fungi, Sebaciniales) as revealed from comparative phylogenetic analyses. 2014 , 23, 4168-83	47
1581	Soil organic carbon and soil structure are driving microbial abundance and community composition across the arid and semi-arid grasslands in northern China. 2014 , 77, 51-57	106
1580	Ecology. Microbes ride the current. 2014 , 345, 1246-7	9
1579	Biogeographic patterns in ocean microbes emerge in a neutral agent-based model. 2014 , 345, 1346-9	109
1578	Spatial scaling effects on soil bacterial communities in Malaysian tropical forests. 2014 , 68, 247-58	28
1577	Bacterial distribution along a 50 °C temperature gradient reveals a parceled out hot spring environment. 2014 , 68, 729-39	13
1576	A molecular survey of protist diversity through the central Arctic Ocean. 2014 , 37, 1271-1287	34
1575	Life in extreme environments: microbial diversity in Great Salt Lake, Utah. 2014 , 18, 525-35	46
1574	Pyrosequencing reveals correlations between extremely acidophilic bacterial communities with hydrogen sulphide concentrations, pH and inert polymer coatings at concrete sewer crown surfaces. 2014 , 117, 50-64	22
1573	The unseen world: environmental microbial sequencing and identification methods for ecologists. 2014 , 12, 224-231	23
1572	Do spatial patterns of benthic diatom assemblages vary across regions and years?. 2014 , 33, 402-416	27
1571	Neotropical Andes hot springs harbor diverse and distinct planktonic microbial communities. 2014 , 89, 56-66	15
1570	Forensic soil DNA analysis using high-throughput sequencing: a comparison of four molecular markers. 2014 , 13, 176-84	42
1569	Bacterial Diversity in Sustainable Agriculture. 2014 ,	5
1568	Morphological delineation and distribution patterns of four newly described species within the <i>Synura petersenii</i> species complex (Chrysophyceae, Stramenopiles). 2014 , 49, 213-229	32
1567	Community history affects the predictability of microbial ecosystem development. 2014 , 8, 19-30	55
1566	Phytoplankton metacommunity structure in subarctic rock pools. 2014 , 73, 81-91	18
1565	What ecologists can tell virologists. 2014 , 68, 117-35	17

1564	Fungal endophyte β diversity associated with Myrtaceae species in an Andean Patagonian forest (Argentina) and an Atlantic forest (Brazil). 2014 , 8, 28-36	25
1563	Bacterial community structure and its regulating factors in the intertidal sediment along the Liaodong Bay of Bohai Sea, China. 2014 , 169, 585-92	67
1562	Abundance of broad bacterial taxa in the sargasso sea explained by environmental conditions but not water mass. 2014 , 80, 2786-95	20
1561	Environmental filtering affects soil fungal community composition more than dispersal limitation at regional scales. 2014 , 12, 14-25	113
1560	Soil properties and tree species drive β diversity of soil bacterial communities. 2014 , 76, 201-209	71
1559	Metacommunity Structure Along Resource and Disturbance Gradients in Everglades Wetlands. 2014 , 34, 135-146	15
1558	Macroecology of methane-oxidizing bacteria: the β diversity of pmoA genotypes in tropical and subtropical rice paddies. 2014 , 16, 72-83	34
1557	References. 222-260	
1556	New insights into relationships between active and dormant organisms, phylogenetic diversity and ecosystem productivity. 2015 , 24, 5767-9	1
1555	Planting increases the abundance and structure complexity of soil core functional genes relevant to carbon and nitrogen cycling. 2015 , 5, 14345	21
1554	Contrasting soil bacterial community structure between the phyla Acidobacteria and Proteobacteria in tropical Southeast Asian and temperate Japanese forests. 2015 , 90, 61-77	17
1553	Evolutionary Ecology of Microorganisms: From the Tamed to the Wild. 2015 , 4.1.2-1-4.1.2-12	2
1552	The Microbial Ecology of Benthic Environments. 2015 , 4.2.1-1-4.2.1-20	3
1551	Biogeography of Nocardiosis strains from hypersaline environments of Yunnan and Xinjiang Provinces, western China. 2015 , 5, 13323	7
1550	Genetic data from algae sedimentary DNA reflect the influence of environment over geography. 2015 , 5, 12924	21
1549	Deep sequencing of amplified Prasinovirus and host green algal genes from an Indian Ocean transect reveals interacting trophic dependencies and new genotypes. 2015 , 7, 979-89	8
1548	High speciation rate at temperate latitudes explains unusual diversity gradients in a clade of ectomycorrhizal fungi. 2015 , 69, 2196-209	20
1547	Uncovering major genomic features of essential genes in Bacteria and a methanogenic Archaea. 2015 , 282, 3395-3411	23

1546	Ecosystem productivity is associated with bacterial phylogenetic distance in surface marine waters. 2015 , 24, 5785-95	19
1545	Inner Mongolian steppe arbuscular mycorrhizal fungal communities respond more strongly to water availability than to nitrogen fertilization. 2015 , 17, 3051-68	46
1544	Bacterial biogeography in the coastal waters of northern Zhejiang, East China Sea is highly controlled by spatially structured environmental gradients. 2015 , 17, 3898-913	56
1543	Two-dimensional distribution of living benthic foraminifera in anoxic sediment layers of an estuarine mudflat (Loire estuary, France). 2015 , 12, 6219-6234	28
1542	Estimating and mapping ecological processes influencing microbial community assembly. 2015 , 6, 370	270
1541	The large-scale distribution of ammonia oxidizers in paddy soils is driven by soil pH, geographic distance, and climatic factors. 2015 , 6, 938	38
1540	Emerging spatial patterns in Antarctic prokaryotes. 2015 , 6, 1058	44
1539	Nutrient-cycling microbes in coastal Douglas-fir forests: regional-scale correlation between communities, in situ climate, and other factors. 2015 , 6, 1097	19
1538	Fractal Hypothesis of the Pelagic Microbial Ecosystem-Can Simple Ecological Principles Lead to Self-Similar Complexity in the Pelagic Microbial Food Web?. 2015 , 6, 1357	4
1537	Differential assemblage of functional units in paddy soil microbiomes. 2015 , 10, e0122221	38
1536	Diversity and Persistence of Salmonella enterica Strains in Rural Landscapes in the Southeastern United States. 2015 , 10, e0128937	31
1535	Impact of Water Chemistry, Pipe Material and Stagnation on the Building Plumbing Microbiome. 2015 , 10, e0141087	82
1534	Relative Roles of Deterministic and Stochastic Processes in Driving the Vertical Distribution of Bacterial Communities in a Permafrost Core from the Qinghai-Tibet Plateau, China. 2015 , 10, e0145747	22
1533	Detrital Dynamics and Cascading Effects on Supporting Ecosystem Services. 2015 , 97-160	15
1532	Microbial Assembly in Agroecosystems [From the Small Arise the Big. 2015 ,	1
1531	Spatial scales of bacterial community diversity at cold seeps (Eastern Mediterranean Sea). 2015 , 9, 1306-18	50
1530	Ocean plankton. Structure and function of the global ocean microbiome. 2015 , 348, 1261359	1261
1529	Who's getting around? Assessing species diversity and phylogeography in the widely distributed lichen-forming fungal genus Montanelia (Parmeliaceae, Ascomycota). 2015 , 90, 85-96	28

1528	Bacterial diversity in soils subjected to long-term chemical fertilization can be more stably maintained with the addition of livestock manure than wheat straw. 2015 , 88, 9-18	351
1527	Microbiome Ecosystem Ecology: Unseen Majority in an Anthropogenic Ecosystem. 2015 , 1-11	2
1526	Variation in recruitment and the establishment of alternative community states. 2015 , 96, 3186-96	23
1525	Independent origins and incipient speciation among host-associated populations of <i>Thielaviopsis ethacetica</i> in Cameroon. 2015 , 119, 957-972	3
1524	Metacommunity organisation, spatial extent and dispersal in aquatic systems: patterns, processes and prospects. 2015 , 60, 845-869	477
1523	Environmental metabarcoding reveals heterogeneous drivers of microbial eukaryote diversity in contrasting estuarine ecosystems. 2015 , 9, 1208-21	93
1522	Environmental rather than spatial factors structure bacterioplankton communities in shallow lakes along a > 6000 km latitudinal gradient in South America. 2015 , 17, 2336-51	53
1521	Multilocus sequence analysis of xanthomonads causing bacterial spot of tomato and pepper plants reveals strains generated by recombination among species and recent global spread of <i>Xanthomonas gardneri</i> . 2015 , 81, 1520-9	50
1520	Strong effect of climate on ectomycorrhizal fungal composition: evidence from range overlap between two mountains. 2015 , 9, 1870-9	48
1519	Patterns of local adaptation in space and time among soil bacteria. 2015 , 185, 317-31	17
1518	Aquatic invasive species: challenges for the future. 2015 , 750, 147-170	222
1517	High-throughput metagenomic technologies for complex microbial community analysis: open and closed formats. 2015 , 6,	265
1516	The effects of local, buffer zone and geographical variables on lake plankton metacommunities. 2015 , 743, 175-188	11
1515	Soil bacterial communities are shaped by temporal and environmental filtering: evidence from a long-term chronosequence. 2015 , 17, 3208-18	71
1514	Marine Actinobacterial Metabolites and their Pharmaceutical Potential. 2015 , 1371-1386	1
1513	Bacterial community structures as a diagnostic tool for watershed quality assessment. 2015 , 166, 38-44	12
1512	Long-term oil contamination increases deterministic assembly processes in soil microbes. 2015 , 25, 1235-43	30
1511	Biotechnological Potential of Marine Microbes. 2015 , 651-661	4

1510	Symbiotic diversity, specificity and distribution of rhizobia in native legumes of the Core Cape Subregion (South Africa). 2015 , 91, 1-17	86
1509	Aquifer environment selects for microbial species cohorts in sediment and groundwater. 2015 , 9, 1846-56	63
1508	Depth shapes β and α diversities of microbial eukaryotes in surficial sediments of coastal ecosystems. 2015 , 17, 3722-37	66
1507	Recent radiation in a marine and freshwater dinoflagellate species flock. 2015 , 9, 1821-34	24
1506	Geochemical niches of iron-oxidizing acidophiles in acidic coal mine drainage. 2015 , 81, 1242-50	47
1505	Metabolic dependence of phytoplankton species richness. 2015 , 24, 472-482	16
1504	Functional congruence of rhizosphere microbial communities associated to leguminous tree from Brazilian semiarid region. 2015 , 7, 95-101	15
1503	Composition of fungal and bacterial communities in forest litter and soil is largely determined by dominant trees. 2015 , 84, 53-64	317
1502	Effects of hydrography on the distribution of bacteria and virus in Cochin estuary, India. 2015 , 30, 85-92	11
1501	Soil pH determines the alpha diversity but not beta diversity of soil fungal community along altitude in a typical Tibetan forest ecosystem. 2015 , 15, 1224-1232	70
1500	The biogeography of abundant and rare bacterioplankton in the lakes and reservoirs of China. 2015 , 9, 2068-77	249
1499	Latitudinal diversity patterns of diatoms in the Southwestern Atlantic and Antarctic waters. 2015 , 37, 659-665	5
1498	Distinct soil bacterial communities along a small-scale elevational gradient in alpine tundra. 2015 , 6, 582	76
1497	Polar front associated variation in prokaryotic community structure in Arctic shelf seafloor. 2015 , 6, 17	22
1496	The Gut Microbiome of Wild Lemurs: A Comparison of Sympatric Lemur catta and Propithecus verreauxi. 2015 , 86, 85-95	37
1495	Control of climate and litter quality on leaf litter decomposition in different climatic zones. 2015 , 128, 791-802	12
1494	Development of Spatial Distribution Patterns by Biofilm Cells. 2015 , 81, 6120-8	25
1493	The spatial organization and microbial community structure of an epilithic biofilm. 2015 , 91,	18

1492	The niche of an invasive marine microbe in a subtropical freshwater impoundment. 2015 , 9, 256-64	35
1491	Interchange of entire communities: microbial community coalescence. 2015 , 30, 470-6	123
1490	Quantifying separation and similarity in a <i>Saccharomyces cerevisiae</i> metapopulation. 2015 , 9, 361-70	57
1489	Dispersal and ecological traits explain differences in beta diversity patterns of European beetles. 2015 , 42, 1526-1537	13
1488	Bacterial and archaeal communities in sediments of the north Chinese marginal seas. 2015 , 70, 105-17	73
1487	Testing ecological theories with sequence similarity networks: marine ciliates exhibit similar geographic dispersal patterns as multicellular organisms. 2015 , 13, 16	35
1486	Multi-scale variability analysis reveals the importance of spatial distance in shaping Arctic soil microbial functional communities. 2015 , 86, 126-134	36
1485	Theories, Mechanisms and Patterns of Microbiome Species Coexistence in an Era of Climate Change. 2015 , 13-53	4
1484	Ecoevolutionary Processes Regulating Microbiome Community Assembly in a Changing Global Ecosystem. 2015 , 55-87	4
1483	Metagenetic tools for the census of marine meiofaunal biodiversity: An overview. 2015 , 24 Pt 1, 11-20	68
1482	Challenges and prospects for interpreting long-term phytoplankton diversity changes in Lake Zurich (Switzerland). 2015 , 60, 1052-1059	15
1481	Biogeography and ecology of the rare and abundant microbial lineages in deep-sea hydrothermal vents. 2015 , 91, 1-11	43
1480	Quantifying the relative roles of selective and neutral processes in defining eukaryotic microbial communities. 2015 , 9, 2003-11	69
1479	Quantifying the effects of geographical and environmental factors on distribution of stream bacterioplankton within nature reserves of Fujian, China. 2015 , 22, 11010-21	17
1478	16S rRNA and As-Related Functional Diversity: Contrasting Fingerprints in Arsenic-Rich Sediments from an Acid Mine Drainage. 2015 , 70, 154-67	17
1477	Parent material and vegetation influence soil microbial community structure following 30-years of rock weathering and pedogenesis. 2015 , 69, 383-94	19
1476	Contrasting spatial patterns and ecological attributes of soil bacterial and archaeal taxa across a landscape. 2015 , 4, 518-31	30
1475	Marked seasonality and high spatial variability of protist communities in shallow freshwater systems. 2015 , 9, 1941-53	81

1474	Over 150 years of long-term fertilization alters spatial scaling of microbial biodiversity. 2015 , 6,	32
1473	Species concepts and speciation factors in cyanobacteria, with connection to the problems of diversity and classification. 2015 , 24, 739-757	84
1472	Local-global overlap in diversity informs mechanisms of bacterial biogeography. 2015 , 9, 2413-22	15
1471	Mapping and determinism of soil microbial community distribution across an agricultural landscape. 2015 , 4, 505-17	49
1470	Vegetation-associated impacts on arctic tundra bacterial and microeukaryotic communities. 2015 , 81, 492-501	60
1469	Vineyard soil bacterial diversity and composition revealed by 16S rRNA genes: Differentiation by geographic features. 2015 , 91, 232-247	82
1468	Scale-dependent effects of climate and geographic distance on bacterial diversity patterns across northern China's grasslands. 2015 , 91,	56
1467	The spatial distribution of exoenzyme activities across the soil micro-landscape, as measured in micro- and macro-aggregates, and ecosystem processes. 2015 , 91, 258-267	15
1466	Microbial evolution in extreme environments: microbial migration, genomic highways, and geochemical barriers in hydrothermal ecosystems. 2015 , 4,	6
1465	Global biogeography of human infectious diseases. 2015 , 112, 12746-51	79
1464	Neutral community model explains the bacterial community assembly in freshwater lakes. 2015 , 91,	29
1463	Antarctic bdelloid rotifers: diversity, endemism and evolution. 2015 , 761, 5-43	36
1462	Freshwater Conservation and Biomonitoring of Structure and Function. 2015 , 241-271	2
1461	Macroecological patterns of archaeal ammonia oxidizers in the Atlantic Ocean. 2015 , 24, 4931-42	15
1460	Microbial invasions: the process, patterns, and mechanisms. 2015 , 23, 719-729	181
1459	Microbial ecology of Antarctic aquatic systems. <i>Nature Reviews Microbiology</i> , 2015 , 13, 691-706	22.2 106
1458	Environmental and not spatial processes (directional and non-directional) shape the phytoplankton composition and functional groups in a large subtropical river basin. 2015 , fbv084	4
1457	Effects of local environmental variables and geographical location on the genetic diversity and composition of <i>Rhizobium leguminosarum</i> nodulating <i>Vicia cracca</i> populations. 2015 , 90, 71-79	22

1456	Biogeography of Viruses in the Sea. 2015 , 2, 41-66	68
1455	Epidemic Clones, Oceanic Gene Pools, and Eco-LD in the Free Living Marine Pathogen <i>Vibrio parahaemolyticus</i> . 2015 , 32, 1396-410	63
1454	Under-detection of endospore-forming Firmicutes in metagenomic data. 2015 , 13, 299-306	65
1453	Landscape position influences microbial composition and function via redistribution of soil water across a watershed. 2015 , 81, 8457-68	19
1452	Extinction risk of soil biota. 2015 , 6, 8862	124
1451	Plant diversity predicts beta but not alpha diversity of soil microbes across grasslands worldwide. 2015 , 18, 85-95	394
1450	Reasons Behind the Long-Term Stability of Dissolved Organic Matter. 2015 , 369-388	50
1449	Local-scale biogeography and spatiotemporal variability in communities of mycorrhizal fungi. 2015 , 205, 1454-63	146
1448	Microbial biogeography: the end of the ubiquitous dispersal hypothesis?. 2015 , 17, 544-6	47
1447	Mechanisms of soil acidification reducing bacterial diversity. 2015 , 81, 275-281	55
1446	Exploring the diversity and metabolic potential of actinomycetes from temperate marine sediments from Newfoundland, Canada. 2015 , 42, 57-72	26
1445	The population biology of fungal invasions. 2015 , 24, 1969-86	123
1444	Do organic inputs alter resistance and resilience of soil microbial community to drying?. 2015 , 81, 58-66	25
1443	Bacterial community of pond's water, sediment and in the guts of tilapia (<i>Oreochromis niloticus</i>) juveniles characterized by fluorescent in situ hybridization technique. 2015 , 46, 707-715	39
1442	Distribution of airborne microbes and antibiotic susceptibility pattern of bacteria during Gwalior trade fair, Central India. 2015 , 114, 639-46	12
1441	Oceanographic structure drives the assembly processes of microbial eukaryotic communities. 2015 , 9, 990-1002	74
1440	Using a "time machine" to test for local adaptation of aquatic microbes to temporal and spatial environmental variation. 2015 , 69, 136-45	11
1439	How do freshwater organisms cross the "dry ocean"? A review on passive dispersal and colonization processes with a special focus on temporary ponds. 2015 , 750, 103-123	143

1438	Species sorting and seasonal dynamics primarily shape bacterial communities in the Upper Mississippi River. 2015 , 505, 435-45	97
1437	Microbial communities associated with human decomposition and their potential use as postmortem clocks. 2015 , 129, 623-32	47
1436	Complex communities of small protists and unexpected occurrence of typical marine lineages in shallow freshwater systems. 2015 , 17, 3610-27	52
1435	Ammonia-oxidizing bacteria and archaea in sediments of the Gulf of Mexico. 2015 , 36, 124-35	20
1434	Investigation of microbial community structure of a shallow lake after one season copper sulfate algaecide treatment. 2015 , 170, 105-13	29
1433	Climate-related range shifts - a global multidimensional synthesis and new research directions. 2015 , 38, 15-28	469
1432	A second horizon scan of biogeography: Golden Ages, Midas touches, and the Red Queen. 2016 , 8,	3
1431	Microbial Diversity of Ammonia Oxidizing Bacteria through Waste Water Genomics. 2016 , 2,	
1430	. 2016 ,	20
1429	Colwellia psychrerythraea Strains from Distant Deep Sea Basins Show Adaptation to Local Conditions. 2016 , 4,	16
1428	Aerobiology Over Antarctica - A New Initiative for Atmospheric Ecology. 2016 , 7, 16	35
1427	Biogeographic Variation in Host Range Phenotypes and Taxonomic Composition of Marine Cyanophage Isolates. 2016 , 7, 983	15
1426	Biogeographic Distribution Patterns of Bacteria in Typical Chinese Forest Soils. 2016 , 7, 1106	55
1425	Dramatic Increases of Soil Microbial Functional Gene Diversity at the Treeline Ecotone of Changbai Mountain. 2016 , 7, 1184	23
1424	Species Divergence vs. Functional Convergence Characterizes Crude Oil Microbial Community Assembly. 2016 , 7, 1254	18
1423	Diversity, Biogeography, and Biodegradation Potential of Actinobacteria in the Deep-Sea Sediments along the Southwest Indian Ridge. 2016 , 7, 1340	46
1422	A Combination of Extreme Environmental Conditions Favor the Prevalence of Endospore-Forming Firmicutes. 2016 , 7, 1707	60
1421	Deconstructing the Bat Skin Microbiome: Influences of the Host and the Environment. 2016 , 7, 1753	50

1420	Editorial: The Role of Microbial Communities in Tropical Ecosystems. 2016 , 7, 1805	18
1419	Local and Regional Diversity Reveals Dispersal Limitation and Drift as Drivers for Groundwater Bacterial Communities from a Fractured Granite Formation. 2016 , 7, 1933	13
1418	Coupling Spatiotemporal Community Assembly Processes to Changes in Microbial Metabolism. 2016 , 7, 1949	57
1417	Local Environmental Conditions Shape Generalist But Not Specialist Components of Microbial Metacommunities in the Baltic Sea. 2016 , 7, 2078	16
1416	Extremophiles in an Antarctic Marine Ecosystem. 2016 , 4,	15
1415	Phytoplankton across Tropical and Subtropical Regions of the Atlantic, Indian and Pacific Oceans. 2016 , 11, e0151699	45
1414	Latitude delineates patterns of biogeography in terrestrial Streptomyces. 2016 , 18, 4931-4945	23
1413	Microbial biogeography of permafrost thaw ponds across the changing northern landscape. 2016 , 39, 609-618	27
1412	Water-energy balance, past ecological perturbations and evolutionary constraints shape the latitudinal diversity gradient of soil testate amoebae in south-western South America. 2016 , 25, 1216-1227	26
1411	Microbiome evolution along divergent branches of the vertebrate tree of life: what is known and unknown. 2016 , 25, 3776-800	178
1410	Biogeographical patterns in fungal communities from soils cultivated with sugarcane. 2016 , 43, 2016-2026	25
1409	Connectivity between surface and deep waters determines prokaryotic diversity in the North Atlantic Deep Water. 2016 , 18, 2052-63	31
1408	High-throughput Sequencing of Trace Quantities of Soil Provides Reproducible and Discriminative Fungal DNA Profiles. 2016 , 61, 478-484	14
1407	A Latitudinal Diversity Gradient in Terrestrial Bacteria of the Genus Streptomyces. 2016 , 7, e02200-15	66
1406	Bacterial community dissimilarity between the surface and subsurface soils equals horizontal differences over several kilometers in the western Tibetan Plateau. 2016 , 18, 1523-33	105
1405	Spatial Ecology of the Fungal Genus Xylaria in a Tropical Cloud Forest. 2016 , 48, 381-393	31
1404	Wind dispersal results in a gradient of dispersal limitation and environmental match among discrete aquatic habitats. 2016 , 39, 726-732	29
1403	Microbial community dynamics in soil aggregates shape biogeochemical gas fluxes from soil profiles - upscaling an aggregate biophysical model. 2016 , 22, 3141-56	77

