

Introducing DOTUR, a Computer Program for Defining Estimating Species Richness

Applied and Environmental Microbiology
71, 1501-1506

DOI: 10.1128/aem.71.3.1501-1506.2005

Citation Report

#	ARTICLE	IF	CITATIONS
1	Status of the Microbial Census. Microbiology and Molecular Biology Reviews, 2004, 68, 686-691.	6.6	455
2	Metagenomics: Advances in ecology and biotechnology. FEMS Microbiology Letters, 2005, 247, 105-111.	1.8	98
3	Diversity of halophilic archaea in the crystallizers of an Adriatic solar saltern. FEMS Microbiology Ecology, 2005, 54, 491-498.	2.7	67
4	Archaeal diversity along a soil salinity gradient prone to disturbance. Environmental Microbiology, 2005, 7, 1655-1666.	3.8	135
6	Bacterial diversity in water samples from uranium wastes as demonstrated by 16S rDNA and ribosomal intergenic spacer amplification retrievals. Canadian Journal of Microbiology, 2005, 51, 910-923.	1.7	25
7	Culture-Independent Characterization of the Microbiota of the Ant Lion Myrmeleon mobilis (Neuroptera: Myrmeleontidae). Applied and Environmental Microbiology, 2005, 71, 8784-8794.	3.1	67
8	Ubiquity and diversity of ammonia-oxidizing archaea in water columns and sediments of the ocean. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 14683-14688.	7.1	2,072
9	Metagenomics for studying unculturable microorganisms: cutting the Gordian knot. Genome Biology, 2005, 6, 229.	9.6	407
10	Assessment of Microbial Phylogenetic Diversity Based on Environmental Nucleic Acids. , 2006, , 219-259.		8
11	Diversity of Basidiomycetes in Michigan Agricultural Soils. Applied and Environmental Microbiology, 2006, 72, 7050-7056.	3.1	95
12	Nitrous Oxide Reductase Genes (nosZ) of Denitrifying Microbial Populations in Soil and the Earthworm Gut Are Phylogenetically Similar. Applied and Environmental Microbiology, 2006, 72, 1019-1026.	3.1	100
13	Phylogenetic and Morphological Diversity of Bacteroidales Members Associated with the Gut Wall of Termites. Bioscience, Biotechnology and Biochemistry, 2006, 70, 211-218.	1.3	34
14	Community Structure Analyses Are More Sensitive to Differences in Soil Bacterial Communities than Anonymous Diversity Indices. Applied and Environmental Microbiology, 2006, 72, 7804-7812.	3.1	163
15	Alkenone producers inferred from well-preserved 18S rDNA in Greenland lake sediments. Journal of Geophysical Research, 2006, 111, .	3.3	39
16	Unexpected Diversity and Complexity of the Guerrero Negro Hypersaline Microbial Mat. Applied and Environmental Microbiology, 2006, 72, 3685-3695.	3.1	435
17	Molecular epidemiology of forest pathogens: from genes to landscape. Canadian Journal of Plant Pathology, 2006, 28, 167-181.	1.4	9
18	Differences between Tissue-Associated Intestinal Microfloras of Patients with Crohn's Disease and Ulcerative Colitis. Journal of Clinical Microbiology, 2006, 44, 4136-4141.	3.9	480
19	Bacterial diversity in the active stage of a bioremediation system for mineral oil hydrocarbon-contaminated soils. Microbiology (United Kingdom), 2006, 152, 3291-3304.	1.8	85

#	ARTICLE	IF	CITATIONS
20	Ecological and Evolutionary Forces Shaping Microbial Diversity in the Human Intestine. <i>Cell</i> , 2006, 124, 837-848.	28.9	2,744
21	Reciprocal Gut Microbiota Transplants from Zebrafish and Mice to Germ-free Recipients Reveal Host Habitat Selection. <i>Cell</i> , 2006, 127, 423-433.	28.9	808
22	Effect of Temporal Sample Preservation on the Molecular Study of a Complex Microbial Community in the Gut of the Termite <i>Microcerotermes</i> sp.. <i>Microbes and Environments</i> , 2006, 21, 78-85.	1.6	12
23	The desert of Tataouine: an extreme environment that hosts a wide diversity of microorganisms and radiotolerant bacteria. <i>Environmental Microbiology</i> , 2006, 8, 514-525.	3.8	192
24	Microbial community dynamics in a humic lake: differential persistence of common freshwater phylotypes. <i>Environmental Microbiology</i> , 2006, 8, 956-970.	3.8	141
25	Microbial diversity in alpine tundra wet meadow soil: novel <i>Chloroflexi</i> from a cold, water-saturated environment. <i>Environmental Microbiology</i> , 2006, 8, 1471-1486.	3.8	147
26	Analysis of mercuric reductase (<i>merA</i>) gene diversity in an anaerobic mercury-contaminated sediment enrichment. <i>Environmental Microbiology</i> , 2006, 8, 1746-1752.	3.8	55
27	Development and evaluation of specific 16S rDNA primers for marine <i>Cytophaga-Flavobacteria</i> cluster. <i>Molecular Ecology Notes</i> , 2006, 6, 1278-1281.	1.7	10
28	Characterization of bacterial populations recovered from the teat canals of lactating dairy and beef cattle by 16S rRNA gene sequence analysis. <i>FEMS Microbiology Ecology</i> , 2006, 56, 471-481.	2.7	44
29	Biogeographical distribution and ecological ranges of benthic cyanobacteria in East Antarctic lakes. <i>FEMS Microbiology Ecology</i> , 2006, 57, 272-289.	2.7	173
30	Diversity estimates of microeukaryotes below the chemocline of the anoxic Mariager Fjord, Denmark. <i>FEMS Microbiology Ecology</i> , 2006, 58, 476-491.	2.7	96
31	<i>Vannella epipetala</i> n. sp. Isolated from the Leaf Surface of <i>Spondias mombin</i> (Anacardiaceae) Growing in the Dry Forest of Costa Rica. <i>Journal of Eukaryotic Microbiology</i> , 2006, 53, 522-530.	1.7	13
32	Abnormal microbiota composition in the ileocolonic mucosa of Crohn's disease patients as revealed by polymerase chain reaction-denaturing gradient gel electrophoresis. <i>Inflammatory Bowel Diseases</i> , 2006, 12, 1136-1145.	1.9	238
33	Diversity and community structure of ectomycorrhizal fungi in a wooded meadow. <i>Mycological Research</i> , 2006, 110, 734-748.	2.5	137
34	FastGroupII: a web-based bioinformatics platform for analyses of large 16S rDNA libraries. <i>BMC Bioinformatics</i> , 2006, 7, 57.	2.6	186
35	Characterization of Gut-Associated Bacteria in Larvae and Adults of the Southern Pine Beetle, <i>Dendroctonus frontalis</i> Zimmermann. <i>Environmental Entomology</i> , 2006, 35, 1710-1717.	1.4	74
36	Characterization of Gut-Associated Bacteria in Larvae and Adults of the Southern Pine Beetle, <i>Dendroctonus frontalis</i> Zimmermann. <i>Environmental Entomology</i> , 2006, 35, 1710-1717.	1.4	41
37	Toward a Census of Bacteria in Soil. <i>PLoS Computational Biology</i> , 2006, 2, e92.	3.2	366

#	ARTICLE	IF	CITATIONS
38	Diversity and Distribution of Planctomycetes and Related Bacteria in the Suboxic Zone of the Black Sea. <i>Applied and Environmental Microbiology</i> , 2006, 72, 3079-3083.	3.1	79
39	What is the extent of prokaryotic diversity?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 2023-2037.	4.0	90
40	Environmental Whole-Genome Amplification To Access Microbial Populations in Contaminated Sediments. <i>Applied and Environmental Microbiology</i> , 2006, 72, 3291-3301.	3.1	213
41	Synthetic Statistical Approach Reveals a High Degree of Richness of Microbial Eukaryotes in an Anoxic Water Column. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6578-6583.	3.1	33
42	DivergentSet, a Tool for Picking Non-redundant Sequences from Large Sequence Collections. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1520-1532.	3.8	13
43	Molecular Characterization of Subject-Specific Oral Microflora during Initial Colonization of Enamel. <i>Applied and Environmental Microbiology</i> , 2006, 72, 2837-2848.	3.1	353
45	Phylogenetic Comparisons of Bacterial Communities from Serpentine and Nonserpentine Soils. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6965-6971.	3.1	52
46	Diversity of Microorganisms within Rock Varnish in the Whipple Mountains, California. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1708-1715.	3.1	73
47	Bacteria Associated with the Guts of Two Wood-Boring Beetles: <i>Anoplophora glabripennis</i> and <i>Saperda vestita</i> (Cerambycidae). <i>Environmental Entomology</i> , 2006, 35, 625-629.	1.4	121
48	Phylogenetic Diversity, Localization, and Cell Morphologies of Members of the Candidate Phylum TC3 and a Subphylum in the Phylum Fibrobacteres, Recently Discovered Bacterial Groups Dominant in Termite Guts. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6780-6788.	3.1	99
49	Diversity of Ammonia-Oxidizing Archaea and Bacteria in the Sediments of a Hypernutrified Subtropical Estuary: Bahía del Tolbari, Mexico. <i>Applied and Environmental Microbiology</i> , 2006, 72, 7767-7777.	3.1	216
50	Introducing TreeClimber, a Test To Compare Microbial Community Structures. <i>Applied and Environmental Microbiology</i> , 2006, 72, 2379-2384.	3.1	97
51	Microeukaryote Community Patterns along an O ₂ /H ₂ S Gradient in a Supersulfidic Anoxic Fjord (Framvaren, Norway). <i>Applied and Environmental Microbiology</i> , 2006, 72, 3626-3636.	3.1	132
52	Microbial diversity in the deep sea and the underexplored "rare biosphere". <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12115-12120.	7.1	3,297
53	The bacteriology of biopsies differs between newly diagnosed, untreated, Crohn's disease and ulcerative colitis patients. <i>Journal of Medical Microbiology</i> , 2006, 55, 1141-1149.	1.8	211
54	Bacteria Associated with Mucus and Tissues of the Coral <i>Oculina patagonica</i> in Summer and Winter. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5254-5259.	3.1	240
55	Denitrifier Community Composition along a Nitrate and Salinity Gradient in a Coastal Aquifer. <i>Applied and Environmental Microbiology</i> , 2006, 72, 2102-2109.	3.1	170
56	NAST: a multiple sequence alignment server for comparative analysis of 16S rRNA genes. <i>Nucleic Acids Research</i> , 2006, 34, W394-W399.	14.5	918

#	ARTICLE	IF	CITATIONS
57	Occurrence of Ammonia-Oxidizing Archaea in Wastewater Treatment Plant Bioreactors. Applied and Environmental Microbiology, 2006, 72, 5643-5647.	3.1	347
58	Introducing SONS, a Tool for Operational Taxonomic Unit-Based Comparisons of Microbial Community Memberships and Structures. Applied and Environmental Microbiology, 2006, 72, 6773-6779.	3.1	239
59	Application of a High-Density Oligonucleotide Microarray Approach To Study Bacterial Population Dynamics during Uranium Reduction and Reoxidation. Applied and Environmental Microbiology, 2006, 72, 6288-6298.	3.1	404
60	Novel Nickel Resistance Genes from the Rhizosphere Metagenome of Plants Adapted to Acid Mine Drainage. Applied and Environmental Microbiology, 2007, 73, 6001-6011.	3.1	117
61	Structure and Function of Methanogens along a Short-Term Restoration Chronosequence in the Florida Everglades. Applied and Environmental Microbiology, 2007, 73, 4135-4141.	3.1	21
62	Potential for Mercury Reduction by Microbes in the High Arctic. Applied and Environmental Microbiology, 2007, 73, 2230-2238.	3.1	88
63	Microbial Community Biofabrics in a Geothermal Mine Adit. Applied and Environmental Microbiology, 2007, 73, 6172-6180.	3.1	76
64	Urban aerosols harbor diverse and dynamic bacterial populations. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 299-304.	7.1	593
65	Phylogenetic Analysis of Bacteria Preserved in a Permafrost Ice Wedge for 25,000 Years. Applied and Environmental Microbiology, 2007, 73, 2360-2363.	3.1	88
66	Salinity Constraints on Subsurface Archaeal Diversity and Methanogenesis in Sedimentary Rock Rich in Organic Matter. Applied and Environmental Microbiology, 2007, 73, 4171-4179.	3.1	115
67	Microbial Diversity in the Deep Marine Sediments from the Qiongdongnan Basin in South China Sea. Geomicrobiology Journal, 2007, 24, 505-517.	2.0	38
68	Diversity and Metabolism of Marine Bacteria Cultivated on Dissolved DNA. Applied and Environmental Microbiology, 2007, 73, 2799-2805.	3.1	59
69	Native Microbial Colonization of <i>Drosophila melanogaster</i> and Its Use as a Model of <i>Enterococcus faecalis</i> Pathogenesis. Infection and Immunity, 2007, 75, 1565-1576.	2.2	271
70	No Evidence of an Impact on the Rhizosphere Diazotroph Community by the Expression of <i>Bacillus thuringiensis</i> Cry1Ab Toxin by Bt White Spruce. Applied and Environmental Microbiology, 2007, 73, 6577-6583.	3.1	35
71	Salinity Constraints on Subsurface Archaeal Diversity and Methanogenesis in Sedimentary Rock Rich in Organic Matter. Applied and Environmental Microbiology, 2007, 73, 5387-5387.	3.1	21
72	Distribution and Diversity of Archaeal Ammonia Monooxygenase Genes Associated with Corals. Applied and Environmental Microbiology, 2007, 73, 5642-5647.	3.1	107
73	Postinoculation Protozoan Establishment and Association Patterns of Methanogenic Archaea in the Ovine Rumen. Applied and Environmental Microbiology, 2007, 73, 4609-4618.	3.1	81
74	Changes in Bacterial Populations and in Biphenyl Dioxygenase Gene Diversity in a Polychlorinated Biphenyl-Polluted Soil after Introduction of Willow Trees for Rhizoremediation. Applied and Environmental Microbiology, 2007, 73, 6224-6232.	3.1	63

#	ARTICLE	IF	CITATIONS
75	The Motility Symbiont of the Termite Gut Flagellate <i>Caduceia versatilis</i> Is a Member of the <i>Synergistes</i> Group. Applied and Environmental Microbiology, 2007, 73, 6270-6276.	3.1	64
76	Isolation of Polymer-Degrading Bacteria and Characterization of the Hindgut Bacterial Community from the Detritus-Feeding Larvae of <i>Tipula abdominalis</i> (Diptera: Tipulidae). Applied and Environmental Microbiology, 2007, 73, 5683-5686.	3.1	22
77	High Temporal but Low Spatial Heterogeneity of Bacterioplankton in the Chesapeake Bay. Applied and Environmental Microbiology, 2007, 73, 6776-6789.	3.1	73
78	Microbial Diversity in Natural Asphalts of the Rancho La Brea Tar Pits. Applied and Environmental Microbiology, 2007, 73, 4579-4591.	3.1	107
79	Geographical Distribution and Diversity of Bacteria Associated with Natural Populations of <i>Drosophila melanogaster</i> . Applied and Environmental Microbiology, 2007, 73, 3470-3479.	3.1	200
80	Detection of Anammox Activity and Diversity of Anammox Bacteria-Related 16S rRNA Genes in Coastal Marine Sediment in Japan. Microbes and Environments, 2007, 22, 232-242.	1.6	129
81	Archaeal and bacterial community composition of a pristine coastal aquifer in Doñana National Park, Spain. Aquatic Microbial Ecology, 2007, 47, 123-139.	1.8	25
82	Archaeal and bacterial community composition of sediment and plankton from a suboxic freshwater pond. Research in Microbiology, 2007, 158, 213-227.	2.1	128
83	Ecological anomalies in the East China Sea: Impacts of the Three Gorges Dam?. Water Research, 2007, 41, 1287-1293.	11.3	138
84	Microbial Population Structures in the Deep Marine Biosphere. Science, 2007, 318, 97-100.	12.6	802
85	The Fecal Microbiota of Irritable Bowel Syndrome Patients Differs Significantly From That of Healthy Subjects. Gastroenterology, 2007, 133, 24-33.	1.3	882
86	Coral mucus-associated bacterial communities from natural and aquarium environments. FEMS Microbiology Letters, 2007, 276, 106-113.	1.8	116
87	Haloarchaeal communities in the crystallizers of two adriatic solar salterns. Canadian Journal of Microbiology, 2007, 53, 8-18.	1.7	34
88	The Last Word: Books as a Statistical Metaphor for Microbial Communities. Annual Review of Microbiology, 2007, 61, 23-34.	7.3	41
89	Phylogenetic Ecology of the Freshwater <i>Actinobacteria</i> Lineage. Applied and Environmental Microbiology, 2007, 73, 7169-7176.	3.1	195
90	The ribosomal database project (RDP-II): introducing myRDP space and quality controlled public data. Nucleic Acids Research, 2007, 35, D169-D172.	14.5	991
91	Loss of Bacterial Diversity during Antibiotic Treatment of Intubated Patients Colonized with <i>Pseudomonas aeruginosa</i> . Journal of Clinical Microbiology, 2007, 45, 1954-1962.	3.9	166
92	Molecular Phylogeny of Uncultivated <i>Crenarchaeota</i> in Great Basin Hot Springs of Moderately Elevated Temperature. Geomicrobiology Journal, 2007, 24, 535-542.	2.0	23

#	ARTICLE	IF	CITATIONS
93	Salmonella enterica Serovar Typhimurium Exploits Inflammation to Compete with the Intestinal Microbiota. PLoS Biology, 2007, 5, e244.	5.6	905
94	Diversidade de bact�rias diazotr�ficas endof�ticas associadas a plantas de milho. Revista Brasileira De Ciencia Do Solo, 2007, 31, 1367-1380.	1.3	15
95	Molecular Characterization of the Microbial Community in Onsite Treatment Units. , 2007, , .		1
96	Adaptation and spectral tuning in divergent marine proteorhodopsins from the eastern Mediterranean and the Sargasso Seas. ISME Journal, 2007, 1, 48-55.	9.8	65
97	Pyrosequencing enumerates and contrasts soil microbial diversity. ISME Journal, 2007, 1, 283-290.	9.8	1,615
98	High diversity of bacterial mercuric reductase genes from surface and sub-surface floodplain soil (Oak Ridge, USA). ISME Journal, 2007, 1, 453-467.	9.8	54
99	The Human Microbiome Project. Nature, 2007, 449, 804-810.	27.8	4,750
100	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. Nature, 2007, 450, 560-565.	27.8	1,181
101	Characterization of bacterial community structure in vestimentiferan tubeworm Ridgeia piscesae trophosomes. Marine Ecology, 2007, 28, 72-85.	1.1	18
102	Analysis of nitrite reductase (nirK and nirS) genes and cultivation reveal depauperate community of denitrifying bacteria in the Black Sea suboxic zone. Environmental Microbiology, 2007, 9, 118-130.	3.8	85
103	Unexpected diversity in populations of the many-celled magnetotactic prokaryote. Environmental Microbiology, 2007, 9, 206-215.	3.8	68
104	Disturbance and recovery of microbial community structure and function following Hurricane Frances. Environmental Microbiology, 2007, 9, 576-583.	3.8	54
105	High local and global diversity of Flavobacteria in marine plankton. Environmental Microbiology, 2007, 9, 1253-1266.	3.8	176
106	Bacterial taxa abundance pattern in an industrial wastewater treatment system determined by the full rRNA cycle approach. Environmental Microbiology, 2007, 9, 1780-1789.	3.8	56
107	Bacterioplankton assemblages transforming dissolved organic compounds in coastal seawater. Environmental Microbiology, 2007, 9, 2025-2037.	3.8	57
108	Frequent occurrence of the human-specific Bacteroides fecal marker at an open coast marine beach: relationship to waves, tides and traditional indicators. Environmental Microbiology, 2007, 9, 2038-2049.	3.8	49
109	Novel hopanoid cyclases from the environment. Environmental Microbiology, 2007, 9, 2175-2188.	3.8	108
110	Viability, diversity and composition of the bacterial community in a high Arctic permafrost soil from Spitsbergen, Northern Norway. Environmental Microbiology, 2007, 9, 2870-2884.	3.8	129

#	ARTICLE	IF	CITATIONS
111	Fungal rDNA signatures in coronary atherosclerotic plaques. <i>Environmental Microbiology</i> , 2007, 9, 3035-3045.	3.8	12
112	Distinct distribution pattern of abundance and diversity of aerobic anoxygenic phototrophic bacteria in the global ocean. <i>Environmental Microbiology</i> , 2007, 9, 3091-3099.	3.8	164
113	Identification of novel perchloroethene- ϵ -respiring microorganisms in anoxic river sediment by RNA- ϵ -based stable isotope probing. <i>Environmental Microbiology</i> , 2008, 10, 31-46.	3.8	51
114	Abundant proteorhodopsin genes in the North Atlantic Ocean. <i>Environmental Microbiology</i> , 2008, 10, 99-109.	3.8	84
115	Diversity and phylogeny of Baltic Sea picocyanobacteria inferred from their ITS and phycobiliprotein operons. <i>Environmental Microbiology</i> , 2008, 10, 174-188.	3.8	77
116	Relationships between bacterial diversity and environmental variables in a tropical marine environment, Rio de Janeiro. <i>Environmental Microbiology</i> , 2008, 10, 189-199.	3.8	52
117	Microbial diversity - insights from population genetics. <i>Environmental Microbiology</i> , 2008, 10, 251-264.	3.8	34
118	Evolutionary trend of phylogenetic diversity of nitrogen fixation genes in the gut community of wood-feeding termites. <i>Molecular Ecology</i> , 2007, 16, 3768-3777.	3.9	64
119	Genetic diversity assessment of anoxygenic photosynthetic bacteria by distance-based grouping analysis of pufM sequences. <i>Letters in Applied Microbiology</i> , 2007, 45, 639-645.	2.2	24
120	16S rRNA gene-based analysis of mucosa-associated bacterial community and phylogeny in the chicken gastrointestinal tracts: from crops to ceca. <i>FEMS Microbiology Ecology</i> , 2007, 59, 147-157.	2.7	268
121	Allochthonous inputs of riverine picocyanobacteria to coastal waters in the Arctic Ocean. <i>FEMS Microbiology Ecology</i> , 2007, 59, 356-365.	2.7	83
122	Succession in the intestinal microbiota of preadolescent turkeys. <i>FEMS Microbiology Ecology</i> , 2007, 60, 136-147.	2.7	64
123	Comparative bacterial diversity in recent Hawaiian volcanic deposits of different ages. <i>FEMS Microbiology Ecology</i> , 2007, 60, 60-73.	2.7	103
124	Diversity of sulfate-reducing bacteria from an extreme hypersaline sediment, Great Salt Lake (Utah). <i>FEMS Microbiology Ecology</i> , 2007, 60, 287-298.	2.7	117
125	The candidate phylum "Termite Group 1" of bacteria: phylogenetic diversity, distribution, and endosymbiont members of various gut flagellated protists. <i>FEMS Microbiology Ecology</i> , 2007, 60, 467-476.	2.7	97
126	Quantitation and diversity analysis of ruminal methanogenic populations in response to the antimethanogenic compound bromochloromethane. <i>FEMS Microbiology Ecology</i> , 2007, 62, 313-322.	2.7	429
127	Influence of high temperature and humidity on rumen bacterial diversity in Holstein heifers. <i>Anaerobe</i> , 2007, 13, 57-64.	2.1	128
128	Nitrogen fertilization reduces diversity and alters community structure of active fungi in boreal ecosystems. <i>Soil Biology and Biochemistry</i> , 2007, 39, 1878-1887.	8.8	255

#	ARTICLE	IF	CITATIONS
129	Prokaryotic community composition and ecology of floating macroscopic filaments from an extreme acidic environment, R��o Tinto (SW, Spain). Systematic and Applied Microbiology, 2007, 30, 601-614.	2.8	92
130	Phylogenetic diversity of planktonic archaea in the estuarine region of East China Sea. Microbiological Research, 2007, 162, 26-36.	5.3	29
131	The phylogeny of fluorescent pseudomonads in an unflooded rice paddy soil. Annals of Microbiology, 2007, 57, 299-306.	2.6	6
132	High-Density Universal 16S rRNA Microarray Analysis Reveals Broader Diversity than Typical Clone Library When Sampling the Environment. Microbial Ecology, 2007, 53, 371-383.	2.8	416
133	Microbial Community Succession in an Unvegetated, Recently Deglaciaded Soil. Microbial Ecology, 2007, 53, 110-122.	2.8	359
134	Novel and Unexpected Prokaryotic Diversity in Water and Sediments of the Alkaline, Hypersaline Lakes of the Wadi An Natrun, Egypt. Microbial Ecology, 2007, 54, 598-617.	2.8	194
135	Bacterial Diversity and Distribution in the Holocene Sediments of a Northern Temperate Lake. Microbial Ecology, 2007, 54, 252-263.	2.8	49
136	Bacterial Diversity in Mine Tailings Compared by Cultivation and Cultivation-independent Methods and their Resistance to Lead and Cadmium. Microbial Ecology, 2007, 54, 705-712.	2.8	55
137	Metagenomics, biotechnology with non-culturable microbes. Applied Microbiology and Biotechnology, 2007, 75, 955-962.	3.6	282
138	Community analysis of hydrogen-producing extreme thermophilic anaerobic microflora enriched from cow manure with five substrates. Applied Microbiology and Biotechnology, 2007, 77, 213-222.	3.6	73
139	Influence of bicarbonate, sulfate, and electron donors on biological reduction of uranium and microbial community composition. Applied Microbiology and Biotechnology, 2007, 77, 713-721.	3.6	54
140	Effect of long-term nitrogen fertilization on mycorrhizal fungi associated with a dominant grass in a semiarid grassland. Plant and Soil, 2007, 296, 65-75.	3.7	101
141	Increases in soil respiration following labile carbon additions linked to rapid shifts in soil microbial community composition. Biogeochemistry, 2007, 82, 229-240.	3.5	378
142	Bacterial diversity associated with the Caribbean tunicate Ecteinascidia turbinata. Antonie Van Leeuwenhoek, 2007, 92, 155-164.	1.7	61
143	Biodiversity of diazotrophic bacteria within the soil, root and stem of field-grown maize. Plant and Soil, 2008, 302, 91-104.	3.7	128
144	Molecular analyses of methanogen diversity associated with cattle dung. World Journal of Microbiology and Biotechnology, 2008, 24, 2973-2979.	3.6	22
145	Diversity of soil fungal communities of Cerrado and its closely surrounding agriculture fields. Archives of Microbiology, 2008, 190, 129-39.	2.2	50
146	Bacterial communities of the marine sponges Hymeniacidon heliophila and Polymastia janeirensis and their environment in Rio de Janeiro, Brazil. Marine Biology, 2008, 155, 135-146.	1.5	25

#	ARTICLE	IF	CITATIONS
147	Bacteria Associated with the Bleached and Cave Coral <i>Oculina patagonica</i> . <i>Microbial Ecology</i> , 2008, 55, 523-529.	2.8	52
148	Intensive Management Affects Composition of Betaproteobacterial Ammonia Oxidizers in Turfgrass Systems. <i>Microbial Ecology</i> , 2008, 56, 178-190.	2.8	13
149	Evidence of Increased Diversity of Methanogenic Archaea with Plant Extract Supplementation. <i>Microbial Ecology</i> , 2008, 56, 234-242.	2.8	107
150	Comparison of the Cecal Microbiota of Domestic and Wild Turkeys. <i>Microbial Ecology</i> , 2008, 56, 322-331.	2.8	118
151	Composition of <i>nifH</i> in a wastewater treatment system reliant on N ₂ fixation. <i>Applied Microbiology and Biotechnology</i> , 2008, 79, 811-818.	3.6	24
152	Fungal Communities in Decaying Sapwood and Heartwood of a Conifer <i>Keteleeria evelyniana</i> . <i>Current Microbiology</i> , 2008, 56, 358-362.	2.2	14
153	Bacterial Growth on Coral Mucus. <i>Current Microbiology</i> , 2008, 56, 481-488.	2.2	53
154	Rapid phylogenetic dissection of prokaryotic community structure in tidal flat using pyrosequencing. <i>Journal of Microbiology</i> , 2008, 46, 357-363.	2.8	71
155	Prokaryotic diversity of a Tunisian multipond solar saltern. <i>Extremophiles</i> , 2008, 12, 505-518.	2.3	93
156	Culturable and molecular phylogenetic diversity of microorganisms in an open-dumped, extremely acidic Pb/Zn mine tailings. <i>Extremophiles</i> , 2008, 12, 657-664.	2.3	50
157	Fungal Taxa Target Different Carbon Sources in Forest Soil. <i>Ecosystems</i> , 2008, 11, 1157-1167.	3.4	174
158	Bacteria Associated with Toxic Clonal Cultures of the Dinoflagellate <i>Ostreopsis lenticularis</i> . <i>Marine Biotechnology</i> , 2008, 10, 492-496.	2.4	16
159	Characterization of a methanogenic consortium enriched from a coalbed methane well in the Powder River Basin, U.S.A.. <i>International Journal of Coal Geology</i> , 2008, 76, 34-45.	5.0	223
160	Investigation of methanogen population structure in biogas reactor by molecular characterization of methyl-coenzyme M reductase A (<i>mcrA</i>) genes. <i>Bioresource Technology</i> , 2008, 99, 5317-5326.	9.6	71
161	Assessment of microbial diversity in effluent treatment plants by culture dependent and culture independent approaches. <i>Bioresource Technology</i> , 2008, 99, 7098-7107.	9.6	74
162	Unexpectedly high bacterial diversity in decaying wood of a conifer as revealed by a molecular method. <i>International Biodeterioration and Biodegradation</i> , 2008, 62, 471-474.	3.9	44
163	Molecular Mechanisms of Plant and Microbe Coexistence. <i>Soil Biology</i> , 2008, , .	0.8	37
164	Novelty and Uniqueness Patterns of Rare Members of the Soil Biosphere. <i>Applied and Environmental Microbiology</i> , 2008, 74, 5422-5428.	3.1	189