1402	Global patterns and drivers of species and trait composition in diatoms. 2016 , 25, 940-950	94
1401	Climate is an important driver for stream diatom distributions. 2016 , 25, 198-206	27
1400	Long-lasting effects of land use history on soil fungal communities in second-growth tropical rain forests. 2016 , 26, 1881-1895	47
1399	Microbial diversity and community structure along a lake elevation gradient in Yosemite National Park, California, USA. 2016 , 18, 1782-91	47
1398	Geological connectivity drives microbial community structure and connectivity in polar, terrestrial ecosystems. 2016 , 18, 1834-49	30
1397	The role of tissue-specific microbiota in initial establishment success of Pacific oysters. 2016 , 18, 970-87	67
1396	Soil microorganisms behave like macroscopic organisms: patterns in the global distribution of soil euglyphid testate amoebae. 2016 , 43, 520-532	34
1395	Microbial eukaryote plankton communities of high-mountain lakes from three continents exhibit strong biogeographic patterns. 2016 , 25, 2286-301	56
1394	Microbial Community Structure of Subalpine Snow in the Sierra Nevada, California. 2016 , 48, 685-701	9
1393	Salinity shapes microbial diversity and community structure in surface sediments of the Qinghai-Tibetan Lakes. 2016 , 6, 25078	103
1392	Marine and giant viruses as indicators of a marine microbial community in a riverine system. 2016 , 5, 1071-1084	8
1391	Inhibitory interactions promote frequent bistability among competing bacteria. 2016 , 7, 11274	52
1390	Soil pH, total phosphorus, climate and distance are the major factors influencing microbial activity at a regional spatial scale. 2016 , 6, 25815	37
1389	The stable microbiome of inter and sub-tidal anemone species under increasing pCO ₂ . 2016 , 6, 37387	8
1388	Summer temperature can predict the distribution of wild yeast populations. 2016 , 6, 1236-50	34
1387	Not poles apart: Antarctic soil fungal communities show similarities to those of the distant Arctic. 2016 , 19, 528-36	61
1386	Distance-Decay Relationship for Biological Wastewater Treatment Plants. 2016 , 82, 4860-6	19
1385	Characterization and bioremediation potential of marine Psychrobacter species. 2016 , 42, 193-203	5

1384	Biogeography of planktonic and coral-associated microorganisms across the Hawaiian Archipelago. 2016 , 92,	7
1383	"Every Gene Is Everywhere but the Environment Selects": Global Geolocalization of Gene Sharing in Environmental Samples through Network Analysis. 2016 , 8, 1388-400	55
1382	Biogeography of sulfur-oxidizing <i>Acidithiobacillus</i> populations in extremely acidic cave biofilms. 2016 , 10, 2879-2891	22
1381	Active populations of rare microbes in oceanic environments as revealed by bromodeoxyuridine incorporation and 454 tag sequencing. 2016 , 576, 650-6	8
1380	Microbiology: Mixing Wine, Chocolate, and Coffee. 2016 , 26, R275-7	3
1379	Patterns and multi-scale drivers of phytoplankton species richness in temperate peri-urban lakes. 2016 , 559, 74-83	15
1378	Experimental demonstration of an Allee effect in microbial populations. 2016 , 12,	16
1377	The efficiency of a new hydrodynamic cavitation pilot system on <i>Artemia salina</i> cysts and natural population of copepods and bacteria under controlled mesocosm conditions. 2016 , 105, 341-50	3
1376	Temporal and spatial assessment of microbial communities in commercial silages from bunker silos. 2016 , 100, 6827-6835	29
1375	Bacterial communities in oil contaminated soils: Biogeography and co-occurrence patterns. 2016 , 98, 64-73	207
1374	Evidence of adaptation, niche separation and microevolution within the genus <i>Polaromonas</i> on Arctic and Antarctic glacial surfaces. 2016 , 20, 403-13	29
1373	Evidence for dispersal and habitat controls on pond diatom communities from the McMurdo Sound Region of Antarctica. 2016 , 39, 2441-2456	20
1372	Geomicrobiology and Metagenomics of Terrestrial Deep Subsurface Microbiomes. 2016 , 94, 1-77	25
1371	Their World: A Diversity of Microbial Environments. 2016 ,	4
1370	Microbes and the Arctic Ocean. 2016 , 341-381	4
1369	Crotalariaeae and Genisteae of the South African Great Escarpment are nodulated by novel <i>Bradyrhizobium</i> species with unique and diverse symbiotic loci. 2016 , 100, 206-218	27
1368	Deterministic assembly processes govern bacterial community structure in the Fynbos, South Africa. 2016 , 72, 313-23	15
1367	Impact of Middle Eastern dust storms on indoor and outdoor composition of bioaerosol. 2016 , 138, 135-143	54

1366	Modeling Soil Processes: Review, Key Challenges, and New Perspectives. 2016 , 15, vzt2015.09.0131	311
1365	Bacterial Community Structure at the Microscale in Two Different Soils. 2016 , 72, 717-24	4
1364	Communities that thrive in extreme conditions captured from a freshwater lake. 2016 , 12,	11
1363	Plant community, geographic distance and abiotic factors play different roles in predicting AMF biogeography at the regional scale in northern China. 2016 , 8, 1048-1057	38
1362	Toxicity of Manufactured Nanomaterials to Microorganisms. 2016 , 320-346	4
1361	Microbial eukaryote communities exhibit robust biogeographical patterns along a gradient of Patagonian and Antarctic lakes. 2016 , 18, 5249-5264	31
1360	Systematics of organic-walled microfossils from the ca. 780-740 Ma Chuar Group, Grand Canyon, Arizona. 2016 , 90, 815-853	36
1359	A Step Forward to Empower Global Microbiome Research Through Local Leadership. 2016 , 24, 767-771	9
1358	Evidence of small-scale spatial structuring of phytoplankton alpha- and beta-diversity in the open ocean. 2016 , 104, 1682-1695	24
1357	Biogeochemical drivers of microbial community convergence across actively retreating glaciers. 2016 , 101, 74-84	30
1356	An equilibrium theory signature in the island biogeography of human parasites and pathogens. 2016 , 25, 107-116	9
1355	Environmental conditions shape soil bacterial community structure in a fragmented landscape. 2016 , 103, 39-45	9
1354	THE POPULATION BIOLOGY OF FUNGAL INVASIONS. 2016 , 81-100	0
1353	Distinct distribution patterns of prokaryotes between sediment and water in the Yellow River estuary. 2016 , 100, 9683-9697	34
1352	Vertical and seasonal dynamics of fungal communities in boreal Scots pine forest soil. 2016 , 92,	55
1351	Landscape-scale spatial abundance distributions discriminate core from random components of boreal lake bacterioplankton. 2016 , 19, 1506-1515	25
1350	Temperature mediates continental-scale diversity of microbes in forest soils. 2016 , 7, 12083	271
1349	Genomic differentiation among wild cyanophages despite widespread horizontal gene transfer. 2016 , 17, 930	75

1348	Decoupling function and taxonomy in the global ocean microbiome. 2016 , 353, 1272-7	880
1347	Bats perceptually weight prey cues across sensory systems when hunting in noise. 2016 , 353, 1277-80	59
1346	A monotonically declining elevational pattern of bacterial diversity in freshwater lake sediments. 2016 , 18, 5175-5186	21
1345	Vertical variation of bacterial community in Nam Co, a large stratified lake in central Tibetan Plateau. 2016 , 109, 1323-35	13
1344	Global biogeography of microbial nitrogen-cycling traits in soil. 2016 , 113, 8033-40	186
1343	Neutral processes and species sorting in benthic microalgal community assembly: effects of tidal resuspension. 2016 , 52, 827-839	10
1342	Biogeography, Microbial. 2016 , 179-185	1
1341	Self-organized patchiness facilitates survival in a cooperatively growing <i>Bacillus subtilis</i> population. 2016 , 1, 16022	38
1340	Planktonic protistan communities in lakes along a large-scale environmental gradient. 2017 , 93,	9
1339	The biogeography of red snow microbiomes and their role in melting arctic glaciers. 2016 , 7, 11968	112
1338	Biogeography and Adaptive evolution of <i>Streptomyces</i> Strains from saline environments. 2016 , 6, 32718	10
1337	Divergent habitat filtering of root and soil fungal communities in temperate beech forests. 2016 , 6, 31439	59
1336	European derived <i>Saccharomyces cerevisiae</i> colonisation of New Zealand vineyards aided by humans. 2016 , 16,	10
1335	Diversity and Biogeography of Picoeukaryotes: New Insights into the Rare Biosphere. 2016 , 315-328	1
1334	The timescales of global surface-ocean connectivity. 2016 , 7, 11239	55
1333	Dust Rains Deliver Diverse Assemblages of Microorganisms to the Eastern Mediterranean. 2016 , 6, 22657	30
1332	Identification of subannual patterns in microbial community signatures from individual sedimentary laminae using a freeze-coring approach. 2016 , 61, 735-747	3
1331	Stream diatom assemblages as predictors of climate. 2016 , 61, 876-886	7

1330	Applying landscape genetics to the microbial world. 2016 , 25, 3266-75	8
1329	Biogeography of Marine Microorganisms. 2016 , 187-207	5
1328	Environmental Filtering Process Has More Important Roles than Dispersal Limitation in Shaping Large-Scale Prokaryotic Beta Diversity Patterns of Grassland Soils. 2016 , 72, 221-230	20
1327	Spring to autumn changes in the arbuscular mycorrhizal fungal community composition in the different propagule types associated to a Mediterranean shrubland. 2016 , 408, 107-120	22
1326	Determinants of the biodiversity patterns of ammonia-oxidizing archaea community in two contrasting forest stands. 2016 , 16, 878-888	2
1325	Widespread green algae <i>Chlorella</i> and <i>Stichococcus</i> exhibit polar-temperate and tropical-temperate biogeography. 2016 , 92,	46
1324	Biogeographical Patterns of Legume-Nodulating <i>Burkholderia</i> spp.: from African Fynbos to Continental Scales. 2016 , 82, 5099-115	39
1323	Site-specific environmental factors control bacterial and viral diversity in stormwater retention ponds. 2016 , 77, 23-36	11
1322	Diversity at low abundance: The phenomenon of the rare bacterial biosphere. 2016 , 85, 272-282	15
1321	Marine yeast biodiversity on seaweeds in New Zealand waters. 2016 , 54, 30-47	9
1320	Comparing how land use change impacts soil microbial catabolic respiration in Southwestern Amazon. 2016 , 47, 63-72	10
1319	Does arsenic play an important role in the soil microbial community around a typical arsenic mining area?. 2016 , 213, 949-956	15
1318	The mutation-drift balance in spatially structured populations. 2016 , 402, 9-17	9
1317	From laboratory to environmental conditions: a new approach for chemical's biodegradability assessment. 2016 , 23, 18684-93	14
1316	Dimensions of biodiversity in the Earth mycobiome. <i>Nature Reviews Microbiology</i> , 2016 , 14, 434-47	22.2 292
1315	The Impact of Selection, Gene Conversion, and Biased Sampling on the Assessment of Microbial Demography. 2016 , 33, 1711-25	41
1314	Ectomycorrhizal fungal richness declines towards the host species' range edge. 2016 , 25, 3224-41	26
1313	Biogeographic patterns of soil diazotrophic communities across six forests in North America. 2016 , 25, 2937-48	57

1312	Decoupled distance-decay patterns between <i>dsrA</i> and 16S rRNA genes among salt marsh sulfate-reducing bacteria. 2016 , 18, 75-86	21
1311	Multispecies Swarms of Social Microorganisms as Moving Ecosystems. 2016 , 24, 257-269	27
1310	Distribution patterns of the abundance of major bacterial and archaeal groups in Patagonian lakes. 2016 , 38, 64-82	13
1309	Epidemiology: A global picture of melioidosis. 2016 , 529, 290-1	25
1308	Salinity is the major factor influencing the sediment bacterial communities in a Mediterranean lagoonal complex (Amvrakikos Gulf, Ionian Sea). 2016 , 28, 71-81	17
1307	Biogeography of thermophilic phototrophic bacteria belonging to <i>Roseiflexus</i> genus. 2016 , 92,	8
1306	Crop rotations alter bacterial and fungal diversity in paddy soils across East Asia. 2016 , 95, 250-261	75
1305	Potential sources of microbial colonizers in an initial soil ecosystem after retreat of an alpine glacier. 2016 , 10, 1625-41	57
1304	Soil microbial communities along the route of a venturous cycling trip. 2016 , 99, 13-18	10
1303	Characterization of the papilionoid-Burkholderia interaction in the Fynbos biome: The diversity and distribution of beta-rhizobia nodulating <i>Podalyria calyptrata</i> (Fabaceae, Podalyrieae). 2016 , 39, 41-8	26
1302	Functional implications of the pH-trait distribution of the microbial community in a re-inoculation experiment across a pH gradient. 2016 , 93, 69-78	22
1301	Bacterial diversity and distribution in seven different estuarine sediments of Poyang Lake, China. 2016 , 75, 1	30
1300	Plankton communities in the five Iles Eparses (Western Indian Ocean) considered to be pristine ecosystems. 2016 , 72, 9-20	9
1299	Biogeographic Patterns Between Bacterial Phyllosphere Communities of the Southern Magnolia (<i>Magnolia grandiflora</i>) in a Small Forest. 2016 , 71, 954-61	17
1298	Unpredictable assembly of arbuscular mycorrhizal fungal communities. 2016 , 59, 11-15	42
1297	Differences in the composition of arbuscular mycorrhizal fungal communities promoted by different propagule forms from a Mediterranean shrubland. 2016 , 26, 489-96	25
1296	Amplicon-Based Pyrosequencing Reveals High Diversity of Protistan Parasites in Ships' Ballast Water: Implications for Biogeography and Infectious Diseases. 2016 , 71, 530-42	37
1295	Interactions between hydrology and water chemistry shape bacterioplankton biogeography across boreal freshwater networks. 2016 , 10, 1755-66	113

1294	Patterns and processes in microbial biogeography: do molecules and morphologies give the same answers?. 2016 , 10, 1779-90		47
1293	Microbial diversity in an anaerobic digester with biogeographical proximity to geothermally active region. 2016 , 37, 2694-702		4
1292	Disentangling the relative importance of host tree community, abiotic environment and spatial factors on ectomycorrhizal fungal assemblages along an elevation gradient. 2016 , 92, fiw044		38
1291	Contrasting factors drive within-lake bacterial community composition and functional traits in a large shallow subtropical lake. 2016 , 778, 105-120		14
1290	Mycelium-Like Networks Increase Bacterial Dispersal, Growth, and Biodegradation in a Model Ecosystem at Various Water Potentials. 2016 , 82, 2902-2908		28
1289	Seasonal dynamics of the soil microbial community structure within the proximal area of tree boles: Possible influence of stemflow. 2016 , 73, 108-118		24
1288	The ecology and biogeochemistry of stream biofilms. <i>Nature Reviews Microbiology</i> , 2016 , 14, 251-63	22.2	494
1287	Application of the Environmental Relative Moldiness Index in Finland. 2016 , 82, 578-84		17
1286	Identification of Specialists and Abundance-Occupancy Relationships among Intestinal Bacteria of Aves, Mammalia, and Actinopterygii. 2015 , 82, 1496-1503		3
1285	The biogeography of polymicrobial infection. <i>Nature Reviews Microbiology</i> , 2016 , 14, 93-105	22.2	161
1284	Latitudinal variation in virus-induced mortality of phytoplankton across the North Atlantic Ocean. 2016 , 10, 500-13		67
1283	Diversity, distribution and biotechnological potential of endophytic fungi. 2016 , 66, 529-542		58
1282	Interference Competition Among Household Strains of Pseudomonas. 2016 , 72, 821-830		8
1281	Bacterial diversity and community composition from seasurface to subseafloor. 2016 , 10, 979-89		133
1280	Microbial biofilms as one of the key elements in modulating ecohydrological processes in both natural and urban water corridors. 2016 , 16, 33-38		3
1279	Carbon Mineralization in Peatlands: Does the Soil Microbial Community Composition Matter?. 2016 , 33, 151-162		6
1278	Leveraging ecological theory to guide natural product discovery. 2016 , 43, 115-28		26
1277	Silica-scaled chrysophytes (Stramenopiles, Ochrophyta) along a salinity gradient: a case study from the Gulf of Bothnia western shore (northern Europe). 2016 , 764, 187-197		11

1276	Microbial Nonlinear Response to a Precipitation Gradient in the Northeastern Tibetan Plateau. 2016 , 33, 85-97	4
1275	Biogeography of aquatic hyphomycetes: Current knowledge and future perspectives. 2016 , 19, 169-181	55
1274	Metadata-mining of 18S rDNA sequences reveals that 'Everything is not everywhere' for glomeromycotan fungi. 2016 , 66, 361-371	4
1273	Shifts in bacterial community composition associated with increased carbon cycling in a mosaic of phytoplankton blooms. 2016 , 10, 39-50	86
1272	Field experimental evidence that stochastic processes predominate in the initial assembly of bacterial communities. 2016 , 18, 1730-9	13
1271	The roles of environmental conditions and geographical distances on the species turnover of the whole phytoplankton and zooplankton communities and their subsets in tropical reservoirs. 2016 , 764, 171-186	30
1270	Drivers of phytoplankton diversity in Patagonian and Antarctic lakes across a latitudinal gradient (2150 km): the importance of spatial and environmental factors. 2016 , 764, 157-170	26
1269	The Succession of Bacterial Community Structure in Groundwater from a 250-m Gallery in the Horonobe Underground Research Laboratory. 2017 , 34, 489-499	4
1268	Enhanced summer warming reduces fungal decomposer diversity and litter mass loss more strongly in dry than in wet tundra. 2017 , 23, 406-420	53
1267	Diversity and composition of cultivable gut bacteria in an endemic island bird and its mainland sister species. 2017 , 71, 155-164	4
1266	Bacterial diversity in the rhizosphere of two phylogenetically closely related plant species across environmental gradients. 2017 , 17, 122-132	8
1265	Chemotype diversity in <i>Planktothrix rubescens</i> (cyanobacteria) populations is correlated to lake depth. 2017 , 9, 158-168	9
1264	Pyrosequencing of <i>rpoB</i> uncovers a significant biogeographical pattern of rhizobial species in soybean rhizosphere. 2017 , 44, 1491-1499	14
1263	From Microhabitat of Floral Nectar Up to Biogeographic Scale: Novel Insights on Neutral and Niche Bacterial Assemblies. 2017 , 74, 128-139	7
1262	Namib Desert edaphic bacterial, fungal and archaeal communities assemble through deterministic processes but are influenced by different abiotic parameters. 2017 , 21, 381-392	22
1261	Ecoimmunology and microbial ecology: Contributions to avian behavior, physiology, and life history. 2017 , 88, 112-121	14
1260	Protistan Biogeography: A Snapshot Across a Major Shipping Corridor Spanning Two Oceans. 2017 , 168, 183-196	2
1259	A community trait-based approach to ecosystem functioning in soil. 2017 , 239, 265-273	13

1258	Bacterial Diversity in Ships' Ballast Water, Ballast-Water Exchange, and Implications for Ship-Mediated Dispersal of Microorganisms. 2017 , 51, 1962-1972	29
1257	Phylogenetic relationships and spatial distributions of putative fungal pathogens of seedlings across a rainfall gradient in Panama. 2017 , 26, 65-73	8
1256	The differentiation of soil bacterial communities along a precipitation and temperature gradient in the eastern Inner Mongolia steppe. 2017 , 152, 47-56	56
1255	The thermal mismatch hypothesis explains host susceptibility to an emerging infectious disease. 2017 , 20, 184-193	93
1254	Metapopulation theory provides new insight into microbial biogeography. 2017 , 19, 849-850	2
1253	Beta diversity of diatoms is driven by environmental heterogeneity, spatial extent and productivity. 2017 , 800, 7-16	26
1252	Habitat-specific patterns and drivers of bacterial diversity in China's drylands. 2017 , 11, 1345-1358	111
1251	Distribution of Ciliates in Intertidal Sediments across Geographic Distances: A Molecular View. 2017 , 168, 171-182	12
1250	The role of dispersal and local environment in urban land snail assemblages: an example of three cities in Central Italy. 2017 , 20, 919-931	13
1249	Plant diversity represents the prevalent determinant of soil fungal community structure across temperate grasslands in northern China. 2017 , 110, 12-21	124
1248	Microdiversity shapes the traits, niche space, and biogeography of microbial taxa. 2017 , 9, 55-70	59
1247	Distinct Biogeographic Patterns for Archaea, Bacteria, and Fungi along the Vegetation Gradient at the Continental Scale in Eastern China. 2017 , 2,	63
1246	The Landscape Ecology and Microbiota of the Human Nose, Mouth, and Throat. 2017 , 21, 421-432	98
1245	Distinct Soil Microbial Communities in habitats of differing soil water balance on the Tibetan Plateau. 2017 , 7, 46407	18
1244	Patterns of Arbuscular Mycorrhizal Fungal Distribution on Mainland and Island Sandy Coastal Plain Ecosystems in Brazil. 2017 , 74, 654-669	13
1243	Patterns and drivers of fungal diversity along an altitudinal gradient on Mount Gongga, China. 2017 , 17, 2856-2865	15
1242	Scale-dependent key drivers controlling methane oxidation potential in Chinese grassland soils. 2017 , 111, 104-114	50
1241	Contribution of different bacterial dispersal sources to lakes: Population and community effects in different seasons. 2017 , 19, 2391-2404	28

1240	Molecular characterisation of protistan species and communities in shipsballast water across three U.S. coasts. 2017 , 23, 680-691	13
1239	Mechanistic modeling of microbial interactions at pore to profile scale resolve methane emission dynamics from permafrost soil. 2017 , 122, 1216-1238	14
1238	Community composition and assembly processes of the free-living and particle-attached bacteria in Taihu Lake. 2017 , 93,	31
1237	Functioning grouped soil microbial communities according to ecosystem type, based on comparison of fallows and meadows in the same region. 2017 , 599-600, 981-991	3
1236	The interacting roles of climate, soils, and plant production on soil microbial communities at a continental scale. 2017 , 98, 1957-1967	45
1235	Subsurface Microbial Ecosystems: A Photon Flux and a Metabolic Cascade. 2017 , 167, 763-776	5
1234	Spatial variation of microbial communities in sediments along the environmental gradients from Xiaoqing River to Laizhou Bay. 2017 , 120, 90-98	21
1233	The Implications of Eco-Evolutionary Processes for the Emergence of Marine Plankton Community Biogeography. 2017 , 190, 116-130	18
1232	Population structure of Rhizobium etli-like strains nodulated with Phaseolus vulgaris in two ecoregions of China. 2017 , 112, 14-23	7
1231	Disentangling multi-scale environmental effects on stream microbial communities. 2017 , 44, 1512-1523	26
1230	Land scale biogeography of arsenic biotransformation genes in estuarine wetland. 2017 , 19, 2468-2482	29
1229	Soil aggregation and associated microbial communities modify the impact of agricultural management on carbon content. 2017 , 19, 3070-3086	99
1228	Drivers of phytoplankton richness and diversity components in Neotropical floodplain lakes, from small to large spatial scales. 2017 , 799, 203-215	18
1227	Vertical zonation of soil fungal community structure in a Korean pine forest on Changbai Mountain, China. 2017 , 33, 12	13
1226	Bacterioplankton assemblages in coastal ponds reflect the influence of hydrology and geomorphological setting. 2017 , 93,	4
1225	Verrucomicrobial elevational distribution was strongly influenced by soil pH and carbon/nitrogen ratio. 2017 , 17, 2449-2456	36
1224	Fundamental differences in diversity and genomic population structure between Atlantic and Pacific Prochlorococcus. 2017 , 11, 1997-2011	35
1223	The heterogeneity of composition and assembly processes of the microbial community between different nutrient loading lake zones in Taihu Lake. 2017 , 101, 5913-5923	29

1222	Thermal barriers constrain microbial elevational range size via climate variability. 2017 , 19, 3283-3296	7
1221	Transition boundaries for protistan species turnover in hypersaline waters of different biogeographic regions. 2017 , 19, 3186-3200	19
1220	Diversity and biogeographical patterns of yeast communities in Antarctic, Patagonian and tropical lakes. 2017 , 28, 33-43	16
1219	Soil fungal diversity in natural grasslands of the Tibetan Plateau: associations with plant diversity and productivity. 2017 , 215, 756-765	130
1218	Microorganisms and ocean global change. 2017 , 2, 17058	166
1217	Industrial Culture Collections: Gateways from Microbial Diversity to Applications. 2017 , 237-255	
1216	Diversity of aromatic hydroxylating dioxygenase genes in mangrove microbiome and their biogeographic patterns across global sites. 2017 , 6, e00490	10
1215	Distance decay relationships in foliar fungal endophytes are driven by rare taxa. 2017 , 19, 2794-2805	31
1214	The microbial habitat in soil: Scale, heterogeneity and functional consequences. 2017 , 180, 425-429	35
1213	Relative roles of competition, environmental selection and spatial processes in structuring soil bacterial communities in the Qinghai-Tibetan Plateau. 2017 , 117-118, 223-232	13
1212	Temporal patterns of phyto- and bacterioplankton and their relationships with environmental factors in Lake Taihu, China. 2017 , 184, 299-308	27
1211	Feeding preference as a main determinant of microscale patchiness among terrestrial nematodes. 2017 , 17, 1257-1270	23
1210	Managing Soil Microbial Biomass for Sustainable Agro-Ecosystems. 2017 , 67-101	1
1209	Common and Rare Taxa of Planktonic Ciliates: Influence of Flood Events and Biogeographic Patterns in Neotropical Floodplains. 2017 , 74, 522-533	10
1208	Competition and niche separation of pelagic bacteria in freshwater habitats. 2017 , 19, 2133-2150	23
1207	Deterministic influences exceed dispersal effects on hydrologically-connected microbiomes. 2017 , 19, 1552-1567	86
1206	History of adaptation determines short-term shifts in performance and community structure of hydrogen-producing microbial communities degrading wheat straw. 2017 , 10, 1569-1580	20
1205	The theory of island biogeography applies to ectomycorrhizal fungi in subalpine tree islands at a fine scale. 2017 , 8, e01677	21

1204	Computational Modeling of Microbial Communities. 2017 , 163-189	4
1203	Association mapping reveals novel serpentine adaptation gene clusters in a population of symbiotic Mesorhizobium. 2017 , 11, 248-262	46
1202	Metapopulation theory identifies biogeographical patterns among core and satellite marine bacteria scaling from tens to thousands of kilometers. 2017 , 19, 1222-1236	20
1201	High taxonomic variability despite stable functional structure across microbial communities. 2016 , 1, 15	198
1200	Endemicity of the cosmopolitan mesophilic chemolithoautotroph Sulfurimonas at deep-sea hydrothermal vents. 2017 , 11, 909-919	19
1199	Genomic evolution of bacterial populations under coselection by antibiotics and phage. 2017 , 26, 1848-1859	9
1198	Evidence for microbial local adaptation in nature. 2017 , 26, 1860-1876	28
1197	Generalist species drive microbial dispersion and evolution. 2017 , 8, 1162	68
1196	The influence of e-waste recycling on the molecular ecological network of soil microbial communities in Pakistan and China. 2017 , 231, 173-181	33
1195	Shift in bacterioplankton diversity and structure: Influence of anthropogenic disturbances along the Yarlung Tsangpo River on the Tibetan Plateau, China. 2017 , 7, 12529	31
1194	The coupling of taxonomy and function in microbiomes. 2017 , 32, 1225-1243	20
1193	Soil pH is a major driver of soil diazotrophic community assembly in Qinghai-Tibet alpine meadows. 2017 , 115, 547-555	67
1192	Stochastic Community Assembly: Does It Matter in Microbial Ecology?. 2017 , 81,	537
1191	The Brazilian Microbiome Project. 2017 , 1-6	2
1190	The Brazilian Soil Microbiome. 2017 , 21-39	1
1189	Fungal community assemblages in a high elevation desert environment: Absence of dispersal limitation and edaphic effects in surface soil. 2017 , 115, 393-402	20
1188	Distinct seasonality of chytrid-dominated benthic fungal communities in the neritic oceans (Bohai Sea and North Yellow Sea). 2017 , 30, 55-66	18
1187	Environmental niches and metabolic diversity in Neoproterozoic lakes. 2017 , 15, 767-783	23

1186	Is microbial terroir related to geographic distance between vineyards?. 2017 , 9, 742-749	40
1185	nirS-type denitrifying bacterial assemblages respond to environmental conditions of a shallow estuary. 2017 , 9, 766-778	5
1184	Inference on Paleoclimate Change Using Microbial Habitat Preference in Arctic Holocene Sediments. 2017 , 7, 9652	2
1183	Bacterial diversity among four healthcare-associated institutes in Taiwan. 2017 , 7, 8230	12
1182	Lineage overwhelms environmental conditions in determining rhizosphere bacterial community structure in a cosmopolitan invasive plant. 2017 , 8, 433	64
1181	Linking bacterial community structure to advection and environmental impact along a coast-fjord gradient of the Sognefjord, western Norway. 2017 , 159, 13-30	10
1180	Long-Distance Dispersal of Fungi. 2017 , 5,	48
1179	Assembly of microbial communities in replicate nutrient-cycling model ecosystems follows divergent trajectories, leading to alternate stable states. 2017 , 19, 3374-3386	23
1178	Fungal communities are differentially affected by conventional and biodynamic agricultural management approaches in vineyard ecosystems. 2017 , 246, 306-313	51
1177	Freshwater diatoms in the Sajama, Quelccaya, and Coropuna glaciers of the South American Andes. 2017 , 32, 153-162	4
1176	Environment and geographic distance differ in relative importance for determining fungal community of rhizosphere and bulk soil. 2017 , 19, 3649-3659	51
1175	Response of microbial community and catabolic genes to simulated petroleum hydrocarbon spills in soils/sediments from different geographic locations. 2017 , 123, 875-885	12
1174	Biophysical processes supporting the diversity of microbial life in soil. 2017 , 41, 599-623	184
1173	Small-scale variation of corticolous microalgal covers: Effects of microhabitat, season, and space. 2017 , 65, 299-311	2
1172	Dispersal limitation promotes the diversification of the mammalian gut microbiota. 2017 , 114, 13768-13773	64
1171	THE IMPACT OF AGRICULTURE ON SOIL MICROBIAL COMMUNITY COMPOSITION AND DIVERSITY IN SOUTHEAST ASIA. 2017 , 25-40	
1170	Microdiversity of an Abundant Terrestrial Bacterium Encompasses Extensive Variation in Ecologically Relevant Traits. 2017 , 8,	32
1169	Changes in the soil bacterial community along a pedogenic gradient. 2017 , 7, 14593	25

1168	Translating Phytobiomes from Theory to Practice: Ecological and Evolutionary Considerations. 2017 , 1, 57-69	35
1167	Environmental filtering by pH and soil nutrients drives community assembly in fungi at fine spatial scales. 2017 , 26, 6960-6973	127
1166	Unravelling direct and indirect effects of hierarchical factors driving microbial stream communities. 2017 , 44, 2376-2385	14
1165	Microbial Biogeography. 2017 , 1-6	2
1164	Effects of habitat constraints on soil microbial community function. 2017 , 7, 4280	37
1163	Introducing the sporobiota and sporobiome. 2017 , 9, 38	30
1162	Do biofilm communities respond to the chemical signatures of fracking? A test involving streams in North-central Arkansas. 2017 , 17, 29	6
1161	Leaf and root C-to-N ratios are poor predictors of soil microbial biomass C and respiration across 32 tree species. 2017 , 65, 1623	11
1160	Bacterial Community Composition and Dynamics Spanning Five Years in Freshwater Bog Lakes. 2017 , 2,	36
1159	Water depth is a strong driver of intra-lake diatom distributions in a small boreal lake. 2017 , 58, 231-241	11
1158	Bacteria as Emerging Indicators of Soil Condition. 2017 , 83,	120
1157	Seasonal and geographical distribution of near-surface small photosynthetic eukaryotes in the western North Pacific determined by pyrosequencing of 18S rDNA. 2017 , 93,	20
1156	Distinct biogeographical patterns of marine bacterial taxonomy and functional genes. 2017 , 26, 177-190	36
1155	Spatial and temporal dynamics of nitrogen fixing, nitrifying and denitrifying microbes in an unfertilized grassland soil. 2017 , 109, 214-226	57
1154	The Role of Oceans in the Origin of Life and in Biological Evolution. 2017 , 209-256	1
1153	Soil enzyme activity and stoichiometry in forest ecosystems along the North-South Transect in eastern China (NSTEC). 2017 , 104, 152-163	143
1152	Bacterial distribution pattern in the surface sediments distinctive among shelf, slope and basin across the western Arctic Ocean. 2017 , 40, 423-436	4
1151	Effects of dispersal and selection on stochastic assembly in microbial communities. 2017 , 11, 176-185	128

1150	Water mass mixing shapes bacterial biogeography in a highly hydrodynamic region of the Southern Ocean. 2017 , 19, 1017-1029	19
1149	Bacterial Diversity Patterns Differ in Soils Developing in Sub-tropical and Cool-Temperate Ecosystems. 2017 , 73, 556-569	9
1148	Biogeography of <i>Oenococcus oeni</i> Reveals Distinctive but Nonspecific Populations in Wine-Producing Regions. 2017 , 83,	26
1147	Structured Populations of <i>Sulfolobus acidocaldarius</i> with Susceptibility to Mobile Genetic Elements. 2017 , 9, 1699-1710	14
1146	Overview of freshwater microbial eukaryotes diversity: a first analysis of publicly available metabarcoding data. 2017 , 93,	67
1145	Microbial diversity in an intensively managed landscape is structured by landscape connectivity. 2017 , 93,	14
1144	Invasive legumes can associate with many mutualists of native legumes, but usually do not. 2017 , 7, 8599-8611	16
1143	Biogeographical Patterns in Myxomycetes. 2017 , 299-331	6
1142	The geographical patterns of Chinese liquors during 1995-2004. 2017 , 13, 107-116	6
1141	Change in Soil Microbial Community Compositions and Diversity Following the Conversion of Tropical Forest to Rubber Plantations in Xishuangbanna, Southwest China. 2017 , 10, 194008291773323	16
1140	Geographical distance and local environmental conditions drive the genetic population structure of a freshwater microalga (Bathycoccaleae; Chlorophyta) in Patagonian lakes. 2017 , 93,	11
1139	Geographical variation in soil bacterial community structure in tropical forests in Southeast Asia and temperate forests in Japan based on pyrosequencing analysis of 16S rRNA. 2017 , 92, 1-20	6
1138	Impact of tropical forest conversion on soil bacterial diversity in tropical region of China. 2017 , 83, 91-97	13
1137	Long-Distance Dispersal of Fungi. 2017 , 309-333	16
1136	Soil Bacterial Diversity Impacted by Conversion of Secondary Forest to Rubber or Eucalyptus Plantations: A Case Study of Hainan Island, South China. 2017 , 63, 87-93	22
1135	Sampling Terrestrial Environments for Bacterial Polyketides. 2017 , 22,	9
1134	Microbial Community and Functional Structure Significantly Varied among Distinct Types of Paddy Soils But Responded Differently along Gradients of Soil Depth Layers. 2017 , 8, 945	40
1133	Eelgrass Leaf Surface Microbiomes Are Locally Variable and Highly Correlated with Epibiotic Eukaryotes. 2017 , 8, 1312	30

1132	Global Biogeographic Analysis of Methanogenic Archaea Identifies Community-Shaping Environmental Factors of Natural Environments. 2017 , 8, 1339	43
1131	Conservation of Species- and Trait-Based Modeling Network Interactions in Extremely Acidic Microbial Community Assembly. 2017 , 8, 1486	8
1130	The Patterns and Drivers of Bacterial and Fungal Diversity in a Typical Dryland Ecosystem of Northwest China. 2017 , 8, 2126	33
1129	Microbial Biogeography ?. 2017 ,	
1128	Picoeukaryotes ?. 2017 ,	
1127	Characterization of spatial distribution of the bacterial community in the South Sea of Korea. 2017 , 12, e0174159	18
1126	City-scale distribution and dispersal routes of mycobiome in residences. 2017 , 5, 131	19
1125	The strength of species sorting of phytoplankton communities is temporally variable in subtropical reservoirs. 2017 , 800, 31-43	19
1124	Characterisation of Arctic Bacterial Communities in the Air above Svalbard. 2017 , 6,	20
1123	Interaction between Salmonella and Plants: Potential Hosts and Vectors for Human Infection. 2017 ,	2
1122	Spatial population genetic structure of a bacterial parasite in close coevolution with its host. 2018 , 27, 1371-1384	7
1121	Microbial community composition along a 50'000-year lacustrine sediment sequence. 2018 , 94,	20
1120	Shrub range expansion alters diversity and distribution of soil fungal communities across an alpine elevation gradient. 2018 , 27, 2461-2476	25
1119	Why do microbes exhibit weak biogeographic patterns?. 2018 , 12, 1404-1413	73
1118	Function and functional redundancy in microbial systems. 2018 , 2, 936-943	423
1117	What will it take to understand the ecology of symbiotic microorganisms?. 2018 , 20, 1920-1924	5
1116	Soil Bacterial Diversity Is Associated with Human Population Density in Urban Greenspaces. 2018 , 52, 5115-5124	21
1115	Multilayer approach for characterization of bacterial diversity in a marginal sea: From surface to seabed. 2018 , 184, 15-27	4

1114	Soil bacterial community composition and diversity in relation to edaphic properties and plant traits in grasslands of southern China. 2018 , 128, 43-53	40
1113	A spatial gradient of bacterial diversity in the human oral cavity shaped by salivary flow. 2018 , 9, 681	64
1112	Extracellular DNA as a genetic recorder of microbial diversity in benthic deep-sea ecosystems. 2018 , 8, 1839	22
1111	Distribution and coexistence patterns of phytoplankton in subtropical shallow lakes and the role of niche-based and spatial processes. 2018 , 814, 233-246	1
1110	Biogeography and ecological processes affecting root-associated bacterial communities in soybean fields across China. 2018 , 627, 20-27	31
1109	Distribution of thermophilic endospores in a temperate estuary indicate that dispersal history structures sediment microbial communities. 2018 , 20, 1134-1147	12
1108	Long-term research in ecology and evolution: a survey of challenges and opportunities. 2018 , 88, 245-258	34
1107	Oxygen modulates bacterial community composition in the coastal upwelling waters off central Chile. 2018 , 156, 68-79	33
1106	References. 2018 , 393-464	
1105	Effects of oak, beech and spruce on the distribution and community structure of fungi in litter and soils across a temperate forest. 2018 , 119, 162-173	34
1104	What role does human activity play in microbial biogeography?: The revealing case of testate amoebae in the soils of Pyramiden, Svalbard. 2018 , 67, 10-15	6
1103	Soil protists: a fertile frontier in soil biology research. 2018 , 42, 293-323	176
1102	Genomic diversity of a nectar yeast clusters into metabolically, but not geographically, distinct lineages. 2018 , 27, 2067-2076	15
1101	Deposition rates of viruses and bacteria above the atmospheric boundary layer. 2018 , 12, 1154-1162	126
1100	Influence of Darkness and Aging on Marine and Freshwater Biofilm Microbial Communities Using Microcosm Experiments. 2018 , 76, 314-327	3
1099	Experimental insights into the importance of ecologically dissimilar bacteria to community assembly along a salinity gradient. 2018 , 20, 1170-1184	22
1098	Bacterial and Fungal Community Composition and Functional Activity Associated with Lake Wetland Water Level Gradients. 2018 , 8, 760	24
1097	Functional biogeography and host specificity of bacterial communities associated with the Marine Green Alga <i>Ulva</i> spp. 2018 , 27, 1952-1965	28

- 1096 First records of testate amoebae from the Novaya Zemlya archipelago (Russian Arctic). **2018**, 41, 1133-1142 5
- 1095 Evaluation of wetted surface area of commercial ships as biofouling habitat flux to the United States. **2018**, 20, 1977-1990 10
- 1094 The Coevolution of Life and Environment on Mars: An Ecosystem Perspective on the Robotic Exploration of Biosignatures. **2018**, 18, 1-27 42
- 1093 Geo-climatic factors drive diatom community distribution in tropical South American freshwaters. **2018**, 106, 1660-1672 16
- 1092 Variation among European beetle taxa in patterns of distance decay of similarity suggests a major role of dispersal processes. **2018**, 41, 1825-1834 37
- 1091 Ecological and biogeographical drivers of freshwater green algae biodiversity: from local communities to large-scale species pools of desmids. **2018**, 186, 1017-1030 10
- 1090 Human dissemination of genes and microorganisms in Earth's Critical Zone. **2018**, 24, 1488-1499 44
- 1089 Co-occurrence patterns of soybean rhizosphere microbiome at a continental scale. **2018**, 118, 178-186 116
- 1088 Large-scale ocean connectivity and planktonic body size. **2018**, 9, 142 53
- 1087 Neutral models of short-term microbiome dynamics with host subpopulation structure and migration limitation. **2018**, 6, 80 12
- 1086 Disentangling the processes driving the biogeography of freshwater diatoms: A multiscale approach. **2018**, 45, 1582-1592 13
- 1085 Microeukaryotic biogeography in the typical subtropical coastal waters with multiple environmental gradients. **2018**, 635, 618-628 25
- 1084 Diversity and assembly patterns of activated sludge microbial communities: A review. **2018**, 36, 1038-1047 85
- 1083 Spatio-temporal dynamics of soil bacterial communities as a function of Amazon forest phenology. **2018**, 8, 4382 21
- 1082 Biodiversity of fungi on *Vitis vinifera* L. revealed by traditional and high-resolution culture-independent approaches. **2018**, 90, 1-84 52
- 1081 Microbial Ecology of Marine Environments Chronically Polluted by Petroleum. **2018**, 1-12
- 1080 Spatial scale affects the relative role of stochasticity versus determinism in soil bacterial communities in wheat fields across the North China Plain. **2018**, 6, 27 152
- 1079 Genetic diversity and symbiotic effectiveness of *Phaseolus vulgaris*-nodulating rhizobia in Kenya. **2018**, 41, 291-299 21

1078	Major changes in the composition of a Southern Ocean bacterial community in response to diatom-derived dissolved organic matter. 2018 , 94,	16
1077	Toward a theory for diversity gradients: the abundance-adaptation hypothesis. 2018 , 41, 255-264	26
1076	Trait-dependent distributional shifts in fruiting of common British fungi. 2018 , 41, 51-61	14
1075	Microbial functional diversity covaries with permafrost thaw-induced environmental heterogeneity in tundra soil. 2018 , 24, 297-307	12
1074	Effects of reclamation years on composition and diversity of soil bacterial communities in Northwest China. 2018 , 64, 28-40	13
1073	From vineyard to winery: a source map of microbial diversity driving wine fermentation. 2018 , 20, 75-84	62
1072	Alterations in soil fungal community composition and network assemblage structure by different long-term fertilization regimes are correlated to the soil ionome. 2018 , 54, 95-106	27
1071	Importance of Local and Regional Scales in Shaping Mycobacterial Abundance in Freshwater Lakes. 2018 , 75, 834-846	5
1070	Host effects on microbiota community assembly. 2018 , 87, 331-340	24
1069	Testing the efficiency of a bacterial community-based index (microgAMBI) to assess distinct impact sources in six locations around the world. 2018 , 85, 594-602	28
1068	Biogeographical patterns of soil microbial community as influenced by soil characteristics and climate across Chinese forest biomes. 2018 , 124, 298-305	19
1067	Forest conversion induces seasonal variation in microbial diversity. 2018 , 20, 111-123	25
1066	A Microbial Analysis Primer for Biogeochemists. 2018 , 599-609	2
1065	Association between temporal and spatial beta diversity in phytoplankton. 2018 , 41, 1345-1356	4
1064	Variation in range size and dispersal capabilities of microbial taxa. 2018 , 99, 322-334	34
1063	Contrasting the relative importance of species sorting and dispersal limitation in shaping marine bacterial versus protist communities. 2018 , 12, 485-494	138
1062	Heterogeneity of methane seep biomes in the Northeast Pacific. 2018 , 150, 195-209	7
1061	Soil organic matter availability and climate drive latitudinal patterns in bacterial diversity from tropical to cold temperate forests. 2018 , 32, 61-70	63

1060	Myxomycete communities occurring in fragmented forest patches in two municipalities of Laguna, Philippines. 2018 , 19, 289-299	4
1059	The genus <i>Eunotia</i> (Bacillariophyta) in the Falkland Islands and species-area relationships in sub-Antarctic islands. 2018 , 33, 413-452	3
1058	Small-Scale Soil Microbial Community Heterogeneity Linked to Landform Historical Events on King George Island, Maritime Antarctica. 2018 , 9, 3065	4
1057	Comparison of Bacterial Diversity in Air and Water of a Major Urban Center. 2018 , 9, 2868	16
1056	Low recovery of bacterial community after an extreme salinization-desalinization cycle. 2018 , 18, 195	3
1055	The Biogeography of Great Salt Lake Halophilic Archaea: Testing the Hypothesis of Avian Mechanical Carriers. 2018 , 10, 124	11
1054	Host diet mediates a negative relationship between abundance and diversity of gut microbiota. 2018 , 8, 9491-9502	18
1053	Local Functioning, Landscape Structuring: Drivers of Soil Microbial Community Structure and Function in Peatlands. 2018 , 9, 2060	2
1052	Impact of hydrologic boundaries on microbial planktonic and biofilm communities in shallow terrestrial subsurface environments. 2018 , 94,	28
1051	Effects of host species, environmental filtering and forest age on community assembly of ectomycorrhizal fungi in fragmented forests. 2018 , 36, 89-98	18
1050	Microcosms and Mesocosms: A Way to Test the Resilience of Microbial Communities in Cuatro Ciñegas. 2018 , 83-102	1
1049	Strain-level diversity drives alternative community types in millimetre-scale granular biofilms. 2018 , 3, 1295-1303	48
1048	Diversity-Function Relationships in Natural, Applied, and Engineered Microbial Ecosystems. 2018 , 105, 131-189	7
1047	Relationships Between Fungal and Plant Communities Differ Between Desert and Grassland in a Typical Dryland Region of Northwest China. 2018 , 9, 2327	7
1046	Two key features influencing community assembly processes at regional scale: Initial state and degree of change in environmental conditions. 2018 , 27, 5238-5251	63
1045	The Biogeographical Distribution of Soil Bacterial Communities in the Loess Plateau as Revealed by High-Throughput Sequencing. 2018 , 9, 2456	19
1044	Mineral Facilitated Horizontal Gene Transfer: A New Principle for Evolution of Life?. 2018 , 9, 2217	7
1043	Fecal source identification using random forest. 2018 , 6, 185	51

1042	Biodiversity-function relationships in methanogenic communities. 2018 , 27, 4641-4651	16
1041	Bacterial community structure in the Bohai Strait provides insights into organic matter niche partitioning. 2018 , 169, 46-54	5
1040	Influence of Environmental Factors on the Structure of Soil Microfungi of Vietnamese Tropical Forests. 2018 , 11, 472-483	
1039	Disentangling protist communities identified from DNA and RNA surveys in the Pearl River-South China Sea Continuum during the wet and dry seasons. 2018 , 27, 4627-4640	9
1038	Seasonal succession of small planktonic eukaryotes inhabiting surface waters of a coastal upwelling system. 2018 , 20, 2955-2973	22
1037	Sporulation of <i>Frankia</i> spp. as a Determinant of Alder-Symbiont Interactions. 2018 , 84,	8
1036	A Reverse Ecology Framework for Bacteria and Archaea. 2018 , 77-96	4
1035	From leaf to continent: The multi-scale distribution of an invasive cryptic pathogen complex on oak. 2018 , 36, 39-50	20
1034	Gut Bacterial Communities of and (Curculionidae: Scolytinae): A Metagenomic Analysis across Different Geographical Locations in Mexico. 2018 , 19,	10
1033	Dispersal Modifies the Diversity and Composition of Active Bacterial Communities in Response to a Salinity Disturbance. 2018 , 9, 2188	22
1032	Macroecology to Unite All Life, Large and Small. 2018 , 33, 731-744	67
1031	Cell size and acid tolerance constrain pond diatom distributions in the subarctic. 2018 , 63, 1569-1578	8
1030	Volume 39 Number 1. 2018 , 39, 1	
1029	The importance of resolving biogeographic patterns of microbial microdiversity. 2018 , 39, 5	13
1028	Using invasion theory to predict the fate of arbuscular mycorrhizal fungal inoculants. 2018 , 20, 2695-2706	12
1027	Deforestation decreases spatial turnover and alters the network interactions in soil bacterial communities. 2018 , 123, 80-86	44
1026	Cosmopolitanism and endemism in free-living nematodes. 2018 , 33,	1
1025	Harmful Algae Introductions: Vectors of Transfer, Mitigation, and Management. 2018 , 493-506	0