#	ARTICLE	IF	CITATIONS
165	Application of self-organizing maps for assessing soil biological quality. Agriculture, Ecosystems and Environment, 2008, 126, 139-152.	5.3	81
166	Bacterial diversity of <i>Taxus</i> rhizosphere: culture-independent and culture-dependent approaches. FEMS Microbiology Letters, 2008, 284, 204-212.	1.8	35
167	Development of an oligonucleotide microarray to detect di- and monooxygenase genes for benzene degradation in soil. FEMS Microbiology Letters, 2008, 285, 111-121.	1.8	15
168	Variability in benthic diazotrophy and cyanobacterial diversity in a tropical intertidal lagoon. FEMS Microbiology Ecology, 2008, 63, 205-221.	2.7	43
169	Diversity and abundance of glycosyl hydrolase family 5 in the North Atlantic Ocean. FEMS Microbiology Ecology, 2008, 63, 316-327.	2.7	26
170	Microbial community succession and bacterial diversity in soils during 77 000 years of ecosystem development. FEMS Microbiology Ecology, 2008, 64, 129-140.	2.7	82
171	Metagenomic analysis of a freshwater toxic cyanobacteria bloom. FEMS Microbiology Ecology, 2008, 64, 9-27.	2.7	64
172	Potential for atmospheric deposition of bacteria to influence bacterioplankton communities. FEMS Microbiology Ecology, 2008, 64, 388-394.	2.7	40
173	Analysis of bacterial diversity in the canine duodenum, jejunum, ileum, and colon by comparative 16S rRNA gene analysis. FEMS Microbiology Ecology, 2008, 66, 567-578.	2.7	194
174	Change of bacterial communities in sediments along Songhua River in Northeastern China after a nitrobenzene pollution event. FEMS Microbiology Ecology, 2008, 65, 494-503.	2.7	41
175	Changes in microbial diversity in industrial wastewater evaporation ponds following artificial salination. FEMS Microbiology Ecology, 2008, 66, 437-446.	2.7	22
176	Molecular-phylogenetic characterization of microbial communities imbalances in the small intestine of dogs with inflammatory bowel disease. FEMS Microbiology Ecology, 2008, 66, 579-589.	2.7	197
177	Comparative analysis of ammonia monooxygenase (<i>amoA</i>) genes in the water column and sediment-water interface of two lakes and the Baltic Sea. FEMS Microbiology Ecology, 2008, 66, 367-378.	2.7	30
178	Assessment of microbial diversity along the feline intestinal tract using 16S rRNA gene analysis. FEMS Microbiology Ecology, 2008, 66, 590-598.	2.7	131
179	Evaluating different approaches that test whether microbial communities have the same structure. ISME Journal, 2008, 2, 265-275.	9.8	164
180	Diversity and abundance of diazotrophic microorganisms in the South China Sea during intermonsoon. ISME Journal, 2008, 2, 954-967.	9.8	176
181	Distantly sampled soils carry few species in common. ISME Journal, 2008, 2, 901-910.	9.8	137
182	The rational exploration of microbial diversity. ISME Journal, 2008, 2, 997-1006.	9.8	190

#	ARTICLE	IF	CITATIONS
183	Bacterial carbon processing by generalist species in the coastal ocean. <i>Nature</i> , 2008, 451, 708-711.	27.8	284
184	Abundance and diversity of microbial life in ocean crust. <i>Nature</i> , 2008, 453, 653-656.	27.8	339
185	DIVERSITY AND HOST SPECIFICITY OF <i>AZOLLA</i> CYANOBIONTS ¹ . <i>Journal of Phycology</i> , 2008, 44, 60-70.	2.3	50
186	PHYLOGENETIC PATTERNS AMONG <i>NOSTOC</i> CYANOBIONTS WITHIN BI- AND TRIPARTITE LICHENS OF THE GENUS <i>PANNARIA</i> ¹ . <i>Journal of Phycology</i> , 2008, 44, 1049-1059.	2.3	42
187	Diversity and mode of transmission of ammonia-oxidizing archaea in marine sponges. <i>Environmental Microbiology</i> , 2008, 10, 1087-1094.	3.8	127
188	Actinorhodopsins: proteorhodopsin-like gene sequences found predominantly in non-marine environments. <i>Environmental Microbiology</i> , 2008, 10, 1039-1056.	3.8	136
189	Shifts in the relative abundance of ammonia-oxidizing bacteria and archaea across physicochemical gradients in a subterranean estuary. <i>Environmental Microbiology</i> , 2008, 10, 1068-1079.	3.8	333
190	Novel uncultured <i>Chloroflexi</i> dechlorinate perchloroethene to <i>trans</i> -dichloroethene in tidal flat sediments. <i>Environmental Microbiology</i> , 2008, 10, 1557-1570.	3.8	68
191	Microbial community composition in soils of Northern Victoria Land, Antarctica. <i>Environmental Microbiology</i> , 2008, 10, 1713-1724.	3.8	182
192	Diversity of microbes associated with the marine sponge, <i>Haliclona simulans</i> , isolated from Irish waters and identification of polyketide synthase genes from the sponge metagenome. <i>Environmental Microbiology</i> , 2008, 10, 1888-1902.	3.8	93
193	Isolation of novel bacteria, including a candidate division, from geothermal soils in New Zealand. <i>Environmental Microbiology</i> , 2008, 10, 2030-2041.	3.8	169
194	It's all relative: ranking the diversity of aquatic bacterial communities. <i>Environmental Microbiology</i> , 2008, 10, 2200-2210.	3.8	159
195	Enriching plant microbiota for a metagenomic library construction. <i>Environmental Microbiology</i> , 2008, 10, 2684-2691.	3.8	59
196	Diversity and expression of nitrogen fixation genes in bacterial symbionts of marine sponges. <i>Environmental Microbiology</i> , 2008, 10, 2910-2921.	3.8	151
197	The species composition of the human intestinal microbiota differs between particle-associated and liquid phase communities. <i>Environmental Microbiology</i> , 2008, 10, 3275-3283.	3.8	135
198	Global distribution and diversity of coral-associated <i>Archaea</i> and their possible role in the coral holobiont nitrogen cycle. <i>Environmental Microbiology</i> , 2008, 10, 2979-2990.	3.8	137
199	The effects of chronic nitrogen fertilization on alpine tundra soil microbial communities: implications for carbon and nitrogen cycling. <i>Environmental Microbiology</i> , 2008, 10, 3093-3105.	3.8	252
200	Microbial diversity and activity through a permafrost/ground ice core profile from the Canadian high Arctic. <i>Environmental Microbiology</i> , 2008, 10, 3388-3403.	3.8	154

#	ARTICLE	IF	CITATIONS
201	Relative abundance and diversity of ammonia-oxidizing archaea and bacteria in the San Francisco Bay estuary. <i>Environmental Microbiology</i> , 2008, 10, 3002-3016.	3.8	342
202	Microbial activity and soil respiration under nitrogen addition in Alaskan boreal forest. <i>Global Change Biology</i> , 2008, 14, 1156-1168.	9.5	330
203	Warming and drying suppress microbial activity and carbon cycling in boreal forest soils. <i>Global Change Biology</i> , 2008, 14, 2898-2909.	9.5	511
204	Translocation of nitrogen and carbon integrates biotic crust and grass production in desert grassland. <i>Journal of Ecology</i> , 2008, 96, 1076-1085.	4.0	134
205	Prevalence and identification of fungal DNA in the small intestine of healthy dogs and dogs with chronic enteropathies. <i>Veterinary Microbiology</i> , 2008, 132, 379-388.	1.9	48
206	A statistical toolbox for metagenomics: assessing functional diversity in microbial communities. <i>BMC Bioinformatics</i> , 2008, 9, 34.	2.6	94
207	XplorSeq: A software environment for integrated management and phylogenetic analysis of metagenomic sequence data. <i>BMC Bioinformatics</i> , 2008, 9, 420.	2.6	47
208	Diversity and seasonal dynamics of bacterial community in indoor environment. <i>BMC Microbiology</i> , 2008, 8, 56.	3.3	235
209	Heterogeneous archaeal communities in the particle-rich environment of an arctic shelf ecosystem. <i>Journal of Marine Systems</i> , 2008, 74, 774-782.	2.1	61
210	Differences in the composition and diversity of bacterial communities from agricultural and forest soils. <i>Soil Biology and Biochemistry</i> , 2008, 40, 1294-1305.	8.8	105
211	Tag-encoded pyrosequencing analysis of bacterial diversity in a single soil type as affected by management and land use. <i>Soil Biology and Biochemistry</i> , 2008, 40, 2762-2770.	8.8	418
212	Relative impacts of land-use, management intensity and fertilization upon soil microbial community structure in agricultural systems. <i>Soil Biology and Biochemistry</i> , 2008, 40, 2843-2853.	8.8	450
213	Bacterial communities and biogeochemical transformations of iron and sulfur in a high saltmarsh soil profile. <i>Soil Biology and Biochemistry</i> , 2008, 40, 2854-2864.	8.8	17
214	Comparative Analysis of Human Gut Microbiota by Barcoded Pyrosequencing. <i>PLoS ONE</i> , 2008, 3, e2836.	2.5	901
215	Long-term fertilization regimes affect bacterial community structure and diversity of an agricultural soil in northern China. <i>Journal of Soils and Sediments</i> , 2008, 8, 43-50.	3.0	177
216	Molecular bacterial diversity and distribution in waste from a steel plant. <i>Canadian Journal of Microbiology</i> , 2008, 54, 996-1005.	1.7	6
217	Rules of Engagement: Interspecies Interactions that Regulate Microbial Communities. <i>Annual Review of Microbiology</i> , 2008, 62, 375-401.	7.3	362
218	The Pervasive Effects of an Antibiotic on the Human Gut Microbiota, as Revealed by Deep 16S rRNA Sequencing. <i>PLoS Biology</i> , 2008, 6, e280.	5.6	2,013

#	ARTICLE	IF	CITATIONS
219	Extreme spatial and temporal variability of hydrothermal microbial mat communities along the Mariana Island Arc and southern Mariana back-arc system. <i>Journal of Geophysical Research</i> , 2008, 113, .	3.3	64
220	Culture-independent characterization of a novel microbial community at a hydrothermal vent at Brothers volcano, Kermadec arc, New Zealand. <i>Journal of Geophysical Research</i> , 2008, 113, .	3.3	23
221	Evidence of a microbial community associated with rock varnish at Yungay, Atacama Desert, Chile. <i>Journal of Geophysical Research</i> , 2008, 113, .	3.3	58
222	Molecular Methods for Studying Microbial Ecology in the Soil and Rhizosphere. <i>Soil Biology</i> , 2008, , 411-436.	0.8	1
223	A renaissance for the pioneering 16S rRNA gene. <i>Current Opinion in Microbiology</i> , 2008, 11, 442-446.	5.1	418
224	Analysis of a diverse assemblage of diazotrophic bacteria from <i>Spartina alterniflora</i> using DGGE and clone library screening. <i>Journal of Microbiological Methods</i> , 2008, 73, 160-171.	1.6	24
225	Species richness in soil bacterial communities: A proposed approach to overcome sample size bias. <i>Journal of Microbiological Methods</i> , 2008, 75, 86-91.	1.6	32
226	Development of group-specific PCR-DGGE fingerprinting for monitoring structural changes of <i>Thauera</i> spp. in an industrial wastewater treatment plant responding to operational perturbations. <i>Journal of Microbiological Methods</i> , 2008, 75, 231-236.	1.6	38
227	Supplemental programs for enhanced recovery of data from the DOTUR application. <i>Journal of Microbiological Methods</i> , 2008, 75, 572-575.	1.6	4
228	Bacterial Tag-Encoded FLX Amplicon Pyrosequencing (bTEFAP) for Microbiome Studies: Bacterial Diversity in the Ileum of Newly Weaned <i>Salmonella</i> -Infected Pigs. <i>Foodborne Pathogens and Disease</i> , 2008, 5, 459-472.	1.8	373
229	Comparative Molecular Analysis of Endoevaporitic Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2008, 74, 6444-6446.	3.1	48
230	Insight into the microbial community structure of a Norwegian deep-water coral reef environment. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2008, 55, 1554-1563.	1.4	36
231	Developing SSU rDNA metagenomic profiles of aquatic microbial communities for environmental assessments. <i>Ecological Indicators</i> , 2008, 8, 442-453.	6.3	22
232	Diet-Induced Obesity Is Linked to Marked but Reversible Alterations in the Mouse Distal Gut Microbiome. <i>Cell Host and Microbe</i> , 2008, 3, 213-223.	11.0	2,535
233	Prokaryotic diversity of arctic ice shelf microbial mats. <i>Environmental Microbiology</i> , 2008, 10, 950-966.	3.8	71
234	Genetic Diversity of Hydrogen-Producing Bacteria in an Acidophilic Ethanol-H ₂ -Coproducting System, Analyzed Using the [Fe]-Hydrogenase Gene. <i>Applied and Environmental Microbiology</i> , 2008, 74, 1232-1239.	3.1	112
235	Dominance of <i>Acidithiobacillus</i> at ore surface of Zijinshan commercial low-grade copper bioleaching heap. <i>Transactions of Nonferrous Metals Society of China</i> , 2008, 18, 1506-1512.	4.2	6
236	Changes in Bacterial and Archaeal Community Structure and Functional Diversity along a Geochemically Variable Soil Profile. <i>Applied and Environmental Microbiology</i> , 2008, 74, 1620-1633.	3.1	439

#	ARTICLE	IF	CITATIONS
237	Characterization of a Bacterial Community in an Abandoned Semiarid Lead-Zinc Mine Tailing Site. Applied and Environmental Microbiology, 2008, 74, 3899-3907.	3.1	162
238	Highly conserved genes in Geobacter species with expression patterns indicative of acetate limitation. Microbiology (United Kingdom), 2008, 154, 2589-2599.	1.8	22
239	Quantitatively evaluating mistaken clone assignments by RFLP analysis of 16S rRNA genes: a case study. Canadian Journal of Microbiology, 2008, 54, 479-482.	1.7	2
240	Geomicrobiological Changes in Two Ephemeral Desert Playa Lakes in the Western United States. Geomicrobiology Journal, 2008, 25, 250-259.	2.0	6
241	Diversity of Human Vaginal Bacterial Communities and Associations with Clinically Defined Bacterial Vaginosis. Applied and Environmental Microbiology, 2008, 74, 4898-4909.	3.1	230
242	Phylogenetic Comparison of the Methanogenic Communities from an Acidic, Oligotrophic Fen and an Anaerobic Digester Treating Municipal Wastewater Sludge. Applied and Environmental Microbiology, 2008, 74, 6663-6671.	3.1	361
243	Diverse and Distinct Bacterial Communities Induced Biofilm Fouling in Membrane Bioreactors Operated under Different Conditions. Environmental Science & Technology, 2008, 42, 8360-8366.	10.0	104
244	Global Occurrence of Archaeal <i>amoA</i> Genes in Terrestrial Hot Springs. Applied and Environmental Microbiology, 2008, 74, 6417-6426.	3.1	189
245	Changes in microbial community structure in the wake of Hurricanes Katrina and Rita. Environmental Science & Technology, 2008, 42, 9072-9078.	10.0	49
246	Diversity and spatial distribution of sediment ammonia-oxidizing crenarchaeota in response to estuarine and environmental gradients in the Changjiang Estuary and East China Sea. Microbiology (United Kingdom), 2008, 154, 2084-2095.	1.8	146
247	Intestinal TM7 bacterial phylogenies in active inflammatory bowel disease. Journal of Medical Microbiology, 2008, 57, 1569-1576.	1.8	164
248	Impact of assembly, testing and launch operations on the airborne bacterial diversity within a spacecraft assembly facility clean-room. International Journal of Astrobiology, 2008, 7, 223-236.	1.6	19
249	Attached Bacterial Populations Shared by Four Species of Aquatic Angiosperms. Applied and Environmental Microbiology, 2008, 74, 5948-5957.	3.1	120
250	Analysis of Bacterial Communities in Soil by Use of Denaturing Gradient Gel Electrophoresis and Clone Libraries, as Influenced by Different Reverse Primers. Applied and Environmental Microbiology, 2008, 74, 2717-2727.	3.1	78
251	Predominant Role of Host Genetics in Controlling the Composition of Gut Microbiota. PLoS ONE, 2008, 3, e3064.	2.5	263
252	<i>Archaea</i> Dominate the Ammonia-Oxidizing Community in the Rhizosphere of the Freshwater Macrophyte <i>Littorella uniflora</i> . Applied and Environmental Microbiology, 2008, 74, 3279-3283.	3.1	167
253	Abundance and diversity of picocyanobacteria in High Arctic lakes and fjords. Algological Studies (Stuttgart, Germany: 2007), 2008, 126, 209-227.	0.4	21
254	Symbiotic gut microbes modulate human metabolic phenotypes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2117-2122.	7.1	994

#	ARTICLE	IF	CITATIONS
255	Microbial Communities in Contaminated Sediments, Associated with Bioremediation of Uranium to Submicromolar Levels. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3718-3729.	3.1	154
256	Genetic and Functional Variation in Denitrifier Populations along a Short-Term Restoration Chronosequence. <i>Applied and Environmental Microbiology</i> , 2008, 74, 5615-5620.	3.1	71
257	A diversity profile of the human skin microbiota. <i>Genome Research</i> , 2008, 18, 1043-1050.	5.5	818
258	Microbes on mountainsides: Contrasting elevational patterns of bacterial and plant diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 11505-11511.	7.1	758
259	Spatial and Temporal Patterns in the Microbial Diversity of a Meromictic Soda Lake in Washington State. <i>Applied and Environmental Microbiology</i> , 2008, 74, 4877-4888.	3.1	73
260	Effects of Transgenic Hybrid Aspen Overexpressing Polyphenol Oxidase on Rhizosphere Diversity. <i>Applied and Environmental Microbiology</i> , 2008, 74, 5340-5348.	3.1	26
261	Diversity and Distribution of Ecotypes of the Aerobic Anoxygenic Phototrophy Gene <i>pufM</i> in the Delaware Estuary. <i>Applied and Environmental Microbiology</i> , 2008, 74, 4012-4021.	3.1	67
262	Bacterial Community in the Crop of the Hoatzin, a Neotropical Folivorous Flying Bird. <i>Applied and Environmental Microbiology</i> , 2008, 74, 5905-5912.	3.1	61
263	Drop-Size Soda Lakes: Transient Microbial Habitats on a Salt-Secreting Desert Tree. <i>Genetics</i> , 2008, 178, 1615-1622.	2.9	46
264	Gut Microbiota of an Invasive Subcortical Beetle, <i>Agrilus planipennis</i> Fairmaire, Across Various Life Stages. <i>Environmental Entomology</i> , 2008, 37, 1344-1353.	1.4	71
265	Quantifying Microbial Utilization of Petroleum Hydrocarbons in Salt Marsh Sediments by Using the ¹³ C Content of Bacterial rRNA. <i>Applied and Environmental Microbiology</i> , 2008, 74, 1157-1166.	3.1	42
266	Miniprimer PCR, a New Lens for Viewing the Microbial World. <i>Applied and Environmental Microbiology</i> , 2008, 74, 840-849.	3.1	94
267	Variation in Prokaryotic Community Composition as a Function of Resource Availability in Tidal Creek Sediments. <i>Applied and Environmental Microbiology</i> , 2008, 74, 1836-1844.	3.1	15
268	Microbial community diversity and heterotrophic production in a coastal Arctic ecosystem: A stamukhi lake and its source waters. <i>Limnology and Oceanography</i> , 2008, 53, 813-823.	3.1	88
269	Diversity of Uncultured <i>Epsilonproteobacteria</i> from Terrestrial Sulfidic Caves and Springs. <i>Applied and Environmental Microbiology</i> , 2008, 74, 4973-4977.	3.1	42
270	Changes in Bacterial Communities of the Marine Sponge <i>Mycale laxissima</i> on Transfer into Aquaculture. <i>Applied and Environmental Microbiology</i> , 2008, 74, 1209-1222.	3.1	79
271	Pyrosequencing analysis of the Oral Microflora of healthy adults. <i>Journal of Dental Research</i> , 2008, 87, 1016-1020.	5.2	574
272	Monitoring Bacterial Diversity of the Marine Sponge <i>Ircinia strobilina</i> upon Transfer into Aquaculture. <i>Applied and Environmental Microbiology</i> , 2008, 74, 4133-4143.	3.1	82

#	ARTICLE	IF	CITATIONS
273	Characterization of the Archaeal Community in a Minerotrophic Fen and Terminal Restriction Fragment Length Polymorphism-Directed Isolation of a Novel Hydrogenotrophic Methanogen. <i>Applied and Environmental Microbiology</i> , 2008, 74, 2059-2068.	3.1	105
274	Actinobacterial Community Structure in Soils Receiving Long-Term Organic and Inorganic Amendments. <i>Applied and Environmental Microbiology</i> , 2008, 74, 526-530.	3.1	37
275	Comparative Characterization of the Microbial Diversities of an Artificial Microbialite Model and a Natural Stromatolite. <i>Applied and Environmental Microbiology</i> , 2008, 74, 7410-7421.	3.1	72
276	Gut Microbiota of an Invasive Subcortical Beetle, <i>Agrilus planipennis</i> Fairmaire, Across Various Life Stages. <i>Environmental Entomology</i> , 2008, 37, 1344-1353.	1.4	64
277	Subsurface Microbial Diversity in Deep-Granitic-Fracture Water in Colorado. <i>Applied and Environmental Microbiology</i> , 2008, 74, 143-152.	3.1	122
278	Decreased Diversity of the Fecal Microbiome in Recurrent <i>Clostridium difficile</i> Associated Diarrhea. <i>Journal of Infectious Diseases</i> , 2008, 197, 435-438.	4.0	954
279	Water masses and biogeography of picoeukaryote assemblages in a cold hydrographically complex system. <i>Limnology and Oceanography</i> , 2008, 53, 922-935.	3.1	86
280	Atmospheric CO and Hydrogen Uptake and CO Oxidizer Phylogeny for Miyake-jima, Japan Volcanic Deposits. <i>Microbes and Environments</i> , 2008, 23, 299-305.	1.6	35
281	Global Sequencing: A Review of Current Molecular Data and New Methods Available to Assess Microbial Diversity. <i>Microbes and Environments</i> , 2008, 23, 253-268.	1.6	64
282	Denitrification Activity and Relevant Bacteria Revealed by Nitrite Reductase Gene Fragments in Soil of Temperate Mixed Forest. <i>Microbes and Environments</i> , 2008, 23, 337-345.	1.6	52
284	Identification and Characterisation of <i>Pseudomonas</i> 16S Ribosomal DNA from Ileal Biopsies of Children with Crohn's Disease. <i>PLoS ONE</i> , 2008, 3, e3578.	2.5	66
285	Temporal Shifts in Microbial Communities in Nonpregnant African-American Women with and without Bacterial Vaginosis. <i>Interdisciplinary Perspectives on Infectious Diseases</i> , 2008, 2008, 1-9.	1.4	17
286	The Human Microbiome and Infectious Diseases: Beyond Koch. <i>Interdisciplinary Perspectives on Infectious Diseases</i> , 2008, 2008, 1-2.	1.4	11
287	The Human Vaginal Bacterial Biota and Bacterial Vaginosis. <i>Interdisciplinary Perspectives on Infectious Diseases</i> , 2008, 2008, 1-22.	1.4	185
289	Identificarion of contaminant bacteria in cachaÃ§a yeast by 16s rDNA gene sequencing. <i>Scientia Agricola</i> , 2008, 65, 508-515.	1.2	10
290	Impact of Organic and Conventional Management on the Phyllosphere Microbial Ecology of an Apple Crop. <i>Journal of Food Protection</i> , 2009, 72, 2321-2325.	1.7	53
291	Influence of Fecal Sample Storage on Bacterial Community Diversity. <i>Open Microbiology Journal</i> , 2009, 3, 40-46.	0.7	118
292	Assessing the diversity of bacterial communities associated with plants. <i>Brazilian Journal of Microbiology</i> , 2009, 40, 417-432.	2.0	78

#	ARTICLE	IF	CITATIONS
293	A Method for Studying Protistan Diversity Using Massively Parallel Sequencing of V9 Hypervariable Regions of Small-Subunit Ribosomal RNA Genes. PLoS ONE, 2009, 4, e6372.	2.5	707
294	Community Analysis of Chronic Wound Bacteria Using 16S rRNA Gene-Based Pyrosequencing: Impact of Diabetes and Antibiotics on Chronic Wound Microbiota. PLoS ONE, 2009, 4, e6462.	2.5	199
295	A High-Throughput DNA Sequence Aligner for Microbial Ecology Studies. PLoS ONE, 2009, 4, e8230.	2.5	280
296	Compared microbiology of granular sludge under autotrophic, mixotrophic and heterotrophic denitrification conditions. Water Science and Technology, 2009, 59, 1227-1236.	2.5	20
297	Coral-Associated Bacteria and Their Role in the Biogeochemical Cycling of Sulfur. Applied and Environmental Microbiology, 2009, 75, 3492-3501.	3.1	395
298	[FeFe] Hydrogenase Genetic Diversity Provides Insight into Molecular Adaptation in a Saline Microbial Mat Community. Applied and Environmental Microbiology, 2009, 75, 4620-4623.	3.1	48
299	Estimation of Pig Fecal Contamination in a River Catchment by Real-Time PCR Using Two Pig-Specific <i>Bacteroidales</i> 16S rRNA Genetic Markers. Applied and Environmental Microbiology, 2009, 75, 3045-3054.	3.1	171
300	Free-Living Protozoa in Two Unchlorinated Drinking Water Supplies, Identified by Phylogenetic Analysis of 18S rRNA Gene Sequences. Applied and Environmental Microbiology, 2009, 75, 4736-4746.	3.1	76
301	Perturbation of the Small Intestine Microbial Ecology by Streptomycin Alters Pathology in a <i>Salmonella enterica</i> Serovar Typhimurium Murine Model of Infection. Infection and Immunity, 2009, 77, 2691-2702.	2.2	116
302	Effect of inulin on the human gut microbiota: stimulation of <i>Bifidobacterium adolescentis</i> and <i>Faecalibacterium prausnitzii</i> . British Journal of Nutrition, 2009, 101, 541-550.	2.3	675
303	Potentially Pathogenic Bacteria in Shower Water and Air of a Stem Cell Transplant Unit. Applied and Environmental Microbiology, 2009, 75, 5363-5372.	3.1	59
304	An ABC Transporter Mutation Alters Root Exudation of Phytochemicals That Provoke an Overhaul of Natural Soil Microbiota. Plant Physiology, 2009, 151, 2006-2017.	4.8	263
305	Effect of Lake Trophic Status and Rooted Macrophytes on Community Composition and Abundance of Ammonia-Oxidizing Prokaryotes in Freshwater Sediments. Applied and Environmental Microbiology, 2009, 75, 3127-3136.	3.1	151
306	Microbial Populations Responsive to Denitrification-Inducing Conditions in Rice Paddy Soil, as Revealed by Comparative 16S rRNA Gene Analysis. Applied and Environmental Microbiology, 2009, 75, 7070-7078.	3.1	94
307	The radiocarbon signature of microorganisms in the mesopelagic ocean. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6513-6518.	7.1	140
308	Diversity of Bacteria in the Marine Sponge <i>Aplysina fulva</i> in Brazilian Coastal Waters. Applied and Environmental Microbiology, 2009, 75, 3331-3343.	3.1	88
309	CO ₂ Uptake and Fixation by a Thermoacidophilic Microbial Community Attached to Precipitated Sulfur in a Geothermal Spring. Applied and Environmental Microbiology, 2009, 75, 4289-4296.	3.1	60
310	Genetic Diversity and Abundance of Flavobacterial Proteorhodopsin in China Seas. Applied and Environmental Microbiology, 2009, 75, 529-533.	3.1	15