1024	Storm Events Restructured Bacterial Community and Their Biogeochemical Potentials. 2018 , 123, 2257-2269	16
1023	Distinct biogeographic patterns of rhizobia and non-rhizobial endophytes associated with soybean nodules across China. 2018 , 643, 569-578	19
1022	Rivers as carriers and potential sentinels for Burkholderia pseudomallei in Laos. 2018 , 8, 8674	8
1021	Biogeography of soil bacteria and archaea across France. 2018 , 4, eaat1808	100
1020	Structure and function of the global topsoil microbiome. 2018 , 560, 233-237	654
1019	Microbes follow Humboldt: temperature drives plant and soil microbial diversity patterns from the Amazon to the Andes. 2018 , 99, 2455-2466	95
1018	Energy Gradients Structure Microbial Communities Across Sediment Horizons in Deep Marine Sediments of the South China Sea. 2018 , 9, 729	9
1017	Taxon-Function Decoupling as an Adaptive Signature of Lake Microbial Metacommunities Under a Chronic Polymetallic Pollution Gradient. 2018 , 9, 869	14
1016	Bacterial Communities in Riparian Sediments: A Large-Scale Longitudinal Distribution Pattern and Response to Dam Construction. 2018 , 9, 999	29
1015	Clean Low-Biomass Procedures and Their Application to Ancient Ice Core Microorganisms. 2018 , 9, 1094	12
1014	Synchrony of Eukaryotic and Prokaryotic Planktonic Communities in Three Seasonally Sampled Austrian Lakes. 2018 , 9, 1290	18
1013	Biodiversity of cultivable Burkholderia species in Argentinean soils under no-till agricultural practices. 2018 , 13, e0200651	8
1012	Microbial Diversity: The Gap between the Estimated and the Known. 2018 , 10, 46	19
1011	Differential Preference of Burkholderia and Mesorhizobium to pH and Soil Types in the Core Cape Subregion, South Africa. 2017 , 9,	11
1010	Linking Uncultivated Microbial Populations and Benthic Carbon Turnover by Using Quantitative Stable Isotope Probing. 2018 , 84,	23
1009	Network hubs in root-associated fungal metacommunities. 2018 , 6, 116	58
1008	A unified conceptual framework for prediction and control of microbiomes. 2018 , 44, 20-27	21
1007	Diel light cycle as a key factor for modelling phytoplankton biogeography and diversity. 2018 , 384, 241-248	6

1006	Microbial diversity and biogeography in Arctic soils. 2018 , 10, 611-625	38
1005	Macroinvertebrate and soil prokaryote communities in the forest-tundra ecotone of the Subarctic Yukon. 2018 , 41, 1619-1633	7
1004	Assessing and Interpreting the Within-Body Biogeography of Human Microbiome Diversity. 2018 , 9, 1619	4
1003	Spatial Patterns and Drivers of Microbial Taxa in a Karst Broadleaf Forest. 2018 , 9, 1691	14
1002	Understanding how microbiomes influence the systems they inhabit. 2018 , 3, 977-982	101
1001	A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. 2018 , 36, 996-1004	1369
1000	Has Submerged Vegetation Loss Altered Sediment Denitrification, N ₂ O Production, and Denitrifying Microbial Communities in Subtropical Lakes?. 2018 , 32, 1195	5
999	Bacterial and ciliate biofilm community structure at different spatial levels of a salt lake meta-community. 2018 , 94,	2
998	Phylogenetic conservatism of thermal traits explains dispersal limitation and genomic differentiation of <i>Streptomyces</i> sister-taxa. 2018 , 12, 2176-2186	15
997	Everything is not everywhere: a tale on the biogeography of cyanobacteria. 2018 , 820, 23-48	26
996	Adaptation to reef habitats through selection on the coral animal and its associated microbiome. 2018 , 27, 2956-2971	42
995	Distance decay as a descriptor of the diatom compositional variation in tropical reservoirs. 2018 , 69, 105	4
994	Continental-scale macrofungal assemblage patterns correlate with climate, soil carbon and nitrogen deposition. 2018 , 45, 1942-1953	24
993	Using collections data to infer biogeographic, environmental, and host structure in communities of endophytic fungi. 2018 , 110, 47-62	14
992	Co-occurrence Networks Among Bacteria and Microbial Eukaryotes of Lake Baikal During a Spring Phytoplankton Bloom. 2019 , 77, 96-109	49
991	Microbiome functioning depends on individual and interactive effects of the environment and community structure. 2019 , 13, 1-11	25
990	The biology of fog: results from coastal Maine and Namib Desert reveal common drivers of fog microbial composition. 2019 , 647, 1547-1556	24
989	Molecular diversity and biogeography of benthic ciliates in the Bohai Sea and Yellow Sea. 2019 , 38, 78-86	1

988	Evaluation of microbial content of indoor air in hot arid climate. 2019 , 16, 5429-5438	3
987	Biogeographical patterns in soil bacterial communities across the Arctic region. 2019 , 95,	25
986	Diversity patterns of planktonic microeukaryote communities in tropical floodplain lakes based on 18S rDNA gene sequences. 2019 , 41, 241-256	7
985	Uncovering the rules of microbial community invasions. 2019 , 3, 1162-1171	17
984	Population Genetic Divergence and Environment Influence the Gut Microbiome in Oregon Threespine Stickleback. 2019 , 10,	14
983	Amazon fish bacterial communities show structural convergence along widespread hydrochemical gradients. 2019 , 28, 3612-3626	9
982	The disappearing periglacial ecosystem atop Mt. Kilimanjaro supports both cosmopolitan and endemic microbial communities. 2019 , 9, 10676	11
981	A biogeographic map of soil bacterial communities in wheats field of the North China Plain. 2019 , 1, 50-58	6
980	Spatio-temporal patterns of zooplankton in a main-stem dam affected tributary: a case study in the Xiangxi River of the Three Gorges Reservoir, China. 2019 , 62, 1058-1069	13
979	Interactome-based abiotic and biotic impacts on biodiversity of plankton communities in disturbed wetlands. 2019 , 25, 1416-1428	1
978	Environmental filtering: A case of bacterial community assembly in soil. 2019 , 136, 107531	11
977	Microbial assembly, interaction, functioning, activity and diversification: a review derived from community compositional data. 2019 , 1, 112-128	40
976	Community Structure, Abundance and Potential Functions of Bacteria and Archaea in the Sansha Yongle Blue Hole, Xisha, South China Sea. 2019 , 10, 2404	11
975	Environmental Filtering Drives Local Soil Fungal beta Diversity More than Dispersal Limitation in Six Forest Types along a Latitudinal Gradient in Eastern China. 2019 , 10, 863	3
974	Microbes and macro-invertebrates show parallel β diversity but contrasting α diversity patterns in a marine natural experiment. 2019 , 286, 20190999	4
973	Not by Salinity Alone: How Environmental Factors Shape Fungal Communities in Saline Soils. 2019 , 83, 1387-1398	7
972	Ecology of Freshwater Diatoms [Current Trends and Applications. 2019 , 289-309	0
971	Bacterial community composition in lakes. 2019 , 1-71	3

970	Selection imposed by local environmental conditions drives differences in microbial community composition across geographically distinct groundwater aquifers. 2019 , 95,	16
969	From the Vineyard to the Winery: How Microbial Ecology Drives Regional Distinctiveness of Wine. 2019 , 10, 2679	43
968	Latitudinal gradient of cyanobacterial diversity in tidal flats. 2019 , 14, e0224444	1
967	Global Distribution of Anaerobic Ammonia Oxidation (Anammox) Bacteria - Field Surveys in Wetland, Dryland, Groundwater Aquifer and Snow. 2019 , 10, 2583	10
966	Metabolic Overlap in Environmentally Diverse Microbial Communities. 2019 , 10, 989	14
965	Incorporating phylogenetic metrics to microbial co-occurrence networks based on amplicon sequences to discern community assembly processes. 2019 , 19, 1552-1564	16
964	Diversity, Ecology, and Prevalence of Antimicrobials in Nature. 2019 , 10, 2518	21
963	Spatial gradients in the characteristics of soil-carbon fractions are associated with abiotic features but not microbial communities. 2019 , 16, 3911-3928	12
962	Dispersal ability and niche breadth act synergistically to determine zooplankton but not phytoplankton metacommunity structure. 2019 , 41, 479-490	3
961	Does Soil Contribute to the Human Gut Microbiome?. 2019 , 7,	43
960	Community phylogenetic structure reveals the imprint of dispersal-related dynamics and environmental filtering by nutrient availability in freshwater diatoms. 2019 , 9, 11590	7
959	Functional Diversity: An Epistemic Roadmap. 2019 , 69, 800-811	10
958	Biogeography of arbuscular mycorrhizal fungal communities in saline ecosystems of northern China. 2019 , 143, 213-221	5
957	Carbon in the Deep Biosphere. 2019 , 480-523	1
956	Population Genomics Insights into Adaptive Evolution and Ecological Differentiation in Streptomyces. 2019 , 85,	12
955	Spatio-temporal population dynamics of six phytoplankton taxa. 2019 , 828, 301-314	3
954	Selfish, sharing and scavenging bacteria in the Atlantic Ocean: a biogeographical study of bacterial substrate utilisation. 2019 , 13, 1119-1132	43
953	Coupled effects of land use pattern and hydrological regime on composition and diversity of riverine eukaryotic community in a coastal watershed of Southeast China. 2019 , 660, 787-798	10

952	Microbial community drivers of PK/NRP gene diversity in selected global soils. 2019 , 7, 78	15
951	Neutral models predict biogeographical patterns of soil microbes at a local scale in Mediterranean heathlands, South Africa. 2019 , 74, 139-150	2
950	Microbial Ecology of Marine Environments Chronically Polluted by Petroleum. 2019 , 51-62	
949	A new DTAR (diversity×time×area relationship) model demonstrated with the indoor microbiome. 2019 , 46, 2024-2041	12
948	When Is A Lineage A Species? A Case Study In Myxocorys gen. nov. (Synechococcales: Cyanobacteria) With The Description of Two New Species From The Americas. 2019 , 55, 976-996	24
947	Pseudomonas strains isolated from different environmental niches exhibit different antagonistic ability. 2019 , 31, 399-420	3
946	Detection limits affect the predictability of the presence of an invasive harmful alga across geographic space. 2019 , 21, 2301-2311	1
945	Legacy of a Pleistocene bacterial community: Patterns in community dynamics through changing ecosystems. 2019 , 226, 65-73	0
944	Phosphorus mediates soil prokaryote distribution pattern along a small-scale elevation gradient in Noijin Kangsang Peak, Tibetan Plateau. 2019 , 95,	7
943	Soil chemical properties and geographical distance exerted effects on arbuscular mycorrhizal fungal community composition in pear orchards in Jiangsu Province, China. 2019 , 142, 18-24	17
942	Modelling the effects of physicochemical variables and anthropogenic activities as ecological drivers of Plesiomonas shigelloides distribution and freshwaters quality. 2019 , 682, 765-778	4
941	A comprehensive census of lake microbial diversity on a global scale. 2019 , 62, 1320-1331	22
940	Spatial differences in bacterial communities preserved in soils archived for a decade. 2019 , 142, 64-71	2
939	Biogeography of the free-living and particle-attached bacteria in Tibetan lakes. 2019 , 95,	11
938	Distinct responses of planktonic and sedimentary bacterial communities to anthropogenic activities: Case study of a tributary of the Three Gorges Reservoir, China. 2019 , 682, 324-332	13
937	Priming effect of litter mineralization: the role of root exudate depends on its interactions with litter quality and soil condition. 2019 , 440, 457-471	18
936	Differences in the Cyanobacterial Community Composition of Biocrusts From the Drylands of Central Mexico. Are There Endemic Species?. 2019 , 10, 937	20
935	Global diversity and biogeography of bacterial communities in wastewater treatment plants. 2019 , 4, 1183-1195	248

934	The spatial scale dependence of diazotrophic and bacterial community assembly in paddy soil. 2019 , 28, 1093	8
933	From ecosystems to human welfare: the role and conservation of biodiversity. 2019 , 49,	1
932	Biogeography and the driving factors affecting forest soil bacteria in an arid area. 2019 , 680, 124-131	32
931	Diversity of nasal microbiota and its interaction with surface microbiota among residents in healthcare institutes. 2019 , 9, 6175	15
930	Genes, geology and germs: gut microbiota across a primate hybrid zone are explained by site soil properties, not host species. 2019 , 286, 20190431	48
929	Establishment Limitation Constrains the Abundance of Lactic Acid Bacteria in the Napa Cabbage Phyllosphere. 2019 , 85,	13
928	Freshwater Bacterioplankton Metacommunity Structure Along Urbanization Gradients in Belgium. 2019 , 10, 743	11
927	Delving into the dark ecology: A continent-wide assessment of patterns of composition in soil fungal communities from Australian tussock grasslands. 2019 , 39, 356-370	4
926	Archaeorhizomycetes Spatial Distribution in Soils Along Wide Elevational and Environmental Gradients Reveal Co-abundance Patterns With Other Fungal Saprobies and Potential Weathering Capacities. 2019 , 10, 656	17
925	Dispersal limitations and historical factors determine the biogeography of specialized terrestrial protists. 2019 , 28, 3089-3100	19
924	Multiscale patterns of rarity in fungi, inferred from fruiting records. 2019 , 28, 1106	3
923	Two sub-Antarctic and Northern Europe distributed diatom species found in a middle-mountain lake in France. 2019 , 166, 212-220	1
922	Climate and soil parameters are more important than denitrifier abundances in controlling potential denitrification rates in Chinese grassland soils. 2019 , 669, 62-69	9
921	Coming to Common Ground: The Challenges of Applying Ecological Theory Developed Aboveground to Rhizosphere Interactions. 2019 , 7,	4
920	Disentangling the effects of dispersal mode on the assembly of macroinvertebrate assemblages in a heterogeneous highland region. 2019 , 38, 170-182	12
919	Drivers of Regional Bacterial Community Structure and Diversity in the Northwest Atlantic Ocean. 2019 , 10, 281	11
918	Impacts of Sampling Design on Estimates of Microbial Community Diversity and Composition in Agricultural Soils. 2019 , 78, 753-763	8
917	Response of dry bean (<i>Phaseolus vulgaris</i> L.) to inoculation with indigenous and commercial <i>Rhizobium</i> strains under organic farming systems in Minnesota. 2019 , 78, 125-134	4

916	Planktonic food web structure and trophic transfer efficiency along a productivity gradient in the tropical and subtropical Atlantic Ocean. 2019 , 9, 2044	43
915	Spatial Variability of Antarctic Surface Snow Bacterial Communities. 2019 , 10, 461	8
914	Historical Factors Associated With Past Environments Influence the Biogeography of Thermophilic Endospores in Arctic Marine Sediments. 2019 , 10, 245	5
913	Divergent national-scale trends of microbial and animal biodiversity revealed across diverse temperate soil ecosystems. 2019 , 10, 1107	51
912	Microbial community composition in alpine lake sediments from the Hengduan Mountains. 2019 , 8, e00832	10
911	Fiddler crab bioturbation determines consistent changes in bacterial communities across contrasting environmental conditions. 2019 , 9, 3749	31
910	Scale dependency of dispersal limitation, environmental filtering and biotic interactions determine the diversity and composition of oribatid mite communities. 2019 , 74, 43-53	5
909	Spatial patterns of fungal endophytes in a subtropical montane rainforest of northern Taiwan. 2019 , 39, 316-327	8
908	Dynamics of the physiochemical and community structures of biofilms under the influence of algal organic matter and humic substances. 2019 , 158, 136-145	13
907	Structure and Diversity of Soil Bacterial Communities in Offshore Islands. 2019 , 9, 4689	11
906	Dispersal homogenizes communities via immigration even at low rates in a simplified synthetic bacterial metacommunity. 2019 , 10, 1314	23
905	Phytoplankton Species Richness along Coastal and Estuarine Salinity Continua. 2019 , 194, E41-E51	11
904	Microbial biogeography of Spanish-style green olive fermentations in the province of Seville, Spain. 2019 , 82, 259-268	14
903	Widespread Distribution of Highly Adapted Species Nodulating Diverse Legumes in Africa. 2019 , 10, 310	25
902	Offspring Microbiomes Differ Across Breeding Sites in a Panmictic Species. 2019 , 10, 35	22
901	Microbiomes of China's Space Station During Assembly, Integration, and Test Operations. 2019 , 78, 631-650	6
900	The effects of environmental factors and geographic distance on species turnover in an agriculturally dominated river network. 2019 , 191, 201	3
899	Community ecology across bacteria, archaea and microbial eukaryotes in the sediment and seawater of coastal Puerto Nuevo, Baja California. 2019 , 14, e0212355	21

898	Variability in the Response of Bacterial Community Assembly to Environmental Selection and Biotic Factors Depends on the Immigrated Bacteria, as Revealed by a Soil Microcosm Experiment. 2019 , 4,	0
897	Australian corticolous myxomycetes: models of distribution and development. 2019 , 67, 617	3
896	Abiotic and biotic drivers of endosymbiont community assembly in <i>Jatropha curcas</i> . 2019 , 10, e02941	3
895	High diatom species turnover in a Baltic Sea rock pool metacommunity. 2019 , 49, 2887-2899	6
894	7. Techniques and approaches to quantify microbial diversity in extreme environments. 2019 , 151-166	
893	Habitat filtering shapes the differential structure of microbial communities in the Xilingol grassland. 2019 , 9, 19326	5
892	Taxa Area and distance Decay relationships of unicellular eukaryotes along an elevation gradient of mountainous freshwater ecosystems. 2019 , 41, 821-834	3
891	Gene gain and loss push prokaryotes beyond the homologous recombination barrier and accelerate genome sequence divergence. 2019 , 10, 5376	24
890	Biogeographic Patterns of Ectomycorrhizal Fungal Communities Associated With Across the Japanese Archipelago. 2019 , 10, 2656	3
889	Prokaryotic Diversity in Mangrove Sediments across Southeastern China Fundamentally Differs from That in Other Biomes. 2019 , 4,	26
888	Bringing Community Ecology to Bear on the Issue of Antimicrobial Resistance. 2019 , 10, 2626	8
887	Tissue-Specific and Geographical Variation in Endophytic Fungi of and Fungal Associations With the Environment. 2019 , 10, 2919	14
886	Shedding Light on Specificity: Population Genomic Structure of a Symbiosis Between a Coral Reef Fish and Luminous Bacterium. 2019 , 10, 2670	2
885	Molecular biogeography of planktonic and benthic diatoms in the Yangtze River. 2019 , 7, 153	21
884	Sketching the Human Microbiome Biogeography with DAR (Diversity-Area Relationship) Profiles. 2019 , 77, 821-838	13
883	Repeated evolutionary transitions of flavobacteria from marine to non-marine habitats. 2019 , 21, 648-666	17
882	Bridging reproductive and microbial ecology: a case study in arbuscular mycorrhizal fungi. 2019 , 13, 873-884	21
881	Microorganisms in ballast water: Disinfection, community dynamics, and implications for management. 2019 , 657, 704-716	37

- 880 Evolutionary constraints on species diversity in marine bacterioplankton communities. **2019**, 13, 1032-1041 8
- 879 Experimental Testing of Dispersal Limitation in Soil Bacterial Communities with a Propagule Addition Approach. **2019**, 77, 905-912 1
- 878 Environmental and spatial variables determine the taxonomic but not functional structure patterns of microbial communities in alpine grasslands. **2019**, 654, 960-968 3
- 877 Community structural differences shape microbial responses to high molecular weight organic matter. **2019**, 21, 557-571 24
- 876 Applying microbial biogeography in soil forensics. **2019**, 38, 195-203 19
- 875 Factors influencing aquatic and terrestrial bacterial community assembly. **2019**, 11, 306-315 70
- 874 Seasonal, sub-seasonal and diurnal variation of soil bacterial community composition in a temperate deciduous forest. **2019**, 95, 9 9
- 873 Geographic distance and soil microbial biomass carbon drive biogeographical distribution of fungal communities in Chinese Loess Plateau soils. **2019**, 660, 1058-1069 26
- 872 Long Term Diversity and Distribution of Non-photosynthetic Cyanobacteria in Peri-Alpine Lakes. **2018**, 9, 3344 23
- 871 Bacterioplankton Metacommunity Processes across Thermal Gradients: Weaker Species Sorting but Stronger Niche Segregation in Summer than in Winter in a Subtropical Bay. **2019**, 85, 11 11
- 870 Biogeography of thermophiles and predominance of *Thermus scotoductus* in domestic water heaters. **2019**, 23, 119-132 3
- 869 Bacterial spores, from ecology to biotechnology. **2019**, 106, 79-111 12
- 868 Strong in combination: Polyphasic approach enhances arguments for cold-assigned cyanobacterial endemism. **2019**, 8, e00729 16
- 867 Grape berry surface bacterial microbiome: impact from the varieties and clones in the same vineyard from central China. **2019**, 126, 204-214 18
- 866 Soil bacterial community structure in Chinese wetlands. **2019**, 337, 290-299 33
- 865 Niche and fitness differences determine invasion success and impact in laboratory bacterial communities. **2019**, 13, 402-412 27
- 864 Assembly processes of trophic guilds in the root mycobiome of temperate forests. **2019**, 28, 348-364 22
- 863 Towards global distribution maps of unicellular organisms such as calcareous dinophytes based on DNA sequence information. **2019**, 49, 749-758 3

862	The drivers of soil bacterial communities in rubber plantation at local and geographic scales. 2020 , 66, 358-369	7
861	Dispersal alters soil microbial community response to drought. 2020 , 22, 905-916	18
860	Potential pathogen communities in highly polluted river ecosystems: Geographical distribution and environmental influence. 2020 , 49, 197-207	10
859	The diversity and biogeography of microeukaryotes in the euphotic zone of the northwestern Pacific Ocean. 2020 , 698, 134289	13
858	Fungal community demonstrates stronger dispersal limitation and less network connectivity than bacterial community in sediments along a large river. 2020 , 22, 832-849	40
857	Global ecotypes in the ubiquitous marine clade SAR86. 2020 , 14, 178-188	16
856	Oceanic Microplankton Do Not Adhere to the Latitudinal Diversity Gradient. 2020 , 79, 511-515	9
855	Contribution of Microbes in the Renovation of Wetlands. 2020 , 101-124	4
854	Rapid Colonization of Uranium Mining-Impacted Waters, the Biodiversity of Successful Lineages of Phytoplankton Extremophiles. 2020 , 79, 576-587	2
853	Small scale fungal community differentiation in a vineyard system. 2020 , 87, 103358	21
852	Regional community assembly drivers and microbial environmental sources shaping bacterioplankton in an alpine lacustrine district (Pyrenees, Spain). 2020 , 22, 297-309	11
851	Significant Bacterial Distance-Decay Relationship in Continuous, Well-Connected Southern Ocean Surface Water. 2020 , 80, 73-80	3
850	Conservation tillage decreases selection pressure on community assembly in the rhizosphere of arbuscular mycorrhizal fungi. 2020 , 710, 136326	13
849	Marine diatom assemblages of the Nosy Be Island coasts, NW Madagascar: species composition and biodiversity using molecular and morphological taxonomy. 2020 , 18, 161-180	7
848	The Best of All Worlds: Conjunctivitis through the Lens of Community Ecology and Microbial Biogeography. 2019 , 8,	3
847	Microbial biogeography and ecology of the mouth and implications for periodontal diseases. 2020 , 82, 26-41	32
846	Depth-Dependent Patterns of Bacterial Communities and Assembly Processes in a Typical Red Soil Critical Zone. 2020 , 37, 201-212	10
845	Mechanisms of soil bacterial and fungal community assembly differ among and within islands. 2020 , 22, 1559-1571	17

844	Temperature drives local contributions to beta diversity in mountain streams: Stochastic and deterministic processes. 2020 , 29, 420-432	14
843	Mountain biodiversity and ecosystem functions: interplay between geology and contemporary environments. 2020 , 14, 931-944	33
842	The life aquatic in high relief: shifts in the physical and biological characteristics of alpine lakes along an elevation gradient in the Rocky Mountains, USA. 2020 , 82, 1	3
841	Development of biological soil crust prompts convergent succession of prokaryotic communities. 2020 , 187, 104360	13
840	Large-scale geographical and environmental drivers of shallow lake diatom metacommunities across Europe. 2020 , 707, 135887	8
839	Biogeographic patterns of microbial association networks in paddy soil within Eastern China. 2020 , 142, 107696	18
838	Rain-Fed Granite Rock Basins Accumulate a High Diversity of Dormant Microbial Eukaryotes. 2020 , 79, 882-897	5
837	Fungi associated with tree species at an Alberta oil sands reclamation area, as determined by sporocarp assessments and high-throughput DNA sequencing. 2020 , 147, 103359	2
836	Microbial rescue effects: How microbiomes can save hosts from extinction. 2020 , 34, 2055-2064	15
835	Microbial Communities across Global Marine Basins Show Important Compositional Similarities by Depth. 2020 , 11,	7
834	Metacommunity Structures of Macroinvertebrates and Diatoms in High Mountain Streams, Yunnan, China. 2020 , 8,	2
833	Soil structure, nutrient status and water holding capacity shape Uruguayan grassland prokaryotic communities. 2020 , 96,	0
832	Effects of water temperature over benthic diatom communities: insights from thermal springs. 2020 , 13, 325-337	2
831	Ecological Synthesis and Its Role in Advancing Knowledge. 2020 ,	2
830	Stochastic Dispersal Rather Than Deterministic Selection Explains the Spatio-Temporal Distribution of Soil Bacteria in a Temperate Grassland. 2020 , 11, 1391	13
829	Ocean currents promote rare species diversity in protists. 2020 , 6, eaaz9037	5
828	Inoculum handling alters the strength and direction of plant-microbe interactions. 2020 , 101, e02994	7
827	Spatiotemporal Patterns in Diversity and Assembly Process of Marine Protist Communities of the Changjiang (Yangtze River) Plume and Its Adjacent Waters. 2020 , 11, 579290	3

826	A Landscape of Opportunities for Microbial Ecology Research. 2020 , 11, 561427	7
825	Diversity and connectivity of microeukaryote communities across multiple habitats from intertidal zone to deep-sea floor in the Western Pacific Ocean. 2020 , 165, 103395	1
824	Microbiome of Drinking Water Biofilters is Influenced by Environmental Factors and Engineering Decisions but has Little Influence on the Microbiome of the Filtrate. 2020 , 54, 11526-11535	8
823	The effects of abiotic and biotic factors on taxonomic and phylogenetic diversity of stream epilithic bacteria around Qiandao Lake. 2020 , 82, 1	2
822	A guide to deciphering microbial interactions and metabolic fluxes in microbiome communities. 2020 , 64, 230-237	21
821	Geographical patterns of root nodule bacterial diversity in cultivated and wild populations of a woody legume crop. 2020 , 96,	2
820	Effects of Different Hosts on Bacterial Communities of Parasitic Wasp. 2020 , 11, 1435	3
819	Comparative Analysis of Microbial Diversity Across Temperature Gradients in Hot Springs From Yellowstone and Iceland. 2020 , 11, 1625	14
818	Whitepaper: Earth Evolution at the dry limit. 2020 , 193, 103275	3
817	Microbial macroecology: In search of mechanisms governing microbial biogeographic patterns. 2020 , 29, 1870-1886	27
816	Implications of bacterial, viral and mycotic microorganisms in vultures for wildlife conservation, ecosystem services and public health. 2020 , 162, 1109-1124	23
815	Fungal communities decline with urbanization-more in air than in soil. 2020 , 14, 2806-2815	21
814	Bacterial Diversity and Interaction Networks of Rhizosphere Differ Significantly From Bulk Soil in the Oligotrophic Basin of Cuatro Ciénegas. 2020 , 11, 1028	8
813	Contrasting responses of above- and below-ground herbivore communities along elevation. 2020 , 194, 515-528	0
812	Evaluating Alternative Metacommunity Hypotheses for Diatoms in the McMurdo Dry Valleys Using Simulations and Remote Sensing Data. 2020 , 8,	1
811	Local community assembly mechanisms shape soil bacterial diversity patterns along a latitudinal gradient. 2020 , 11, 5428	9
810	Range-wide Phylogeography of a Nivicolous Protist <i>Didymium nivicola</i> Meyl. (Myxomycetes, Amoebozoa): Striking Contrasts Between the Northern and the Southern Hemisphere. 2020 , 171, 125771	5
809	Rapid Isolation, Propagation, and Online Analysis of a Small Number of Therapeutic Staphylococcal Bacteriophages from a Complex Matrix. 2020 , 6, 2745-2755	3

808	The Fungal Microbiome Is an Important Component of Vineyard Ecosystems and Correlates with Regional Distinctiveness of Wine. 2020 , 5,	25
807	Antibiotic Resistance: Moving From Individual Health Norms to Social Norms in One Health and Global Health. 2020 , 11, 1914	24
806	Distribution of Viable Bacteria in the Dust-Generating Natural Source Area of the Gobi Region, Mongolia. 2020 , 11, 893	3
805	Centers of endemism of freshwater protists deviate from pattern of taxon richness on a continental scale. 2020 , 10, 14431	3
804	Spatial patterns of microbial communities across surface waters of the Great Barrier Reef. 2020 , 3, 442	8
803	Early ecological succession patterns of bacterial, fungal and plant communities along a chronosequence in a recently deglaciated area of the Italian Alps. 2020 , 96,	9
802	Spatial diversity of planktonic protists in the Lagoon of Venice (LTER-Italy) based on 18S rDNA. 2020 , 11,	1
801	Microbial Diversity of Fermented Greek Table Olives of Halkidiki and Konservolia Varieties from Different Regions as Revealed by Metagenomic Analysis. 2020 , 8,	11
800	Association of insularity and body condition to cloacal bacteria prevalence in a small shorebird. 2020 , 15, e0237369	1
799	A core phyllosphere microbiome exists across distant populations of a tree species indigenous to New Zealand. 2020 , 15, e0237079	6
798	A re-investigation of lake sediment diatoms from the Vestfold Hills, Antarctica, using an updated, fine-grained taxonomy. 2020 , 35, 231-254	1
797	Organism body size structures the soil microbial and nematode community assembly at a continental and global scale. 2020 , 11, 6406	28
796	Implications of increasing Atlantic influence for Arctic microbial community structure. 2020 , 10, 19262	3
795	Taxonomic Diversity of Pico-/Nanoeukaryotes Is Related to Dissolved Oxygen and Productivity, but Functional Composition Is Shaped by Limiting Nutrients in Eutrophic Coastal Oceans. 2020 , 11, 601037	3
794	Habitat type and interannual variation shape unique fungal pathogen communities on a California native bunchgrass. 2020 , 48,	0
793	Mechanisms governing avian phyllosymbiosis: Genetic dissimilarity based on neutral and MHC regions exhibits little relationship with gut microbiome distributions of Galápagos mockingbirds. 2020 , 10, 13345-13354	2
792	Microbial community structure across grazing treatments and environmental gradients in the Serengeti. 2020 , 1	0
791	Homogeneous selection shapes free-living and particle-associated bacterial communities in subtropical coastal waters. 2020 , 27, 1904	2

790	Slope aspect influences soil microbial community structure and composition in the Israel arid Mediterranean. 2020 , 67, 23-28	1
789	Biogeographic Patterns in Members of Globally Distributed and Dominant Taxa Found in Port Microbial Communities. 2020 , 5,	6
788	The relative influence of the environment, land use, and space on the functional and taxonomic structures of phytoplankton and zooplankton metacommunities in tropical reservoirs. 2020 , 39, 321-333	5
787	Unraveling the Microbiota of Natural Black cv. Kalamata Fermented Olives through 16S and ITS Metataxonomic Analysis. 2020 , 8,	12
786	Genotypic and phenotypic analyses reveal distinct population structures and ecotypes for sugar beet-associated in Oxford and Auckland. 2020 , 10, 5963-5975	0
785	The streptococcal multidomain fibrillar adhesin CshA has an elongated polymeric architecture. 2020 , 295, 6689-6699	3
784	Microbial functional gene diversity in natural secondary forest Ultisols. 2020 , 105, 103575	1
783	Prokaryotic Diversity and Composition of Sediments From Prydz Bay, the Antarctic Peninsula Region, and the Ross Sea, Southern Ocean. 2020 , 11, 783	2
782	Differences in the soil microbiomes of <i>Pentaclethra macroloba</i> across tree size and in contrasting land use histories. 2020 , 452, 329-345	1
781	Biogeography of soil microbial habitats across France. 2020 , 29, 1399-1411	9
780	Biogeographic patterns of microbial co-occurrence ecological networks in six American forests. 2020 , 148, 107897	27
779	<i>Mesorhizobium jarvisii</i> is a dominant and widespread species symbiotically efficient on <i>Astragalus sinicus</i> L. in the Southwest of China. 2020 , 43, 126102	
778	Antibiotic resistomes in drinking water sources across a large geographical scale: Multiple drivers and co-occurrence with opportunistic bacterial pathogens. 2020 , 183, 116088	37
777	A Systematic Review of Sources of Variability and Uncertainty in eDNA Data for Environmental Monitoring. 2020 , 8,	16
776	Disentangling Large- and Small-Scale Abiotic and Biotic Factors Shaping Soil Microbial Communities in an Alpine Cushion Plant System. 2020 , 11, 925	10
775	Hospital-Associated Multidrug-Resistant MRSA Lineages Are Trophic to the Ocular Surface and Cause Severe Microbial Keratitis. 2020 , 8, 204	5
774	Geographical separation and physiology drive differentiation of microbial communities of two discrete populations of the bat <i>Leptonycteris yerbabuenae</i> . 2020 , 9, 1113-1127	7
773	Biogeography of American Northwest Hot Spring A/B-Lineage Populations. 2020 , 11, 77	6

772	Random sampling in metagenomic sequencing leads to overestimated spatial scaling of microbial diversity. 2020 , 22, 2140-2149	1
771	Minerals play key roles in driving prokaryotic and fungal communities in the surface sediments of the Qinghai-Tibetan lakes. 2020 , 96,	7
770	A framework to bridge scales in distribution modeling of soil microbiota. 2020 , 96,	5
769	Soil biological characteristic, nutrient contents and stoichiometry as affected by different types of remediation in a smelter-impacted soil. 2020 , 36, 419-433	4
768	Factors shaping community patterns of protists and bacteria on a European scale. 2020 , 22, 2243-2260	19
767	The diversity and distribution of endophytes across biomes, plant phylogeny and host tissues: how far have we come and where do we go from here?. 2020 , 22, 2107-2123	44
766	Predicting Microbiome Function Across Space Is Confounded by Strain-Level Differences and Functional Redundancy Across Taxa. 2020 , 11, 101	19
765	Soil Microbial Community Assembly and Interactions Are Constrained by Nitrogen and Phosphorus in Broadleaf Forests of Southern China. 2020 , 11, 285	3
764	Impacts of the Zhe-Min Coastal Current on the biogeographic pattern of microbial eukaryotic communities. 2020 , 183, 102309	2
763	Habitat-specific environmental factors regulate spatial variability of soil bacterial communities in biocrusts across northern China's drylands. 2020 , 719, 137479	11
762	Population structure and adaptation of a bacterial pathogen in California grapevines. 2020 , 22, 2625-2638	11
761	Spatiotemporal dynamics of the archaeal community in coastal sediments: assembly process and co-occurrence relationship. 2020 , 14, 1463-1478	56
760	Soil properties rather than climate and ecosystem type control the vertical variations of soil organic carbon, microbial carbon, and microbial quotient. 2020 , 148, 107905	27
759	Comparative Metabarcoding and Metatranscriptomic Analysis of Microeukaryotes Within Coastal Surface Waters of West Greenland and Northwest Iceland. 2020 , 7,	1
758	Microbial and Geochemical Dynamics of an Aquifer Stimulated for Microbial Induced Calcite Precipitation (MICP). 2020 , 11, 1327	7
757	Prairie plants harbor distinct and beneficial root-endophytic bacterial communities. 2020 , 15, e0234537	
756	MicroNiche: an R package for assessing microbial niche breadth and overlap from amplicon sequencing data. 2020 , 96,	7
755	Microbial diversity and functional potential in wetland ecosystems. 2020 , 289-314	2

754	Genetically diverse lentil- and faba bean-nodulating rhizobia are present in soils across Central and Southern Ethiopia. 2020 , 96,	4
753	Genome Resolved Biogeography of Mamiellales. 2020 , 11,	5
752	Biogeographic pattern of the nirS gene-targeted anammox bacterial community and composition in the northern South China Sea and a coastal Mai Po mangrove wetland. 2020 , 104, 3167-3181	2
751	Bacterioplankton community variation in Bohai Bay (China) is explained by joint effects of environmental and spatial factors. 2020 , 9, e997	5
750	Coevolution of Resistance Against Antimicrobial Peptides. 2020 , 26, 880-899	3
749	Using null models to compare bacterial and microeukaryotic metacommunity assembly under shifting environmental conditions. 2020 , 10, 2455	27
748	Comparing Morphological and Molecular Estimates of Species Diversity in the Freshwater Genus <i>Synura</i> (Stramenopiles): A Model for Understanding Diversity of Eukaryotic Microorganisms. 2020 , 56, 574-591	11
747	Transient invaders can induce shifts between alternative stable states of microbial communities. 2020 , 6, eaay8676	38
746	A Montero Auction Mechanism to Regulate Antimicrobial Consumption in Agriculture. 2020 , 102, 1448-1467	2
745	A toxic grass <i>Achnatherum inebrians</i> serves as a diversity refuge for the soil fungal community in rangelands of northern China. 2020 , 448, 425-438	5
744	Geographic Patterns of Bacterioplankton among Lakes of the Middle and Lower Reaches of the Yangtze River Basin, China. 2020 , 86,	9
743	Comparative phylogeography of two free-living cosmopolitan cyanobacteria: Insights on biogeographic and latitudinal distribution. 2020 , 47, 1106-1118	4
742	Turnover is replaced by nestedness with increasing geographical distance in bacterial communities of coastal shallow lakes. 2020 , 71, 1086	0
741	Temporal and spatial variations in the bacterial community composition in Lake Bosten, a large, brackish lake in China. 2020 , 10, 304	13
740	Integrating Computational Methods to Investigate the Macroecology of Microbiomes. 2019 , 10, 1344	3
739	Plant functional traits regulate soil bacterial diversity across temperate deserts. 2020 , 715, 136976	14
738	Shifts in microbial communities and networks are correlated with the soil ionome in a kiwifruit orchard under different fertilization regimes. 2020 , 149, 103517	7
737	Revealing Fungal Communities in Alpine Wetlands Through Species Diversity, Functional Diversity and Ecological Network Diversity. 2020 , 8,	4

736	Arbuscular mycorrhizal fungal communities in the rhizospheric soil of litchi and mango orchards as affected by geographic distance, soil properties and manure input. 2020 , 152, 103593	16
735	Biogeography and Assembly of Microbial Communities in Wastewater Treatment Plants in China. 2020 , 54, 5884-5892	13
734	Linking microbial communities to ecosystem functions: what we can learn from genotype-phenotype mapping in organisms. 2020 , 375, 20190244	12
733	Spatial Structure of Marine Host-Associated Microbiomes: Effect of Taxonomy, Species Traits, and Study Design. 2020 , 7,	1
732	Distance from the Forest Edge Influences Soil Fungal Communities Colonizing a Reclaimed Soil Borrow Site in Boreal Mixedwood Forest. 2020 , 11, 427	2
731	Functional Genomics Differentiate Inherent and Environmentally Influenced Traits in Dinoflagellate and Diatom Communities. 2020 , 8,	6
730	Ecoregional Characteristics Drive the Distribution Patterns of Neotropical Stream Diatoms. 2020 , 56, 1053-1065	5
729	Island biogeography of soil bacteria and fungi: similar patterns, but different mechanisms. 2020 , 14, 1886-1896	8
728	Different community assembly mechanisms underlie similar biogeography of bacteria and microeukaryotes in Tibetan lakes. 2020 , 96,	17
727	Spatial Patterns of Soil Fungal Communities Are Driven by Dissolved Organic Matter (DOM) Quality in Semi-Arid Regions. 2021 , 82, 202-214	6
726	Biogeography and emerging significance of Actinobacteria in Australia and Northern Antarctica soils. 2020 , 146, 107805	16
725	Impacts of copper and lead exposure on prokaryotic communities from contaminated contrasted coastal seawaters: the influence of previous metal exposure. 2020 , 96,	4
724	Temperature and Nutrient Levels Correspond with Lineage-Specific Microdiversification in the Ubiquitous and Abundant Freshwater Genus. 2020 , 86,	6
723	Vertical Beta-Diversity of Bacterial Communities Depending on Water Stratification. 2020 , 11, 449	5
722	Ecological factors shaping cyanobacterial assemblages in a coastal lake system. 2020 , 847, 2225-2239	
721	Biogeographic patterns of abundant and rare bacterial and microeukaryotic subcommunities in connected freshwater lake zones subjected to different levels of nutrient loading. 2021 , 130, 123-132	2
720	Phytoplankton in Antarctic lakes: biodiversity and main ecological features. 2021 , 848, 177-207	5
719	Relationship between severity of trunk decay of <i>Pinus koraiensis</i> and soil properties around roots. 2021 , 32, 1213-1220	0

7 ¹⁸	Environmental and Spatial Influences on Biogeography and Community Structure of Saltmarsh Benthic Diatoms. 2021 , 44, 147-161	4
7 ¹⁷	Plant and Soil Drivers of Whole-Plant Microbiomes: Variation in Switchgrass Fungi from Coastal to Mountain Sites. 2021 , 5, 69-79	5
7 ¹⁶	Local and Geographic Factors Shape the Occupancy-Frequency Distribution of Freshwater Bacteria. 2021 , 81, 26-35	1
7 ¹⁵	Decoupled diversity patterns in microbial geographic distributions on the arid area (the Loess Plateau). 2021 , 196, 104922	6
7 ¹⁴	Microbial diversity accumulates in a downstream direction in the Three Gorges Reservoir. 2021 , 101, 156-167	8
7 ¹³	Identification of microbial strategies for labile substrate utilization at phylogenetic classification using a microcosm approach. 2021 , 153, 107970	14
7 ¹²	Bacteria in the lakes of the Tibetan Plateau and polar regions. 2021 , 754, 142248	2
7 ¹¹	History of petroleum disturbance triggering the depth-resolved assembly process of microbial communities in the vadose zone. 2021 , 402, 124060	15
7 ¹⁰	Novel Cyanobacterial Diversity Found in Costa Rican Thermal Springs Associated with Rincon de la Vieja and Miravalles Volcanoes: A Polyphasic Approach. 2021 , 57, 183-198	3
7 ⁰⁹	Fifteen-year no tillage of a Mollisol with residue retention indirectly affects topsoil bacterial community by altering soil properties. 2021 , 205, 104804	5
7 ⁰⁸	Microeukaryotic Communities Associated With the Seagrass <i>Zostera marina</i> Are Spatially Structured. 2021 , 68, e12827	4
7 ⁰⁷	The relative contribution of non-selection and selection processes in marine benthic assemblages. 2021 , 163, 105223	
7 ⁰⁶	Taxonomy and diversity of bacterial communities associated with marine sediments from Chilean salmonid farms. 2021 , 52, 1605-1620	0
7 ⁰⁵	Distinct assembly processes shape bacterial communities along unsaturated, groundwater fluctuated, and saturated zones. 2021 , 761, 143303	9
7 ⁰⁴	Microbial mutualist distribution limits spread of the invasive legume <i>Medicago polymorpha</i> . 2021 , 23, 843-856	5
7 ⁰³	Microbial Inoculants: Silver Bullet or Microbial Jurassic Park?. 2021 , 29, 299-308	13
7 ⁰²	Scale-dependent patterns of metacommunity structuring in aquatic organisms across floodplain systems. 2021 , 48, 872-885	9
7 ⁰¹	The bacterial and fungal communities associated with <i>Anthurium</i> spp. leaves: Insights into plant endemism and microbe association. 2021 , 244, 126667	2

700	Rates and microbial communities of denitrification and anammox across coastal tidal flat lands and inland paddy soils in East China. 2021 , 157, 103768	7
699	Developing a method for exploiting soil bacterial communities as evidence in environmental forensic investigations. 2021 , 22, 385-392	3
698	Bathymetric gradient shapes the community composition rather than the species richness of deep-sea benthic ciliates. 2021 , 755, 142623	1
697	Phylogeography and Symbiotic Effectiveness of Rhizobia Nodulating Chickpea (<i>Cicer arietinum</i> L.) in Ethiopia. 2021 , 81, 703-716	2
696	A guide to metabolic flux analysis in metabolic engineering: Methods, tools and applications. 2021 , 63, 2-12	15
695	Lakes in the era of global change: moving beyond single-lake thinking in maintaining biodiversity and ecosystem services. 2021 , 96, 89-106	38
694	Depth-Dependent Variables Shape Community Structure and Functionality in the Prince Edward Islands. 2021 , 81, 396-409	1
693	Stochastic processes shape the biogeographic variations in core bacterial communities between aerial and belowground compartments of common bean. 2021 , 23, 949-964	13
692	Niche-neutral theoretic approach to mechanisms underlying the biodiversity and biogeography of human microbiomes. 2021 , 14, 322-334	5
691	Understanding response of microbial communities to saltwater intrusion through microcosms. 2021 , 19, 929-933	1
690	Environmental influences shaping microbial communities in low oxygen, highly stratified marine embayment.	0
689	Framework for Studying Rhizospheric Microflora Under the Effect of Improved Crop Variety. 2021 , 251-261	
688	Latent extinction risk of soil fauna in Beijing: a 4-year study from 2013 to 2016. 2021 , 7, 1878934	1
687	Spatial Variability in Streambed Microbial Community Structure Across Two Watersheds.	
686	Full Issue PDF. 2021 , 5, 1-120	
685	Virtually engaging students through collaborative investigation of scientific literature, a case study. 2021 , 50, e20051	2
684	Microdiversity and phylogeographic diversification of bacterioplankton in pelagic freshwater systems revealed through long-read amplicon sequencing. 2021 , 9, 24	5
683	Multi-Scale Biophysical Factors Driving Litter Dynamics in Streams. 2021 , 7-21	1