#	ARTICLE	IF	CITATIONS
311	High-Throughput Quantitative Analysis of the Human Intestinal Microbiota with a Phylogenetic Microarray. Applied and Environmental Microbiology, 2009, 75, 3572-3579.	3.1	93
312	RAML: a tool for identification and characterization of phylogenetic clusters in microbial communities. Bioinformatics, 2009, 25, 736-742.	4.1	54
313	Impact of an 8-Year-Old Transgenic Poplar Plantation on the Ectomycorrhizal Fungal Community. Applied and Environmental Microbiology, 2009, 75, 7527-7536.	3.1	41
314	Bacteroidales Diversity in Ring-Billed Gulls (<i>Larus delawarensis</i>) Residing at Lake Michigan Beaches. Applied and Environmental Microbiology, 2009, 75, 1525-1533.	3.1	31
315	Molecular diversity of visual pigments in Stomatopoda (Crustacea). Visual Neuroscience, 2009, 26, 255-265.	1.0	55
316	Diversity of <i>Frankia</i> Populations in Root Nodules of Geographically Isolated Arizona Alder Trees in Central Arizona (United States). Applied and Environmental Microbiology, 2009, 75, 6913-6918.	3.1	27
317	Molecular Comparison of Bacterial Communities within Iron-Containing Flocculent Mats Associated with Submarine Volcanoes along the Kermadec Arc. Applied and Environmental Microbiology, 2009, 75, 1650-1657.	3.1	49
319	Microbial Diversity in Endostromatolites (<i>cf.</i> Fissure Calcretes) and in the Surrounding Permafrost Landscape, Houghton Impact Structure Region, Devon Island, Canada. Astrobiology, 2009, 9, 807-822.	3.0	17
320	Investigating repetitively matching short sequencing reads: The enigmatic nature of H3K9me3. Epigenetics, 2009, 4, 476-486.	2.7	11
321	Statistical Methods for Detecting Differentially Abundant Features in Clinical Metagenomic Samples. PLoS Computational Biology, 2009, 5, e1000352.	3.2	1,495
322	Novel Alkane Hydroxylase Gene (<i>alkB</i>) Diversity in Sediments Associated with Hydrocarbon Seeps in the Timor Sea, Australia. Applied and Environmental Microbiology, 2009, 75, 7391-7398.	3.1	80
323	Assessment of the Diversity, Abundance, and Ecological Distribution of Members of Candidate Division SR1 Reveals a High Level of Phylogenetic Diversity but Limited Morphotypic Diversity. Applied and Environmental Microbiology, 2009, 75, 4139-4148.	3.1	46
324	Diets Enriched in Oat Bran or Wheat Bran Temporally and Differentially Alter the Composition of the Fecal Community of Rats. Journal of Nutrition, 2009, 139, 2024-2031.	2.9	61
325	New Insights into the Diversity of Marine Picoeukaryotes. PLoS ONE, 2009, 4, e7143.	2.5	221
326	Protistan diversity in suboxic and anoxic waters of the Gotland Deep (Baltic Sea) as revealed by 18S rRNA clone libraries. Aquatic Microbial Ecology, 2009, 55, 267-284.	1.8	77
327	Modern Subsurface Bacteria in Pristine 2.7 Ga-Old Fossil Stromatolite Drillcore Samples from the Fortescue Group, Western Australia. PLoS ONE, 2009, 4, e5298.	2.5	23
328	Extensive Phylogenetic Analysis of a Soil Bacterial Community Illustrates Extreme Taxon Evenness and the Effects of Amplicon Length, Degree of Coverage, and DNA Fractionation on Classification and Ecological Parameters. Applied and Environmental Microbiology, 2009, 75, 668-675.	3.1	56
329	Evaluation of Swine-Specific PCR Assays Used for Fecal Source Tracking and Analysis of Molecular Diversity of Swine-Specific <i>Bacteroidales</i> Populations. Applied and Environmental Microbiology, 2009, 75, 5787-5796.	3.1	43

#	ARTICLE	IF	CITATIONS
330	Comprehensive Census of Bacteria in Clean Rooms by Using DNA Microarray and Cloning Methods. Applied and Environmental Microbiology, 2009, 75, 6559-6567.	3.1	80
331	Alteration of the Ileal Microbiota of Weanling Piglets by the Growth-Promoting Antibiotic Chlortetracycline. Applied and Environmental Microbiology, 2009, 75, 5489-5495.	3.1	88
332	Long-Term Monensin Supplementation Does Not Significantly Affect the Quantity or Diversity of Methanogens in the Rumen of the Lactating Dairy Cow. Applied and Environmental Microbiology, 2009, 75, 374-380.	3.1	127
333	Selection of <i>Sphingomonadaceae</i> at the Base of <i>Laccaria proxima</i> and <i>Russula exalbicans</i> Fruiting Bodies. Applied and Environmental Microbiology, 2009, 75, 1979-1989.	3.1	47
334	Defining DNA-Based Operational Taxonomic Units for Microbial-Eukaryote Ecology. Applied and Environmental Microbiology, 2009, 75, 5797-5808.	3.1	185
335	Assessment of Microbial Communities by Graph Partitioning in a Study of Soil Fungi in Two Alpine Meadows. Applied and Environmental Microbiology, 2009, 75, 5863-5870.	3.1	21
336	Antibiotic Treatment of <i>Clostridium difficile</i> Carrier Mice Triggers a Supershedder State, Spore-Mediated Transmission, and Severe Disease in Immunocompromised Hosts. Infection and Immunity, 2009, 77, 3661-3669.	2.2	315
337	Diverse and Novel <i>nifH</i> and <i>nifH</i> -Like Gene Sequences in the Deep-Sea Methane Seep Sediments of the Okhotsk Sea. Applied and Environmental Microbiology, 2009, 75, 2238-2245.	3.1	61
338	A Vaccine against Rumen Methanogens Can Alter the Composition of Archaeal Populations. Applied and Environmental Microbiology, 2009, 75, 1860-1866.	3.1	114
339	A Cryptoendolithic Community in Volcanic Glass. Astrobiology, 2009, 9, 369-381.	3.0	55
340	Molecular phylogenetic diversity of bacteria associated with soil of the savanna-like Cerrado vegetation. Microbiological Research, 2009, 164, 59-70.	5.3	52
341	Novel methanotroph diversity evidenced by molecular characterization of particulate methane monooxygenase A (pmoA) genes in a biogas reactor. Microbiological Research, 2009, 164, 536-544.	5.3	16
342	Vertical distribution and phylogenetic composition of bacteria in the Eastern Tropical North Pacific Ocean. Microbiological Research, 2009, 164, 624-633.	5.3	18
343	Diversity and evolutionary origins of fungi associated with seeds of a neotropical pioneer tree: a case study for analysing fungal environmental samples. Mycological Research, 2009, 113, 432-449.	2.5	131
344	Photoacceleration of plant litter decomposition in an arid environment. Soil Biology and Biochemistry, 2009, 41, 1433-1441.	8.8	127
345	Differences in the activity and bacterial community structure of drained grassland and forest peat soils. Soil Biology and Biochemistry, 2009, 41, 1874-1881.	8.8	48
346	Temporal shifts in diversity and quantity of nirS and nirK in a rice paddy field soil. Soil Biology and Biochemistry, 2009, 41, 2044-2051.	8.8	168
347	Molecular diversity of Bacteroides spp. in human fecal microbiota as determined by group-specific 16S rRNA gene clone library analysis. Systematic and Applied Microbiology, 2009, 32, 193-200.	2.8	19

#	ARTICLE	IF	CITATIONS
348	A supervised learning approach for taxonomic classification of core-photosystem-II genes and transcripts in the marine environment. BMC Genomics, 2009, 10, 229.	2.8	17
349	Zooplankton diversity analysis through single-gene sequencing of a community sample. BMC Genomics, 2009, 10, 438.	2.8	62
350	Defining the healthy "core microbiome" of oral microbial communities. BMC Microbiology, 2009, 9, 259.	3.3	989
351	Sequence analysis of percent G+C fraction libraries of human faecal bacterial DNA reveals a high number of Actinobacteria. BMC Microbiology, 2009, 9, 68.	3.3	57
352	Bacterial diversity analysis of larvae and adult midgut microflora using culture-dependent and culture-independent methods in lab-reared and field-collected Anopheles stephensi-an Asian malarial vector. BMC Microbiology, 2009, 9, 96.	3.3	287
353	A new procedure to optimize the selection of groups in a classification tree: Applications for ecological data. Ecological Modelling, 2009, 220, 451-461.	2.5	9
354	In-feed administered sub-therapeutic chlortetracycline alters community composition and structure but not the abundance of community resistance determinants in the fecal flora of the rat. Anaerobe, 2009, 15, 145-154.	2.1	15
355	Isolation and characterization of cellulose-degrading bacteria from the deep subsurface of the Homestake gold mine, Lead, South Dakota, USA. Journal of Industrial Microbiology and Biotechnology, 2009, 36, 585-598.	3.0	117
356	Bacterial diversity in the snow over Tibetan Plateau Glaciers. Extremophiles, 2009, 13, 411-423.	2.3	114
357	Microbiology and geochemistry of great boiling and mud hot springs in the United States Great Basin. Extremophiles, 2009, 13, 447-459.	2.3	157
358	Changes in the bacterial populations of the highly alkaline saline soil of the former lake Texcoco (Mexico) following flooding. Extremophiles, 2009, 13, 609-621.	2.3	106
359	Diversity of Actinobacterial community in saline sediments from Yunnan and Xinjiang, China. Extremophiles, 2009, 13, 623-632.	2.3	32
360	Characterization of the intestinal microbiota of two Antarctic notothenioid fish species. Extremophiles, 2009, 13, 679-685.	2.3	130
361	Microbial activity and diversity during extreme freeze-thaw cycles in periglacial soils, 5400m elevation, Cordillera Vilcanota, Peru. Extremophiles, 2009, 13, 807-816.	2.3	71
362	Study of the diversity of culturable actinomycetes in the North Pacific and Caribbean coasts of Costa Rica. Antonie Van Leeuwenhoek, 2009, 96, 71-78.	1.7	18
363	Characterisation of the effect of a simulated hydrocarbon spill on diazotrophs in mangrove sediment mesocosm. Antonie Van Leeuwenhoek, 2009, 96, 343-354.	1.7	30
364	Integrating engineering design improvements with exoelectrogen enrichment process to increase power output from microbial fuel cells. Journal of Power Sources, 2009, 191, 520-527.	7.8	86
365	Seasonal changes in bacterial diversity in the Salton Sea. Hydrobiologia, 2009, 632, 49-64.	2.0	46

#	ARTICLE	IF	CITATIONS
366	Ecology, DNA, and the Future of Microbial Source Tracking. <i>Water, Air, and Soil Pollution</i> , 2009, 201, 219-232.	2.4	4
367	Extracellular hydrolytic enzyme screening of culturable heterotrophic bacteria from deep-sea sediments of the Southern Okinawa Trough. <i>World Journal of Microbiology and Biotechnology</i> , 2009, 25, 71-79.	3.6	62
368	Fine-scale vertical distribution of bacteria in the East Pacific deep-sea sediments determined via 16S rRNA gene T-RFLP and clone library analyses. <i>World Journal of Microbiology and Biotechnology</i> , 2009, 25, 179-188.	3.6	26
369	Could nested PCR be applicable for the study of microbial diversity?. <i>World Journal of Microbiology and Biotechnology</i> , 2009, 25, 1447-1452.	3.6	14
370	Diversity of microorganisms in solar salterns of Tamil Nadu, India. <i>World Journal of Microbiology and Biotechnology</i> , 2009, 25, 1007-1017.	3.6	32
371	Phylogenetic profiling of bacterial community from two intimately located sites in Balramgari, North-East coast of India. <i>Indian Journal of Microbiology</i> , 2009, 49, 169-187.	2.7	2
372	Towards bioremediation of toxic unresolved complex mixtures of hydrocarbons: identification of bacteria capable of rapid degradation of alkyltetralins. <i>Journal of Soils and Sediments</i> , 2009, 9, 129-136.	3.0	15
373	Abundance and diversity of snow bacteria in two glaciers at the Tibetan Plateau. <i>Frontiers of Earth Science</i> , 2009, 3, 80-90.	0.5	5
374	Molecular analysis of prokaryotic diversity in the deep subsurface of the former Homestake gold mine, South Dakota, USA. <i>Journal of Microbiology</i> , 2009, 47, 371-384.	2.8	56
375	Functional shifts in unvegetated, perhumid, recently-deglaciated soils do not correlate with shifts in soil bacterial community composition. <i>Journal of Microbiology</i> , 2009, 47, 673-681.	2.8	70
376	Bacterial, archaeal and eukaryotic diversity in Arctic sediment as revealed by 16S rRNA and 18S rRNA gene clone libraries analysis. <i>Polar Biology</i> , 2009, 32, 93-103.	1.2	65
377	Diverse communities of active Bacteria and Archaea along oxygen gradients in coral reef sediments. <i>Coral Reefs</i> , 2009, 28, 15-26.	2.2	30
378	Reef-associated crustacean fauna: biodiversity estimates using semi-quantitative sampling and DNA barcoding. <i>Coral Reefs</i> , 2009, 28, 977-986.	2.2	106
379	Genetic diversity of aerobic anoxygenic photosynthetic bacteria in open ocean surface waters and upper twilight zones. <i>Marine Biology</i> , 2009, 156, 425-437.	1.5	11
380	Oxygen and Guanine/Cytosine Profiles in Marine Environments. <i>Journal of Molecular Evolution</i> , 2009, 69, 203-206.	1.8	23
381	Diversity of Aerobic Methanotrophic Bacteria in a Permafrost Active Layer Soil of the Lena Delta, Siberia. <i>Microbial Ecology</i> , 2009, 57, 25-35.	2.8	96
382	Diversity and Distribution of Sediment NirS-Encoding Bacterial Assemblages in Response to Environmental Gradients in the Eutrophied Jiaozhou Bay, China. <i>Microbial Ecology</i> , 2009, 58, 161-169.	2.8	82
383	The Diverse Bacterial Community in Intertidal, Anaerobic Sediments at Sapelo Island, Georgia. <i>Microbial Ecology</i> , 2009, 58, 244-261.	2.8	37

#	ARTICLE	IF	CITATIONS
384	Denitrifying Bacterial Community Composition Changes Associated with Stages of Denitrification in Oxygen Minimum Zones. <i>Microbial Ecology</i> , 2009, 58, 350-362.	2.8	89
385	Archaeal Diversity at the Great Salt Plains of Oklahoma Described by Cultivation and Molecular Analyses. <i>Microbial Ecology</i> , 2009, 58, 519-528.	2.8	37
386	Bacterial Community Composition in Brazilian Anthrosols and Adjacent Soils Characterized Using Culturing and Molecular Identification. <i>Microbial Ecology</i> , 2009, 58, 23-35.	2.8	256
387	Bacterial Community and Nitrogen Fixation in the Red Turpentine Beetle, <i>Dendroctonus valens</i> LeConte (Coleoptera: Curculionidae: Scolytinae). <i>Microbial Ecology</i> , 2009, 58, 879-891.	2.8	144
388	Microbial Community Response to Seawater Amendment in Low-Salinity Tidal Sediments. <i>Microbial Ecology</i> , 2009, 58, 558-568.	2.8	70
389	Development of a Bacterial Cell Enrichment Method and its Application to the Community Analysis in Soybean Stems. <i>Microbial Ecology</i> , 2009, 58, 703-714.	2.8	108
390	Enhancement of the microbial community biomass and diversity during air sparging bioremediation of a soil highly contaminated with kerosene and BTEX. <i>Applied Microbiology and Biotechnology</i> , 2009, 82, 565-577.	3.6	52
391	Molecular identification and dynamics of microbial communities in reactor treating organic household waste. <i>Applied Microbiology and Biotechnology</i> , 2009, 84, 777-789.	3.6	73
392	Diversity of Bacteria and Fungi in Aerosols During Screening in a Green Waste Composting Plant. <i>Current Microbiology</i> , 2009, 59, 326-335.	2.2	39
393	Microbial community analysis reveals high level phylogenetic alterations in the overall gastrointestinal microbiota of diarrhoea-predominant irritable bowel syndrome sufferers. <i>BMC Gastroenterology</i> , 2009, 9, 95.	2.0	252
394	Environmentally-acquired bacteria influence microbial diversity and natural innate immune responses at gut surfaces. <i>BMC Biology</i> , 2009, 7, 79.	3.8	228
395	Controlling accumulation of fermentation inhibitors in biorefinery recycle water using microbial fuel cells. <i>Biotechnology for Biofuels</i> , 2009, 2, 7.	6.2	72
396	The structure of the bacterial and archaeal community in a biogas digester as revealed by denaturing gradient gel electrophoresis and 16S rDNA sequencing analysis. <i>Journal of Applied Microbiology</i> , 2009, 106, 952-966.	3.1	130
397	Bacterial diversity associated with the Brazilian endemic reef coral <i>Mussismilia braziliensis</i> . <i>Journal of Applied Microbiology</i> , 2009, 106, 1378-1387.	3.1	60
398	Diversity and spatial distribution of <i>amoA</i> -encoding archaea in the deep-sea sediments of the tropical West Pacific Continental Margin. <i>Journal of Applied Microbiology</i> , 2009, 106, 1482-1493.	3.1	52
399	Waiting for fungi: the ectomycorrhizal invasion of lowland heathlands. <i>Journal of Ecology</i> , 2009, 97, 950-963.	4.0	105
400	Biodiversity in microbial communities: system scale patterns and mechanisms. <i>Molecular Ecology</i> , 2009, 18, 1455-1462.	3.9	41
401	Hidden <i>Wolbachia</i> diversity in field populations of the European cherry fruit fly, <i>Rhagoletis cerasi</i> (Diptera, Tephritidae). <i>Molecular Ecology</i> , 2009, 18, 3816-3830.	3.9	96

#	ARTICLE	IF	CITATIONS
402	Diversity rankings among bacterial lineages in soil. ISME Journal, 2009, 3, 305-313.	9.8	100
403	Determining the specific microbial populations and their spatial distribution within the stromatolite ecosystem of Shark Bay. ISME Journal, 2009, 3, 383-396.	9.8	125
404	Colorful microdiversity of <i>Synechococcus</i> strains (picocyanobacteria) isolated from the Baltic Sea. ISME Journal, 2009, 3, 397-408.	9.8	115
405	Bacterial diversity and White Plague Disease-associated community changes in the Caribbean coral <i>Montastraea faveolata</i> . ISME Journal, 2009, 3, 512-521.	9.8	364
406	Bacterial community succession during <i>in situ</i> uranium bioremediation: spatial similarities along controlled flow paths. ISME Journal, 2009, 3, 47-64.	9.8	90
407	Evidence for the functional significance of diazotroph community structure in soil. ISME Journal, 2009, 3, 124-136.	9.8	224
408	Towards the definition of a core of microorganisms involved in anaerobic digestion of sludge. ISME Journal, 2009, 3, 700-714.	9.8	728
409	Unique archaeal assemblages in the Arctic Ocean unveiled by massively parallel tag sequencing. ISME Journal, 2009, 3, 860-869.	9.8	163
410	Biogeography of two cold-adapted genera: <i>Psychrobacter</i> and <i>Exiguobacterium</i> . ISME Journal, 2009, 3, 658-665.	9.8	78
411	Characterization of the complex bacterial communities colonizing biliary stents reveals a host-dependent diversity. ISME Journal, 2009, 3, 797-807.	9.8	21
412	16S rRNA gene-based analysis of fecal microbiota from preterm infants with and without necrotizing enterocolitis. ISME Journal, 2009, 3, 944-954.	9.8	508
413	Rumen-like methanogens identified from the crop of the folivorous South American bird, the hoatzin (<i>Opisthocomus hoazin</i>). ISME Journal, 2009, 3, 1120-1126.	9.8	52
414	Abundance, composition, diversity and novelty of soil <i>Proteobacteria</i> . ISME Journal, 2009, 3, 992-1000.	9.8	409
415	Changes in land use alter the structure of bacterial communities in Western Amazon soils. ISME Journal, 2009, 3, 1004-1011.	9.8	342
416	Abundant transposases encoded by the metagenome of a hydrothermal chimney biofilm. ISME Journal, 2009, 3, 1420-1424.	9.8	112
417	Matriptase-Deficient Mice Exhibit Ichthyotic Skin with a Selective Shift in Skin Microbiota. Journal of Investigative Dermatology, 2009, 129, 2435-2442.	0.7	60
418	Accurate determination of microbial diversity from 454 pyrosequencing data. Nature Methods, 2009, 6, 639-641.	19.0	895
419	PCR-Based Diversity Estimates of Artificial and Environmental 18S rRNA Gene Libraries. Journal of Eukaryotic Microbiology, 2009, 56, 174-181.	1.7	77

#	ARTICLE	IF	CITATIONS
420	Changes in soil <i>Acidobacteria</i> communities after 2,4,6-trinitrotoluene contamination. FEMS Microbiology Letters, 2009, 296, 159-166.	1.8	38
421	Haloarchaeal assimilatory nitrate-reducing communities from a saline alkaline soil. FEMS Microbiology Letters, 2009, 298, 56-66.	1.8	11
422	Integrative approaches for assessing the ecological sustainability of <i>in situ</i> bioremediation. FEMS Microbiology Reviews, 2009, 33, 324-375.	8.6	142
423	Spatial comparison of total vs. active bacterial populations by coupling genetic fingerprinting and clone library analyses in the NW Mediterranean Sea. FEMS Microbiology Ecology, 2009, 67, 30-42.	2.7	27
424	Temporal and spatial variability in nearshore bacterioplankton communities of Lake Michigan. FEMS Microbiology Ecology, 2009, 67, 511-522.	2.7	86
425	Microbial diversity in sediments associated with a shallow methane seep in the tropical Timor Sea of Australia reveals a novel aerobic methanotroph diversity. FEMS Microbiology Ecology, 2009, 68, 142-151.	2.7	39
426	Molecular characterization of bacteria associated with the trophosome and the tube of <i>Lamellibrachia</i> sp., a siboglinid annelid from cold seeps in the eastern Mediterranean. FEMS Microbiology Ecology, 2009, 69, 395-409.	2.7	56
427	Termination of belowground C allocation by trees alters soil fungal and bacterial communities in a boreal forest. FEMS Microbiology Ecology, 2009, 70, 151-162.	2.7	117
428	Seasonal and spatial variations in microbial community structure and diversity in the acid stream draining across an ongoing surface mining site. FEMS Microbiology Ecology, 2009, 70, 277-285.	2.7	49
429	Bacterial diversity of water and sediment in the Changjiang estuary and coastal area of the East China Sea. FEMS Microbiology Ecology, 2009, 70, 236-248.	2.7	185
430	Pan-oceanic distribution of new highly diverse clades of deep-sea diplomonads. Environmental Microbiology, 2009, 11, 47-55.	3.8	82
431	The diversity and abundance of bacteria inhabiting seafloor lavas positively correlate with rock alteration. Environmental Microbiology, 2009, 11, 86-98.	3.8	100
432	Microbial eukaryotes in the hypersaline anoxic L'Atalante deep-sea basin. Environmental Microbiology, 2009, 11, 360-381.	3.8	134
433	Taxonomic resolution, ecotypes and the biogeography of <i>Prochlorococcus</i> . Environmental Microbiology, 2009, 11, 823-832.	3.8	188
434	Insights into networks of functional microbes catalysing methanization of cellulose under mesophilic conditions. Environmental Microbiology, 2009, 11, 889-904.	3.8	105
435	The phylogeography of Adelie penguin faecal flora. Environmental Microbiology, 2009, 11, 577-588.	3.8	69
436	Archaeal diversity and a gene for ammonia oxidation are coupled to oceanic circulation. Environmental Microbiology, 2009, 11, 971-980.	3.8	77
437	New <i>alk</i> genes detected in Antarctic marine sediments. Environmental Microbiology, 2009, 11, 669-673.	3.8	63

#	ARTICLE	IF	CITATIONS
438	Vertical structure of archaeal communities and the distribution of ammonia monooxygenase A gene variants in two meromictic High Arctic lakes. <i>Environmental Microbiology</i> , 2009, 11, 687-699.	3.8	97
439	Biogeographical distribution of diverse anaerobic ammonium oxidizing (anammox) bacteria in Cape Fear River Estuary. <i>Environmental Microbiology</i> , 2009, 11, 1194-1207.	3.8	199
440	Effect of PCR amplicon size on assessments of clone library microbial diversity and community structure. <i>Environmental Microbiology</i> , 2009, 11, 1292-1302.	3.8	133
441	Microbial biodiversity of thermophilic communities in hot mineral soils of Tramway Ridge, Mount Erebus, Antarctica. <i>Environmental Microbiology</i> , 2009, 11, 715-728.	3.8	97
442	An interlaboratory comparison of 16S rRNA gene-based terminal restriction fragment length polymorphism and sequencing methods for assessing microbial diversity of seafloor basalts. <i>Environmental Microbiology</i> , 2009, 11, 1728-1735.	3.8	32
443	Diversity and abundance of freshwater <i>Actinobacteria</i> along environmental gradients in the brackish northern Baltic Sea. <i>Environmental Microbiology</i> , 2009, 11, 2042-2054.	3.8	73
444	Microbial communities in iron-silica-rich microbial mats at deep-sea hydrothermal fields of the Southern Mariana Trough. <i>Environmental Microbiology</i> , 2009, 11, 2094-2111.	3.8	124
445	The role of pH in determining the species composition of the human colonic microbiota. <i>Environmental Microbiology</i> , 2009, 11, 2112-2122.	3.8	587
446	Metagenomic approach studying the taxonomic and functional diversity of the bacterial community in a mesotrophic lake (Lac du Bourget – France). <i>Environmental Microbiology</i> , 2009, 11, 2412-2424.	3.8	135
447	Archaeal communities associated with shallow to deep subseafloor sediments of the New Caledonia Basin. <i>Environmental Microbiology</i> , 2009, 11, 2446-2462.	3.8	49
448	Evidence for structuring of bacterial community composition by organic carbon source in temperate lakes. <i>Environmental Microbiology</i> , 2009, 11, 2463-2472.	3.8	123
449	Short-term microbial and physicochemical variability in low-temperature hydrothermal fluids near 5Â°S on the Mid-Atlantic Ridge. <i>Environmental Microbiology</i> , 2009, 11, 2526-2541.	3.8	44
450	Towards the human intestinal microbiota phylogenetic core. <i>Environmental Microbiology</i> , 2009, 11, 2574-2584.	3.8	773
451	Microbial diversity in modern marine stromatolites, Highborne Cay, Bahamas. <i>Environmental Microbiology</i> , 2009, 11, 2710-2719.	3.8	95
452	Bacterial, archaeal and eukaryal community structures throughout soil horizons of harvested and naturally disturbed forest stands. <i>Environmental Microbiology</i> , 2009, 11, 3045-3062.	3.8	184
453	The seasonal structure of microbial communities in the Western English Channel. <i>Environmental Microbiology</i> , 2009, 11, 3132-3139.	3.8	384
454	Eukaryotic diversity and phylogeny using small- and large-subunit ribosomal RNA genes from environmental samples. <i>Environmental Microbiology</i> , 2009, 11, 3179-3188.	3.8	64
455	Light-dependent growth and proteorhodopsin expression by <i>Flavobacteria</i> and SAR11 in experiments with Delaware coastal waters. <i>Environmental Microbiology</i> , 2009, 11, 3201-3209.	3.8	62

#	ARTICLE	IF	CITATIONS
456	Abundance of <i>Zetaproteobacteria</i> within crustal fluids in back-arc hydrothermal fields of the Southern Mariana Trough. <i>Environmental Microbiology</i> , 2009, 11, 3210-3222.	3.8	93
457	Phylogenetic diversity of transition and anoxic zone bacterial communities within a near-shore anoxic basin: Nitinat Lake. <i>Environmental Microbiology</i> , 2009, 11, 3233-3251.	3.8	26
458	Deep sequencing reveals exceptional diversity and modes of transmission for bacterial sponge symbionts. <i>Environmental Microbiology</i> , 2010, 12, 2070-2082.	3.8	394
459	Disclosing arbuscular mycorrhizal fungal biodiversity in soil through a land-use gradient using a pyrosequencing approach. <i>Environmental Microbiology</i> , 2010, 12, 2165-2179.	3.8	313
460	Metabolic responses of novel cellulolytic and saccharolytic agricultural soil <i>Bacteria</i> to oxygen. <i>Environmental Microbiology</i> , 2010, 12, 845-861.	3.8	138
461	Biogeography of wetland rice methanotrophs. <i>Environmental Microbiology</i> , 2010, 12, 862-872.	3.8	92
462	Biogeochemical changes induced in uranium mining waste pile samples by uranyl nitrate treatments under anaerobic conditions. <i>Geobiology</i> , 2009, 7, 282-294.	2.4	22
463	Analyses of microbial consortia in the starter of Fen Liquor. <i>Letters in Applied Microbiology</i> , 2009, 48, 478-485.	2.2	51
464	Molecular detection of nifH gene-containing <i>Paenibacillus</i> in the rhizosphere of sorghum (<i>Sorghum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.2	12
465	Identification and phylogeny of eukaryotic 18S rDNA phylotypes detected in chlorinated finished drinking water samples from three Parisian surface water treatment plants. <i>Letters in Applied Microbiology</i> , 2009, 49, 589-595.	2.2	30
466	Aromatic hydrocarbon degradation genes from chronically polluted Subantarctic marine sediments. <i>Letters in Applied Microbiology</i> , 2009, 49, 602-608.	2.2	38
467	Bacterial community structure change during pyrite bioleaching process: Effect of pH and aeration. <i>Hydrometallurgy</i> , 2009, 95, 267-272.	4.3	26
468	Microbial community variation and functions to excess sludge reduction in a novel gravel contact oxidation reactor. <i>Journal of Hazardous Materials</i> , 2009, 165, 1083-1090.	12.4	15
469	Improving power production in acetate-fed microbial fuel cells via enrichment of exoelectrogenic organisms in flow-through systems. <i>Biochemical Engineering Journal</i> , 2009, 48, 71-80.	3.6	110
470	Electricity generation using chocolate industry wastewater and its treatment in activated sludge based microbial fuel cell and analysis of developed microbial community in the anode chamber. <i>Bioresource Technology</i> , 2009, 100, 5132-5139.	9.6	242
471	Molecular Studies on the Microbial Diversity Associated with Mining-Impacted Coeur d'Alene River Sediments. <i>Microbial Ecology</i> , 2009, 58, 129-139.	2.8	24
472	Prokaryotic Community Structure and Sulfate Reducer Activity in Water from High-Temperature Oil Reservoirs with and without Nitrate Treatment. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7086-7096.	3.1	177
473	Dominance of a clonal green sulfur bacterial population in a stratified lake. <i>FEMS Microbiology Ecology</i> , 2009, 70, 30-41.	2.7	54

#	ARTICLE	IF	CITATIONS
474	A nonparametric lower bound for the number of species shared by multiple communities. Journal of Agricultural, Biological, and Environmental Statistics, 2009, 14, 452-468.	1.4	16
475	Bacterial and archaeal communities in the surface sediment from the northern slope of the South China Sea. Journal of Zhejiang University: Science B, 2009, 10, 890-901.	2.8	24
476	Fumarole-Supported Islands of Biodiversity within a Hyperarid, High-Elevation Landscape on Socompa Volcano, Puna de Atacama, Andes. Applied and Environmental Microbiology, 2009, 75, 735-747.	3.1	133
477	Topographical and Temporal Diversity of the Human Skin Microbiome. Science, 2009, 324, 1190-1192.	12.6	2,280
478	Human gut microbiota in obesity and after gastric bypass. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2365-2370.	7.1	1,641
479	The Role of Biofilms in the Sedimentology of Actively Forming Gypsum Deposits at Guerrero Negro, Mexico. Astrobiology, 2009, 9, 875-893.	3.0	31
480	Pyrosequencing of the Chaperonin-60 Universal Target as a Tool for Determining Microbial Community Composition. Applied and Environmental Microbiology, 2009, 75, 2889-2898.	3.1	102
481	Assessment of the Microbial Ecology of Ruminal Methanogens in Cattle with Different Feed Efficiencies. Applied and Environmental Microbiology, 2009, 75, 6524-6533.	3.1	280
482	Biocorrosive Thermophilic Microbial Communities in Alaskan North Slope Oil Facilities. Environmental Science & Technology, 2009, 43, 7977-7984.	10.0	195
483	Tracking the influence of long-term chromium pollution on soil bacterial community structures by comparative analyses of 16S rRNA gene phylotypes. Research in Microbiology, 2009, 160, 1-9.	2.1	120
484	Microbial community dynamics in replicate membrane bioreactors â€“ Natural reproducible fluctuations. Water Research, 2009, 43, 842-852.	11.3	65
485	Memory and learning behavior in mice is temporally associated with diet-induced alterations in gut bacteria. Physiology and Behavior, 2009, 96, 557-567.	2.1	215
486	Metagenomic study of the oral microbiota by Illumina high-throughput sequencing. Journal of Microbiological Methods, 2009, 79, 266-271.	1.6	289
487	Comparison of bacterial communities in fish farm sediments along an organic enrichment gradient. Aquaculture, 2009, 287, 107-113.	3.5	71
488	Microbial Biogeography of Six Salt Lakes in Inner Mongolia, China, and a Salt Lake in Argentina. Applied and Environmental Microbiology, 2009, 75, 5750-5760.	3.1	119
489	Community proteogenomics reveals insights into the physiology of phyllosphere bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16428-16433.	7.1	774
490	Microbial community profiling for human microbiome projects: Tools, techniques, and challenges. Genome Research, 2009, 19, 1141-1152.	5.5	805
491	The occupant as a source of house dust bacteria. Journal of Allergy and Clinical Immunology, 2009, 124, 834-840.e47.	2.9	180

#	ARTICLE	IF	CITATIONS
492	ESPRIT: estimating species richness using large collections of 16S rRNA pyrosequences. <i>Nucleic Acids Research</i> , 2009, 37, e76-e76.	14.5	232
493	Metagenomic Pyrosequencing and Microbial Identification. <i>Clinical Chemistry</i> , 2009, 55, 856-866.	3.2	459
494	Phylogenetic Diversity and Metabolic Potential Revealed in a Glacier Ice Metagenome. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7519-7526.	3.1	213
495	Response of Archaeal Community Structure to Environmental Changes in Lakes on the Tibetan Plateau, Northwestern China. <i>Geomicrobiology Journal</i> , 2009, 26, 289-297.	2.0	41
496	Influence of Species Specificity and Other Factors on Bacteria Associated with the Coral <i>Stylophora pistillata</i> in Taiwan. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7797-7806.	3.1	73
497	Reproducible Community Dynamics of the Gastrointestinal Microbiota following Antibiotic Perturbation. <i>Infection and Immunity</i> , 2009, 77, 2367-2375.	2.2	489
498	Effect of Host Tree Species on Cellulase Activity and Bacterial Community Composition in the Gut of Larval Asian Longhorned Beetle. <i>Environmental Entomology</i> , 2009, 38, 686-699.	1.4	64
499	Microcosm-based Study of the Attenuation of an Acid Mine Drainage-Impacted Site through Biological Sulfate and Iron Reduction. <i>Geomicrobiology Journal</i> , 2009, 26, 9-20.	2.0	18
500	Low Taxon Richness of Bacterioplankton in High-Altitude Lakes of the Eastern Tibetan Plateau, with a Predominance of <i>Bacteroidetes</i> and <i>Synechococcus</i> spp. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7017-7025.	3.1	100
501	Introducing mothur: Open-Source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7537-7541.	3.1	18,390
502	Ammonia-Oxidizing Bacteria and Archaea in Groundwater Treatment and Drinking Water Distribution Systems. <i>Applied and Environmental Microbiology</i> , 2009, 75, 4687-4695.	3.1	140
503	Gut-Associated Denitrification and In Vivo Emission of Nitrous Oxide by the Earthworm Families Megascolecidae and Lumbricidae in New Zealand. <i>Applied and Environmental Microbiology</i> , 2009, 75, 3430-3436.	3.1	38
504	Prokaryotic Genomes and Diversity in Surface Ocean Waters: Interrogating the Global Ocean Sampling Metagenome. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2221-2229.	3.1	188
505	Highly specialized microbial diversity in hyper-arid polar desert. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 19964-19969.	7.1	393
506	Archaeal Lipids and 16S rRNA Genes Characterizing Non-hydrate and Hydrate-Impacted Sediments in the Gulf of Mexico. <i>Geomicrobiology Journal</i> , 2009, 26, 227-237.	2.0	10
507	Gene-centric metagenomics of the fiber-adherent bovine rumen microbiome reveals forage specific glycoside hydrolases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1948-1953.	7.1	669
508	Comparison of Species Richness Estimates Obtained Using Nearly Complete Fragments and Simulated Pyrosequencing-Generated Fragments in 16S rRNA Gene-Based Environmental Surveys. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5227-5236.	3.1	362
509	<i>Zeta-Proteobacteria</i> Dominate the Colonization and Formation of Microbial Mats in Low-Temperature Hydrothermal Vents at Loihi Seamount, Hawaii. <i>Geomicrobiology Journal</i> , 2009, 26, 623-638.	2.0	57

#	ARTICLE	IF	CITATIONS
510	Bacterial Variability within an Iron-Silica-Manganese-rich Hydrothermal Mound Located Off-axis at the Cleft Segment, Juan de Fuca Ridge. <i>Geomicrobiology Journal</i> , 2009, 26, 570-580.	2.0	41
511	Archaeal Methane Cycling Communities Associated with Gassy Subsurface Sediments of Marennes-Oléron Bay (France). <i>Geomicrobiology Journal</i> , 2009, 26, 31-43.	2.0	45
512	Microbial Ecology of Fe (hydr)oxide Mats and Basaltic Rock from Vailulu'u Seamount, American Samoa. <i>Geomicrobiology Journal</i> , 2009, 26, 581-596.	2.0	70
513	Prokaryotic diversity in continuous cropping and rotational cropping soybean soil. <i>FEMS Microbiology Letters</i> , 2009, 298, 267-273.	1.8	18
514	Spatial distribution, diversity and composition of bacterial communities in sub-seafloor fluids at a deep-sea hydrothermal field of the Suiyo Seamount. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2009, 56, 1844-1855.	1.4	21
515	EnvDB, a database for describing the environmental distribution of prokaryotic taxa. <i>Environmental Microbiology Reports</i> , 2009, 1, 191-197.	2.4	39
516	Identification of active methylotrophic bacteria inhabiting surface sediment of a marine estuary. <i>Environmental Microbiology Reports</i> , 2009, 1, 424-433.	2.4	28
517	Novel diversity of bacterial communities associated with bottlenose dolphin upper respiratory tracts. <i>Environmental Microbiology Reports</i> , 2009, 1, 555-562.	2.4	42
518	Extreme diversity in noncalcifying haptophytes explains a major pigment paradox in open oceans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12803-12808.	7.1	263
519	Nodulation-Dependent Communities of Culturable Bacterial Endophytes from Stems of Field-Grown Soybeans. <i>Microbes and Environments</i> , 2009, 24, 253-258.	1.6	32
520	Comparison of free-living, suspended particle, and aggregate-associated Bacterial and Archaeal communities in the Laptev Sea. <i>Aquatic Microbial Ecology</i> , 2009, 57, 1-18.	1.8	90
521	Bacterial Diversity in <i>Amblyomma americanum</i> (Acari: Ixodidae) With a Focus on Members of the Genus <i>Rickettsia</i> . <i>Journal of Medical Entomology</i> , 2010, 47, 258-268.	1.8	75
522	Inter-annual recurrence of archaeal assemblages in the coastal NW Mediterranean Sea (Blanes Bay) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 351 131		
523	Biogeography of terrestrial cyanobacteria from Antarctic ice-free areas. <i>Annals of Glaciology</i> , 2010, 51, 171-177.	1.4	50
524	The Bacteriology of Pouchitis. <i>Annals of Surgery</i> , 2010, 252, 90-98.	4.2	99
525	Subcuticular Bacteria Associated With Two Common New Zealand Echinoderms: Characterization Using 16S rRNA Sequence Analysis and Fluorescence <i>in situ</i> Hybridization. <i>Biological Bulletin</i> , 2010, 218, 95-104.	1.8	12
526	Population Dynamics of Crenarchaeota and Euryarchaeota in the Mixing Front of River and Marine Waters. <i>Microbes and Environments</i> , 2010, 25, 126-132.	1.6	10
527	Comprehensive Detection of Phototrophic Sulfur Bacteria Using PCR Primers That Target Reverse Dissimilatory Sulfite Reductase Gene. <i>Microbes and Environments</i> , 2010, 25, 190-196.	1.6	23

#	ARTICLE	IF	CITATIONS
528	Altitudinal Changes in a Bacterial Community on Gulkana Glacier in Alaska. <i>Microbes and Environments</i> , 2010, 25, 171-182.	1.6	33
529	Soil Clone Library Analyses to Evaluate Specificity and Selectivity of PCR Primers Targeting Fungal 18S rDNA for Denaturing-Gradient Gel Electrophoresis (DGGE). <i>Microbes and Environments</i> , 2010, 25, 281-287.	1.6	26
530	Diversity and Community Structure of Archaea in Deep Subsurface Sediments from the Tropical Western Pacific. <i>Current Microbiology</i> , 2010, 60, 439-445.	2.2	15
531	Influence of Soil Characteristics on the Diversity of Bacteria in the Southern Brazilian Atlantic Forest. <i>Applied and Environmental Microbiology</i> , 2010, 76, 4744-4749.	3.1	189
532	A Molecular Survey of the Diversity of Microbial Communities in Different Amazonian Agricultural Model Systems. <i>Diversity</i> , 2010, 2, 787-809.	1.7	64
533	Microbiology and geochemistry of smith creek and grass valley hot springs: Emerging evidence for wide distribution of novel thermophilic lineages in the US Great Basin. <i>Journal of Earth Science (Wuhan, China)</i> , 2010, 21, 315-318.	3.2	9
534	The Spatial Factor, Rather than Elevated CO ₂ , Controls the Soil Bacterial Community in a Temperate Forest Ecosystem. <i>Applied and Environmental Microbiology</i> , 2010, 76, 7429-7436.	3.1	33
535	Soil Type-Dependent Responses to Phenanthrene as Revealed by Determining the Diversity and Abundance of Polycyclic Aromatic Hydrocarbon Ring-Hydroxylating Dioxygenase Genes by Using a Novel PCR Detection System. <i>Applied and Environmental Microbiology</i> , 2010, 76, 4765-4771.	3.1	98
536	Comparative Analysis of Acidobacterial Genomic Fragments from Terrestrial and Aquatic Metagenomic Libraries, with Emphasis on <i>Acidobacteria</i> Subdivision 6. <i>Applied and Environmental Microbiology</i> , 2010, 76, 6769-6777.	3.1	31
537	Detection of Fiber-Digesting Bacteria in the Ceca of Ostrich Using Specific Primer Sets. <i>Current Microbiology</i> , 2010, 60, 112-116.	2.2	13
538	Microbiomic Comparison of the Intestine of the Earthworm <i>Eisenia fetida</i> Fed Ergovaline. <i>Current Microbiology</i> , 2010, 60, 229-235.	2.2	15
539	Bacterial diversity in the rumen of Indian Surti buffalo (<i>Bubalus bubalis</i>), assessed by 16S rDNA analysis. <i>Journal of Applied Genetics</i> , 2010, 51, 395-402.	1.9	41
540	Environmental <i>Escherichia coli</i> occur as natural plant growth-promoting soil bacterium. <i>Archives of Microbiology</i> , 2010, 192, 185-193.	2.2	46
541	Bacterial Community Diversity in Undisturbed Perhumid Montane Forest Soils in Taiwan. <i>Microbial Ecology</i> , 2010, 59, 369-378.	2.8	43
542	Relationship Between Soil Properties and Patterns of Bacterial α -diversity Across Reclaimed and Natural Boreal Forest Soils. <i>Microbial Ecology</i> , 2010, 59, 563-573.	2.8	93
543	Robustness of the Bacterial Community in the Cabbage White Butterfly Larval Midgut. <i>Microbial Ecology</i> , 2010, 59, 199-211.	2.8	142
544	Microbial Diversity in Uranium Mining-Impacted Soils as Revealed by High-Density 16S Microarray and Clone Library. <i>Microbial Ecology</i> , 2010, 59, 94-108.	2.8	102
545	Archaea, Bacteria, and Algal Plastids Associated with the Reef-Building Corals <i>Siderastrea stellata</i> and <i>Mussismilia hispida</i> from Búzios, South Atlantic Ocean, Brazil. <i>Microbial Ecology</i> , 2010, 59, 523-532.	2.8	40

#	ARTICLE	IF	CITATIONS
546	Diversity and Community Structure of Archaea Inhabiting the Rhizoplane of Two Contrasting Plants from an Acidic Bog. <i>Microbial Ecology</i> , 2010, 59, 757-767.	2.8	36
547	The Influence of Different Land Uses on the Structure of Archaeal Communities in Amazonian Anthrosols Based on 16S rRNA and amoA Genes. <i>Microbial Ecology</i> , 2010, 59, 734-743.	2.8	61
548	Bacterial Community Associated with Healthy and Diseased Reef Coral <i>Mussismilia hispida</i> from Eastern Brazil. <i>Microbial Ecology</i> , 2010, 59, 658-667.	2.8	84
549	Pyrosequencing Reveals a Highly Diverse and Cultivar-Specific Bacterial Endophyte Community in Potato Roots. <i>Microbial Ecology</i> , 2010, 60, 157-166.	2.8	256
550	Soil Microbial Communities Associated with Douglas-fir and Red Alder Stands at High- and Low-Productivity Forest Sites in Oregon, USA. <i>Microbial Ecology</i> , 2010, 60, 606-617.	2.8	43
551	Bacterial Diversity of Weathered Terrestrial Icelandic Volcanic Glasses. <i>Microbial Ecology</i> , 2010, 60, 740-752.	2.8	66
552	Community Analysis Reveals Close Affinities Between Endophytic and Endolichenic Fungi in Mosses and Lichens. <i>Microbial Ecology</i> , 2010, 60, 340-353.	2.8	191
553	Temporal Patterns in Glycolate-Utilizing Bacterial Community Composition Correlate with Phytoplankton Population Dynamics in Humic Lakes. <i>Microbial Ecology</i> , 2010, 60, 406-418.	2.8	37
554	Competitiveness of Diverse <i>Methylobacterium</i> Strains in the Phyllosphere of <i>Arabidopsis thaliana</i> and Identification of Representative Models, Including <i>M. extorquens</i> PA1. <i>Microbial Ecology</i> , 2010, 60, 440-452.	2.8	102
555	Molecular Detection of Anaerobic Ammonium-Oxidizing (Anammox) Bacteria in High-Temperature Petroleum Reservoirs. <i>Microbial Ecology</i> , 2010, 60, 771-783.	2.8	131
556	Community Structure of Archaea from Deep-Sea Sediments of the South China Sea. <i>Microbial Ecology</i> , 2010, 60, 796-806.	2.8	25
557	Bacterial Community Diversity in the Brazilian Atlantic Forest Soils. <i>Microbial Ecology</i> , 2010, 60, 840-849.	2.8	70
558	Bacterial diversity in water injection systems of Brazilian offshore oil platforms. <i>Applied Microbiology and Biotechnology</i> , 2010, 85, 791-800.	3.6	53
559	Identifying diazotrophs by incorporation of nitrogen from $^{15}\text{N}_2$ into RNA. <i>Applied Microbiology and Biotechnology</i> , 2010, 87, 2313-2322.	3.6	13
560	Characterization of thermostable cellulases produced by <i>Bacillus</i> and <i>Geobacillus</i> strains. <i>Bioresource Technology</i> , 2010, 101, 8798-8806.	9.6	229
561	Microbial diversity in the anaerobic tank of a full-scale produced water treatment plant. <i>Process Biochemistry</i> , 2010, 45, 744-751.	3.7	24
562	Microbial sequences retrieved from environmental samples from seasonal Arctic snow and meltwater from Svalbard, Norway. <i>Extremophiles</i> , 2010, 14, 205-212.	2.3	100
563	Diversity of Crenarchaeota in terrestrial hot springs in Tengchong, China. <i>Extremophiles</i> , 2010, 14, 287-296.	2.3	49

#	ARTICLE	IF	CITATIONS
564	Planktonic actinobacterial diversity along a salinity gradient of a river and five lakes on the Tibetan Plateau. <i>Extremophiles</i> , 2010, 14, 367-376.	2.3	35
565	Variations of bacterial 16S rDNA phylotypes prior to and after chlorination for drinking water production from two surface water treatment plants. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2010, 37, 117-128.	3.0	55
566	Bacterial communities associated with the rhizosphere of pioneer plants (<i>Bahia xylopoda</i> and <i>Viguiera</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.7	71
567	The bacterial diversity in a Brazilian non-disturbed mangrove sediment. <i>Antonie Van Leeuwenhoek</i> , 2010, 98, 541-551.	1.7	61
568	Slowed decomposition is biotically mediated in an ectomycorrhizal, tropical rain forest. <i>Oecologia</i> , 2010, 164, 785-795.	2.0	84
569	Microbial community response to a simulated hydrocarbon spill in mangrove sediments. <i>Journal of Microbiology</i> , 2010, 48, 7-15.	2.8	72
570	Bacterial diversity in the sediment from polymetallic nodule fields of the Clarion-Clipperton Fracture Zone. <i>Journal of Microbiology</i> , 2010, 48, 573-585.	2.8	21
571	Microbial community on healthy and diseased leaves of an invasive plant <i>Eupatorium adenophorum</i> in Southwest China. <i>Journal of Microbiology</i> , 2010, 48, 139-145.	2.8	24
572	Assessment of soil fungal communities using pyrosequencing. <i>Journal of Microbiology</i> , 2010, 48, 284-289.	2.8	116
573	Diversity analysis of nitrite reductase genes (<i>nirS</i>) in black soil under different long-term fertilization conditions. <i>Annals of Microbiology</i> , 2010, 60, 97-104.	2.6	22
574	Fungal diversity associated with Brazilian energy transmission towers. <i>Fungal Diversity</i> , 2010, 44, 53-63.	12.3	19
575	Cultivation of hitherto-uncultured bacteria belonging to the Verrucomicrobia subdivision 1 from the potato (<i>Solanum tuberosum</i> L.) rhizosphere. <i>Journal of Soils and Sediments</i> , 2010, 10, 326-339.	3.0	52
576	Metagenomics: Facts and Artifacts, and Computational Challenges. <i>Journal of Computer Science and Technology</i> , 2010, 25, 71-81.	1.5	132
577	Influence of copper solvent extractant on microbial community structure of acidophilic microorganisms. <i>Central South University</i> , 2010, 17, 1196-1200.	0.5	3
578	Phylogenetic analysis of 16S rRNA gene sequences reveals distal gut bacterial diversity in wild wolves (<i>Canis lupus</i>). <i>Molecular Biology Reports</i> , 2010, 37, 4013-4022.	2.3	38
579	Influence of the bacterioplankton community of a tropical eutrophic lagoon on the bacterial community of its neighbouring ocean. <i>World Journal of Microbiology and Biotechnology</i> , 2010, 26, 1865-1873.	3.6	2
580	Molecular characterization of soil bacterial communities in contrasting zero tillage systems. <i>Plant and Soil</i> , 2010, 329, 127-137.	3.7	45
581	Bacterial community of very wet and acidic subalpine forest and fire-induced grassland soils. <i>Plant and Soil</i> , 2010, 332, 417-427.	3.7	9

#	ARTICLE	IF	CITATIONS
582	Bacterial soil community in a Brazilian sugarcane field. <i>Plant and Soil</i> , 2010, 336, 337-349.	3.7	16
583	Sulfide formation in freshwater sediments, by sulfate-reducing microorganisms with diverse tolerance to salt. <i>Science of the Total Environment</i> , 2010, 409, 134-139.	8.0	22
584	Development of soil microbial communities during tallgrass prairie restoration. <i>Soil Biology and Biochemistry</i> , 2010, 42, 302-312.	8.8	85
585	Bacterial diversity in cucumber (<i>Cucumis sativus</i>) rhizosphere in response to salinity, soil pH, and boron. <i>Soil Biology and Biochemistry</i> , 2010, 42, 567-575.	8.8	118
586	Nitrogen alters carbon dynamics during early succession in boreal forest. <i>Soil Biology and Biochemistry</i> , 2010, 42, 1157-1164.	8.8	96
587	Resistance of microbial and soil properties to warming treatment seven years after boreal fire. <i>Soil Biology and Biochemistry</i> , 2010, 42, 1872-1878.	8.8	81
588	Bacterioplankton diversity and community composition in the Southern Lagoon of Venice. <i>Systematic and Applied Microbiology</i> , 2010, 33, 128-138.	2.8	30
589	Seasonal and regional diversity of maple sap microbiota revealed using community PCR fingerprinting and 16S rRNA gene clone libraries. <i>Systematic and Applied Microbiology</i> , 2010, 33, 165-173.	2.8	34
590	Alignment and clustering of phylogenetic markers - implications for microbial diversity studies. <i>BMC Bioinformatics</i> , 2010, 11, 152.	2.6	63
591	VITCOMIC: visualization tool for taxonomic compositions of microbial communities based on 16S rRNA gene sequences. <i>BMC Bioinformatics</i> , 2010, 11, 332.	2.6	25
592	Molecular evidence for a diverse green algal community growing in the hair of sloths and a specific association with <i>Trichophilus welckeri</i> (Chlorophyta, Ulvophyceae). <i>BMC Evolutionary Biology</i> , 2010, 10, 86.	3.2	58
593	Molecular analysis of the diversity of vaginal microbiota associated with bacterial vaginosis. <i>BMC Genomics</i> , 2010, 11, 488.	2.8	284
594	Microbiological pattern of arterial catheters in the intensive care unit. <i>BMC Microbiology</i> , 2010, 10, 266.	3.3	16
595	CANGS: a user-friendly utility for processing and analyzing 454 GS-FLX data in biodiversity studies. <i>BMC Research Notes</i> , 2010, 3, 3.	1.4	50
596	Fermented liquid feed enhances bacterial diversity in piglet intestine. <i>Anaerobe</i> , 2010, 16, 6-11.	2.1	22
597	Microbial diversity in ostrich ceca as revealed by 16S ribosomal RNA gene clone library and detection of novel <i>Fibrobacter</i> species. <i>Anaerobe</i> , 2010, 16, 83-93.	2.1	60
598	Diversity and abundance of the bacterial 16S rRNA gene sequences in forestomach of alpacas (<i>Lama</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.1	46
599	Bacterial community analysis of a gas-phase biotrickling filter for biogas mimics desulfurization through the rRNA approach. <i>Chemosphere</i> , 2010, 80, 872-880.	8.2	56

#	ARTICLE	IF	CITATIONS
600	Molecular analysis of bacterial population structure and dynamics during cold storage of untreated and treated milk. <i>International Journal of Food Microbiology</i> , 2010, 138, 108-118.	4.7	105
601	Molecular analysis of the bacterial microbiota in duodenal biopsies from dogs with idiopathic inflammatory bowel disease. <i>Veterinary Microbiology</i> , 2010, 142, 394-400.	1.9	155
602	Molecular characterization of the cloacal microbiota of wild and captive parrots. <i>Veterinary Microbiology</i> , 2010, 146, 320-325.	1.9	102
603	The phage-driven microbial loop in petroleum bioremediation. <i>Microbial Biotechnology</i> , 2010, 3, 467-472.	4.2	27
604	Alteration of the murine gut microbiota during infection with the parasitic helminth <i>Heligmosomoides polygyrus</i> . <i>Inflammatory Bowel Diseases</i> , 2010, 16, 1841-1849.	1.9	276
605	Diversity of nitrifying bacteria in a full-scale petroleum refinery wastewater treatment plant experiencing unstable nitrification. <i>Journal of Hazardous Materials</i> , 2010, 181, 281-288.	12.4	48
606	Bioleaching of chalcocite started at different pH: Response of the microbial community to environmental stress and leaching kinetics. <i>Hydrometallurgy</i> , 2010, 103, 1-6.	4.3	27
607	<i>Leptospirillum</i> forms a minor portion of the population in Zijinshan commercial non-aeration copper bioleaching heap identified by 16S rRNA clone libraries and real-time PCR. <i>Hydrometallurgy</i> , 2010, 104, 399-403.	4.3	38
608	Community dynamics and phylogenetics of bacteria fouling Jet A and JP-8 aviation fuel. <i>International Biodeterioration and Biodegradation</i> , 2010, 64, 253-261.	3.9	29
609	Anaerobic degradation of linear alkylbenzene sulfonate (LAS) in fluidized bed reactor by microbial consortia in different support materials. <i>Bioresource Technology</i> , 2010, 101, 5112-5122.	9.6	59
610	Evaluating wastewater stabilizing constructed wetland, through diversity and abundance of the nitrite reductase gene <i>nirS</i> , with regard to nitrogen control. <i>Desalination</i> , 2010, 264, 201-205.	8.2	14
611	Microbiology and geochemistry of Little Hot Creek, a hot spring environment in the Long Valley Caldera. <i>Geobiology</i> , 2010, 8, 140-154.	2.4	91
612	Biogeochemical cycling and microbial diversity in the thrombolitic microbialites of Highborne Cay, Bahamas. <i>Geobiology</i> , 2010, 8, 337-354.	2.4	84
613	Bacterial diversity in Fe-rich hydrothermal sediments at two South Tonga Arc submarine volcanoes. <i>Geobiology</i> , 2010, 8, 417-432.	2.4	52
614	Characterization of monooxygenase gene diversity in benzene-amended soils. <i>Letters in Applied Microbiology</i> , 2010, 50, 138-145.	2.2	1
615	The bacterial community in "taberna"™ a traditional beverage of Southern Mexico. <i>Letters in Applied Microbiology</i> , 2010, 51, 558-563.	2.2	45
616	Stramenopile Microorganisms Associated with the Massive Coral <i>Favia</i> sp.. <i>Journal of Eukaryotic Microbiology</i> , 2010, 57, 236-244.	1.7	32
617	Diversity of microbial communities colonizing the walls of a Karstic cave in Slovenia. <i>FEMS Microbiology Ecology</i> , 2010, 71, 50-60.	2.7	88