682	Drivers of inter-population variation in the gut microbiomes of sister species of <i>Phanaeus dung</i> beetles.	1
681	Characteristics of planktonic and sediment bacterial communities in a heavily polluted urban river. 2021 , 9, e10866	2
680	The impact of invader number on whole community invasions in biomethane-producing communities.	
679	A latitudinal gradient of microbial diversity in continental paddy soils. 2021 , 30, 909-919	3
678	Spatial scale structure soil bacterial communities across an Arctic landscape. 2020 ,	3
677	Microbial, environmental and anthropogenic factors influencing the indoor microbiome of the built environment. 2021 , 61, 267-292	7
676	Soil properties and root traits jointly shape fine-scale spatial patterns of bacterial community and metabolic functions within a Korean pine forest. 2021 , 9, e10902	1
675	Diatoms from small ponds and terrestrial habitats in Deserta Grande Island (Madeira Archipelago). 2021 , 9, e59898	1
674	DNA barcoding of phytopathogens for disease diagnostics and bio-surveillance. 2021 , 37, 54	3
673	Soil microbial composition and carbon mineralization are associated with vegetation type and temperature regime in mesocosms of a semiarid ecosystem. 2021 , 368,	1
672	Environmental risk characterization and ecological process determination of bacterial antibiotic resistome in lake sediments. 2021 , 147, 106345	15
671	Controls on diatom biogeography on South Carolina (USA) barrier island beaches. 2021 , 661, 17-33	1
670	Exploring the microdiversity within marine bacterial taxa: Towards an integrated biogeography in the Southern Ocean.	
669	Selective constraints on global plankton dispersal. 2021 , 118,	4
668	Population structure, pathogenicity, and fungicide sensitivity of <i>Colletotrichum siamense</i> from different hosts in Hainan, China. 2021 , 70, 1158-1167	0
667	Priority effects alter interaction outcomes in a legume-rhizobium mutualism. 2021 , 288, 20202753	4
666	Phylogeographic distribution of rhizobia nodulating common bean (<i>Phaseolus vulgaris</i> L.) in Ethiopia. 2021 , 97,	1
665	Composition of woody plant communities drives macrofungal community composition in three climatic regions. 2021 , 32, e13001	1

- 664 Transient surface hydration impacts biogeography and intercellular interactions of non-motile bacteria. **2021**,
- 663 Spatiotemporal patterns of rhizosphere microbiome assembly: From ecological theory to agricultural application. **2021**, 58, 894-904 7
- 662 Microbial biogeography through the lens of exotic species: the recent introduction and spread of the freshwater diatom *Discostella asterocostata* in the United States. **2021**, 23, 2191-2204 0
- 661 Variations in soil nutrient dynamics and bacterial communities in long-term tea monoculture production systems.
- 660 The Utility of Macroecological Rules for Microbial Biogeography. **2021**, 9, 8
- 659 Alterations to the Gut Microbiota of a Wild Juvenile Passerine in an Urban Mosaic.
- 658 Microbe-mediated adaptation in plants. **2021**, 24, 1302-1317 7
- 657 Quantifying microbial control of soil organic matter dynamics at macrosystem scales. **2021**, 156, 19-40 10
- 656 Multi-scale and multi-system perspectives of zooplankton structure and function in Canadian freshwaters. 1-20 2
- 655 Global Trends of Benthic Bacterial Diversity and Community Composition Along Organic Enrichment Gradients of Salmon Farms. **2021**, 12, 637811 2
- 654 Microbial ecology of coral-dominated reefs in the Federated States of Micronesia. **2021**, 86, 115-136 4
- 653 Deep-sea shipwrecks represent island-like ecosystems for marine microbiomes. **2021**, 15, 2883-2891 4
- 652 Topsoil microbial community structure responds to land cover type and environmental zone in the Western Pacific region. **2021**, 764, 144349 2
- 651 Diversity and functional characterization of endophytic *Methylobacterium* isolated from banana cultivars of South India and its impact on early growth of tissue culture banana plantlets. **2021**, 131, 2448-2465⁰
- 650 Rare Bacteria Assembly in Soils Is Mainly Driven by Deterministic Processes. **2021**, 1 2
- 649 Environmental association of heterotrophic micro-eukaryotes in the varying biogeochemical regimes of the Arabian Sea, resolved via high-throughput sequencing. **2021**, 55, 807-824
- 648 Distinct microhabitats affect the relative balance of ecological processes shaping the spatial distribution of bacterial communities in lakeshore habitats. **2021**, 66, 1475-1489 1
- 647 Deep-sea mussels from a hybrid zone on the Mid-Atlantic Ridge host genetically indistinguishable symbionts. **2021**, 15, 3076-3083 2

646	The Investigation of the Connections Among Hydrogeological Factors and the Emissions of Two Greenhouse Gases in Lake Sediment. 2021 , 57, e2020WR029375	0
645	Seasonal Climate Variations Promote Bacterial Diversity in Soil. 2021 , 1	1
644	Vertical diversity and association pattern of total, abundant and rare microbial communities in deep-sea sediments. 2021 , 30, 2800-2816	5
643	All together now: Limitations and recommendations for the simultaneous analysis of all eukaryotic soil sequences. 2021 , 21, 1759-1771	3
642	Highest Composition Dissimilarity among Phytoplankton Communities at Intermediate Environmental Distances across High-Altitude Tropical Lakes. 2021 , 13, 1378	0
641	Biogeographic Role of the Kuroshio Current Intrusion in the Microzooplankton Community in the Boundary Zone of the Northern South China Sea. 2021 , 9,	3
640	Assessment of the Effect of Application of the Herbicide S-Metolachlor on the Activity of Some Enzymes Found in Soil. 2021 , 11, 469	2
639	Diversity and distribution of harmful microalgae in the Gulf of Thailand assessed by DNA metabarcoding. 2021 , 106, 102063	4
638	Climate-driven divergence in plant-microbiome interactions generates range-wide variation in bud break phenology. 2021 , 4, 748	3
637	Airborne bacteria over the oceans shed light on global biogeodiversity patterns.	1
636	Dissolved organic matter (DOM) quality drives biogeographic patterns of soil bacterial communities and their association networks in semi-arid regions. 2021 , 97,	3
635	Multi-omics profiling of Earth's biomes reveals that microbial and metabolite composition are shaped by the environment.	3
634	"Everything is not everywhere": Time-calibrated phylogeography of the genus Milnesium (Tardigrada). 2021 , 30, 3590-3609	6
633	Hydrographic fronts shape productivity, nitrogen fixation, and microbial community composition in the southern Indian Ocean and the Southern Ocean. 2021 , 18, 3733-3749	2
632	The impact of propagule pressure on whole community invasions in biomethane-producing communities. 2021 , 24, 102659	2
631	Complex Interaction Networks Among Cyanolichens of a Tropical Biodiversity Hotspot. 2021 , 12, 672333	5
630	Geographic Distance and Habitat Type Influence Fungal Communities in the Arctic and Antarctic Sites. 2021 , 82, 224-232	1
629	Photo-movement of coral larvae influences vertical positioning in the ocean. 2021 , 40, 1297-1306	2

628	Mass-immigration determines the assembly of activated sludge microbial communities. 2021 , 118,	9
627	Interplay of Various Evolutionary Modes in Genome Diversification and Adaptive Evolution of the Family. 2021 , 12, 639995	0
626	Exposure to a fungal pathogen increases the critical thermal minimum of two frog species. 2021 , 11, 9589-9598	1
625	Fungal alpha diversity influences stochasticity of bacterial and fungal community assemblies in soil aggregates in an apple orchard. 2021 , 162, 103878	5
624	Nutrient improvement and soil acidification inducing contrary effects on bacterial community structure following application of hairy vetch (<i>Vicia villosa</i> Roth L.) in Ultisol. 2021 , 312, 107348	5
623	Assessing biogeographic survey gaps in bacterial diversity knowledge: A global synthesis of freshwaters. 2021 , 66, 1595-1605	1
622	Patterns of protist distribution and diversification in alpine lakes across Europe. 2021 , 10, e1216	1
621	Exploring the Microdiversity Within Marine Bacterial Taxa: Toward an Integrated Biogeography in the Southern Ocean. 2021 , 12, 703792	2
620	From the ground up: Building predictions for how climate change will affect belowground mutualisms, floral traits, and bee behavior. 2021 , 1, 100013	4
619	Dispersal Limitation Expands the Diversity of Coral Microbiome Metacommunity in the South China Sea. 2021 , 8,	1
618	Partners in space: Discordant population structure between legume hosts and rhizobium symbionts in their native range.	0
617	Assembly of the amphibian microbiome is influenced by the effects of land-use change on environmental reservoirs. 2021 , 23, 4595-4611	2
616	Glacier ice archives nearly 15,000-year-old microbes and phages. 2021 , 9, 160	7
615	Stochastic processes drive bacterial and fungal community assembly in sustainable intensive agricultural soils of Shanghai, China. 2021 , 778, 146021	7
614	Spatial turnover of multiple ecosystem functions is more associated with plant than soil microbial diversity. 2021 , 12, e03644	1
613	Historical contingency impacts on community assembly and ecosystem function in chemosynthetic marine ecosystems. 2021 , 11, 13994	0
612	Effects of dispersal on species distribution, abundance, diversity and interaction in a bacterial biofilm metacommunity. 2021 ,	0
611	Procyanidin inhibited N ₂ O emissions from paddy soils by affecting nitrate reductase activity and nirS- and nirK-denitrifier populations. 2021 , 57, 935-947	1

610	The rates of global bacterial and archaeal dispersal. 2021 ,	2
609	Changes in Soil Microbial Community Structure Following Different Tree Species Functional Traits Afforestation. 2021 , 12, 1018	
608	Money Kills Native Ecosystems: European Crayfish as an Example. 2021 , 9,	9
607	Impact of Landscape on Host-Parasite Genetic Diversity and Distribution Using the -Bank Vole System. 2021 , 9,	0
606	Shift in archaeal community along a soil profile in coastal wheat-maize rotation fields of different reclamation ages. 2021 , 32, 4162-4173	2
605	Changes in protist communities in drainages across the Pearl River Delta under anthropogenic influence. 2021 , 200, 117294	5
604	Small-scale variation in a pristine montane cloud forest: evidence on high soil fungal diversity and biogeochemical heterogeneity. 2021 , 9, e11956	0
603	Habitability Models for Astrobiology. 2021 , 21, 1017-1027	2
602	The role of soils in provision of genetic, medicinal and biochemical resources. 2021 , 376, 20200183	3
601	Bacterial and Fungal Diversity in Sediment and Water Column From the Abyssal Regions of the Indian Ocean. 2021 , 8,	
600	Divergent drivers determine soil bacterial diversity of forest and grassland ecosystems in Northwest China. 2021 , 28, e01622	1
599	Response of Soil Microbial Community to Vegetation Reconstruction Modes in Mining Areas of the Loess Plateau, China. 2021 , 12, 714967	0
598	Effects of <i>Bacillus subtilis</i> NCD-2 and broccoli residues return on potato <i>Verticillium</i> wilt and soil fungal community structure. 2021 , 159, 104628	6
597	Potential niche displacement in species of aquatic bdelloid rotifers between temperate and tropical areas. 2021 , 848, 4903-4918	1
596	Comparative Genomics of Reveals What Makes a Cosmopolitan Bacterium. 2021 , 6, e0038321	2
595	Removal efficacy of opportunistic pathogen gene markers in drinking water supply systems: an in situ and large-scale molecular investigation. 2021 , 28, 54153-54160	
594	Preferential associations of soil fungal taxa under mixed compositions of eastern American tree species.	
593	Biogeography rather than substrate type determines bacterial colonization dynamics of marine plastics. 2021 , 9, e12135	1

592	Soil greenhouse gas fluxes from tropical coastal wetlands and alternative agricultural land uses. 2021 , 18, 5085-5096	3
591	Microbiome-mediated effects of habitat fragmentation on native plant performance. 2021 , 232, 1823-1838	1
590	Spatio-temporal dynamics of bacterial communities in the shoreline of Laurentian great Lake Erie and Lake St. Clair's large freshwater ecosystems. 2021 , 21, 253	0
589	Contrasting the assembly of phytoplankton and zooplankton communities in a polluted semi-closed sea: Effects of marine compartments and environmental selection. 2021 , 285, 117256	2
588	The shifts of maize soil microbial community and networks are related to soil properties under different organic fertilizers. 2021 , 19, 100388	5
587	Planktonic protist diversity across contrasting Subtropical and Subantarctic waters of the southwest Pacific.	
586	Peatland microhabitat heterogeneity drives phototrophic microbe distribution and photosynthetic activity. 2021 , 23, 6811-6827	1
585	Geostatistical modelling and mapping of nematode-based soil ecological quality indices in a polluted nature reserve. 2021 , 31, 670-682	0
584	Predictors of soil fungal biomass and community composition in temperate mountainous forests in Central Europe. 2021 , 161, 108366	2
583	On the suitability of using vegetation indices to monitor the response of Africa's terrestrial ecoregions to drought. 2021 , 792, 148282	7
582	Microbiological assessment of ecological status in the Pearl River Estuary, China. 2021 , 130, 108084	2
581	Soil properties and geography shape arbuscular mycorrhizal fungal communities in black land of China. 2021 , 167, 104109	3
580	Meadow degradation increases spatial turnover rates of the fungal community through both niche selection and dispersal limitation. 2021 , 798, 149362	2
579	Rhizosphere bacterial and fungal spatial distribution and network pattern of <i>Astragalus mongholicus</i> in representative planting sites differ the bulk soil. 2021 , 168, 104114	4
578	Plastisphere in freshwaters: An emerging concern. 2021 , 290, 118123	4
577	Biogeographical patterns in myxomycetes. 2022 , 377-416	
576	Soil type and pH mediated arable soil bacterial compositional variation across geographic distance in North China Plain. 2022 , 169, 104220	1
575	Functional filtering and random processes affect the assembly of microbial communities of snow algae blooms at Maritime Antarctic. 2022 , 805, 150305	0

574	Drivers of microbial beta-diversity in wastewater treatment plants in China.. 2022 , 115, 341-349	0
573	Ecology of Fishes of Rivers: Functional Roles. 2021 , 187-286	
572	Beneficial Plant-Associated Microorganisms From Semiarid Regions and Seasonally Dry Environments: A Review. 2020 , 11, 553223	7
571	Palaeomycology: a modern mycological view of fungal palynomorphs. 2021 , 511, 91-120	3
570	Are recently deglaciated areas at both poles colonised by the same bacteria?. 2021 , 368,	0
569	Genetic diversity and distribution of rhizobia associated with soybean in red soil in Hunan Province. 2021 , 203, 1971-1980	3
568	Uncovering multi-faceted taxonomic and functional diversity of soil bacteriomes in tropical Southeast Asian countries. 2021 , 11, 582	1
567	The influence of mycorrhizal fungi on rhizosphere bacterial communities in forests. 2021 , 257-275	
566	Relationships between plant diversity and soil microbial diversity vary across taxonomic groups and spatial scales. 2020 , 11, e02999	23
565	On the Eco-Evolutionary Relationships of Fresh and Salt Water Bacteria and the Role of Gene Transfer in Their Adaptation. 2013 , 55-77	19
564	Diatom Diversity and Biogeography Across Tropical South America. 2020 , 121-143	1
563	The Prokaryotic Species Concept and Challenges. 2020 , 21-49	3
562	Overview of Phylogenetic Approaches to Mycorrhizal Biogeography, Diversity and Evolution. 2017 , 1-37	5
561	Aeromicrobiology. 2017 , 41-55	3
560	Extreme Views on Prokaryote Evolution. 2008 , 45-70	21
559	Utility of Molecular Tools in Monitoring Large Scale Composting. 2010 , 135-151	7
558	The diversity and distribution of diatoms: from cosmopolitanism to narrow endemism. 2007 , 159-171	2
557	Distribution and diversity of aquatic protists: an evolutionary and ecological perspective. 2007 , 9-25	1

556	Watershed land use types as drivers of freshwater phytoplankton structure. 2012 , 121-131	3
555	Functional structure, taxonomic composition and the dominant assembly processes of soil prokaryotic community along an altitudinal gradient. 2020 , 155, 103647	3
554	Do shared traits create the same fates? Examining the link between morphological type and the biogeography of fungal and bacterial communities. 2020 , 46, 100948	10
553	Global biogeography of fungal and bacterial biomass carbon in topsoil. 2020 , 151, 108024	21
552	The Diatoms: Applications for the Environmental and Earth Sciences. 560-569	14
551	Environmental heterogeneity determines the ecological processes that govern bacterial metacommunity assembly in a floodplain river system. 2020 , 14, 2951-2966	30
550	Biodiversity, Ecosystem Functioning, and Human Wellbeing. 2009 ,	191
549	Consequences of species loss for ecosystem functioning: meta-analyses of data from biodiversity experiments. 2009 , 14-29	55
548	Biodiversity-ecosystem function research and biodiversity futures: early bird catches the worm or a day late and a dollar short?. 2009 , 30-45	4
547	Forecasting decline in ecosystem services under realistic scenarios of extinction. 2009 , 60-77	14
546	Biodiversity and the stability of ecosystem functioning. 2009 , 78-93	49
545	The analysis of biodiversity experiments: from pattern toward mechanism. 2009 , 94-104	17
544	Towards a food web perspective on biodiversity and ecosystem functioning. 2009 , 105-120	18
543	Biodiversity as spatial insurance: the effects of habitat fragmentation and dispersal on ecosystem functioning. 2009 , 134-146	34
542	Incorporating biodiversity in climate change mitigation initiatives. 2009 , 149-166	14
541	Restoring biodiversity and ecosystem function: will an integrated approach improve results?. 2009 , 167-177	10
540	Managed ecosystems: biodiversity and ecosystem functions in landscapes modified by human use. 2009 , 178-194	8
539	Understanding the role of species richness for crop pollination services. 2009 , 195-208	21

538	Biodiversity and ecosystem function: perspectives on disease. 2009 , 209-216	4
537	Opening communities to colonization [the impacts of invaders on biodiversity and ecosystem functioning. 2009 , 217-229	4
536	The economics of biodiversity and ecosystem services. 2009 , 230-247	4
535	The valuation of ecosystem services. 2009 , 248-262	23
534	Modelling biodiversity and ecosystem services in coupled ecological-economic systems. 2009 , 263-278	1
533	TraitNet: furthering biodiversity research through the curation, discovery, and sharing of species trait data. 2009 , 281-289	9
532	Can we predict the effects of global change on biodiversity loss and ecosystem functioning?. 2009 , 290-298	5
531	Dormancy dampens the microbial distance-decay relationship. 2020 , 375, 20190243	19
530	<i>Haloparvum sedimenti</i> gen. nov., sp. nov., a member of the family Haloferacaceae. 2016 , 66, 2327-2334	17
529	Latitude delineates patterns of biogeography in terrestrial <i>Streptomyces</i> .	1
528	Understanding How Microbiomes Influence The Systems They Inhabit: Moving From A Correlative To A Causal Research Framework.	5
527	Microbes follow Humboldt: temperature drives plant and soil microbial diversity patterns from the Amazon to the Andes.	4
526	There and back again [unraveling mechanisms of bacterial biogeography in the North Pacific Subtropical Gyre to and from station ALOHA.	1
525	Epiphytic Microbiome of Grapes Berries Varies Between Phenological Timepoints, Growing Seasons and Regions.	1
524	Vineyard ecosystems are structured and distinguished by fungal communities impacting the flavour and quality of wine.	1
523	Glacier ice archives fifteen-thousand-year-old viruses.	9
522	Ocean currents promote rare species diversity in protists.	1
521	Geological degassing enhances microbial metabolism in the continental subsurface.	4

520	Microdiversity and phylogeographic diversification of bacterioplankton in pelagic freshwater systems revealed through long-read amplicon sequencing.	3
519	Deep-sea mussels from a hybrid zone on the Mid-Atlantic Ridge host genetically indistinguishable symbionts.	3
518	Simulation of bacterial populations with SLiM.	0
517	Comparative genomics of <i>Exiguobacterium</i> reveals what makes a cosmopolitan bacterium.	1
516	Assembly of the amphibian microbiome is influenced by the effects of land-use change on environmental reservoirs.	1
515	A proposal for a standardized bacterial taxonomy based on genome phylogeny.	32
514	Network hubs in root-associated fungal metacommunities.	1
513	Small-scale soil microbial community heterogeneity linked to landforms on King George Island, maritime Antarctica.	2
512	Different processes shape prokaryotic and picoeukaryotic assemblages in the sunlit ocean microbiome.	5
511	Biogeography and Microscale Diversity Shape the Biosynthetic Potential of Fungus-growing Ant-associated <i>Pseudonocardia</i> .	8
510	Biogeographic patterns of ectomycorrhizal fungal communities associated with <i>Castanopsis sieboldii</i> across the Japanese archipelago.	1
509	Metabolic overlap in environmentally diverse microbial communities.	1
508	Transient invaders can induce shifts between alternative stable states of microbial communities.	2
507	Population genomics of a bioluminescent symbiosis sheds light on symbiont transmission and specificity.	1
506	Diversity patterns of marine heterotrophic culturable bacteria along vertical and latitudinal gradients.	1
505	Comparative analysis of microbial diversity across temperature gradients in hot springs from Yellowstone and Iceland.	1
504	Genomic evidence for global ocean plankton biogeography shaped by large-scale current systems.	20
503	Contrasting patterns and drivers of soil bacterial and fungal diversity across a mountain gradient. 2020 , 22, 3287-3301	33

502	Microbial Biogeography: Patterns in Microbial Diversity across Space and Time. 95-115	62
501	Why Cooperate? The Ecology and Evolution of Myxobacteria. 17-40	4
500	Diversity and Environmental Distribution of Ammonia-Oxidizing Bacteria. 39-55	18
499	DNA Barcoding on Bacteria: A Review. 2014 , 2014, 1-9	26
498	Predicting prokaryotic ecological niches using genome sequence analysis. 2007 , 2, e743	23
497	Valinomycin biosynthetic gene cluster in <i>Streptomyces</i> : conservation, ecology and evolution. 2009 , 4, e7194	35
496	Lack of phylogeographic structure in the freshwater cyanobacterium <i>Microcystis aeruginosa</i> suggests global dispersal. 2011 , 6, e19561	91
495	Evidence of weak habitat specialisation in microscopic animals. 2011 , 6, e23969	26
494	Validation and application of a PCR primer set to quantify fungal communities in the soil environment by real-time quantitative PCR. 2011 , 6, e24166	145
493	Substrate type determines metagenomic profiles from diverse chemical habitats. 2011 , 6, e25173	24
492	Genetic diversity and population structure of <i>Saccharomyces cerevisiae</i> strains isolated from different grape varieties and winemaking regions. 2012 , 7, e32507	64
491	Contrasted effects of diversity and immigration on ecological insurance in marine bacterioplankton communities. 2012 , 7, e37620	13
490	Post-fire spatial patterns of soil nitrogen mineralization and microbial abundance. 2012 , 7, e50597	21
489	Digging the New York City Skyline: soil fungal communities in green roofs and city parks. 2013 , 8, e58020	135
488	Spatial and temporal biogeography of soil microbial communities in arid and semiarid regions. 2013 , 8, e69705	70
487	Architectural design drives the biogeography of indoor bacterial communities. 2014 , 9, e87093	129
486	The role of abiotic environmental conditions and herbivory in shaping bacterial community composition in floral nectar. 2014 , 9, e99107	34
485	Assessment of species diversity and distribution of an ancient diatom lineage using a DNA metabarcoding approach. 2014 , 9, e103810	34

484	How does conversion of natural tropical rainforest ecosystems affect soil bacterial and fungal communities in the Nile river watershed of Uganda?. 2014 , 9, e104818	13
483	Niche-partitioning of edaphic microbial communities in the Namib Desert gravel plain Fairy Circles. 2014 , 9, e109539	17
482	Distance-decay and taxa-area relationships for bacteria, archaea and methanogenic archaea in a tropical lake sediment. 2014 , 9, e110128	30
481	Multivariate and phylogenetic analyses assessing the response of bacterial mat communities from an ancient oligotrophic aquatic ecosystem to different scenarios of long-term environmental disturbance. 2015 , 10, e0119741	10
480	Estimating bacterial diversity for ecological studies: methods, metrics, and assumptions. 2015 , 10, e0125356	55
479	Archaeal and Bacterial Communities Associated with the Surface Mucus of Caribbean Corals Differ in Their Degree of Host Specificity and Community Turnover Over Reefs. 2016 , 11, e0144702	17
478	Hydrology Affects Environmental and Spatial Structuring of Microalgal Metacommunities in Tropical Pacific Coast Wetlands. 2016 , 11, e0149505	17
477	Assessing Low-Intensity Relationships in Complex Networks. 2016 , 11, e0152536	13
476	Patterns of variation in diversity of the Mississippi river microbiome over 1,300 kilometers. 2017 , 12, e0174890	21
475	Factors limiting sulfolane biodegradation in contaminated subarctic aquifer substrate. 2017 , 12, e0181462	19
474	Assigning ecological roles to the populations belonging to a phenanthrene-degrading bacterial consortium using omic approaches. 2017 , 12, e0184505	26
473	Mapping and predictive variations of soil bacterial richness across France. 2017 , 12, e0186766	55
472	Biogeography of freshwater diatoms Bacillariophyta. Main concepts and approaches. 2014 , 24, 125-146	5
471	Inclusion of myxomycetes in the Red Data Book of Ukraine: feasibility, selection criteria and recommended species. 2020 , 77, 189-203	2
470	The Amphibian Skin Microbiome and Its Protective Role Against Chytridiomycosis. 2020 , 76, 167	20
469	DNA Sequencing: Strategies for Soil Microbiology. 2007 , 71, 592-600	23
468	Bacteriophages presence in nature and their role in the natural selection of bacterial populations. 2020 , 91, e2020024	4
467	Worldwide Distribution of Major Clones of <i>Listeria monocytogenes</i> . 2011 , 17, 1110-1112	141

466	Microbial biogeography during austral summer 2007 in the surface waters around the South Shetland Islands, Antarctica. 2013 , 70, 131-140	5
465	Small-scale temporal and spatial variations in protistan community composition at the San Pedro Ocean Time-series station off the coast of southern California. 2013 , 70, 93-110	20
464	Inter-taxonomic differences in bacterioplankton community assembly in oligotrophic mountain lakes of east Japan. 2015 , 75, 251-257	3
463	The legacy of the past: effects of historical processes on microbial metacommunities. 2017 , 79, 13-19	26
462	Microbial community assembly in marine sediments. 2017 , 79, 177-195	64
461	Bacterial communities associated with lionfish in their native and invaded ranges. 2015 , 531, 253-262	6
460	Bacterial communities and their hydrocarbon bioremediation potential in the Bohai Sea, China. 2015 , 538, 117-130	2
459	Latitudinal variation in the microbiome of the sponge <i>Ircinia campana</i> correlates with host haplotype but not anti-predatory chemical defense. 2017 , 565, 53-66	14
458	Spatial patterns of functional diversity and composition in marine benthic ciliates along the coast of China. 2019 , 627, 49-60	4
457	Biodiversity and biogeography of marine microbenthos: progress and prospect. 2012 , 19, 661-675	1
456	Secondary metabolites of impact the assembly of soil-derived semisynthetic bacterial communities. 2020 , 16, 2983-2998	5
455	Insight of Proteomics and Genomics in Environmental Bioremediation. 2017 , 46-69	2
454	Melioidosis in the Torres Strait Islands, Australia: Exquisite Interplay between Pathogen, Host, and Environment. 2019 , 100, 517-521	4
453	Bacteria in the global atmosphere [Part 1: Review and synthesis of literature data for different ecosystems.	14
452	DNA from lake sediments reveals the long-term dynamics and diversity of <i>Synechococcus</i> assemblages.	19
451	The effect of resource history on the functioning of soil microbial communities is maintained across time.	8
450	Biogeography in the air: fungal diversity over land and oceans.	6
449	Response of bacterioplankton community structure to an artificial gradient of $p\text{CO}_2$ in the Arctic Ocean.	9

448	Paleoenvironmental imprint on seafloor microbial communities in Western Mediterranean Sea Quaternary sediments.	1
447	Composition and dynamics of microeukaryote communities in the River Danube.. 2010 , 10, 99-113	2
446	Alder and the Golden Fleece: high diversity of and ectomycorrhizal fungi revealed from subsp. roots close to a Tertiary and glacial refugium. 2017 , 5, e3479	11
445	Distribution of bacterial communities along the spatial and environmental gradients from Bohai Sea to northern Yellow Sea. 2018 , 6, e4272	23
444	Salt marsh sediment bacterial communities maintain original population structure after transplantation across a latitudinal gradient. 2018 , 6, e4735	7
443	Bacterial and archaeal spatial distribution and its environmental drivers in an extremely haloalkaline soil at the landscape scale. 2019 , 7, e6127	5
442	Phytobiomes are compositionally nested from the ground up. 2019 , 7, e6609	19
441	Metabarcoding advances for ecology and biogeography of Neotropical protists: what do we know, where do we go?. 2021 , 21,	0
440	The East Asian gut microbiome is distinct from colocalized White subjects and connected to metabolic health. 2021 , 10,	6
439	Editorial: Microbial Landscape Ecology: Highlights on the Invisible Corridors. 2021 , 9,	0
438	Bacterial Communities Present Distinct Co-occurrence Networks in Sediment and Water of the Thermokarst Lakes in the Yellow River Source Area. 2021 , 12, 716732	1
437	Microbial Community Composition in Municipal Wastewater Treatment Bioreactors Follows a Distance Decay Pattern Primarily Controlled by Environmental Heterogeneity. 2021 , 6, e0064821	0
436	Are microorganisms everywhere they can be?. 2021 , 23, 6355-6363	0
435	Diversity and ecology of protists revealed by metabarcoding. 2021 , 31, R1267-R1280	10
434	Microcoleus (Cyanobacteria) form watershed-wide populations without strong gradients in population structure. 2021 , 31, 86	1
433	Microbial stowaways in waterbirds as dispersal vectors of aquatic pro- and microeukaryotic communities.	
432	Wastewater constituents impact biofilm microbial community in receiving streams. 2021 , 151080	0
431	Some Observations on Phytoplankton Community Structure, Dynamics and Their Relationship to Water Quality in Five Santiago Island Reservoirs, Cape Verde. 2021 , 13, 2888	

- 430 Co-occurrence of planktonic bacteria and archaea affects their biogeographic patterns in China's coastal wetlands. **2021**, 16, 19 1
- 429 Protistan-Bacterial Microbiota Exhibit Stronger Species Sorting and Greater Network Connectivity Offshore than Nearshore across a Coast-to-Basin Continuum. **2021**, 6, e0010021 3
- 428 Towards revealing the global diversity and community assembly of soil eukaryotes. **2022**, 25, 65-76 2
- 427 Biogeographical distributions of nitrogen-cycling functional genes in a subtropical estuary. 2
- 426 Impacts of environmental stress on resistance and resilience of algal-associated bacterial communities. **2021**, 11, 15004-15019 0
- 425 Soil mapping, digital soil mapping and soil monitoring over large areas and the dimensions of soil security [A review](#). **2021**, 5, 100018 1
- 424 Microbial biodiversity. **2007**, 1-9 1
- 423 Introduction and Overview: Soil, Rhizosphere, and Phyllosphere. **2007**, 595-596
- 422 Prokaryotic Diversity: Form, Ecophysiology, and Habitat. **2007**, 20-34
- 421 From Genetics to Genomics. 255-266
- 420 Towards an Ecosystem Approach to Cheese Microbiology. 311-321 1
- 419 Do climate factors govern soil microbial community composition and biomass at a regional scale?. 1
- 418 Two-dimensional distribution of living benthic foraminifera in anoxic sediment layers of an estuarine mudflat (Loire Estuary, France).
- 417 Microbiome engineers: Grazers, browsers, and the phytobiome stampede.
- 416 Deterministic influences exceed dispersal effects on hydrologically-connected microbiomes.
- 415 Evolutionary Biology of Drug Resistance. **2017**, 9-36 1
- 414 Full Issue PDF. **2017**, 1, 55-114 1
- 413 Eelgrass leaf surface microbiomes are locally variable and highly correlated with epibiotic eukaryotes. 0

- 412 Defining marine microbial biomes from environmental and dispersal filtered metapopulations.
- 411 Habitat diversification promotes environmental selection in planktonic prokaryotes and ecological drift in microbial eukaryotes. 0
- 410 Rolling a mycobiome down a hill: endophytes in the Taiwanese Cloud Forest.
- 409 Strain-level diversity drives alternative community types in millimeter scale granular biofilms.
- 408 Microbial Forensics: Bioterrorism and Biocrime. **2018**, 24, 55-63
- 407 Geographic Patterns of Bacterioplankton among Lakes of the Middle and Lower Reaches of the Yangtze River Basin, China.
- 406 Habitat type and interannual variation shape unique fungal pathogen communities on a California native bunchgrass.
- 405 Microbial biogeography and ecology of the mouth and implications for periodontal diseases.
- 404 Biogeographical patterns in soil bacterial communities across the Arctic region. 1
- 403 Global ecotypes in the ubiquitous marine clade SAR86.
- 402 Dormancy dampens the microbial distance-decay relationship. 1
- 401 Linking microbial communities to ecosystem functions: what we can learn from genotype-phenotype mapping in organisms. 1
- 400 Using null models to compare bacterial and microeukaryotic metacommunity assembly under shifting environmental conditions. 0
- 399 Describing macroecological patterns in microbes: Approaches for comparative analyses of operational taxonomic unit read number distribution with a case study of global oceanic bacteria.
- 398 Beyond taxonomic identification: integration of ecological responses to a soil bacterial 16S rRNA gene database.
- 397 Temperature and nutrient gradients correspond with lineage-specific microdiversification in the ubiquitous and abundant *Limnohabitans* freshwater genus.
- 396 Ecological patterns of root nodule diversity in cultivated and wild rooibos populations: a community prediction approach.
- 395 Community succession of the grapevine fungal microbiome in the annual growth cycle. 2

- 394 Towards a unifying diversity-area relationship (DAR) of species- and gene-diversity.
- 393 Secondary metabolites of *Bacillus subtilis* impact soil-derived semi-synthetic bacterial community assembly.
- 392 Seasonal climate variations promote bacterial diversity in soil.
- 391 Global drivers of eukaryotic plankton biogeography in the sunlit ocean. **2021**, 374, 594-599 3
- 390 Diversity and Biogeography of Bathyal and Abyssal Seafloor Bacteria and Archaea Along a Mediterranean-Atlantic Gradient. **2021**, 12, 702016
- 389 Molecular identification and antimicrobial activity of endophytic fungi isolated from *Heritiera fomes* (Buch. -Ham), a mangrove plant of the Sundarbans. **2020**, 9, 2
- 388 The current state of research on the evolutionary ecology of invasive species. **2022**, 99-133
- 387 Environmental heterogeneity ruling the action of ecological processes over the bacterial metacommunity assembly.
- 386 Aquatic microbial community is partially functionally redundant: insights from an in situ reciprocal transplant experiment.
- 385 PLANT BIODIVERSITY OF MONITORING POINTS V.AMANGELDY ALMATY REGION. **2020**, 2, 48-55
- 384 Bacterial Characteristics of Dust Particle Saltation in Gobi Dust Sites, Mongolia. **2021**, 12, 1456 0
- 383 Drivers of bacterial colonization patterns in stream biofilms. **2010**,
- 382 Differences in the gut microbiomes of distinct ethnicities within the same geographic area are linked to host metabolic health.
- 381 Actinomycetes from sediments in the Trondheim fjord, Norway: diversity and biological activity. **2008**, 6, 12-24 47
- 380 Freshwater biodiversity of Guam. 1. Introduction, with new records of ciliates and a heliozoan. **2008**, 40, 273-293 2
- 379 An horizon scan of biogeography. **2013**, 5, 3
- 378 The INDUSEM Position Paper on the Emerging Electronic Waste Management Emergency. **2020**, 13, 25-29
- 377 Habitat-specific microbial community associated with the biodiversity hotspot. **2022**, 25-43

- 376 Exploration of microbial ecology and diversity in hotspots. **2022**, 1-23
- 375 Large-scale homogenization of soil bacterial communities in response to agricultural practices in paddy fields, China. **2022**, 164, 108490 2
- 374 Soil environment influences plant growth-promotion traits of isolated rhizobacteria. **2022**, 90, 150785 0
- 373 Selected rhizosphere bacteria are associated with endangered species - *Scutellaria tsinyunensis* via comparative microbiome analysis.. **2021**, 258, 126917 1
- 372 Heterogeneity across Neotropical aquatic environments affects prokaryotic and eukaryotic biodiversity based on environmental DNA.
- 371 Decay of similarity across tropical forest communities: integrating spatial distance with soil nutrients. **2021**, e03599 1
- 370 Dynamics of local adaptation in a stable environmental gradient. **2021**, 3,
- 369 Soil Bacterial Biogeography at the Scale of France. **2021**, 165-192
- 368 Small-scale agricultural grassland management can affect soil fungal community structure as much as continental scale geographic patterns. **2021**, 1 1
- 367 Edaphoclimatic Descriptors of Wild Tomato Species (Sect. *Lycopersicon*) and Closely Related Species (Sect. *Juglandifolia* and Sect. *Lycopersicoides*) in South America. **2021**, 12, 748979 0
- 366 Toward a unified diversity-area relationship (DAR) of species and gene diversity illustrated with the human gut metagenome. **2021**, 12, e03807
- 365 Blowin' in the wind: Dispersal, structure, and metacommunity dynamics of aeolian diatoms in the McMurdo Sound region, Antarctica. **2021**, 1 1
- 364 The Biogeography of Forest Soil Microbial Functional Diversity Responds to Forest Types across Guangxi, Southwest China. **2021**, 12, 1578 0
- 363 Soil Microbial Biomass as an Index of Soil Quality and Fertility in Different Land Use Systems of Northeast India. **2021**, 91-110 1
- 362 Contrasting Effects of Local Environmental and Biogeographic Factors on the Composition and Structure of Bacterial Communities in Arid Monospecific Mangrove Soils.. **2022**, e0090321 1
- 361 Simulation of bacterial populations with SLiM. 2, 2
- 360 Phyllosphere fungal communities of rubber trees exhibited biogeographical patterns, but not bacteria.. **2022**, 2
- 359 Contrasting Community Assembly Mechanisms Underlie Similar Biogeographic Patterns of Surface Microbiota in the Tropical North Pacific Ocean.. **2022**, e0079821 0

358	Diversity of soil fungi in the vineyards of Changli region in China.. 2022,	1
357	Microbiome Development of Seawater-Incubated Pre-production Plastic Pellets Reveals Distinct and Predictive Community Compositions. 2022, 8,	1
356	Disentangling the Ecological Processes Shaping the Latitudinal Pattern of Phytoplankton Communities in the Pacific Ocean.. 2022, e0120321	0
355	Habitat Adaptation Drives Speciation of a Species with Distinct Habitats and Disparate Geographic Origins.. 2022, e0278121	4
354	How habitat heterogeneity shapes bacterial and protistan communities in temperate coastal areas near estuaries.. 2022,	2
353	Current Status, Recent Advances, and Main Challenges on Table Olive Fermentation: The Present Meets the Future.. 2021, 12, 797295	5
352	Intra species diversity of <i>Helicoverpa armigera</i> (Hübner) (Lepidoptera: Noctuidae) in relation to geography and host plants affiliation in Uttarakhand Himalayan population, India. 1	0
351	Fish Skin Microbiomes Are Highly Variable Among Individuals and Populations but Not Within Individuals.. 2021, 12, 767770	1
350	Aquaculture drives distinct patterns of planktonic and sedimentary bacterial communities: insights into co-occurrence pattern and assembly processes.. 2022,	1
349	Molecular Phylogenetics, Speciation, and Long Distance Dispersal in Tardigrade Evolution: A case study of the genus <i>Milnesium</i> .. 2022, 169, 107401	0
348	Soil NO emission in <i>Cinnamomum camphora</i> plantations along an urbanization gradient altered by changes in litter input and microbial community composition.. 2022, 299, 118876	0
347	Biogeographic patterns of soil microbe communities in the deserts of the Hexi Corridor, northern China. 2022, 211, 106026	0
346	Global patterns and predictors of soil microbial biomass carbon, nitrogen, and phosphorus in terrestrial ecosystems. 2022, 211, 106037	1
345	The biogeography of infection revisited.. <i>Nature Reviews Microbiology</i> , 2022, 22.2	1
344	Non-invasive monitoring of multiple wildlife health factors by fecal microbiome analysis.. 2022, 12, e8564	2
343	The effect of vine variety and vintage on wine yeast community structure of grapes and ferments.. 2022,	1
342	Diversity of Microbial Communities of var. at Spatial Scale.. 2022, 10,	0
341	Environmental structure impacts microbial composition and secondary metabolism. 2022, 2,	2

- 340 A framework for integrating microbial dispersal modes into soil ecosystem ecology.. **2022**, 25, 103887 ○
- 339 Phytoplankton community structure and driving mechanism of its construction process in autumn in Zhelin Reservoir, Lake Poyang Basin. **2022**, 34, 433-444 ○
- 338 Does the thermal mismatch hypothesis predict disease outcomes in different morphs of a terrestrial salamander?. **2022**, 1
- 337 Salinity Gradient Controls Microbial Community Structure and Assembly in Coastal Solar Salterns.. **2022**, 13, ○
- 336 Characterization and genomic analysis of a Demereciviridae phage SP76 with lytic multiple-serotypes of Salmonella.. **2022**, 204, 175 1
- 335 Considerations on Field Methodology for Macrofungi Studies in Fragmented Forests of Mediterranean Agricultural Landscapes. **2022**, 12, 528 ○
- 334 Construction of Environmental Synthetic Microbial Consortia: Based on Engineering and Ecological Principles.. **2022**, 13, 829717 4
- 333 Sargasso Sea bacterioplankton community structure and drivers of variance as revealed by DNA metabarcoding analysis.. **2022**, 10, e12835
- 332 Functional Traits Resolve Mechanisms Governing the Assembly and Distribution of Nitrogen-Cycling Microbial Communities in the Global Ocean.. **2022**, e0383221 1
- 331 Seasonal variability in environmental parameters influence bacterial communities in mangrove sediments along an estuarine gradient. **2022**, 107791 ○
- 330 MOLECULAR INSIGHT REVEALS BROAD-SCALE SPATIAL PATTERNS IN FLOODPLAIN CILIATE COMMUNITIES, WHILE MORPHOLOGY REFLECTS LOCAL ENVIRONMENTAL CONTROLS.
- 329 Spatiotemporal Dynamics of Bacterial Taxonomic and Functional Profiles in Estuarine Intertidal Soils of China Coastal Zone.. **2022**, 1 1
- 328 Prevalence of Wheat Associated spp. and Their Bio-Control Efficacy Against Root Rot.. **2021**, 12, 798619 1
- 327 Composition and functionality of bacterioplankton communities in marine coastal zones adjacent to finfish aquaculture.
- 326 Microbial Dispersal, Including Bison Dung Vected Dispersal, Increases Soil Microbial Diversity in a Grassland Ecosystem.. **2022**, 13, 825193 ○
- 325 Biogeography of reef water microbes from within-reef to global scales. **2022**, 88, 81-94 1
- 324 Homogeneous selection is not always important in bacterial community in the eutrophic enclosed bay. **2022**, 11,
- 323 A framework for soil microbial ecology in urban ecosystems. **2022**, 13, ○

- 322 Deciphering the distinct mechanisms shaping the broomcorn millet rhizosphere bacterial and fungal communities in a typical agricultural ecosystem of Northern China. 1 0
- 321 Relationships Between Soil Microbial Diversities Across an Aridity Gradient in Temperate Grasslands : Soil Microbial Diversity Relationships.. **2022**, 1
- 320 Salinity and host drive *Ulva* associated bacterial communities across the Atlantic-Baltic Sea gradient.. **2022**, 0
- 319 Precipitation balances deterministic and stochastic processes of bacterial community assembly in grassland soils. **2022**, 168, 108635 0
- 318 Rare biosphere regulates the planktonic and sedimentary bacteria by disparate ecological processes in a large source water reservoir.. **2022**, 216, 118296 1
- 317 Landscape context determines soil fungal diversity in a fragmented habitat. **2022**, 213, 106163 2
- 316 Climate and landscape changes enhance the global spread of a bloom-forming dinoflagellate related to fish kills and water quality deterioration. **2021**, 133, 108408 0
- 315 Spatial Variability in Streambed Microbial Community Structure across Two Watersheds.. **2021**, 9, e0197221 0
- 314 Genomes of keystone *Mortierella* species lead to better in silico prediction of soil mycobiome functions from Taiwan's offshore islands.
- 313 Spatial Distribution and Influencing Factors of Soil Fungi in a Degraded Alpine Meadow Invaded by *Stellera chamaejasme*. **2021**, 11, 1280 1
- 312 Biogeography of culturable marine bacteria from both poles reveals that 'everything is not everywhere' at the genomic level.. **2021**, 1 1
- 311 Depth dependence of climatic controls on soil microbial community activity and composition. **2021**, 1, 1 1
- 310 The influence of aboveground and belowground species composition on spatial turnover in nutrient pools in alpine grasslands. **2022**, 31, 486-500 0
- 309 Effects of Magnetic Minerals Exposure and Microbial Responses in Surface Sediment across the Bohai Sea.. **2021**, 10, 0
- 308 Archaeal and Bacterial Diversity and Distribution Patterns in Mediterranean-Climate Vernal Pools of Mexico and the Western USA.. **2021**, 1
- 307 Tumors are evolutionary island-like ecosystems. **2021**,
- 306 Diatom biogeography in freshwaters: new insights from between-region comparisons and the role of unmeasured environmental factors. 1-8 0
- 305 Microbial landscape ecology: landscape structure better predicts soil protist diversity than local edaphic variables in alpine meadows.