#	ARTICLE	IF	CITATIONS
618	Fungal diversity in oxygen-depleted regions of the Arabian Sea revealed by targeted environmental sequencing combined with cultivation. FEMS Microbiology Ecology, 2010, 71, 399-412.	2.7	120
619	Molecular diversity of arbuscular mycorrhizal fungi and their distribution patterns related to host-plants and habitats in a hot and arid ecosystem, southwest China. FEMS Microbiology Ecology, 2010, 71, 418-427.	2.7	71
620	Biogeography of thermophilic cyanobacteria: insights from the Zerka Ma'in hot springs (Jordan). FEMS Microbiology Ecology, 2010, 72, 103-113.	2.7	55
621	Spatio-temporal variations in protistan communities along an O ₂ /H ₂ S gradient in the anoxic Framvaren Fjord (Norway). FEMS Microbiology Ecology, 2010, 72, 89-102.	2.7	67
622	Diversity, abundance and distribution of amoA-encoding archaea in deep-sea methane seep sediments of the Okhotsk Sea. FEMS Microbiology Ecology, 2010, 72, 370-385.	2.7	68
623	Cyanotoxins are not implicated in the etiology of coral black band disease outbreaks on Pelorus Island, Great Barrier Reef. FEMS Microbiology Ecology, 2010, 73, no-no.	2.7	16
624	Abundance, diversity, and activity of microbial assemblages associated with coral reef fish guts and feces. FEMS Microbiology Ecology, 2010, 73, no-no.	2.7	113
625	Seasonal succession and UV sensitivity of marine bacterioplankton at an Antarctic coastal site. FEMS Microbiology Ecology, 2010, 73, no-no.	2.7	14
626	Expression of acetate permease-like (apl) genes in subsurface communities of Geobacter species under fluctuating acetate concentrations. FEMS Microbiology Ecology, 2010, 73, no-no.	2.7	20
627	Structural shifts of gut microbiota as surrogate endpoints for monitoring host health changes induced by carcinogen exposure. FEMS Microbiology Ecology, 2010, 73, no-no.	2.7	44
628	Diversity of nitrogen-fixing bacteria in cyanobacterial mats. FEMS Microbiology Ecology, 2010, 73, no-no.	2.7	43
629	Inter- and intraspecific comparison of the bacterial assemblages in the hindgut of humivorous scarab beetle larvae (Pachnoda spp.). FEMS Microbiology Ecology, 2010, 74, 439-449.	2.7	51
630	Composition, spatial distribution, and diversity of the bacterial communities in the rumen of cows fed different forages. FEMS Microbiology Ecology, 2010, 74, 612-622.	2.7	211
631	Bacterial community changes during bioremediation of aliphatic hydrocarbon-contaminated soil. FEMS Microbiology Ecology, 2010, 74, 669-681.	2.7	125
632	Ultrasequencing of the meiofaunal biosphere: practice, pitfalls and promises. Molecular Ecology, 2010, 19, 4-20.	3.9	309
633	Diversity in a hidden world: potential and limitation of next-generation sequencing for surveys of molecular diversity of eukaryotic microorganisms. Molecular Ecology, 2010, 19, 32-40.	3.9	330
634	Bacterial diversity in a glacier foreland of the high Arctic. Molecular Ecology, 2010, 19, 54-66.	3.9	139
635	Phylogenetic similarity and structure of Agaricomycotina communities across a forested landscape. Molecular Ecology, 2010, 19, 1469-1482.	3.9	43

#	ARTICLE	IF	CITATIONS
636	The microbial signature of aerosols produced during the thermophilic phase of composting. Journal of Applied Microbiology, 2010, 108, 325-340.	3.1	61
637	Phylogenetic analysis of <i>Bacteroidales</i> 16S rRNA gene sequences from human and animal effluents and assessment of ruminant faecal pollution by real-time PCR. Journal of Applied Microbiology, 2010, 108, 974-984.	3.1	99
638	Gene-targeted-metagenomics reveals extensive diversity of aromatic dioxygenase genes in the environment. ISME Journal, 2010, 4, 279-285.	9.8	121
639	Archaeal ammonia oxidizers and <i>nirS</i> -type denitrifiers dominate sediment nitrifying and denitrifying populations in a subtropical macrotidal estuary. ISME Journal, 2010, 4, 286-300.	9.8	170
640	Bacterial diversity and biogeography in deep-sea surface sediments of the South Atlantic Ocean. ISME Journal, 2010, 4, 159-170.	9.8	227
641	Global ecological patterns in uncultured Archaea. ISME Journal, 2010, 4, 182-190.	9.8	406
642	Interactions between gut microbiota, host genetics and diet relevant to development of metabolic syndromes in mice. ISME Journal, 2010, 4, 232-241.	9.8	845
643	Global distribution of cyanobacterial ecotypes in the cold biosphere. ISME Journal, 2010, 4, 191-202.	9.8	194
644	Bacteriophage predation regulates microbial abundance and diversity in a full-scale bioreactor treating industrial wastewater. ISME Journal, 2010, 4, 327-336.	9.8	138
645	Community shifts of soybean stem-associated bacteria responding to different nodulation phenotypes and N levels. ISME Journal, 2010, 4, 315-326.	9.8	63
646	Exposure of different bacterial inocula to newborn chicken affects gut microbiota development and ileum gene expression. ISME Journal, 2010, 4, 367-376.	9.8	102
647	Microbial methane production in deep aquifer associated with the accretionary prism in Southwest Japan. ISME Journal, 2010, 4, 531-541.	9.8	53
648	Hydrography shapes bacterial biogeography of the deep Arctic Ocean. ISME Journal, 2010, 4, 564-576.	9.8	179
649	Distinct flavobacterial communities in contrasting water masses of the North Atlantic Ocean. ISME Journal, 2010, 4, 472-487.	9.8	143
650	Activity profiles for marine sponge-associated bacteria obtained by 16S rRNA vs 16S rRNA gene comparisons. ISME Journal, 2010, 4, 498-508.	9.8	132
651	Evolutionary divergence and biogeography of sympatric niche-differentiated bacterial populations. ISME Journal, 2010, 4, 488-497.	9.8	61
652	Developmental microbial ecology of the crop of the folivorous hoatzin. ISME Journal, 2010, 4, 611-620.	9.8	55
653	Investigation of archaeal and bacterial diversity in fermented seafood using barcoded pyrosequencing. ISME Journal, 2010, 4, 1-16.	9.8	256

#	ARTICLE	IF	CITATIONS
654	Diversity of aerobic and anaerobic ammonia-oxidizing bacteria in marine sponges. ISME Journal, 2010, 4, 38-48.	9.8	193
655	Molecular characterization of the spatial diversity and novel lineages of mycoplankton in Hawaiian coastal waters. ISME Journal, 2010, 4, 111-120.	9.8	96
656	Linking phylogenetic and functional diversity to nutrient spiraling in microbial mats from Lower Kane Cave (USA). ISME Journal, 2010, 4, 98-110.	9.8	70
657	Nitrogen and phosphorus enrichment alter the composition of ammonia-oxidizing bacteria in salt marsh sediments. ISME Journal, 2010, 4, 933-944.	9.8	41
658	PANGEA: pipeline for analysis of next generation amplicons. ISME Journal, 2010, 4, 852-861.	9.8	103
659	Diversity of active marine picoeukaryotes in the Eastern Mediterranean Sea unveiled using photosystem-II <i>psbA</i> transcripts. ISME Journal, 2010, 4, 1044-1052.	9.8	43
660	Bacterial diversity in the oral cavity of 10 healthy individuals. ISME Journal, 2010, 4, 962-974.	9.8	541
661	Bacterial diversity in rhizosphere soil from Antarctic vascular plants of Admiralty Bay, maritime Antarctica. ISME Journal, 2010, 4, 989-1001.	9.8	295
662	Microbial characterization of a subzero, hypersaline methane seep in the Canadian High Arctic. ISME Journal, 2010, 4, 1326-1339.	9.8	76
663	Spatial structure and persistence of methanogen populations in humic bog lakes. ISME Journal, 2010, 4, 764-776.	9.8	19
664	Active methylotrophs in the sediments of Lonar Lake, a saline and alkaline ecosystem formed by meteor impact. ISME Journal, 2010, 4, 1470-1480.	9.8	59
665	[FeFe]-hydrogenase in Yellowstone National Park: evidence for dispersal limitation and phylogenetic niche conservatism. ISME Journal, 2010, 4, 1485-1495.	9.8	63
666	Bioturbating shrimp alter the structure and diversity of bacterial communities in coastal marine sediments. ISME Journal, 2010, 4, 1531-1544.	9.8	103
667	Community structures of ammonia-oxidizing archaea and bacteria in high-altitude lakes on the Tibetan Plateau. Freshwater Biology, 2010, 55, 2375-2390.	2.4	65
668	Enteric defensins are essential regulators of intestinal microbial ecology. Nature Immunology, 2010, 11, 76-82.	14.5	1,013
669	Nitrogen availability is a primary determinant of conifer mycorrhizas across complex environmental gradients. Ecology Letters, 2010, 13, 1103-1113.	6.4	204
670	Diversity of human colonic butyrate-producing bacteria revealed by analysis of the butyryl-CoA:acetate CoA-transferase gene. Environmental Microbiology, 2010, 12, 304-314.	3.8	599
671	Diversity and population structure of sewage-derived microorganisms in wastewater treatment plant influent. Environmental Microbiology, 2010, 12, 378-392.	3.8	342

#	ARTICLE	IF	CITATIONS
672	Biomass production and energy source of thermophiles in a Japanese alkaline geothermal pool. <i>Environmental Microbiology</i> , 2010, 12, 480-489.	3.8	16
673	Effect of the herbicide glyphosate on glyphosate-tolerant maize rhizobacterial communities: a comparison with pre-emergence applied herbicide consisting of a combination of acetochlor and terbuthylazine. <i>Environmental Microbiology</i> , 2010, 12, 1021-1030.	3.8	57
674	Karst pools in subsurface environments: collectors of microbial diversity or temporary residence between habitat types. <i>Environmental Microbiology</i> , 2010, 12, 1061-1074.	3.8	55
675	The structure of bacterial communities in the western Arctic Ocean as revealed by pyrosequencing of 16S rRNA genes. <i>Environmental Microbiology</i> , 2010, 12, 1132-1143.	3.8	223
676	Microbial diversity and biogeochemistry of the Guaymas Basin deep-sea hydrothermal plume. <i>Environmental Microbiology</i> , 2010, 12, 1334-1347.	3.8	105
677	Persistence of bacterial and archaeal communities in sea ice through an Arctic winter. <i>Environmental Microbiology</i> , 2010, 12, 1828-1841.	3.8	147
678	The effect of nutrient deposition on bacterial communities in Arctic tundra soil. <i>Environmental Microbiology</i> , 2010, 12, 1842-1854.	3.8	323
679	Distribution and diversity of carbon monoxide-oxidizing bacteria and bulk bacterial communities across a succession gradient on a Hawaiian volcanic deposit. <i>Environmental Microbiology</i> , 2010, 12, 1855-1867.	3.8	60
680	Activity, abundance and diversity of nitrifying archaea and bacteria in the central California Current. <i>Environmental Microbiology</i> , 2010, 12, 1989-2006.	3.8	364
681	Halophilic archaea in the human intestinal mucosa. <i>Environmental Microbiology</i> , 2010, 12, 2398-2410.	3.8	105
682	Comparative analysis between protist communities from the deep-sea pelagic ecosystem and specific deep hydrothermal habitats. <i>Environmental Microbiology</i> , 2010, 12, 2946-2964.	3.8	80
683	GeneFISH – an <i>in situ</i> technique for linking gene presence and cell identity in environmental microorganisms. <i>Environmental Microbiology</i> , 2010, 12, 3057-3073.	3.8	75
684	Methanogenesis, sulfate reduction and crude oil biodegradation in hot Alaskan oilfields. <i>Environmental Microbiology</i> , 2010, 12, 3074-3086.	3.8	162
685	Threatened Corals Provide Underexplored Microbial Habitats. <i>PLoS ONE</i> , 2010, 5, e9554.	2.5	273
686	Robust Computational Analysis of rRNA Hypervariable Tag Datasets. <i>PLoS ONE</i> , 2010, 5, e15220.	2.5	15
687	Environmental Shaping of Sponge Associated Archaeal Communities. <i>PLoS ONE</i> , 2010, 5, e15774.	2.5	84
688	Phylogenetic Characterization of Fecal Microbial Communities of Dogs Fed Diets with or without Supplemental Dietary Fiber Using 454 Pyrosequencing. <i>PLoS ONE</i> , 2010, 5, e9768.	2.5	223
689	Molecular analysis of the bacterial diversity in a specialized consortium for diesel oil degradation. <i>Revista Brasileira De Ciencia Do Solo</i> , 2010, 34, 773-781.	1.3	14

#	ARTICLE	IF	CITATIONS
690	Simulated Atmospheric Nitrogen Deposition Alters Actinobacterial Community Composition in Forest Soils. Soil Science Society of America Journal, 2010, 74, 1157-1166.	2.2	81
691	A Clustering Optimization Strategy for Molecular Taxonomy Applied to Planktonic Foraminifera SSU rDNA. Evolutionary Bioinformatics, 2010, 6, EBO.S5504.	1.2	27
692	Association of Novel and Highly Diverse Acid-Tolerant Denitrifiers with N ₂ O Fluxes of an Acidic Fen. Applied and Environmental Microbiology, 2010, 76, 1125-1134.	3.1	58
693	Antibiotic Manipulation of Intestinal Microbiota To Identify Microbes Associated with <i>Campylobacter jejuni</i> Exclusion in Poultry. Applied and Environmental Microbiology, 2010, 76, 8026-8032.	3.1	29
694	Changes in the Structure and Function of Microbial Communities in Drinking Water Treatment Bioreactors upon Addition of Phosphorus. Applied and Environmental Microbiology, 2010, 76, 7473-7481.	3.1	60
695	Archaeal and Bacterial Communities Respond Differently to Environmental Gradients in Anoxic Sediments of a California Hypersaline Lake, the Salton Sea. Applied and Environmental Microbiology, 2010, 76, 757-768.	3.1	115
696	Bacterial Symbionts of the Brown Planthopper, <i>Nilaparvata lugens</i> (Homoptera: Delphacidae). Applied and Environmental Microbiology, 2010, 76, 1740-1745.	3.1	88
697	Large-scale patterns in biodiversity of microbial eukaryotes from the abyssal sea floor. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 115-120.	7.1	104
698	Estimating DNA coverage and abundance in metagenomes using a gamma approximation. Bioinformatics, 2010, 26, 295-301.	4.1	31
699	Detection of Protozoan Hosts for <i>Legionella pneumophila</i> in Engineered Water Systems by Using a Biofilm Batch Test. Applied and Environmental Microbiology, 2010, 76, 7144-7153.	3.1	54
700	RNA-Based Investigation of Ammonia-Oxidizing Archaea in Hot Springs of Yunnan Province, China. Applied and Environmental Microbiology, 2010, 76, 4538-4541.	3.1	81
701	Inhospitable sweetness: nectar filtering of pollinator-borne inocula leads to impoverished, phylogenetically clustered yeast communities. Proceedings of the Royal Society B: Biological Sciences, 2010, 277, 747-754.	2.6	127
702	Biogeography and Biodiversity in Sulfide Structures of Active and Inactive Vents at Deep-Sea Hydrothermal Fields of the Southern Mariana Trough. Applied and Environmental Microbiology, 2010, 76, 2968-2979.	3.1	88
703	Thaumarchaeal Ammonia Oxidation in an Acidic Forest Peat Soil Is Not Influenced by Ammonium Amendment. Applied and Environmental Microbiology, 2010, 76, 7626-7634.	3.1	180
704	Community Structure of Subsurface Biofilms in the Thermal Sulfidic Caves of Acquasanta Terme, Italy. Applied and Environmental Microbiology, 2010, 76, 5902-5910.	3.1	72
705	Characterization of Bacterial Community Structure in a Drinking Water Distribution System during an Occurrence of Red Water. Applied and Environmental Microbiology, 2010, 76, 7171-7180.	3.1	111
706	Diversity, Abundance, and Spatial Distribution of Sediment Ammonia-Oxidizing <i>Betaproteobacteria</i> in Response to Environmental Gradients and Coastal Eutrophication in Jiaozhou Bay, China. Applied and Environmental Microbiology, 2010, 76, 4691-4702.	3.1	155
707	Phylogenetic and Multivariate Analyses To Determine the Effects of Different Tillage and Residue Management Practices on Soil Bacterial Communities. Applied and Environmental Microbiology, 2010, 76, 3685-3691.	3.1	153

#	ARTICLE	IF	CITATIONS
708	Different Atmospheric Methane-Oxidizing Communities in European Beech and Norway Spruce Soils. Applied and Environmental Microbiology, 2010, 76, 3228-3235.	3.1	138
709	Adaptation to herbivory by the Tammar wallaby includes bacterial and glycoside hydrolase profiles different from other herbivores. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 14793-14798.	7.1	234
710	Advanced computational algorithms for microbial community analysis using massive 16S rRNA sequence data. Nucleic Acids Research, 2010, 38, e205-e205.	14.5	43
711	Diversity of Dissimilatory Sulfite Reductase Genes (<i>dsrAB</i>) in a Salt Marsh Impacted by Long-Term Acid Mine Drainage. Applied and Environmental Microbiology, 2010, 76, 4819-4828.	3.1	48
712	Microbial Community Composition as Affected by Dryland Cropping Systems and Tillage in a Semiarid Sandy Soil. Diversity, 2010, 2, 910-931.	1.7	66
713	Transcriptional activity of the dominant gut mucosal microbiota in chronic inflammatory bowel disease patients. Journal of Medical Microbiology, 2010, 59, 1114-1122.	1.8	121
714	Diversity, abundance and novel 16S rRNA gene sequences of methanogens in rumen liquid, solid and epithelium fractions of Jinnan cattle. Animal, 2010, 4, 20-29.	3.3	55
715	nirK-Harboring Denitrifiers Are More Responsive to Denitrification- Inducing Conditions in Rice Paddy Soil Than nirS-Harboring Bacteria. Microbes and Environments, 2010, 25, 45-48.	1.6	85
716	Bacterial Diversity in <i>Amblyomma americanum</i> (Acari: Ixodidae) With a Focus on Members of the Genus <i>Rickettsia</i> . Journal of Medical Entomology, 2010, 47, 258-268.	1.8	60
717	Soil Microbial Community Responses to Multiple Experimental Climate Change Drivers. Applied and Environmental Microbiology, 2010, 76, 999-1007.	3.1	690
718	Diversity of Anaerobic Microbes in Spacecraft Assembly Clean Rooms. Applied and Environmental Microbiology, 2010, 76, 2837-2845.	3.1	50
719	Culture-Independent Estimation of Optimal and Maximum Growth Temperatures of Archaea in Subsurface Habitats Based on the G+C Content in 16S rRNA Gene Sequences. Geomicrobiology Journal, 2010, 27, 114-122.	2.0	17
720	High-Density 16S Microarray and Clone Library-Based Microbial Community Composition of the Phoenix Spacecraft Assembly Clean Room. Astrobiology, 2010, 10, 499-508.	3.0	37
721	Tapping the Subsurface Ocean Crust Biosphere: Low Biomass and Drilling-Related Contamination Calls for Improved Quality Controls. Geomicrobiology Journal, 2010, 27, 158-169.	2.0	54
722	Application of Molecular Techniques To Elucidate the Influence of Cellulosic Waste on the Bacterial Community Structure at a Simulated Low-Level-Radioactive-Waste Site. Applied and Environmental Microbiology, 2010, 76, 3106-3115.	3.1	39
723	Environmental Factors Shape Sediment Anammox Bacterial Communities in Hypertrophic Jiaozhou Bay, China. Applied and Environmental Microbiology, 2010, 76, 7036-7047.	3.1	140
724	Animal-to-Animal Variation in Fecal Microbial Diversity among Beef Cattle. Applied and Environmental Microbiology, 2010, 76, 4858-4862.	3.1	146
725	Functional diversity in resource use by fungi. Ecology, 2010, 91, 2324-2332.	3.2	133

#	ARTICLE	IF	CITATIONS
726	Finding Biologically Accurate Clusterings in Hierarchical Tree Decompositions Using the Variation of Information. <i>Journal of Computational Biology</i> , 2010, 17, 503-516.	1.6	29
727	Horizon-Specific Bacterial Community Composition of German Grassland Soils, as Revealed by Pyrosequencing-Based Analysis of 16S rRNA Genes. <i>Applied and Environmental Microbiology</i> , 2010, 76, 6751-6759.	3.1	312
728	Commensal bacteria play a role in mating preference of <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 20051-20056.	7.1	752
729	Longitudinal shift in diabetic wound microbiota correlates with prolonged skin defense response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14799-14804.	7.1	189
730	Hepatitis C Virus Transmission Bottlenecks Analyzed by Deep Sequencing. <i>Journal of Virology</i> , 2010, 84, 6218-6228.	3.4	135
731	Microbial Community Changes in Response to Ethanol or Methanol Amendments for U(VI) Reduction. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5728-5735.	3.1	38
732	Clonal Analysis of the Microbiota of Severe Early Childhood Caries. <i>Caries Research</i> , 2010, 44, 485-497.	2.0	205
733	Imaging Marine Bacteria with Unique 16S rRNA V6 Sequences by Fluorescence <i>in situ</i> Hybridization and Spectral Analysis. <i>Geomicrobiology Journal</i> , 2010, 27, 251-260.	2.0	7
734	Abundance of Novel and Diverse <i>tfdA</i> -Like Genes, Encoding Putative Phenoxyalkanoic Acid Herbicide-Degrading Dioxygenases, in Soil. <i>Applied and Environmental Microbiology</i> , 2010, 76, 119-128.	3.1	57
735	Interrelations between the Microbiotas in the Litter and in the Intestines of Commercial Broiler Chickens. <i>Applied and Environmental Microbiology</i> , 2010, 76, 6572-6582.	3.1	157
736	Intestinal dysbiosis in irritable bowel syndrome: etiological factor or epiphenomenon?. <i>Expert Review of Molecular Diagnostics</i> , 2010, 10, 389-393.	3.1	19
737	Spatial Bacterial Diversity in a Recent Freshwater Tufa Deposit. <i>Geomicrobiology Journal</i> , 2010, 27, 275-291.	2.0	9
738	Molecular Characterization of the Archaeal Community in an Amazonian Wetland Soil and Culture-Dependent Isolation of Methanogenic Archaea. <i>Diversity</i> , 2010, 2, 1026-1047.	1.7	28
739	Effects of Plant Genotype and Growth Stage on the Betaproteobacterial Communities Associated with Different Potato Cultivars in Two Fields. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3675-3684.	3.1	215
740	Phylogenetic evidence of noteworthy microflora from the subsurface of the former Homestake gold mine, Lead, South Dakota. <i>Environmental Technology (United Kingdom)</i> , 2010, 31, 979-991.	2.2	8
741	Which Microbial Communities Are Present? Sequence-Based Metagenomics. , 2010, , 63-76.		1
742	Mineral and Bacterial Diversities of Desert Sand Grains from South-East Morocco. <i>Geomicrobiology Journal</i> , 2010, 27, 76-92.	2.0	27
743	Responses of Ammonia-Oxidizing Bacterial and Archaeal Populations to Organic Nitrogen Amendments in Low-Nutrient Groundwater. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2517-2523.	3.1	39

#	ARTICLE	IF	CITATIONS
744	Indoor fungal composition is geographically patterned and more diverse in temperate zones than in the tropics. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 13748-13753.	7.1	335
745	Diversity of rock varnish bacterial communities from Black Canyon, New Mexico. Journal of Geophysical Research, 2010, 115, .	3.3	63
746	Pyrosequencing Analysis of Bacterial Biofilm Communities in Water Meters of a Drinking Water Distribution System. Applied and Environmental Microbiology, 2010, 76, 5631-5635.	3.1	166
747	Response of Aerobic Anoxygenic Phototrophic Bacterial Diversity to Environment Conditions in Saline Lakes and Daotang River on the Tibetan Plateau, NW China. Geomicrobiology Journal, 2010, 27, 400-408.	2.0	26
748	Microbial community of salt crystals processed from Mediterranean seawater based on 16S rRNA analysis. Canadian Journal of Microbiology, 2010, 56, 44-51.	1.7	30
749	Endotracheal tube biofilm inoculation of oral flora and subsequent colonization of opportunistic pathogens. International Journal of Medical Microbiology, 2010, 300, 503-511.	3.6	67
750	Bacterial community composition in faeces from pigs in an outdoor production system without prophylactic or growth-promoting antibiotics. Livestock Science, 2010, 133, 110-112.	1.6	3
751	A general suite of fungal endophytes dominate the roots of two dominant grasses in a semiarid grassland. Journal of Arid Environments, 2010, 74, 35-42.	2.4	103
752	Exploring the identity of the Greek Dinophysis cf. acuminata. Harmful Algae, 2010, 10, 1-8.	4.8	17
753	Biochemical and microbial features of shallow marine sediments along the Terra Nova Bay (Ross Sea,) Tj ETQq1 1 0.784314 rgBT /Ove	1.8	85
754	Impact of natural oil and higher hydrocarbons on microbial diversity, distribution, and activity in Gulf of Mexico cold-seep sediments. Deep-Sea Research Part II: Topical Studies in Oceanography, 2010, 57, 2008-2021.	1.4	171
755	Phylogenetic diversity and evolutionary relatedness of alkenone-producing haptophyte algae in lakes: Implications for continental paleotemperature reconstructions. Earth and Planetary Science Letters, 2010, 300, 311-320.	4.4	119
756	Bacterial communities from soil sediments of a mountain oasis in northern Oman. Catena, 2010, 82, 102-111.	5.0	3
757	Phylogenetic diversity of archaeal 16S rRNA and ammonia monooxygenase genes from tropical estuarine sediments on the central west coast of India. Research in Microbiology, 2010, 161, 177-186.	2.1	36
758	The community composition of soil-denitrifying bacteria from a turfgrass environment. Research in Microbiology, 2010, 161, 315-325.	2.1	18
759	Novel prokaryotic diversity in sediments of Tunisian multipond solar saltern. Research in Microbiology, 2010, 161, 573-582.	2.1	50
760	Impact of microfiltration treatment of secondary wastewater effluent on biofouling of reverse osmosis membranes. Water Research, 2010, 44, 167-176.	11.3	76
761	Identification of bacterial populations in drinking water using 16S rRNA-based sequence analyses. Water Research, 2010, 44, 1353-1360.	11.3	96

#	ARTICLE	IF	CITATIONS
762	Bioaugmentation for improved recovery of anaerobic digesters after toxicant exposure. <i>Water Research</i> , 2010, 44, 3555-3564.	11.3	99
763	Constitutive Expression of the Proteorhodopsin Gene by a <i>Flavobacterium</i> Strain Representative of the Proteorhodopsin-Producing Microbial Community in the North Sea. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3187-3197.	3.1	49
764	Molecular diversity of arbuscular mycorrhizal fungi associated with two dominant xerophytes in a valley-type savanna, southwest China. <i>Applied Soil Ecology</i> , 2010, 44, 61-66.	4.3	12
765	Pyrosequencing analysis for characterization of soil bacterial populations as affected by an integrated livestock-cotton production system. <i>Applied Soil Ecology</i> , 2010, 45, 13-25.	4.3	105
766	Sediment-associated microdiversity within the Marine Group I Crenarchaeota. <i>Environmental Microbiology Reports</i> , 2010, 2, 693-703.	2.4	77
767	Novel Microbial Diversity Retrieved by Autonomous Robotic Exploration of the World's Deepest Vertical Phreatic Sinkhole. <i>Astrobiology</i> , 2010, 10, 201-213.	3.0	39
768	Characterization of cyanobacterial communities from high-elevation lakes in the Bolivian Andes. <i>Journal of Geophysical Research</i> , 2010, 115, .	3.3	23
769	Morphology, phylogeny and toxin analysis of <i>Pseudo-nitzschia pseudodelicatissima</i> (<i>Bacillariophyceae</i>) isolated from the Thermaikos Gulf, Greece. <i>Phycologia</i> , 2010, 49, 260-273.	1.4	32
770	Diversity of Bacteria and Glycosyl Hydrolase Family 48 Genes in Cellulolytic Consortia Enriched from Thermophilic Biocompost. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3545-3553.	3.1	63
771	Archaea and bacteria with surprising microdiversity show shifts in dominance over 1,000-year time scales in hydrothermal chimneys. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1612-1617.	7.1	181
772	Alteration of Microbial Communities Colonizing Leaf Litter in a Temperate Woodland Stream by Growth of Trees under Conditions of Elevated Atmospheric CO ₂ . <i>Applied and Environmental Microbiology</i> , 2010, 76, 4950-4959.	3.1	26
773	Recurrent Isolation of Extremotolerant Bacteria from the Clean Room Where Phoenix Spacecraft Components Were Assembled. <i>Astrobiology</i> , 2010, 10, 325-335.	3.0	67
774	Symbioses and Stress. <i>Cellular Origin and Life in Extreme Habitats</i> , 2010, , .	0.3	10
775	Clone Libraries of Ribosomal RNA Gene Sequences for Characterization of Bacterial and Fungal Communities. , 2010, , 3969-3993.		9
776	<i>Microbes at Work</i> . , 2010, , .		34
777	Second-generation environmental sequencing unmasks marine metazoan biodiversity. <i>Nature Communications</i> , 2010, 1, 98.	12.8	321
778	Effect of Earthworm Feeding Guilds on Ingested Dissimilatory Nitrate Reducers and Denitrifiers in the Alimentary Canal of the Earthworm. <i>Applied and Environmental Microbiology</i> , 2010, 76, 6205-6214.	3.1	24
779	Distinct Patterns of Picocyanobacterial Communities in Winter and Summer in the Chesapeake Bay. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2955-2960.	3.1	61