304 Grape Cultivar Features Differentiate the Grape Rhizosphere Microbiota.. **2022**, 11,

2

303 Data_Sheet_1.docx. **2020**,

302 Data_Sheet_1.DOCX. **2019**,

301 Data_Sheet_1.DOC. **2018**,

300 Image_1.JPEG. **2018**,

299 Image_2.TIFF. **2018**,

298 Image_3.TIF. **2018**,

297 Image_4.JPEG. **2018**,

296 Data_Sheet_1.docx. **2019**,

295 DataSheet1.docx. **2018**,

294 DataSheet2.csv. **2018**,

293 DataSheet3.csv. **2018**,

292 Data_Sheet_1.PDF. **2018**,

291 Data_Sheet_2.xls. **2018**,

290 Data_Sheet_1.PDF. **2019**,

289 Image_1.TIFF. **2019**,

288 Image_2.TIFF. **2019**,

287 Image_3.TIFF. **2019**,

286 Image_4.TIFF. 2019,

285 Data_Sheet_1.docx. 2018,

284 Table_1.DOCX. 2018,

283 Table_2.XLSX. 2018,

282 Presentation_1.PDF. 2018,

281 Data_Sheet_1.XLSX. 2018,

280 Data_Sheet_2.XLSX. 2018,

279 Data_Sheet_3.XLSX. 2018,

278 Data_Sheet_4.XLSX. 2018,

277 Data_Sheet_5.xlsx. 2018,

276 Data_Sheet_6.XLSX. 2018,

275 Data_Sheet_7.XLSX. 2018,

274 Image_1.PDF. 2018,

273 Image_10.PDF. 2018,

272 Image_11.PDF. 2018,

271 Image_2.PDF. 2018,

270 Image_3.PDF. 2018,

269 Image_4.PDF. 2018,

268 Image_5.PDF. 2018,

267 Image_6.PDF. 2018,

266 Image_7.PDF. 2018,

265 Image_8.PDF. 2018,

264 Image_9.PDF. 2018,

263 Data_Sheet_1.pdf. 2020,

262 Table_1.XLSX. 2020,

261 Table_2.XLSX. 2020,

260 DataSheet_1.xlsx. 2019,

259 Image_1.tif. 2019,

258 Image_2.tif. 2019,

257 Image_3.tif. 2019,

256 Image_4.tif. 2019,

255 Image_1.JPEG. 2020,

254 Image_2.JPEG. 2020,

253 Image_3.JPEG. 2020,

252 Image_4.JPEG. 2020,

251 Image_5.JPEG. 2020,

250 Table_1.DOCX. 2020,

249 Table_2.DOCX. 2020,

248 Table_3.XLSX. 2020,

247 Table_4.XLSX. 2020,

246 Image_1.pdf. 2019,

245 Image_2.pdf. 2019,

244 Image_3.pdf. 2019,

243 Data_Sheet_1.pdf. 2019,

242 Table_1.xlsx. 2019,

241 Table_2.xlsx. 2019,

240 Table_3.xlsx. 2019,

239 Data_Sheet_1.PDF. 2019,

238 Table_2.xls. 2019,

237 Table_3.xlsx. 2019,

236 Table_5.xlsx. 2019,

235 Presentation_1.PDF. 2018,

234 Data_Sheet_1.PDF. 2020,

233 Data_Sheet_1.DOCX. 2020,

232 Table_2.xlsx. 2020,

231 Table_4.xlsx. 2020,

230 Data_Sheet_1.PDF. 2018,

229 Data_Sheet_2.XLSX. 2018,

228 Data_Sheet_3.XLSX. 2018,

227 Data_Sheet_4.XLSX. 2018,

226 Data_Sheet_5.XLSX. 2018,

225 Data_Sheet_1.docx. 2020,

224 Data_Sheet_1.PDF. 2018,

223 Data_Sheet_1.CSV. 2019,

222 Image_1.TIFF. 2019,

221 Image_2.JPEG. 2019,

220 Image_3.TIFF. 2019,

219 Data_Sheet_1.docx. 2020,

218 Image_1.tiff. 2020,

217 Image_2.tif. 2020,

216 Image_3.tif. 2020,

215 Table_1.docx. 2018,

214 Table_2.XLSX. 2018,

213 Table_3.DOCX. 2018,

212 Data_Sheet_1.CSV. 2020,

211 Data_Sheet_2.CSV. 2020,

210 Data_Sheet_3.CSV. 2020,

209 Data_Sheet_4.CSV. 2020,

208 Table_1.docx. 2020,

207 Presentation_1.pdf. 2020,

206 Image_1.PDF. 2018,

205 Image_2.PDF. 2018,

204 Image_3.PDF. 2018,

203 Image_4.PDF. 2018,

202 Image_5.PDF. 2018,

201 Table_1.PDF. 2018,

200 Table_2.PDF. 2018,

199 Data_Sheet_1.pdf. 2018,

198 Data_Sheet_2.pdf. 2018,

197 Image_1.TIF. 2018,

196 Image_2.TIF. **2018,**

195 Image_3.TIF. **2018,**

194 Image_4.TIF. **2018,**

193 Image_5.TIF. **2018,**

192 Image_6.TIF. **2018,**

191 Image_7.TIF. **2018,**

190 Table_1.DOCX. **2018,**

189 Table_2.XLSX. **2018,**

188 Table_3.DOCX. **2018,**

187 Table_4.XLSX. **2018,**

186 Table_5.XLSX. **2018,**

185 Data_Sheet_1.PDF. **2018,**

184 Data_Sheet_1.pdf. **2019,**

183 Data_Sheet_1.pdf. **2019,**

182 Table_1.docx. **2019,**

181 Data_Sheet_1.xlsx. **2019,**

180 Data_Sheet_2.docx. **2019,**

179 Data_Sheet_1.pdf. **2019,**

178 Table_1.XLSX. 2019,

177 Data_Sheet_1.PDF. 2020,

176 Data_Sheet_2.pdf. 2020,

175 Data_Sheet_1.PDF. 2020,

174 Data_Sheet_1.docx. 2020,

173 Data_Sheet_2.xlsx. 2020,

172 Data_Sheet_1.docx. 2020,

171 Table_1.docx. 2020,

170 Image_1.JPEG. 2020,

169 Image_2.JPEG. 2020,

168 Image_3.JPEG. 2020,

167 Image_4.JPEG. 2020,

166 Image_5.JPEG. 2020,

165 Image_6.JPEG. 2020,

164 Image_7.JPEG. 2020,

163 Table_1.XLSX. 2020,

162 Table_2.XLSX. 2020,

161 Table_3.XLS. 2020,

160	DataSheet_1.xlsx. 2020,	
159	DataSheet_2.xlsx. 2020,	
158	Image_1.TIFF. 2020,	
157	The INDUSEM position paper on the emerging electronic waste management emergency. 2020, 13, 25	0
156	Metagenomic Profiling of Antibiotic Resistomes in Soil Biocrusts from Urban Green Spaces at the Continental Scale: Driving Factors, Co-Occurrence Patterns, and Assembly Processes.	
155	Changes to the gut microbiota of a wild juvenile passerine in a multidimensional urban mosaic.. 2022, 12, 6872	1
154	Adaptive Pathways of Microorganisms to Cope With the Shift From P- to N-Limitation in Subtropical Plantations.. 2022, 13, 870667	0
153	Bacterial communities associated with hydromedusa <i>Gonionemus vertens</i> in different regions in Chinese coastal waters.	1
152	Determinants of Soil Bacterial Diversity in a Black Soil Region in a Large-Scale Area. 2022, 11, 731	1
151	Bacterial and Protistan Community Variation across the Changjiang Estuary to the Ocean with Multiple Environmental Gradients. 2022, 10, 991	2
150	Microbial stowaways: Waterbirds as dispersal vectors of aquatic pro- and microeukaryotic communities.	1
149	Preferential associations of soil fungal taxa under mixed compositions of eastern American tree species.. 2022,	
148	Landscape connectivity for the invisibles.	1
147	Elevational Gradients Impose Dispersal Limitation on .. 2022, 13, 856263	
146	Composition and spatial-temporal dynamics of phytoplankton community shaped by environmental selection and interactions in the Jiaozhou Bay.. 2022, 218, 118488	2
145	Phylogenetic and sequence profile analysis of Non-Ribosomal Polyketide Synthase-Adenylation (NRPS) domain from .. 2021, 17, 809-813	
144	Terrestrial and marine influence on atmospheric bacterial diversity over the north Atlantic and Pacific Oceans. 2022, 3,	1
143	Effects of environmental factors on the distribution of microbial communities across soils and lake sediments in the Hoh Xil Nature Reserve of the Qinghai-Tibetan Plateau. 2022, 838, 156148	1

- 142 Planktonic protist diversity across contrasting Subtropical and Subantarctic waters of the southwest Pacific. **2022**, 102809 ○
- 141 Metagenomics Unveils Microbial Diversity and Their Biogeochemical Roles in Water and Sediment of Thermokarst Lakes in the Yellow River Source Area. ○
- 140 Microbial Community Structure Is Mostly Strongly Associated With Geographical Distance and pH in Salt Lake Sediments. **2022**, 13,
- 139 Microbial community assembly and co-occurrence relationship in sediments of the river-dominated estuary and the adjacent shelf in the wet season. **2022**, 119572 1
- 138 In-vitro toxicity assessment of Eucalyptus robusta Smith extracts via whole-cell bioreporter. **2022**, 240, 113704
- 137 Diversity of lytic bacteriophages against XDR Klebsiella pneumoniae sequence type 16 recovered from sewage samples in different parts of the world. **2022**, 839, 156074 1
- 136 Soil Fungi's More Sensitive to High-Altitude Change than Soil Bacteria in Abies Smithii Forest.
- 135 Biogeographic Patterns and Elevational Differentiation of Sedimentary Bacterial Communities across River Systems in China.
- 134 Long-Term Fertilizer Use Altered Soil Microbial Community Structure but Not Diversity in Subtropical Southwestern China.
- 133 Historic Wooden Shipwrecks Influence Dispersal of Deep-Sea Biofilms. 9,
- 132 Diversity and biogeography of plant leaf bacteria along a latitudinal gradient.
- 131 Spatial Patterns and Composition Traits of Soil Microbial Nitrogen-Metabolism Genes in the Robinia pseudoacacia Forests at a Regional Scale. 13,
- 130 Variations in Soil Nutrient Dynamics and Bacterial Communities After the Conversion of Forests to Long-Term Tea Monoculture Systems. 13, ○
- 129 Geographic Dispersal Limitation Dominated Assembly Processes of Bacterial Communities on Microplastics Compared to Water and Sediment. 1
- 128 Microbiome assembly in thawing permafrost and its feedbacks to climate. 1
- 127 Heavy metal(loid)s shape the soil bacterial community and functional genes of desert grassland in a gold mining area in the semi-arid region. **2022**, 113749 1
- 126 Competing drivers of soil microbial community assembly in a cold arid zone and their implications on constraints of n-alkane proxies. **2022**, 606, 120985 ○
- 125 Contrasting assembly mechanisms explain the biogeographic patterns of benthic bacterial and fungal communities on the Tibetan Plateau. **2022**, 113836 ○

- 124 Advection and Composition of Dinophysis spp. Populations Along the European Atlantic Shelf. 9,
- 123 Riverine bacterioplankton and phytoplankton assembly along an environmental gradient induced by urbanization. 0
- 122 Biogeographic responses and niche occupancy of microbial communities following long-term land-use change.
- 121 Routes and rates of bacterial dispersal impact surface soil microbiome composition and functioning. 0
- 120 Response of soil microbial biomass C, N, and P and microbial quotient to agriculture and agricultural abandonment in a meadow steppe of northeast China. **2022**, 223, 105475 0
- 119 Soil pH Determines the Spatial Distribution, Assembly Processes, and Co-existence Networks of Microeukaryotic Community in Wheat Fields of the North China Plain. 13,
- 118 Novel Interactions Between Phytoplankton and Bacteria Shape Microbial Seasonal Dynamics in Coastal Ocean Waters. 9, 0
- 117 Türkiye'deki 25 Nehir Havzasından Türkiye Tatlısu Alg Florasının Yeni Kayıtları, Bölüm I: Bacillariophyta.
- 116 Spatial and environmental variables structure sponge symbiont communities.
- 115 Composition and functionality of bacterioplankton communities in marine coastal zones adjacent to finfish aquaculture. **2022**, 182, 113957
- 114 Contributors. **2009**, viii-x
- 113 Copyright Page. **2009**, iv-iv
- 112 Preface. **2009**, xi-xiii
- 111 Soil protists. **2022**,
- 110 Effect of Climate on Bacterial and Archaeal Diversity of Moroccan Marine Microbiota. **2022**, 10, 1622 1
- 109 Global beta diversity patterns of microbial communities in the surface and deep ocean. 0
- 108 A ridge-to-reef ecosystem microbial census reveals environmental reservoirs for animal and plant microbiomes. **2022**, 119, 0
- 107 Genomic evidence for global ocean plankton biogeography shaped by large-scale current systems. 11, 2

106	Free-living and particle-attached bacterial community composition, assembly processes and determinants across spatiotemporal scales in a macrotidal temperate estuary. 2022 , 12,	2
105	Cascading effects of habitat loss on ectoparasite-associated bacterial microbiomes. 2022 , 2,	1
104	Geography, not lifestyle, explains the population structure of free-living and host-associated deep-sea hydrothermal vent snail symbionts.	0
103	The overlooked dimension: soil depth drives microbial community structure and function along a salinity gradient.	0
102	Unravelling how biochar and dung amendments determine the functional structure and community assembly related to methane metabolisms in grassland soils. 2022 , 4,	0
101	Local adaptation of host-species specific gut microbiota.	0
100	Different Responses of Bacteria and Microeukaryote to Assembly Processes and Co-occurrence Pattern in the Coastal Upwelling.	1
99	Three-dimensional mapping of carbon, nitrogen, and phosphorus in soil microbial biomass and their stoichiometry at the global scale.	0
98	Propagule limitation affects the response of soil methane oxidizer community to increased salinity. 2022 , 426, 116082	
97	Convergent community assembly among globally separated acidic cave biofilms.	0
96	The hierarchy of factors predicting the latitudinal diversity gradient. 2022 ,	0
95	Neighbourhood effect of weeds on wheat root endospheric mycobiota.	0
94	Aerobiology over the Southern Ocean ¶Implications for bacterial colonization of Antarctica. 2022 , 169, 107492	0
93	Biogeographical Patterns of Patagonian Freshwater Microbiota. 2022 , 93-116	0
92	Microbial community diversity and eco-genomics functions across sediment regimen of a saline lake. 2022 , 58, 10	0
91	Soil Microbial Community Responds to Elevation Gradient in an Arid Montane Ecosystem in Northwest China. 2022 , 13, 1360	0
90	Application of Microbiome in Forensics. 2022 ,	0
89	Ecological corridors homogenize plant root endospheric mycobiota.	0

- 88 Biogeographic patterns of potential pathogenic bacteria in the middle and lower reaches of the Yangtze River as well as its two adjoining lakes, China. 13, 0
- 87 Comparison of assembly process and co-occurrence pattern between planktonic and benthic microbial communities in the Bohai Sea. 13, 0
- 86 Random sampling associated with microbial profiling leads to overestimated stochasticity inference in community assembly. 13, 0
- 85 Ecological processes differ in community assembly of Archaea, Bacteria and Eukaryotes in a biogeographical survey of groundwater habitats in the Quebec region (Canada). 1
- 84 Microbiome network in the pelagic and benthic offshore systems of the northern Adriatic Sea (Mediterranean Sea). **2022**, 12, 0
- 83 Effects of close-to-nature management of plantation on the structure and ecological functions of soil microorganisms with different habitat specialization. 0
- 82 Discordant population structure among rhizobium divided genomes and their legume hosts. 0
- 81 Towards quantifying microbial dispersal in the environment. 0
- 80 Identification of shared bacterial strains in the vaginal microbiota of related and unrelated reproductive-age mothers and daughters using genome-resolved metagenomics. **2022**, 17, e0275908 0
- 79 Microbial diversity and biogeochemical cycling potential in deep-sea sediments associated with seamount, trench, and cold seep ecosystems. 13, 0
- 78 Biogeographic Distribution of Five Antarctic Cyanobacteria Using Large-Scale k-mer Searching with sourmash branchwater. 0
- 77 Forecasting of a complex microbial community using meta-omics. 0
- 76 Changes of Arbuscular Mycorrhizal Fungal Community and Glomalin in the Rhizosphere along the Distribution Gradient of Zonal Stipa Populations across the Arid and Semiarid Steppe. **2022**, 10, 0
- 75 Scaling up and down: movement ecology for microorganisms. **2022**, 0
- 74 Effects of species richness and nutrient availability on the invasibility of experimental microalgal microcosms. **2022**, 39, e02304 0
- 73 Multiomics Characterization of the Canada Goose Fecal Microbiome Reveals Selective Efficacy of Simulated Metagenomes. 2
- 72 Bacterial communities in ballast tanks of cargo vessels - Shaped by salinity, treatment and the point of origin of the water but ~~Batch~~its typical microbiome. **2022**, 324, 116403 0
- 71 Heavy metal contamination affects the core microbiome and assembly processes in metal mine soils across Eastern China. **2023**, 443, 130241 0

- 70 Geodiversity influences limnological conditions and freshwater ostracode species distributions across broad spatial scales in the northern Neotropics. **2022**, 19, 5167-5185 ○
- 69 Biogeographical patterns of abundant and rare bacterial biospheres in paddy soils across East Asia. ○
- 68 Infection density pattern of *Cardinium* affects the responses of bacterial communities in an invasive whitefly under heat conditions. ○
- 67 Ecological corridors homogenize plant root endospheric mycobiota. ○
- 66 Molecular diversity and biogeography of benthic microeukaryotes in temperate seagrass (*Zostera japonica*) systems of northern China. **2022**, 41, 115-125 ○
- 65 Response of bacterial communities to shrub encroachment and forage planting in alpine grassland of the Qinghai-Tibetan Plateau. **2023**, 186, 106837 ○
- 64 Water mass-driven multiple ecological effects determine the biodiversity and community assembly of microbial flagellates in subtropic-tropic marginal seas of China. **2023**, 280, 108166 ○
- 63 Data-driven discoveries on widespread contamination of freshwater reservoirs by dominant antibiotic resistance genes. **2023**, 229, 119466 ○
- 62 Stochastic processes contribute to arbuscular mycorrhizal fungal community assembly in paddy soils along middle and lower Yangtze River. **2023**, 183, 104759 ○
- 61 Interplay of broccoli/broccoli sprout bioactives with gut microbiota in reducing inflammation in inflammatory bowel diseases. **2023**, 113, 109238 ○
- 60 Distinct distribution patterns of the abundant and rare bacteria in high plateau hot spring sediments. **2023**, 863, 160832 ○
- 59 Metabarcoding reveals the differential sensitivity of planktonic microbiome to environmental filtering and biointeraction in Sansha Yongle blue hole. 9, ○
- 58 Standardized multi-omics of Earth's microbiomes reveals microbial and metabolite diversity. **2022**, 7, 2128-2150 ○
- 57 Heterogeneous selection dominated the temporal variation of the planktonic prokaryotic community during different seasons in the coastal waters of Bohai Bay. **2022**, 12, ○
- 56 Ocean kinetic energy and photosynthetic biomass are important drivers of planktonic foraminifera diversity in the Atlantic Ocean. 9, ○
- 55 Habitats modulate influencing factors shaping the spatial distribution of bacterial communities along a Tibetan Plateau riverine wetland. **2022**, 160418 ○
- 54 The effects of environmental, climatic and spatial factors on diatom diversity in Sphagnum peatlands in central and northeastern China. ○
- 53 Space Rather than Seasonal Changes Explained More of the Spatiotemporal Variation of Tropical Soil Microbial Communities. **2022**, 10, ○

- 52 A shift from inorganic to organic nitrogen-dominance shapes soil microbiome composition and co-occurrence networks. 13, ○
- 51 Salinity Shapes the Microbial Communities in Surface Sediments of Salt Lakes on the Tibetan Plateau, China. **2022**, 14, 4043 ○
- 50 Distribution of methanogenic and methanotrophic consortia at soil-water interfaces in rice paddies across climate zones. **2022**, 105851 ○
- 49 Microbial communities and biogeochemical functioning across peatlands in the Athabasca Oil Sands region of Canada: Implications for reclamation and management. ○
- 48 Diversity and Biogeography of Soil Bacterial Communities. **2023**, 1-13 ○
- 47 Biogeographic Pattern and Network of Rhizosphere Fungal and Bacterial Communities in Panicum miliaceum Fields: Roles of Abundant and Rare Taxa. **2023**, 11, 134 ○
- 46 Microcystis pangenome reveals cryptic diversity within and across morphospecies. **2023**, 9, ○
- 45 Convergent Community Assembly among Globally Separated Acidic Cave Biofilms. ○
- 44 Burning questions: How do soil microbes shape ecosystem biogeochemistry in the context of global change?. ○
- 43 Fermented table olives from Cyprus: Microbiota profile of three varieties from different regions through metabarcoding sequencing. 13, ○
- 42 Phytoplankton diversity and chemotaxonomy in contrasting North Pacific ecosystems. 11, e14501 ○
- 41 Landscape structure is a key driver of soil protist diversity in meadows in the Swiss Alps. ○
- 40 Plant Community Associates with Rare Rather than Abundant Fungal Taxa in Alpine Grassland Soils. ○
- 39 Quantifying relative contributions of biotic interactions to bacterial diversity and community assembly by using community characteristics of microbial eukaryotes. **2023**, 146, 109841 ○
- 38 Insight into universality and characteristics of nitrate reduction coupled with arsenic oxidation in different paddy soils. **2023**, 866, 161342 ○
- 37 Spatial and diel variations of the prokaryotic community in the Phaeocystis globosa blooms area of Beibu Gulf, China. **2022**, 41, 87-97 ○
- 36 Environmental Filtering Drives Fungal Phyllosphere Community in Regional Agricultural Landscapes. **2023**, 12, 507 ○
- 35 Biogeography and potential ecological functions of prokaryotes in the hydrothermal and non-hydrothermal field sediments of the Indian Ocean Ridges. 9, ○

- 34 Global scale phylogeography of functional traits and microdiversity in *Prochlorococcus*. ○
- 33 Phylogenetic diversity of stochasticity-dominated predatory myxobacterial community drives multi-nutrient cycling in typical farmland soils. **2023**, 871, 161680 ○
- 32 Progress in understanding the methane sink and methanotrophs in karst caves. ○
- 31 Those Nematode-Trapping Fungi That are not Everywhere: Hints Towards Soil Microbial Biogeography. ○
- 30 Novel Clinical mNGS-Based Machine Learning Model for Rapid Antimicrobial Susceptibility Testing of *Acinetobacter baumannii*. ○
- 29 Weathering extents and anthropogenic influences shape the soil bacterial community along a subsurface zonation. **2023**, 876, 162570 ○
- 28 Local conditions matter: Minimal and variable effects of soil disturbance on microbial communities and functions in European vineyards. **2023**, 18, e0280516 ○
- 27 No home-field advantage in litter decomposition from the desert to temperate forest. ○
- 26 Will free-living microbial community composition drive biogeochemical responses to global change?. **2023**, 162, 285-307 ○
- 25 Spatial distribution patterns across multiple microbial taxonomic groups. **2023**, 223, 115470 ○
- 24 Environmental DNA sequencing reveals the regional difference in diversity and community assembly mechanisms of eukaryotic plankton in coastal waters. 14, ○
- 23 Cloacal microbiota are biogeographically structured in larks from desert, tropical and temperate areas. **2023**, 23, ○
- 22 Environmental DNA metabarcoding reveals the influence of human activities on microeukaryotic plankton along the Chinese coastline. **2023**, 233, 119730 1
- 21 Toxicity Characterization of Environment-Related Pollutants Using a Biospectroscopy-Bioreporter-Coupling Approach: Potential for Real-World Toxicity Determination and Source Apportionment of Multiple Pollutants. **2023**, 95, 4291-4300 ○
- 20 Towards an Understanding of Large-Scale Biodiversity Patterns on Land and in the Sea. **2023**, 12, 339 ○
- 19 Distinct Ecological Processes Mediate Domain-Level Differentiation in Microbial Spatial Scaling. **2023**, 89, ○
- 18 Ancient Rapid Radiation Explains Most Conflicts Among Gene Trees and Well-Supported Phylogenomic Trees of Nostocalean Cyanobacteria. ○
- 17 Soil bacterial diversity in the tropical dry deciduous forest of Ajodhya hills, Purulia, West Bengal. **2023**, ○

- 16 Dominant Role of Stochastic Processes in Soil Fungal Communities in Pioneer Forests at a Regional Scale. ○
- 15 Biotic interactions contribute more than environmental factors and geographic distance to biogeographic patterns of soil prokaryotic and fungal communities. 14, ○
- 14 From river to ocean: Connectivity and heterogeneity of aquatic ecosystems depicted by planktonic microeukaryotes. **2023**, 148, 110136 ○
- 13 The biogeography of host-associated bacterial microbiomes: Revisiting classic biodiversity patterns. ○
- 12 Composition and spore abundance of arbuscular mycorrhizal fungi in sweet potato producing areas in Uganda. 3, ○
- 11 Fragmentation disrupts microbial effects on native plant community productivity. ○
- 10 Microbial Communities in Phyllosphere. **2023**, 154-192 ○
- 9 Changes in Soil Rhizobia Diversity and Their Effects on the Symbiotic Efficiency of Soybean Intercropped with Maize. **2023**, 13, 997 ○
- 8 Distinct Assembly Mechanisms for Prokaryotic and Microeukaryotic Communities in the Water of Qinghai Lake. ○
- 7 Soil depth and geographic distance modulate bacterial diversity in deep soil profiles throughout the U.S. Corn Belt. ○
- 6 Phyllosphere Mycobiome: Diversity and Function. **2023**, 63-120 ○
- 5 Variation in *Sphingomonas* traits across habitats and phylogenetic clades. 14, ○
- 4 Uncovering the biogeographic pattern of the widespread nematode-trapping fungi *Arthrobotrys oligospora*: watershed is the key. 14, ○
- 3 Biogeographical and Biodiversity Patterns of Marine Planktonic Bacteria Spanning from the South China Sea across the Gulf of Bengal to the Northern Arabian Sea. ○
- 2 Spatial scale impacts microbial community composition and distribution within and across stream ecosystems in North and Central America. ○
- 1 Geography, not lifestyle, explains the population structure of free-living and host-associated deep-sea hydrothermal vent snail symbionts. **2023**, 11, ○