#	ARTICLE	IF	CITATIONS
780	Detection of WWE2-related <i>Lentisphaerae</i> by 16S rRNA gene sequencing and fluorescence in situ hybridization in landfill leachate. Canadian Journal of Microbiology, 2010, 56, 846-852.	1.7	11
781	Spatial and Temporal Analysis of the Microbial Community in the Tailings of a Pb-Zn Mine Generating Acidic Drainage. Applied and Environmental Microbiology, 2011, 77, 5540-5544.	3.1	68
782	Bacterial Community Analysis of Beef Cattle Feedlots Reveals That Pen Surface Is Distinct from Feces. Foodborne Pathogens and Disease, 2011, 8, 647-649.	1.8	23
783	Metabolite-based mutualism between <i>Pseudomonas aeruginosa</i> PA14 and <i>Enterobacter aerogenes</i> enhances current generation in bioelectrochemical systems. Energy and Environmental Science, 2011, 4, 4550.	30.8	109
785	Responses of Aerobic and Anaerobic Ammonia/Ammonium-Oxidizing Microorganisms to Anthropogenic Pollution in Coastal Marine Environments. Methods in Enzymology, 2011, 496, 35-62.	1.0	33
786	Community Structures of Fecal Bacteria in Cattle from Different Animal Feeding Operations. Applied and Environmental Microbiology, 2011, 77, 2992-3001.	3.1	342
787	Cytochrome <i>cd1</i> -Containing Nitrite Reductase Encoding Gene <i>nirS</i> as a New Functional Biomarker for Detection of Anaerobic Ammonium Oxidizing (Anammox) Bacteria. Environmental Science & Technology, 2011, 45, 3547-3553.	10.0	73
788	Molecular Tools for Investigating ANME Community Structure and Function. Methods in Enzymology, 2011, 494, 75-90.	1.0	3
789	Nod2 is essential for temporal development of intestinal microbial communities. Gut, 2011, 60, 1354-1362.	12.1	278
790	Exploring preserved fossil dinoflagellate and haptophyte DNA signatures to infer ecological and environmental changes during deposition of sapropel S1 in the eastern Mediterranean. Paleoceanography, 2011, 26, .	3.0	18
801	Anammox Bacterial Abundance, Biodiversity and Activity in a Constructed Wetland. Environmental Science & Technology, 2011, 45, 9951-9958.	10.0	124
802	Clustering 16S rRNA for OTU prediction: a method of unsupervised Bayesian clustering. Bioinformatics, 2011, 27, 611-618.	4.1	226
803	Assessing and Improving Methods Used in Operational Taxonomic Unit-Based Approaches for 16S rRNA Gene Sequence Analysis. Applied and Environmental Microbiology, 2011, 77, 3219-3226.	3.1	631
804	Evidence of cellulose metabolism by the giant panda gut microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17714-17719.	7.1	455
805	Diversity of the Human Skin Microbiome Early in Life. Journal of Investigative Dermatology, 2011, 131, 2026-2032.	0.7	402
806	Molecular characterisation of the small-eukaryote community in a tropical Great Lake (Lake Tj ETQq1 1 0.784314 r _g BT /Overlock 10 T _g 13	1.8	13
807	Microbial diversity of active layer and permafrost in an acidic wetland from the Canadian High Arctic. Canadian Journal of Microbiology, 2011, 57, 303-315.	1.7	156
809	Soil bacterial communities in native and regenerated perhumid montane forests. Applied Soil Ecology, 2011, 47, 111-118.	4.3	27

#	ARTICLE	IF	CITATIONS
810	Differences in bacterial community composition in Baltic Sea sediment in response to fish farming. <i>Aquaculture</i> , 2011, 313, 15-23.	3.5	51
811	Revealing archaeal diversity patterns and methane fluxes in Admiralty Bay, King George Island, and their association to Brazilian Antarctic Station activities. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2011, 58, 128-138.	1.4	12
812	Marine bacterioplankton biomass, activity and community structure in the vicinity of Antarctic icebergs. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2011, 58, 1407-1421.	1.4	17
813	Towards a new role for vector systematics in parasite control. <i>Parasitology</i> , 2011, 138, 1723-1729.	1.5	6
814	Integrative analysis of environmental sequences using MEGAN4. <i>Genome Research</i> , 2011, 21, 1552-1560.	5.5	1,245
815	Isolation of <i>Succinivibrionaceae</i> Implicated in Low Methane Emissions from Tammar Wallabies. <i>Science</i> , 2011, 333, 646-648.	12.6	179
816	Integrating High-Throughput Pyrosequencing and Quantitative Real-Time PCR to Analyze Complex Microbial Communities. <i>Methods in Molecular Biology</i> , 2011, 733, 107-128.	0.9	22
817	Ancient origins determine global biogeography of hot and cold desert cyanobacteria. <i>Nature Communications</i> , 2011, 2, 163.	12.8	203
818	Effects of elevated atmospheric CO ₂ on rhizosphere soil microbial communities in a Mojave Desert ecosystem. <i>Journal of Arid Environments</i> , 2011, 75, 917-925.	2.4	32
819	Evaluation of different partial 16S rRNA gene sequence regions for phylogenetic analysis of microbiomes. <i>Journal of Microbiological Methods</i> , 2011, 84, 81-87.	1.6	274
820	Correlation of bacterial communities supported by different organic materials with sulfate reduction in metal-rich landfill leachate. <i>Water Research</i> , 2011, 45, 1115-1128.	11.3	27
821	Biodiversity and population dynamics of microorganisms in a full-scale membrane bioreactor for municipal wastewater treatment. <i>Water Research</i> , 2011, 45, 1129-1138.	11.3	97
822	Kinetic modelling and microbial community assessment of anaerobic biphasic fixed film bioreactor treating distillery spent wash. <i>Water Research</i> , 2011, 45, 4248-4259.	11.3	50
823	Bacterial community characteristics under long-term antibiotic selection pressures. <i>Water Research</i> , 2011, 45, 6063-6073.	11.3	116
824	Phylogenetic diversity of bacterial communities in South China Sea mesoscale cyclonic eddy perturbations. <i>Research in Microbiology</i> , 2011, 162, 320-329.	2.1	26
825	Taxonomic and functional prokaryote diversity in mildly arsenic-contaminated sediments. <i>Research in Microbiology</i> , 2011, 162, 877-887.	2.1	51
826	Characterization of specificity of bacterial community structure within the burrow environment of the marine polychaete <i>Hediste (Nereis) diversicolor</i> . <i>Research in Microbiology</i> , 2011, 162, 1033-1042.	2.1	30
827	Delimiting operational taxonomic units for assessing ciliate environmental diversity using small subunit rRNA gene sequences. <i>Environmental Microbiology Reports</i> , 2011, 3, 154-158.	2.4	68

#	ARTICLE	IF	CITATIONS
828	Compositional differences in particle-associated and free-living microbial assemblages from an extreme deep-ocean environment. <i>Environmental Microbiology Reports</i> , 2011, 3, 449-458.	2.4	189
829	The active methanotrophic community in a wetland from the High Arctic. <i>Environmental Microbiology Reports</i> , 2011, 3, 466-472.	2.4	91
830	The larval sponge holobiont exhibits high thermal tolerance. <i>Environmental Microbiology Reports</i> , 2011, 3, 756-762.	2.4	66
831	Probing Individual Environmental Bacteria for Viruses by Using Microfluidic Digital PCR. <i>Science</i> , 2011, 333, 58-62.	12.6	210
832	Bacterial Communities of Diverse <i>Drosophila</i> Species: Ecological Context of a Host-Microbe Model System. <i>PLoS Genetics</i> , 2011, 7, e1002272.	3.5	650
833	The Effects of Above- and Belowground Mutualisms on Orchid Speciation and Coexistence. <i>American Naturalist</i> , 2011, 177, E54-E68.	2.1	182
835	Comparison of bacterial communities in the Solimões and Negro River tributaries of the Amazon River based on small subunit rRNA gene sequences. <i>Genetics and Molecular Research</i> , 2011, 10, 3783-3793.	0.2	8
836	Molecular profiling of bacterial species in the geese cecum. <i>Czech Journal of Animal Science</i> , 2011, 56, 192-203.	1.3	11
837	Soil Habitat and Horizon Properties Impact Bacterial Diversity and Composition. <i>Soil Science Society of America Journal</i> , 2011, 75, 1440-1448.	2.2	10
838	Distribution of typical denitrifying functional genes and diversity of the <i>nirS</i> -encoding bacterial community related to environmental characteristics of river sediments. <i>Biogeosciences</i> , 2011, 8, 3041-3051.	3.3	67
839	Bacterial diversity of subgingival plaque in 6 healthy Chinese individuals. <i>Experimental and Therapeutic Medicine</i> , 2011, 2, 1023-1029.	1.8	12
840	Variability and Diversity of Nasopharyngeal Microbiota in Children: A Metagenomic Analysis. <i>PLoS ONE</i> , 2011, 6, e17035.	2.5	399
841	CORE: A Phylogenetically-Curated 16S rDNA Database of the Core Oral Microbiome. <i>PLoS ONE</i> , 2011, 6, e19051.	2.5	154
842	Allele Intersection Analysis: A Novel Tool for Multi Locus Sequence Assignment in Multiply Infected Hosts. <i>PLoS ONE</i> , 2011, 6, e22198.	2.5	22
843	Impacts of Poultry House Environment on Poultry Litter Bacterial Community Composition. <i>PLoS ONE</i> , 2011, 6, e24785.	2.5	79
844	Establishment of Normal Gut Microbiota Is Compromised under Excessive Hygiene Conditions. <i>PLoS ONE</i> , 2011, 6, e28284.	2.5	120
845	Development of a Novel Strategy to Cultivate Enhanced Biological Phosphorus Removal (EBPR) Microorganisms. <i>Proceedings of the Water Environment Federation</i> , 2011, 2011, 4833-4851.	0.0	1
846	Phylogenetic distance in Great Salt Lake microbial communities. <i>Aquatic Microbial Ecology</i> , 2011, 64, 267-273.	1.8	16

#	ARTICLE	IF	CITATIONS
847	Membrane-Based Desalination. Water Intelligence Online, 2011, 10, 9781780400914.	0.3	5
848	Contribution of Anammox Bacteria to Benthic Nitrogen Cycling in a Mangrove Forest and Shrimp Ponds, Haiphong, Vietnam. Microbes and Environments, 2011, 26, 1-6.	1.6	57
849	16S rRNA Gene Microarray Analysis of Microbial Communities in Ethanol-Stimulated Subsurface Sediment. Microbes and Environments, 2011, 26, 261-265.	1.6	2
850	Exploring Soil Bacterial Communities in Different Peanut-Cropping Sequences Using Multiple Molecular Approaches. Phytopathology, 2011, 101, 819-827.	2.2	17
851	Molecular identification of methanogenic archaea from Surti buffaloes (<i>bubalus bubalis</i>), reveals more hydrogenotrophic methanogens phylotypes. Brazilian Journal of Microbiology, 2011, 42, 132-139.	2.0	14
853	Seasonal Dynamics of Anammox Bacteria in Estuarial Sediment of the Mai Po Nature Reserve Revealed by Analyzing the 16S rRNA and Hydrazine Oxidoreductase (<i>hzo</i>) Genes. Microbes and Environments, 2011, 26, 15-22.	1.6	90
854	Diversity of Culturable Chitinolytic Bacteria from Rhizospheres of Agronomic Plants in Japan. Microbes and Environments, 2011, 26, 7-14.	1.6	40
855	Distribution and Diversity of Anaerobic Ammonium Oxidation (Anammox) Bacteria in the Sediment of a Eutrophic Freshwater Lake, Lake Kitauro, Japan. Microbes and Environments, 2011, 26, 189-197.	1.6	113
856	Molecular Characterization of Soil Bacterial Community in a Perhumid, Low Mountain Forest. Microbes and Environments, 2011, 26, 325-331.	1.6	4
857	Community Variability of Bacteria in Alpine Snow (Mont Blanc) Containing Saharan Dust Deposition and Their Snow Colonisation Potential. Microbes and Environments, 2011, 26, 237-247.	1.6	46
858	Fish Farming Affects the Abundance and Diversity of the Mercury Resistance Gene <i>merA</i> in Marine Sediments. Microbes and Environments, 2011, 26, 205-211.	1.6	11
859	Genes for selenium dependent and independent formate dehydrogenase in the gut microbial communities of three lower, wood-feeding termites and a wood-feeding roach. Environmental Microbiology, 2011, 13, 307-323.	3.8	13
860	Depicting more accurate pictures of protistan community complexity using pyrosequencing of hypervariable SSU rRNA gene regions. Environmental Microbiology, 2011, 13, 340-349.	3.8	178
861	Diversity, abundance and characterization of ruminal cysteine phytases suggest their important role in phytate degradation. Environmental Microbiology, 2011, 13, 747-757.	3.8	31
862	Novel groups of <i>Gammaproteobacteria</i> catalyse sulfur oxidation and carbon fixation in a coastal, intertidal sediment. Environmental Microbiology, 2011, 13, 758-774.	3.8	136
863	Microbial communities in bulk fluids and biofilms of an oil facility have similar composition but different structure. Environmental Microbiology, 2011, 13, 1078-1090.	3.8	66
864	Bacteria associated with an encrusting sponge (<i>Terpios hoshinota</i>) and the corals partially covered by the sponge. Environmental Microbiology, 2011, 13, 1179-1191.	3.8	31
865	Composition and dynamics of the gill microbiota of an invasive Indo-Pacific oyster in the eastern Mediterranean Sea. Environmental Microbiology, 2011, 13, 1467-1476.	3.8	70

#	ARTICLE	IF	CITATIONS
866	Yellowstone Lake: high-energy geochemistry and rich bacterial diversity. <i>Environmental Microbiology</i> , 2011, 13, 2172-2185.	3.8	52
867	Hydrothermal ecotones and streamer biofilm communities in the Lower Geyser Basin, Yellowstone National Park. <i>Environmental Microbiology</i> , 2011, 13, 2216-2231.	3.8	85
868	Unveiling microbial life in new deep-sea hypersaline Lake <i>Thetis</i>. Part I: Prokaryotes and environmental settings. <i>Environmental Microbiology</i> , 2011, 13, 2250-2268.	3.8	86
869	A global census of nitrogenase diversity. <i>Environmental Microbiology</i> , 2011, 13, 1790-1799.	3.8	155
870	Drivers of bacterial diversity dynamics in permeable carbonate and silicate coral reef sands from the Red Sea. <i>Environmental Microbiology</i> , 2011, 13, 1815-1826.	3.8	45
871	Environmental evidence for net methane production and oxidation in putative ANaerobic MEthanotrophic (ANME) archaea. <i>Environmental Microbiology</i> , 2011, 13, 2548-2564.	3.8	146
872	Molecular diversity of the foregut bacteria community in the dromedary camel (<i>Camelus</i>). <i>Journal of Applied Microbiology</i> , 2011, 110, 1284-1296.	3.8	74
873	Molecular characterization of putative biocorroding microbiota with a novel niche detection of <i>Epsilon</i>- and <i>Zetaproteobacteria</i> in Pacific Ocean coastal seawaters. <i>Environmental Microbiology</i> , 2011, 13, 3059-3074.	3.8	124
874	Culture-dependent and culture-independent assessment of bacteria in the apple phyllosphere. <i>Journal of Applied Microbiology</i> , 2011, 110, 1284-1296.	3.1	95
875	Continuous feeding of antimicrobial growth promoters to commercial swine during the growing/finishing phase does not modify faecal community erythromycin resistance or community structure. <i>Journal of Applied Microbiology</i> , 2011, 110, 1414-1425.	3.1	26
876	Multiresistance, beta-lactamase-encoding genes and bacterial diversity in hospital wastewater in Rio de Janeiro, Brazil. <i>Journal of Applied Microbiology</i> , 2011, 111, 572-581.	3.1	135
877	Fungal community composition and function after long-term exposure of northern forests to elevated atmospheric CO ₂ and tropospheric O ₃ . <i>Global Change Biology</i> , 2011, 17, 2184-2195.	9.5	45
878	Preservation, origin and genetic imprint of extracellular DNA in permanently anoxic deep-sea sediments. <i>Molecular Ecology</i> , 2011, 20, 642-654.	3.9	148
879	Species delimitation in fungal endophyte diversity studies and its implications in ecological and biogeographic inferences. <i>Molecular Ecology</i> , 2011, 20, 3001-3013.	3.9	197
880	Preservation potential of ancient plankton DNA in Pleistocene marine sediments. <i>Geobiology</i> , 2011, 9, 377-393.	2.4	76
881	Archaeal diversity in a terrestrial acidic spring field revealed by a novel PCR primer targeting archaeal 16S rRNA genes. <i>FEMS Microbiology Letters</i> , 2011, 319, 34-43.	1.8	49
882	Molecular characterization of the microbial community in hydrogenetic ferromanganese crusts of the Takuyo-Daigo Seamount, northwest Pacific. <i>FEMS Microbiology Letters</i> , 2011, 321, 121-129.	1.8	45
883	Supervised classification of human microbiota. <i>FEMS Microbiology Reviews</i> , 2011, 35, 343-359.	8.6	377

#	ARTICLE	IF	CITATIONS
884	Effects of estuarine sediment hypoxia on nitrogen fluxes and ammonia oxidizer gene transcription. FEMS Microbiology Ecology, 2011, 75, 111-122.	2.7	49
885	Hydrology is reflected in the functioning and community composition of methanotrophs in the littoral wetland of a boreal lake. FEMS Microbiology Ecology, 2011, 75, 430-445.	2.7	69
886	Impact of endochitinase-transformed white spruce on soil fungal communities under greenhouse conditions. FEMS Microbiology Ecology, 2011, 76, 199-208.	2.7	17
887	Evidence for syntrophic butyrate metabolism under sulfate-reducing conditions in a hydrocarbon-contaminated aquifer. FEMS Microbiology Ecology, 2011, 76, 289-300.	2.7	23
888	Massive parallel 16S rRNA gene pyrosequencing reveals highly diverse fecal bacterial and fungal communities in healthy dogs and cats. FEMS Microbiology Ecology, 2011, 76, 301-310.	2.7	324
889	The impact of different soil parameters on the community structure of dominant bacteria from nine different soils located on Livingston Island, South Shetland Archipelago, Antarctica. FEMS Microbiology Ecology, 2011, 76, 476-491.	2.7	107
890	Diversity and function in microbial mats from the Lucky Strike hydrothermal vent field. FEMS Microbiology Ecology, 2011, 76, 524-540.	2.7	53
891	ThermoPhyl: a software tool for selecting phylogenetically optimized conventional and quantitative-PCR taxon-targeted assays for use with complex samples. FEMS Microbiology Ecology, 2011, 77, 17-27.	2.7	6
892	Organic acids and ethanol inhibit the oxidation of methane by mire methanotrophs. FEMS Microbiology Ecology, 2011, 77, 28-39.	2.7	52
893	Diversity of Archaea in Icelandic hot springs based on 16S rRNA and chaperonin genes. FEMS Microbiology Ecology, 2011, 77, 165-175.	2.7	27
894	Low cyanobacterial diversity in biotopes of the Transantarctic Mountains and Shackleton Range (80-82°S), Antarctica. FEMS Microbiology Ecology, 2011, 77, 503-517.	2.7	32
895	Identification of microbial communities involved in the methane cycle of a freshwater meromictic lake. FEMS Microbiology Ecology, 2011, 77, 533-545.	2.7	110
896	Comparison of microbial communities associated with three Atlantic ultramafic hydrothermal systems. FEMS Microbiology Ecology, 2011, 77, 647-665.	2.7	40
897	Genetic diversity of cyanobacteria in four eutrophic lakes. FEMS Microbiology Ecology, 2011, 78, 336-348.	2.7	27
898	Diversity and distribution of diazotrophic communities in the South China Sea deep basin with mesoscale cyclonic eddy perturbations. FEMS Microbiology Ecology, 2011, 78, 417-427.	2.7	50
899	Biodiversity, abundance, and activity of nitrogen-fixing bacteria during primary succession on a copper mine tailings. FEMS Microbiology Ecology, 2011, 78, 439-450.	2.7	65
900	Microbial diversity in deep-sea sediment from the cobalt-rich crust deposit region in the Pacific Ocean. FEMS Microbiology Ecology, 2011, 78, 565-585.	2.7	56
901	Metabolic strategies of free-living and aggregate-associated bacterial communities inferred from biologic and chemical profiles in the Black Sea suboxic zone. FEMS Microbiology Ecology, 2011, 78, 586-603.	2.7	94

#	ARTICLE	IF	CITATIONS
902	Microbial diversity in saliva of oral squamous cell carcinoma. FEMS Immunology and Medical Microbiology, 2011, 61, 269-277.	2.7	142
903	The impact of reduced pH on the microbial community of the coral <i>Acropora eurystoma</i> . ISME Journal, 2011, 5, 51-60.	9.8	217
904	Sequence diversity and novelty of natural assemblages of picoeukaryotes from the Indian Ocean. ISME Journal, 2011, 5, 184-195.	9.8	50
905	Vertical stratification of microbial communities in the Red Sea revealed by 16S rDNA pyrosequencing. ISME Journal, 2011, 5, 507-518.	9.8	151
906	Comparative metagenomics of bathypelagic plankton and bottom sediment from the Sea of Marmara. ISME Journal, 2011, 5, 285-304.	9.8	140
907	Dominant and diet-responsive groups of bacteria within the human colonic microbiota. ISME Journal, 2011, 5, 220-230.	9.8	1,352
908	Patterns of fungal diversity and composition along a salinity gradient. ISME Journal, 2011, 5, 379-388.	9.8	160
909	The dynamics of microbial partnerships in the coral <i>Isopora palifera</i> . ISME Journal, 2011, 5, 728-740.	9.8	105
910	Elevated seawater temperature causes a microbial shift on crustose coralline algae with implications for the recruitment of coral larvae. ISME Journal, 2011, 5, 759-770.	9.8	145
911	Capturing diversity of marine heterotrophic protists: one cell at a time. ISME Journal, 2011, 5, 674-684.	9.8	86
912	Pyrosequencing reveals highly diverse and species-specific microbial communities in sponges from the Red Sea. ISME Journal, 2011, 5, 650-664.	9.8	265
913	Partitioning core and satellite taxa from within cystic fibrosis lung bacterial communities. ISME Journal, 2011, 5, 780-791.	9.8	222
914	Coral-mucus-associated <i>Vibrio</i> integrons in the Great Barrier Reef: genomic hotspots for environmental adaptation. ISME Journal, 2011, 5, 962-972.	9.8	37
915	Contribution of crenarchaeal autotrophic ammonia oxidizers to the dark primary production in Tyrrhenian deep waters (Central Mediterranean Sea). ISME Journal, 2011, 5, 945-961.	9.8	109
916	Nitrogen fixation and nitrogenase (<i>nifH</i>) expression in tropical waters of the eastern North Atlantic. ISME Journal, 2011, 5, 1201-1212.	9.8	111
917	Response of <i>Prochlorococcus</i> ecotypes to co-culture with diverse marine bacteria. ISME Journal, 2011, 5, 1125-1132.	9.8	142
918	Stochastic and deterministic processes interact in the assembly of desert microbial communities on a global scale. ISME Journal, 2011, 5, 1406-1413.	9.8	301
919	Ovine pedomics: the first study of the ovine foot 16S rRNA-based microbiome. ISME Journal, 2011, 5, 1426-1437.	9.8	46

#	ARTICLE	IF	CITATIONS
920	Agriculture's impact on microbial diversity and associated fluxes of carbon dioxide and methane. ISME Journal, 2011, 5, 1683-1691.	9.8	138
921	Analysis of bacterial and archaeal diversity in coastal microbial mats using massive parallel 16S rRNA gene tag sequencing. ISME Journal, 2011, 5, 1701-1712.	9.8	157
922	Optimizing the indirect extraction of prokaryotic DNA from soils. Soil Biology and Biochemistry, 2011, 43, 736-748.	8.8	44
923	Distinctive fungal and bacterial communities are associated with mats formed by ectomycorrhizal fungi. Soil Biology and Biochemistry, 2011, 43, 1042-1050.	8.8	41
924	Land-use history has a stronger impact on soil microbial community composition than aboveground vegetation and soil properties. Soil Biology and Biochemistry, 2011, 43, 2184-2193.	8.8	362
925	Microbial ecology of autothermal thermophilic aerobic digester (ATAD) systems for treating waste activated sludge. Systematic and Applied Microbiology, 2011, 34, 127-138.	2.8	28
926	Predicting relatedness of bacterial genomes using the chaperonin-60 universal target (cpn60 UT): Application to Thermoanaerobacter species. Systematic and Applied Microbiology, 2011, 34, 171-179.	2.8	40
927	Bacterial community structure of a full-scale biofilter treating pig house exhaust air. Systematic and Applied Microbiology, 2011, 34, 344-352.	2.8	32
928	Diversity of methanogenic archaea in a biogas reactor fed with swine feces as the mono-substrate by mcrA analysis. Microbiological Research, 2011, 166, 27-35.	5.3	63
929	Diversity and abundance of ammonia-oxidizing archaea in the Dongjiang River, China. Microbiological Research, 2011, 166, 337-345.	5.3	63
930	Highly Diverse and Seasonally Dynamic Protist Community in a Pristine Peat Bog. Protist, 2011, 162, 14-32.	1.5	74
931	Microbial communities in the tonsils of healthy pigs. Veterinary Microbiology, 2011, 147, 346-357.	1.9	63
932	Longitudinal investigation of the age-related bacterial diversity in the feces of commercial pigs. Veterinary Microbiology, 2011, 153, 124-133.	1.9	274
933	Assessment of bacterial diversity in the cattle tick Rhipicephalus (Boophilus) microplus through tag-encoded pyrosequencing. BMC Microbiology, 2011, 11, 6.	3.3	263
934	High-throughput clone library analysis of the mucosa-associated microbiota reveals dysbiosis and differences between inflamed and non-inflamed regions of the intestine in inflammatory bowel disease. BMC Microbiology, 2011, 11, 7.	3.3	596
935	CANGS DB: a stand-alone web-based database tool for processing, managing and analyzing 454 data in biodiversity studies. BMC Research Notes, 2011, 4, 227.	1.4	4
936	Identification of anthracene degraders in leachate-contaminated aquifer using stable isotope probing. International Biodeterioration and Biodegradation, 2011, 65, 1224-1228.	3.9	42
937	Electricity generation and microbial community changes in microbial fuel cells packed with different anodic materials. Bioresource Technology, 2011, 102, 10886-10891.	9.6	86

#	ARTICLE	IF	CITATIONS
938	Geochemical and microbiological processes contributing to the transformation of hexahydro-1,3,5-trinitro-1,3,5-triazine (RDX) in contaminated aquifer material. <i>Chemosphere</i> , 2011, 84, 1223-1230.	8.2	29
939	Cultivation-independent methods applied to the microbial prospection of oil and gas in soil from a sedimentary basin in Brazil. <i>AMB Express</i> , 2011, 1, 35.	3.0	22
940	Ammonia-oxidizing Archaea in Kamchatka Hot Springs. <i>Geomicrobiology Journal</i> , 2011, 28, 149-159.	2.0	21
941	A Guide to the Natural History of Freshwater Lake Bacteria. <i>Microbiology and Molecular Biology Reviews</i> , 2011, 75, 14-49.	6.6	1,356
942	Mangrove trees affect the community structure and distribution of anammox bacteria at an anthropogenic-polluted mangrove in the Pearl River Delta reflected by 16S rRNA and hydrazine oxidoreductase (HZO) encoding gene analyses. <i>Ecotoxicology</i> , 2011, 20, 1780-1790.	2.4	71
943	Comparison of an inactive submarine spring with an active nearshore anchialine spring in Florida. <i>Hydrobiologia</i> , 2011, 677, 65-87.	2.0	21
944	Influence of Different Substrates in Wetland Soils on Denitrification. <i>Water, Air, and Soil Pollution</i> , 2011, 215, 549-560.	2.4	10
945	Structures of bacterial communities on the surface of <i>Ulva prolifera</i> and in seawaters in an <i>Ulva</i> blooming region in Jiaozhou Bay, China. <i>World Journal of Microbiology and Biotechnology</i> , 2011, 27, 1703-1712.	3.6	58
946	Cyanobacteria and chloroflexi-dominated hypolithic colonization of quartz at the hyper-arid core of the Atacama Desert, Chile. <i>Extremophiles</i> , 2011, 15, 31-38.	2.3	97
947	Microbial diversity in the snow, a moraine lake and a stream in Himalayan glacier. <i>Extremophiles</i> , 2011, 15, 411-421.	2.3	44
948	Bacterial diversity in five Icelandic geothermal waters: temperature and sinter growth rate effects. <i>Extremophiles</i> , 2011, 15, 473-485.	2.3	64
949	Archaeal and bacterial diversity in hot springs on the Tibetan Plateau, China. <i>Extremophiles</i> , 2011, 15, 549-563.	2.3	80
950	Distribution of denitrifying bacterial communities in the stratified water column and sediment-water interface in two freshwater lakes and the Baltic Sea. <i>Aquatic Ecology</i> , 2011, 45, 99-112.	1.5	32
951	Bacterial community associated with the trunk latex of <i>Hancornia speciosa</i> Gomes (Apocynaceae) grown in the northeast of Brazil. <i>Antonie Van Leeuwenhoek</i> , 2011, 99, 523-532.	1.7	17
952	Impact of redox-stratification on the diversity and distribution of bacterial communities in sandy reef sediments in a microcosm. <i>Chinese Journal of Oceanology and Limnology</i> , 2011, 29, 1209-1223.	0.7	7
953	The community structure of arbuscular mycorrhizal fungi in roots of maize grown in a 50-year monoculture. <i>Biology and Fertility of Soils</i> , 2011, 47, 167-176.	4.3	34
954	Diversity of the Formyltetrahydrofolate Synthetase (FTHFS) Gene in the Proximal and Mid Ostrich Colon. <i>Current Microbiology</i> , 2011, 62, 1-6.	2.2	8
955	Composition of Bacterial Communities Associated with a Plant-Parasitic Nematode <i>Bursaphelenchus mucronatus</i> . <i>Current Microbiology</i> , 2011, 62, 117-125.	2.2	33

#	ARTICLE	IF	CITATIONS
956	Species Richness of Yeast Communities in Floral Nectar of Southern Spanish Plants. <i>Microbial Ecology</i> , 2011, 61, 82-91.	2.8	120
957	Substitution by Inosine at the 3'â€²-Ultimate and Penultimate Positions of 16S rRNA Gene Universal Primers. <i>Microbial Ecology</i> , 2011, 61, 1-6.	2.8	8
958	Anammox Bacterial Diversity in Various Aquatic Ecosystems Based on the Detection of Hydrazine Oxidase Genes (hzoA/hzoB). <i>Microbial Ecology</i> , 2011, 61, 264-276.	2.8	93
959	Change in Bacterial Community Structure in Response to Disturbance of Natural Hardwood and Secondary Coniferous Forest Soils in Central Taiwan. <i>Microbial Ecology</i> , 2011, 61, 429-437.	2.8	35
960	Identification of Sulfur-Cycle Prokaryotes in a Low-Sulfate Lake (Lake Pavin) Using aprA and 16S rRNA Gene Markers. <i>Microbial Ecology</i> , 2011, 61, 313-327.	2.8	47
961	Bacterial Community Structure Along Moisture Gradients in the Parafluvial Sediments of Two Ephemeral Desert Streams. <i>Microbial Ecology</i> , 2011, 61, 543-556.	2.8	107
962	Investigation of Microbial Populations in the Extremely Metal-Contaminated Coeur d'Alene River Sediments. <i>Microbial Ecology</i> , 2011, 62, 1-13.	2.8	47
963	Environmental Constraints Underpin the Distribution and Phylogenetic Diversity of nifH in the Yellowstone Geothermal Complex. <i>Microbial Ecology</i> , 2011, 61, 860-870.	2.8	40
964	Residence of Habitat-Specific Anammox Bacteria in the Deep-Sea Subsurface Sediments of the South China Sea: Analyses of Marker Gene Abundance with Physical Chemical Parameters. <i>Microbial Ecology</i> , 2011, 62, 36-47.	2.8	104
965	Bacterial Diversity of Terrestrial Crystalline Volcanic Rocks, Iceland. <i>Microbial Ecology</i> , 2011, 62, 69-79.	2.8	51
966	Community Structure and Function of Planktonic Crenarchaeota: Changes with Depth in the South China Sea. <i>Microbial Ecology</i> , 2011, 62, 549-563.	2.8	72
967	Bacterial Community Composition of Biological Degreasing Systems and Health Risk Assessment for Workers. <i>Microbial Ecology</i> , 2011, 62, 868-881.	2.8	3
968	Environmental Conditions Constrain the Distribution and Diversity of Archaeal merA in Yellowstone National Park, Wyoming, U.S.A.. <i>Microbial Ecology</i> , 2011, 62, 739-752.	2.8	33
970	Taxonomic and Functional Metagenomic Profiling of the Microbial Community in the Anoxic Sediment of a Sub-saline Shallow Lake (Laguna de Carrizo, Central Spain). <i>Microbial Ecology</i> , 2011, 62, 824-837.	2.8	51
971	Change in ammonia-oxidizing microorganisms in enriched nitrifying activated sludge. <i>Applied Microbiology and Biotechnology</i> , 2011, 89, 843-853.	3.6	43
972	Diversity and abundance of anammox bacterial community in the deep-ocean surface sediment from equatorial Pacific. <i>Applied Microbiology and Biotechnology</i> , 2011, 89, 1233-1241.	3.6	40
973	Spatial distribution and abundances of ammonia-oxidizing archaea (AOA) and ammonia-oxidizing bacteria (AOB) in mangrove sediments. <i>Applied Microbiology and Biotechnology</i> , 2011, 89, 1243-1254.	3.6	135
974	Quantitative analyses of ammonia-oxidizing Archaea and bacteria in the sediments of four nitrogen-rich wetlands in China. <i>Applied Microbiology and Biotechnology</i> , 2011, 90, 779-787.	3.6	123

#	ARTICLE	IF	CITATIONS
975	A diverse bacterial community in an anoxic quinoline-degrading bioreactor determined by using pyrosequencing and clone library analysis. <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 425-434.	3.6	40
976	Dynamic microbial response of sulfidogenic wastewater biofilm to nitrate. <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 1647-1657.	3.6	36
977	Diversity and phylogeny of bacteria on Zimbabwe tobacco leaves estimated by 16S rRNA sequence analysis. <i>Applied Microbiology and Biotechnology</i> , 2011, 92, 1033-1044.	3.6	43
978	Isolation and Partial Characterization of Halotolerant Lactic Acid Bacteria from Two Mexican Cheeses. <i>Applied Biochemistry and Biotechnology</i> , 2011, 164, 889-905.	2.9	65
979	Archaeal communities in the sediments of three contrasting mangroves. <i>Journal of Soils and Sediments</i> , 2011, 11, 1466-1476.	3.0	50
980	16s rDNA based microbial diversity analysis of eleven acid mine drainages obtained from three Chinese copper mines. <i>Central South University</i> , 2011, 18, 1930-1939.	0.5	5
981	CLOTU: An online pipeline for processing and clustering of 454 amplicon reads into OTUs followed by taxonomic annotation. <i>BMC Bioinformatics</i> , 2011, 12, 182.	2.6	66
982	DNACLUSt: accurate and efficient clustering of phylogenetic marker genes. <i>BMC Bioinformatics</i> , 2011, 12, 271.	2.6	167
983	Estimation of bacterial diversity using next generation sequencing of 16S rDNA: a comparison of different workflows. <i>BMC Bioinformatics</i> , 2011, 12, 473.	2.6	57
984	The nonadaptive nature of the H1N1 2009 Swine Flu pandemic contrasts with the adaptive facilitation of transmission to a new host. <i>BMC Evolutionary Biology</i> , 2011, 11, 6.	3.2	10
985	Analysis of 16S rRNA environmental sequences using MEGAN. <i>BMC Genomics</i> , 2011, 12, S17.	2.8	71
986	Uncultured bacterial diversity in tropical maize (<i>Zea mays</i> L.) rhizosphere. <i>Journal of Basic Microbiology</i> , 2011, 51, 15-32.	3.3	33
987	Highlighting new phylogenetic specificities of Crohn's disease microbiota. <i>Inflammatory Bowel Diseases</i> , 2011, 17, 185-192.	1.9	235
988	Cold temperature decreases bacterial species richness in nitrogen-removing bioreactors treating inorganic mine waters. <i>Biotechnology and Bioengineering</i> , 2011, 108, 2876-2883.	3.3	51
989	Abundance of amoA genes of ammonia-oxidizing archaea and bacteria in activated sludge of full-scale wastewater treatment plants. <i>Bioresource Technology</i> , 2011, 102, 3694-3701.	9.6	187
990	Enhancement in current density and energy conversion efficiency of 3-dimensional MFC anodes using pre-enriched consortium and continuous supply of electron donors. <i>Bioresource Technology</i> , 2011, 102, 5098-5104.	9.6	40
991	Performance and spatial community succession of an anaerobic baffled reactor treating acetone-butanol-ethanol fermentation wastewater. <i>Bioresource Technology</i> , 2011, 102, 7407-7414.	9.6	45
992	Enhancing bioremediation of diesel-fuel-contaminated soil in a boreal climate: Comparison of biostimulation and bioaugmentation. <i>International Biodeterioration and Biodegradation</i> , 2011, 65, 359-368.	3.9	161

#	ARTICLE	IF	CITATIONS
993	The Utility of Functional Gene Arrays for Assessing Community Composition, Relative Abundance, and Distribution of Ammonia-Oxidizing Bacteria and Archaea. <i>Methods in Enzymology</i> , 2011, 496, 373-396.	1.0	20
994	Influence of Molecular Resolution on Sequence-Based Discovery of Ecological Diversity among <i>Synechococcus</i> Populations in an Alkaline Siliceous Hot Spring Microbial Mat. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1359-1367.	3.1	44
995	Biodiversity and Emerging Biogeography of the Neutrophilic Iron-Oxidizing Zetaproteobacteria. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5445-5457.	3.1	125
996	Microbial eukaryotic distribution in a dynamic Beaufort Sea and the Arctic Ocean. <i>Journal of Plankton Research</i> , 2011, 33, 431-444.	1.8	84
997	Recovery of As-Yet-Uncultured Soil Acidobacteria on Dilute Solid Media. <i>Applied and Environmental Microbiology</i> , 2011, 77, 8184-8188.	3.1	64
998	Niche Partitioning of Marine Group I Crenarchaeota in the Euphotic and Upper Mesopelagic Zones of the East China Sea. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7469-7478.	3.1	53
999	Isolation and Characterization of <i>Methanothermobacter crinale</i> sp. nov., a Novel Hydrogenotrophic Methanogen from the Shengli Oil Field. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5212-5219.	3.1	87
1000	Microorganisms with Novel Dissimilatory (Bi)Sulfite Reductase Genes Are Widespread and Part of the Core Microbiota in Low-Sulfate Peatlands. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1231-1242.	3.1	49
1001	Microbial Diversity of a Brazilian Coastal Region Influenced by an Upwelling System and Anthropogenic Activity. <i>PLoS ONE</i> , 2011, 6, e16553.	2.5	47
1002	Identification and Targeted Cultivation of Abundant Novel Freshwater Sphingomonads and Analysis of Their Population Substructure. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7355-7364.	3.1	22
1003	Diversity, Abundance, and Potential Activity of Nitrifying and Nitrate-Reducing Microbial Assemblages in a Subglacial Ecosystem. <i>Applied and Environmental Microbiology</i> , 2011, 77, 4778-4787.	3.1	119
1004	Soil Rhizosphere Microbial Communities and Enzyme Activities under Organic Farming in Alabama. <i>Diversity</i> , 2011, 3, 308-328.	1.7	45
1005	Potential for Direct Interspecies Electron Transfer in Methanogenic Wastewater Digester Aggregates. <i>MBio</i> , 2011, 2, e00159-11.	4.1	472
1006	Pyrosequencing-Based Assessment of Bacterial Community Structure Along Different Management Types in German Forest and Grassland Soils. <i>PLoS ONE</i> , 2011, 6, e17000.	2.5	480
1007	Pattern Recognition in Bioinformatics. <i>Lecture Notes in Computer Science</i> , 2011, , .	1.3	1
1008	<i>Applied Microbiology and Molecular Biology in Oilfield Systems.</i> , 2011, , .		15
1009	Quantitative dominance of seasonally persistent filamentous cyanobacteria (<i>Planktothrix</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 97-109.	3.1	49
1010	Phylogenetic diversity and spatio-temporal distribution of nitrogenase genes (<i>nifH</i>) in the northern South China Sea. <i>Aquatic Microbial Ecology</i> , 2011, 65, 15-27.	1.8	43

#	ARTICLE	IF	CITATIONS
1011	Spatial Variability in Nitrification Rates and Ammonia-Oxidizing Microbial Communities in the Agriculturally Impacted Elkhorn Slough Estuary, California. <i>Applied and Environmental Microbiology</i> , 2011, 77, 269-280.	3.1	98
1012	Abundance, Diversity, and Activity of Ammonia-Oxidizing Prokaryotes in the Coastal Arctic Ocean in Summer and Winter. <i>Applied and Environmental Microbiology</i> , 2011, 77, 2026-2034.	3.1	97
1013	Relationships between Free-Living Protozoa, Cultivable <i>Legionella</i> spp., and Water Quality Characteristics in Three Drinking Water Supplies in the Caribbean. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7321-7328.	3.1	50
1014	Ammonia-Oxidizing Bacteria in Biofilters Removing Trihalomethanes Are Related to <i>Nitrosomonas oligotropha</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 2537-2540.	3.1	17
1015	Temporal Variability of Coastal Planctomycetes Clades at Kabeltonne Station, North Sea. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5009-5017.	3.1	52
1016	Autoregulation of Nodulation Interferes with Impacts of Nitrogen Fertilization Levels on the Leaf-Associated Bacterial Community in Soybeans. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1973-1980.	3.1	50
1017	Comparison of the Specificities and Efficacies of Primers for Aromatic Dioxygenase Gene Analysis of Environmental Samples. <i>Applied and Environmental Microbiology</i> , 2011, 77, 3551-3557.	3.1	64
1018	Diversity and distribution of soil fungal communities in a semiarid grassland. <i>Mycologia</i> , 2011, 103, 10-21.	1.9	153
1019	Production Processes Affected Prokaryotic <i>amoA</i> Gene Abundance and Distribution in High-Temperature Petroleum Reservoirs. <i>Geomicrobiology Journal</i> , 2011, 28, 692-704.	2.0	42
1020	JAGLIC – A SOFTWARE PACKAGE FOR ENVIRONMENTAL DIVERSITY ANALYSES. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 749-773.	0.8	42
1021	Following the Kinetics: Iron-Oxidizing Microbial Mats in Cold Icelandic Volcanic Habitats and Their Rock-Associated Carbonaceous Signature. <i>Astrobiology</i> , 2011, 11, 679-694.	3.0	21
1022	Molecular community analysis of magnesium-rich bittern brine recovered from a Tunisian solar saltern. <i>Canadian Journal of Microbiology</i> , 2011, 57, 975-981.	1.7	15
1023	Molecular analysis of microbial diversity in corrosion samples from energy transmission towers. <i>Biofouling</i> , 2011, 27, 435-447.	2.2	13
1024	Microbial Community Composition and Function in Permanently Cold Seawater and Sediments from an Arctic Fjord of Svalbard. <i>Applied and Environmental Microbiology</i> , 2011, 77, 2008-2018.	3.1	126
1026	Experimental Evidence for Microbially Mediated Carbonate Dissolution from the Saline Water Zone of the Edwards Aquifer, Central Texas. <i>Geomicrobiology Journal</i> , 2011, 28, 313-327.	2.0	22
1027	PhylOTU: A High-Throughput Procedure Quantifies Microbial Community Diversity and Resolves Novel Taxa from Metagenomic Data. <i>PLoS Computational Biology</i> , 2011, 7, e1001061.	3.2	73
1028	Concentration and Diversity of Uncultured <i>Legionella</i> spp. in Two Unchlorinated Drinking Water Supplies with Different Concentrations of Natural Organic Matter. <i>Applied and Environmental Microbiology</i> , 2011, 77, 634-641.	3.1	76
1029	ESPRIT-Tree: hierarchical clustering analysis of millions of 16S rRNA pyrosequences in quasilinear computational time. <i>Nucleic Acids Research</i> , 2011, 39, e95-e95.	14.5	131

#	ARTICLE	IF	CITATIONS
1030	Comparative 16S rRNA gene surveys of granular sludge from three upflow anaerobic bioreactors treating purified terephthalic acid (PTA) wastewater. <i>Water Science and Technology</i> , 2011, 64, 1406-1412.	2.5	14
1031	Distribution and Abundance of Archaea in South China Sea Sponge <i>Holoxea</i> sp. and the Presence of Ammonia-Oxidizing Archaea in Sponge Cells. <i>Evidence-based Complementary and Alternative Medicine</i> , 2011, 2011, 1-5.	1.2	8
1032	Composition and stability of bacterial communities associated with granular activated carbon and anthracite filters in a pilot scale municipal drinking water treatment facility. <i>Journal of Water and Health</i> , 2012, 10, 244-255.	2.6	13
1033	Revealing the Diversity and Quantity of Peritrich Ciliates in Environmental Samples Using Specific Primer-based PCR and Quantitative PCR. <i>Microbes and Environments</i> , 2012, 27, 497-503.	1.6	18
1034	Acquisition of epibiotic bacteria along the life cycle of the hydrothermal shrimp <i>Rimicaris exoculata</i> . <i>ISME Journal</i> , 2012, 6, 597-609.	9.8	75
1035	Low Diversity Bacterial Community and the Trapping Activity of Metabolites from Cultivable Bacteria Species in the Female Reproductive System of the Oriental Fruit Fly, <i>Bactrocera dorsalis</i> Hendel (Diptera: Tephritidae). <i>International Journal of Molecular Sciences</i> , 2012, 13, 6266-6278.	4.1	56
1036	Targeted Restoration of the Intestinal Microbiota with a Simple, Defined Bacteriotherapy Resolves Relapsing <i>Clostridium difficile</i> Disease in Mice. <i>PLoS Pathogens</i> , 2012, 8, e1002995.	4.7	504
1037	Structural Changes of Gut Microbiota during Berberine-Mediated Prevention of Obesity and Insulin Resistance in High-Fat Diet-Fed Rats. <i>PLoS ONE</i> , 2012, 7, e42529.	2.5	435
1038	Cultivation-Independent Methods Reveal Differences among Bacterial Gut Microbiota in Triatomine Vectors of Chagas Disease. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1631.	3.0	92
1039	Microbial diversity of biofilm communities in microniches associated with the didemnid ascidian <i>Lissoclinum patella</i> . <i>ISME Journal</i> , 2012, 6, 1222-1237.	9.8	82
1040	Cyanobacterial diversity for an anthropogenic impact assessment in the SÄr Rondane Mountains area, Antarctica. <i>Antarctic Science</i> , 2012, 24, 229-242.	0.9	10
1041	Equine Stomachs Harbor an Abundant and Diverse Mucosal Microbiota. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2522-2532.	3.1	60
1042	Natural Product Biosynthetic Gene Diversity in Geographically Distinct Soil Microbiomes. <i>Applied and Environmental Microbiology</i> , 2012, 78, 3744-3752.	3.1	96
1043	Temporal Variability of Bacterial Diversity in a Chlorinated Drinking Water Distribution System. <i>Journal of Environmental Engineering, ASCE</i> , 2012, 138, 786-795.	1.4	37
1044	Shifts in bacterial communities of two caribbean reef-building coral species affected by white plague disease. <i>ISME Journal</i> , 2012, 6, 502-512.	9.8	155
1045	Efficient Clustering of Metagenomic Sequences using Locality Sensitive Hashing. , 2012, , .		8
1046	DACIDR. , 2012, , .		10
1047	Abundance and community composition of ammonia-oxidizing archaea and bacteria in two different zones of Lake Taihu. <i>Canadian Journal of Microbiology</i> , 2012, 58, 1018-1026.	1.7	37

#	ARTICLE	IF	CITATIONS
1048	Evidence for Cascades of Perturbation and Adaptation in the Metabolic Genes of Higher Termite Gut Symbionts. MBio, 2012, 3, .	4.1	13
1049	Microbially Induced Iron Precipitation Associated with a Neutrophilic Spring at Borra Caves, Vishakhapatnam, India. Astrobiology, 2012, 12, 327-346.	3.0	16
1050	Microbial shifts in the swine distal gut in response to the treatment with antimicrobial growth promoter, tylosin. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15485-15490.	7.1	231
1051	The Archaeal Diversity and Population in a Drained Alkaline Saline Soil of the Former Lake Texcoco (Mexico). Geomicrobiology Journal, 2012, 29, 18-22.	2.0	11
1052	Cow Teat Skin, a Potential Source of Diverse Microbial Populations for Cheese Production. Applied and Environmental Microbiology, 2012, 78, 326-333.	3.1	123
1053	The intestinal microbiome of the pig. Animal Health Research Reviews, 2012, 13, 100-109.	3.1	304
1054	Environmental Factors Affect Acidobacterial Communities below the Subgroup Level in Grassland and Forest Soils. Applied and Environmental Microbiology, 2012, 78, 7398-7406.	3.1	272
1055	Structural resilience of the gut microbiota in adult mice under high-fat dietary perturbations. ISME Journal, 2012, 6, 1848-1857.	9.8	407
1056	Actinobacterial Diversity in Microbial Mats of Five Hot Springs in Central and Central-Eastern Tibet, China. Geomicrobiology Journal, 2012, 29, 520-527.	2.0	17
1057	Composition of the archaeal community involved in methane production during the decomposition of <i>Microcystis</i> blooms in the laboratory. Canadian Journal of Microbiology, 2012, 58, 1153-1158.	1.7	22
1058	Detection of methanogenic archaea in the pitchers of the Northern pitcher plant (<i>Sarracenia</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342	1.7	6
1059	Pyrosequencing as a tool for better understanding of human microbiomes. Journal of Oral Microbiology, 2012, 4, 10743.	2.7	121
1060	Impact of supragingival therapy on subgingival microbial profile in smokers versus non-smokers with severe chronic periodontitis. Journal of Oral Microbiology, 2012, 4, 8640.	2.7	16
1061	Molecular characterization of ancient algal mats from the <i>McMurdo Dry</i> Valleys, Antarctica. Antarctic Science, 2012, 24, 139-146.	0.9	7
1062	SSuMMo: rapid analysis, comparison and visualization of microbial communities. Bioinformatics, 2012, 28, 679-686.	4.1	5
1063	Seed-Colonizing Bacterial Communities Associated with the Suppression of Pythium Seedling Disease in a Municipal Biosolids Compost. Phytopathology, 2012, 102, 478-489.	2.2	23
1064	Global dispersion of bacterial cells on Asian dust. Scientific Reports, 2012, 2, 525.	3.3	174
1065	Soil Diffusion System Enriches the Growth of Diverse and Previously Uncultivated Bacterial Taxa. Soil Science Society of America Journal, 2012, 76, 463-474.	2.2	7

#	ARTICLE	IF	CITATIONS
1066	Comparison of Sulphate-reducing Bacterial Communities in Japanese Fish Farm Sediments with Different Levels of Organic Enrichment. <i>Microbes and Environments</i> , 2012, 27, 193-199.	1.6	23
1067	Identification of Active Denitrifiers in Rice Paddy Soil by DNA- and RNA-Based Analyses. <i>Microbes and Environments</i> , 2012, 27, 456-461.	1.6	77
1068	Microbial life at $\sim 13^{\circ}\text{C}$ in the brine of an ice-sealed Antarctic lake. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20626-20631.	7.1	151
1069	Molecular Methods to Measure Intestinal Bacteria: A Review. <i>Journal of AOAC INTERNATIONAL</i> , 2012, 95, 5-23.	1.5	42
1070	An untapped bacterial cellulolytic community enriched from coastal marine sediment under anaerobic and thermophilic conditions. <i>FEMS Microbiology Letters</i> , 2012, 335, 39-46.	1.8	17
1071	Co-occurrence and distribution of nitrite-dependent anaerobic ammonium and methane-oxidizing bacteria in a paddy soil. <i>FEMS Microbiology Letters</i> , 2012, 336, 79-88.	1.8	201
1072	Increased Abundance of <i>Gallionella</i> spp., <i>Leptothrix</i> spp. and Total Bacteria in Response to Enhanced Mn and Fe Concentrations in a Disturbed Southern Appalachian High Elevation Wetland. <i>Geomicrobiology Journal</i> , 2012, 29, 124-138.	2.0	26
1073	Abundance and Distribution of Tetracycline Resistance Genes and Mobile Elements in an Oxytetracycline Production Wastewater Treatment System. <i>Environmental Science & Technology</i> , 2012, 46, 7551-7557.	10.0	201
1074	Comparison of soil bacterial communities between coastal and inland forests in a subtropical area. <i>Applied Soil Ecology</i> , 2012, 60, 49-55.	4.3	18
1075	Succession of Denitrifying Community Composition in Coastal Wetland Soils Along a Salinity Gradient. <i>Pedosphere</i> , 2012, 22, 367-374.	4.0	18
1076	Molecular Characterisation of Gastrointestinal Microbiota of Children With Autism (With and Without) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 347 419-427.	3.8	166
1077	Bacterial diversity in different regions of gastrointestinal tract of <i>Giant African Snail</i> (<i>Gastrophysa</i> <i>chatina fulica</i>). <i>MicrobiologyOpen</i> , 2012, 1, 415-426.	3.0	43
1078	Phylogenetic characterisation of <i>Onobrychis</i> species with special focus on the forage crop <i>Onobrychis viciifolia</i> Scop.. <i>Genetic Resources and Crop Evolution</i> , 2012, 59, 1777-1788.	1.6	22
1079	Hydrogeochemistry and microbial contamination of groundwater from Lower Ponnaiyar Basin, Cuddalore District, Tamil Nadu, India. <i>Environmental Earth Sciences</i> , 2012, 67, 867-887.	2.7	39
1080	LSH-Div: Species diversity estimation using locality sensitive hashing. , 2012, , .		12
1081	The Response of Potentially Active Planktonic Actinobacteria to the Construction of Three Gorges Dam of the Yangtze River, China. <i>Geomicrobiology Journal</i> , 2012, 29, 114-123.	2.0	4
1082	Linking bacterial diversity and geochemistry of uranium-contaminated groundwater. <i>Environmental Technology (United Kingdom)</i> , 2012, 33, 1629-1640.	2.2	24
1083	Molecular Detection of Novel Anammox Bacterial Clusters in the Sediments of the Shallow Freshwater Lake Taihu. <i>Geomicrobiology Journal</i> , 2012, 29, 852-859.	2.0	19

#	ARTICLE	IF	CITATIONS
1084	Ultrafast clustering algorithms for metagenomic sequence analysis. <i>Briefings in Bioinformatics</i> , 2012, 13, 656-668.	6.5	403
1085	Phylogenetic Microarray Analysis of a Microbial Community Performing Reductive Dechlorination at a TCE-Contaminated Site. <i>Environmental Science & Technology</i> , 2012, 46, 1044-1054.	10.0	36
1086	Microbial Communities Involved in Methane Production from Hydrocarbons in Oil Sands Tailings. <i>Environmental Science & Technology</i> , 2012, 46, 9802-9810.	10.0	102
1087	Methanogen diversity in the rumen of Indian Surti buffalo (<i>Bubalus bubalis</i>), assessed by 16S rDNA analysis. <i>Research in Veterinary Science</i> , 2012, 92, 451-455.	1.9	32
1088	The structure and spatio-temporal distribution of the Archaea in a horizontal subsurface flow constructed wetland. <i>Science of the Total Environment</i> , 2012, 435-436, 465-471.	8.0	17
1089	Bacterial and Archaeal Symbionts in the South China Sea Sponge <i>Phakellia fusca</i> : Community Structure, Relative Abundance, and Ammonia-Oxidizing Populations. <i>Marine Biotechnology</i> , 2012, 14, 701-713.	2.4	27
1090	Environmental constraints defining the distribution, composition, and evolution of chlorophototrophs in thermal features of Yellowstone National Park. <i>Geobiology</i> , 2012, 10, 236-249.	2.4	42
1091	Microbial Community Composition in Acid Mine Drainage Lake of Xiang Mountain Sulfide Mine in Anhui Province, China. <i>Geomicrobiology Journal</i> , 2012, 29, 886-895.	2.0	18
1092	Changes in soil bacterial communities following liming of acidified forests. <i>Applied Soil Ecology</i> , 2012, 59, 116-123.	4.3	24
1093	Bioavailability of jarosite for stimulating acid mine drainage attenuation. <i>Geochimica Et Cosmochimica Acta</i> , 2012, 78, 65-76.	3.9	23
1094	Diversity of microbial plankton across the Three Gorges Dam of the Yangtze River, China. <i>Geoscience Frontiers</i> , 2012, 3, 335-349.	8.4	35
1095	Microbial diversity in cold seep sediments from the northern South China Sea. <i>Geoscience Frontiers</i> , 2012, 3, 301-316.	8.4	47
1096	Microbial diversity in two cold springs on the Qinghai-Tibetan Plateau. <i>Geoscience Frontiers</i> , 2012, 3, 317-325.	8.4	10
1097	Variation of culturable bacteria along depth in the East Rongbuk ice core, Mt. Everest. <i>Geoscience Frontiers</i> , 2012, 3, 327-334.	8.4	17
1098	Comparison of metagenomic samples using sequence signatures. <i>BMC Genomics</i> , 2012, 13, 730.	2.8	74
1099	Short-term responses of unicellular planktonic eukaryotes to increases in temperature and UVB radiation. <i>BMC Microbiology</i> , 2012, 12, 202.	3.3	5
1100	Changes in human gut flora with age: an Indian familial study. <i>BMC Microbiology</i> , 2012, 12, 222.	3.3	36
1101	High-resolution deep sequencing reveals biodiversity, population structure, and persistence of HIV-1 quasispecies within host ecosystems. <i>Retrovirology</i> , 2012, 9, 108.	2.0	27

#	ARTICLE	IF	CITATIONS
1102	Microbial community analysis in biocathode microbial fuel cells packed with different materials. <i>AMB Express</i> , 2012, 2, 21.	3.0	61
1103	Uncovering the origin of the black stains in <i>Leptothrix ascaux</i> in <i>Leptothrix</i> range. <i>Environmental Microbiology</i> , 2012, 14, 3220-3231.	3.8	55
1104	Anammox Bacterial Abundance, Activity, and Contribution in Riparian Sediments of the Pearl River Estuary. <i>Environmental Science & Technology</i> , 2012, 46, 8834-8842.	10.0	175
1105	Meta-analyses of environmental sequence data identify anoxia and salinity as parameters shaping ciliate communities. <i>Systematics and Biodiversity</i> , 2012, 10, 277-288.	1.2	31
1106	Huanglongbing alters the structure and functional diversity of microbial communities associated with citrus rhizosphere. <i>ISME Journal</i> , 2012, 6, 363-383.	9.8	162
1107	Bacterial Communities and the Nitrogen Cycle in the Gypsum Soils of Cuatro CiÃ©negas Basin, Coahuila: A Mars Analogue. <i>Astrobiology</i> , 2012, 12, 699-709.	3.0	59
1108	Microbial community changes in aquifer sediment microcosm for anaerobic anthracene biodegradation under methanogenic condition. <i>Journal of Environmental Sciences</i> , 2012, 24, 1498-1503.	6.1	27
1109	Bacterial diversity of siliciclastic sediments in a <i>Thalassia testudinum</i> meadow and the implications for <i>Luciniscas nassula</i> chemosymbiosis. <i>Estuarine, Coastal and Shelf Science</i> , 2012, 112, 153-161.	2.1	11
1110	Higher nitrate-reducer diversity in macrophyte-colonized compared to unvegetated freshwater sediment. <i>Systematic and Applied Microbiology</i> , 2012, 35, 465-472.	2.8	21
1111	Phylogenetic diversity of ammonia-oxidizing archaea and bacteria in biofilters of recirculating aquaculture systems. <i>Marine Genomics</i> , 2012, 7, 27-31.	1.1	24
1112	Methanogenesis pathways in a stratified eutrophic alpine lake (Lake Bled, Slovenia). <i>Limnology and Oceanography</i> , 2012, 57, 868-880.	3.1	22
1113	Abundance and diversity of candidate division JS1- and Chloroflexi-related bacteria in cold seep sediments of the northern South China Sea. <i>Frontiers of Earth Science</i> , 2012, 6, 373-382.	2.1	7
1114	Co-occurrence of nitrite-dependent anaerobic methane oxidizing and anaerobic ammonia oxidizing bacteria in two Qinghai-Tibetan saline lakes. <i>Frontiers of Earth Science</i> , 2012, 6, 383-391.	2.1	53
1115	Heterogeneity of microbial community structures inside the up-flow biological activated carbon (BAC) filters for the treatment of drinking water. <i>Biotechnology and Bioprocess Engineering</i> , 2012, 17, 881-886.	2.6	38
1116	A large-scale benchmark study of existing algorithms for taxonomy-independent microbial community analysis. <i>Briefings in Bioinformatics</i> , 2012, 13, 107-121.	6.5	133
1117	High-Throughput Characterization and Comparison of Microbial Communities. , 2012, , 37-57.		0
1118	Backwash intensity and frequency impact the microbial community structure and function in a fixed-bed biofilm reactor. <i>Applied Microbiology and Biotechnology</i> , 2012, 96, 815-827.	3.6	15
1119	Bacterial and archaeal phylogenetic diversity associated with swine sludge from an anaerobic treatment lagoon. <i>World Journal of Microbiology and Biotechnology</i> , 2012, 28, 3187-3195.	3.6	23

#	ARTICLE	IF	CITATIONS
1120	Effects of different management practices on arbuscular mycorrhizal fungal diversity in maize fields by a molecular approach. <i>Biology and Fertility of Soils</i> , 2012, 48, 911-922.	4.3	95
1121	Molecular analysis of gut microbiota in obesity among Indian individuals. <i>Journal of Biosciences</i> , 2012, 37, 647-657.	1.1	142
1122	Comparative analysis of fecal microflora of healthy full-term Indian infants born with different methods of delivery (vaginal vs cesarean): <i>Acinetobacter</i> sp. prevalence in vaginally born infants. <i>Journal of Biosciences</i> , 2012, 37, 989-998.	1.1	57
1123	Gut microbiota: methodological aspects to describe taxonomy and functionality. <i>Briefings in Bioinformatics</i> , 2012, 13, 747-750.	6.5	7
1124	Amelioration of free copper by hydrothermal vent microbes as a response to high copper concentrations. <i>Chemistry and Ecology</i> , 2012, 28, 405-420.	1.6	19
1125	Comparative analysis of methanogen diversity in the rumen of crossbred buffalo and cattle in the Philippines by using the functional gene <i>mcrA</i> . <i>Molecular Biology Reports</i> , 2012, 39, 10769-10774.	2.3	8
1126	Spatial distribution of prokaryotic symbionts and ammoxidation, denitrifier bacteria in marine sponge <i>Astrosclera willeyana</i> . <i>Scientific Reports</i> , 2012, 2, 528.	3.3	23
1127	Ray Meta: scalable de novo metagenome assembly and profiling. <i>Genome Biology</i> , 2012, 13, R122.	9.6	549
1128	Abrolhos Bank Reef Health Evaluated by Means of Water Quality, Microbial Diversity, Benthic Cover, and Fish Biomass Data. <i>PLoS ONE</i> , 2012, 7, e36687.	2.5	125
1129	Coordinating Environmental Genomics and Geochemistry Reveals Metabolic Transitions in a Hot Spring Ecosystem. <i>PLoS ONE</i> , 2012, 7, e38108.	2.5	97
1130	Soil Eukaryotic Microorganism Succession as Affected by Continuous Cropping of Peanut - Pathogenic and Beneficial Fungi were Selected. <i>PLoS ONE</i> , 2012, 7, e40659.	2.5	91
1131	Abundance and Genetic Diversity of Microbial Polygalacturonase and Pectate Lyase in the Sheep Rumen Ecosystem. <i>PLoS ONE</i> , 2012, 7, e40940.	2.5	9
1132	Effect of Different Ammonia Concentrations on Community Succession of Ammonia-oxidizing Microorganisms in a Simulated Paddy Soil Column. <i>PLoS ONE</i> , 2012, 7, e44122.	2.5	30
1133	Statistical Object Data Analysis of Taxonomic Trees from Human Microbiome Data. <i>PLoS ONE</i> , 2012, 7, e48996.	2.5	15
1134	Multivariate Approach for Studying Interactions between Environmental Variables and Microbial Communities. <i>PLoS ONE</i> , 2012, 7, e50267.	2.5	21
1135	Hypothesis Testing and Power Calculations for Taxonomic-Based Human Microbiome Data. <i>PLoS ONE</i> , 2012, 7, e52078.	2.5	289
1136	Widespread <i>Oceanospirillaceae</i> Bacteria in <i>Porites</i> spp.. <i>Journal of Marine Biology</i> , 2012, 2012, 1-7.	1.0	35
1137	Diversity and Activity of Denitrifiers of Chilean Arid Soil Ecosystems. <i>Frontiers in Microbiology</i> , 2012, 3, 101.	3.5	38

#	ARTICLE	IF	CITATIONS
1138	Trace Elements Affect Methanogenic Activity and Diversity in Enrichments from Subsurface Coal Bed Produced Water. <i>Frontiers in Microbiology</i> , 2012, 3, 175.	3.5	72
1139	Microbial communities at the borehole observatory on the Costa Rica Rift flank (Ocean Drilling) Tj ETQq1 1 0.784314 rgBT / Overlock 10	3.5	20
1140	Stratified active archaeal communities in the sediments of Jiulong River estuary, China. <i>Frontiers in Microbiology</i> , 2012, 3, 311.	3.5	39
1141	Bacterial Diversity in an Amazonian Mangrove Ecosystem. <i>Aquatic Science and Technology</i> , 2012, 1, .	0.1	1
1142	Effects of long-term fertilization on nifH gene diversity in agricultural black soil. <i>African Journal of Microbiology Research</i> , 2012, 6, .	0.4	0
1143	Molecular diversity of bacterial community of dye wastewater in an anaerobic sequencing batch reactor. <i>African Journal of Microbiology Research</i> , 2012, 6, .	0.4	14
1144	Metagenomics in Polluted Aquatic Environments. , 0, , .		1
1145	Prokaryotic Diversity of the TucuruÃ-Hydropower Plant Reservoir in the Brazilian Amazon. <i>Aquatic Science and Technology</i> , 2012, 1, .	0.1	6
1146	Computational methods for the analysis of tag sequences in metagenomics studies. <i>Frontiers in Bioscience - Scholar</i> , 2012, S4, 1333-1343.	2.1	2
1147	Diversity and three-dimensional structures of the alpha Mcr of the methanogenic Archaea from the anoxic region of TucuruÃ-Lake, in Eastern Brazilian Amazonia. <i>Genetics and Molecular Biology</i> , 2012, 35, 126-133.	1.3	2
1148	Bacterial diversity in the saliva of patients with different oral hygiene indexes. <i>Brazilian Dental Journal</i> , 2012, 23, 409-416.	1.1	11
1149	Cascade cell lyses and DNA extraction for identification of genes and microorganisms in kefir grains. <i>Journal of Dairy Research</i> , 2012, 79, 26-32.	1.4	11
1150	Diversity of Bacteria and Archaea in hypersaline sediment from Death Valley National Park, California. <i>MicrobiologyOpen</i> , 2012, 1, 135-148.	3.0	21
1151	Structural segregation of gut microbiota between colorectal cancer patients and healthy volunteers. <i>ISME Journal</i> , 2012, 6, 320-329.	9.8	1,038
1152	Application of bio-organic fertilizer can control Fusarium wilt of cucumber plants by regulating microbial community of rhizosphere soil. <i>Biology and Fertility of Soils</i> , 2012, 48, 807-816.	4.3	262
1153	Molecular diversity of nitrogen-fixing bacteria associated with <i>Chrysopogon zizanioides</i> (L.) Roberty (vetiver), an essential oil producer plant. <i>Plant and Soil</i> , 2012, 356, 101-111.	3.7	7
1154	Molecular characterisation of the diazotrophic bacterial community in uninoculated and inoculated field-grown sugarcane (<i>Saccharum</i> sp.). <i>Plant and Soil</i> , 2012, 356, 83-99.	3.7	105
1155	Bacterial community in the rhizosphere of the cactus species <i>Mammillaria carnea</i> during dry and rainy seasons assessed by deep sequencing. <i>Plant and Soil</i> , 2012, 357, 275-288.	3.7	38

#	ARTICLE	IF	CITATIONS
1156	Evolving Concepts of Bacterial Species. <i>Evolutionary Biology</i> , 2012, 39, 148-157.	1.1	33
1157	Molecular typing of fecal eukaryotic microbiota of human infants and their respective mothers. <i>Journal of Biosciences</i> , 2012, 37, 221-226.	1.1	39
1158	Anthracene biodegradation under nitrate-reducing condition and associated microbial community changes. <i>Biotechnology and Bioprocess Engineering</i> , 2012, 17, 371-376.	2.6	21
1159	Effect of salinity on nitrogenase activity and composition of the active diazotrophic community in intertidal microbial mats. <i>Archives of Microbiology</i> , 2012, 194, 483-491.	2.2	43
1160	Microbial biodiversity in a Malaysian oil field and a systematic comparison with oil reservoirs worldwide. <i>Archives of Microbiology</i> , 2012, 194, 513-523.	2.2	49
1161	Geographic Specific Coral-Associated Ammonia-Oxidizing Archaea in the Northern Gulf of Eilat (Red Tj ETQq1 1 0.784314 rgBT / Overbo	2.8	21
1162	Genotypic Distribution of a Specialist Model Microorganism, <i>Methanosaeta</i> , along an Estuarine Gradient: Does Metabolic Restriction Limit Niche Differentiation Potential?. <i>Microbial Ecology</i> , 2012, 63, 856-864.	2.8	5
1163	First Prokaryotic Biodiversity Assessment Using Molecular Techniques of an Acidic River in Neuqu�n, Argentina. <i>Microbial Ecology</i> , 2012, 64, 91-104.	2.8	39
1164	Gut-Associated Bacteria Throughout the Life Cycle of the Bark Beetle <i>Dendroctonus rhizophagus</i> Thomas and Bright (Curculionidae: Scolytinae) and Their Cellulolytic Activities. <i>Microbial Ecology</i> , 2012, 64, 268-278.	2.8	139
1165	<i>Exitomelita sigynae</i> gen. et sp. nov.: a new amphipod from the Arctic Loki Castle vent field with potential gill ectosymbionts. <i>Polar Biology</i> , 2012, 35, 705-716.	1.2	20
1166	Comparative microbial diversity analyses of modern marine thrombolitic mats by barcoded pyrosequencing. <i>Environmental Microbiology</i> , 2012, 14, 82-100.	3.8	56
1167	Phylogenetic and functional diversity of Bacteria and Archaea in a unique stratified lagoon, the Clipperton atoll (N Pacific). <i>FEMS Microbiology Ecology</i> , 2012, 79, 203-217.	2.7	25
1168	Genetic characterization of denitrifier communities with contrasting intrinsic functional traits. <i>FEMS Microbiology Ecology</i> , 2012, 79, 542-554.	2.7	56
1169	Phylogenetic characterization of bacteria in the gut of house flies (<i>Musca domestica</i> L.). <i>FEMS Microbiology Ecology</i> , 2012, 79, 581-593.	2.7	144
1170	Phylogenetic diversity, composition and distribution of bacterioplankton community in the Dongjiang River, China. <i>FEMS Microbiology Ecology</i> , 2012, 80, 30-44.	2.7	81
1171	Molecular diversity of methanogens and identification of <i>Methanolobus</i> sp. as active methylotrophic Archaea in Lonar crater lake sediments. <i>FEMS Microbiology Ecology</i> , 2012, 81, 43-51.	2.7	56
1172	Structure and diversity of bacterial, eukaryotic and archaeal communities in glacial cryoconite holes from the Arctic and the Antarctic. <i>FEMS Microbiology Ecology</i> , 2012, 82, 254-267.	2.7	136
1173	Nectar yeasts of two southern Spanish plants: the roles of immigration and physiological traits in community assembly. <i>FEMS Microbiology Ecology</i> , 2012, 80, 281-293.	2.7	109

#	ARTICLE	IF	CITATIONS
1174	Cyanobacterial diversity in the phyllosphere of a mangrove forest. FEMS Microbiology Ecology, 2012, 80, 312-322.	2.7	65
1175	Community structure of bacteria and fungi in aerosols of a pig confinement building. FEMS Microbiology Ecology, 2012, 80, 390-401.	2.7	35
1176	Methane-cycling communities in a permafrost-affected soil on Herschel Island, Western Canadian Arctic: active layer profiling of <i>mcrA</i> and <i>pmoA</i> genes. FEMS Microbiology Ecology, 2012, 82, 287-302.	2.7	72
1177	Assessment of bacterial communities and characterization of lead-resistant bacteria in the rhizosphere soils of metal-tolerant <i>Chenopodium ambrosioides</i> grown on lead-zinc mine tailings. Chemosphere, 2012, 87, 1171-1178.	8.2	86
1178	Heterogeneity of ammonia-oxidizing community structures in a pilot-scale drinking water biofilter. International Biodeterioration and Biodegradation, 2012, 70, 148-152.	3.9	25
1179	Correlation between microbial community structure and biofouling in a laboratory scale membrane bioreactor with synthetic wastewater. Desalination, 2012, 287, 209-215.	8.2	98
1181	Performance and bacterial compositions of aged refuse reactors treating mature landfill leachate. Bioresource Technology, 2012, 103, 71-77.	9.6	76
1182	Various voltage productions by microbial fuel cells with sedimentary inocula taken from different sites in one freshwater lake. Bioresource Technology, 2012, 108, 68-75.	9.6	33
1183	Spatial distribution of archaeal and bacterial ammonia oxidizers in the littoral buffer zone of a nitrogen-rich lake. Journal of Environmental Sciences, 2012, 24, 790-799.	6.1	32
1184	Ecology of the microbiome of the infected root canal system: a comparison between apical and coronal root segments. International Endodontic Journal, 2012, 45, 530-541.	5.0	103
1185	The <i>mcrA</i> gene and 16S rRNA gene in the phylogenetic analysis of methanogens in the rumen of faunated and unfauinated cattle. Animal Science Journal, 2012, 83, 727-734.	1.4	11
1186	Ruminal fermentation and microbial ecology of buffaloes and cattle fed the same diet. Animal Science Journal, 2012, 83, 767-776.	1.4	12
1187	COVER: <i>a priori</i> estimation of coverage for metagenomic sequencing. Environmental Microbiology Reports, 2012, 4, 335-341.	2.4	13
1188	Distribution and Diversity of a Protist Predator <i>Cryothecomonas</i> (Cercozoa) in Arctic Marine Waters. Journal of Eukaryotic Microbiology, 2012, 59, 291-299.	1.7	35
1189	Origin and fate of acetate in an acidic fen. FEMS Microbiology Ecology, 2012, 81, 339-354.	2.7	38
1190	The Pyramid Trough Wetland: environmental and biological diversity in a newly created Antarctic protected area. FEMS Microbiology Ecology, 2012, 82, 356-366.	2.7	30
1191	Diverse and highly active diazotrophic assemblages inhabit ephemeral wetted soils of the Antarctic Dry Valleys. FEMS Microbiology Ecology, 2012, 82, 376-390.	2.7	59
1192	Molecular characterization of the microbial communities in the subcaudal gland secretion of the European badger (<i>Meles meles</i>). FEMS Microbiology Ecology, 2012, 81, 648-659.	2.7	38

#	ARTICLE	IF	CITATIONS
1193	Eukaryotes in Arctic and Antarctic cyanobacterial mats. FEMS Microbiology Ecology, 2012, 82, 416-428.	2.7	52
1194	Aerobic and anaerobic methane oxidation in terrestrial mud volcanoes in the Northern Apennines. Sedimentary Geology, 2012, 263-264, 210-219.	2.1	34
1195	Pyrosequencing and mid-infrared spectroscopy reveal distinct aggregate stratification of soil bacterial communities and organic matter composition. Soil Biology and Biochemistry, 2012, 46, 63-72.	8.8	228
1196	Different biogeographic patterns of prokaryotes and microbial eukaryotes in epilithic biofilms. Molecular Ecology, 2012, 21, 3852-3868.	3.9	57
1197	Massively parallel rRNA gene sequencing exacerbates the potential for biased community diversity comparisons due to variable library sizes. Environmental Microbiology, 2012, 14, 285-290.	3.8	386
1198	Environmental factors determining ammonia-oxidizing organism distribution and diversity in marine environments. Environmental Microbiology, 2012, 14, 714-729.	3.8	146
1199	The response of marine picoplankton to ocean acidification. Environmental Microbiology, 2012, 14, 2293-2307.	3.8	124
1200	Analysis of the salivary microbiome using culture-independent techniques. Journal of Clinical Bioinformatics, 2012, 2, 4.	1.2	54
1201	Characterization of the Gastrointestinal Microbiota in Health and Inflammatory Bowel Disease. Inflammatory Bowel Diseases, 2012, 18, 372-390.	1.9	91
1202	Diversity and distribution of proteorhodopsin-containing microorganisms in marine environments. Frontiers of Environmental Science and Engineering, 2012, 6, 98-106.	6.0	0
1203	Changes of Fecal Bifidobacterium Species in Adult Patients with Hepatitis B Virus-Induced Chronic Liver Disease. Microbial Ecology, 2012, 63, 304-313.	2.8	111
1204	Analysis of Extensive [FeFe] Hydrogenase Gene Diversity Within the Gut Microbiota of Insects Representing Five Families of Dictyoptera. Microbial Ecology, 2012, 63, 586-595.	2.8	12
1205	In-depth Characterization via Complementing Culture-Independent Approaches of the Microbial Community in an Acidic Hot Spring of the Colombian Andes. Microbial Ecology, 2012, 63, 103-115.	2.8	111
1206	Comparative Geochemical and Microbiological Characterization of Two Thermal Pools in the Uzon Caldera, Kamchatka, Russia. Microbial Ecology, 2012, 63, 471-489.	2.8	59
1207	Methanotrophic community structure and activity under warming and grazing of alpine meadow on the Tibetan Plateau. Applied Microbiology and Biotechnology, 2012, 93, 2193-2203.	3.6	87
1208	Benthic mats in Antarctica: biophysical coupling of sea-bed hypoxia and sediment communities. Polar Biology, 2012, 35, 107-116.	1.2	11
1209	Nicomache (Loxochona) lokii sp. nov. (Annelida: Polychaeta: Maldanidae) from the Loki's Castle vent field: an important structure builder in an Arctic vent system. Polar Biology, 2012, 35, 161-170.	1.2	28
1210	Assessment of soil bacterial communities on Alexander Island (in the maritime and continental) Tj ETQq1 1 0.784314 rgBT / Overlock 1047	1.2	47

#	ARTICLE	IF	CITATIONS
1211	Low-diversity fungal assemblage in an Antarctic Dry Valleys soil. <i>Polar Biology</i> , 2012, 35, 567-574.	1.2	65
1212	Diversity of bacterial communities related to the nitrogen cycle in a coastal tropical bay. <i>Molecular Biology Reports</i> , 2012, 39, 3401-3407.	2.3	2
1213	Microbial diversity and activity in hypersaline high Arctic spring channels. <i>Extremophiles</i> , 2012, 16, 177-191.	2.3	33
1214	Diversity of culturable halophilic archaea isolated from Rambla Salada, Murcia (Spain). <i>Extremophiles</i> , 2012, 16, 205-213.	2.3	18
1215	Archaeal <i>amoA</i> gene diversity points to distinct biogeography of ammonia-oxidizing <i>Crenarchaeota</i> in the ocean. <i>Environmental Microbiology</i> , 2013, 15, 1647-1658.	3.8	169
1216	Microbial diversity in the sediment of a crab pond in Nanjing, China. <i>Aquaculture Research</i> , 2013, 44, 321-325.	1.8	12
1217	Culture-independent analysis of <i>Pseudomonas</i> community structures in fertilized and unfertilized agricultural soils. <i>Annals of Microbiology</i> , 2013, 63, 323-333.	2.6	4
1218	Late Holocene changes in cyanobacterial community structure in maritime Antarctic lakes. <i>Journal of Paleolimnology</i> , 2013, 50, 15-31.	1.6	14
1219	Characterization of microbial communities in a granular activated carbon-sand dual media filter for drinking water treatment. <i>International Journal of Environmental Science and Technology</i> , 2013, 10, 917-922.	3.5	42
1220	Filamentous fungi from the Atlantic marine sponge <i>Dragmacidon reticulatum</i> . <i>Archives of Microbiology</i> , 2013, 195, 99-111.	2.2	60
1221	Phylogenetic Diversity of Actinobacteria Associated with Soft Coral <i>Alcyonium gracilimum</i> and Stony Coral <i>Tubastraea coccinea</i> in the East China Sea. <i>Microbial Ecology</i> , 2013, 66, 189-199.	2.8	29
1222	Nitrogen-Fixing and Uricolytic Bacteria Associated with the Gut of <i>Dendroctonus rhizophagus</i> and <i>Dendroctonus valens</i> (Curculionidae: Scolytinae). <i>Microbial Ecology</i> , 2013, 66, 200-210.	2.8	121
1223	The Ecological Perspective of Microbial Communities in Two Pairs of Competitive Hawaiian Native and Invasive Macroalgae. <i>Microbial Ecology</i> , 2013, 65, 361-370.	2.8	3
1224	Elevated Atmospheric CO ₂ Impacts Abundance and Diversity of Nitrogen Cycling Functional Genes in Soil. <i>Microbial Ecology</i> , 2013, 65, 394-404.	2.8	14
1225	Deep Sequencing of <i>Myxilla</i> (Ectyomyxilla) methanophila, an Epibiotic Sponge on Cold-Seep Tubeworms, Reveals Methylophilic, Thiotrophic, and Putative Hydrocarbon-Degrading Microbial Associations. <i>Microbial Ecology</i> , 2013, 65, 450-461.	2.8	25
1226	Bacterial Consortium of <i>Millepora dichotoma</i> Exhibiting Unusual Multifocal Lesion Event in the Gulf of Eilat, Red Sea. <i>Microbial Ecology</i> , 2013, 65, 50-59.	2.8	10
1227	Species diversity of culturable endophytic fungi from Brazilian mangrove forests. <i>Current Genetics</i> , 2013, 59, 153-166.	1.7	78
1228	Microbial communities on deteriorated artistic tiles from Pena National Palace (Sintra, Portugal). <i>International Biodeterioration and Biodegradation</i> , 2013, 84, 322-332.	3.9	42

#	ARTICLE	IF	CITATIONS
1229	Contrasting Patterns of Community Assembly in the Stratified Water Column of Great Salt Lake, Utah. <i>Microbial Ecology</i> , 2013, 66, 268-280.	2.8	64
1230	Community Structures and Distribution of Anaerobic Ammonium Oxidizing and nirS-Encoding Nitrite-Reducing Bacteria in Surface Sediments of the South China Sea. <i>Microbial Ecology</i> , 2013, 66, 281-296.	2.8	57
1231	Taxonomic and functional metagenomic profiling of gastrointestinal tract microbiome of the farmed adult turbot (<i>Scophthalmus maximus</i>). <i>FEMS Microbiology Ecology</i> , 2013, 86, 432-443.	2.7	149
1232	The Ammonia Oxidizing and Denitrifying Prokaryotes Associated with Sponges from Different Sea Areas. <i>Microbial Ecology</i> , 2013, 66, 427-436.	2.8	36
1233	M-pick, a modularity-based method for OTU picking of 16S rRNA sequences. <i>BMC Bioinformatics</i> , 2013, 14, 43.	2.6	33
1234	A unique midgut-associated bacterial community hosted by the cave beetle <i>Cansiliella servadeii</i> (Coleoptera: Leptodirini) reveals parallel phylogenetic divergences from universal gut-specific ancestors. <i>BMC Microbiology</i> , 2013, 13, 129.	3.3	11
1235	Bacterial community changes along a salinity gradient in a Chinese wetland. <i>Canadian Journal of Microbiology</i> , 2013, 59, 611-619.	1.7	19
1236	PhyloPhlAn is a new method for improved phylogenetic and taxonomic placement of microbes. <i>Nature Communications</i> , 2013, 4, 2304.	12.8	797
1237	Mineralogy Drives Bacterial Biogeography of Hydrothermally Inactive Seafloor Sulfide Deposits. <i>Geomicrobiology Journal</i> , 2013, 30, 313-326.	2.0	52
1238	Dark Carbon Fixation in the Columbia River's Estuarine Turbidity Maxima: Molecular Characterization of Red-Type <i>cbbL</i> Genes and Measurement of DIC Uptake Rates in Response to Added Electron Donors. <i>Estuaries and Coasts</i> , 2013, 36, 1073-1083.	2.2	16
1239	Phylogenetic diversity of microbial communities in real drinking water distribution systems. <i>Biotechnology and Bioengineering</i> , 2013, 18, 119-124.	2.6	32
1240	Succession of bacterial communities during composting process as detected by 16S rRNA clone libraries analysis. <i>International Biodeterioration and Biodegradation</i> , 2013, 78, 58-66.	3.9	123
1241	Using the variation of anammox bacteria community structures as a bio-indicator for anthropogenic/terrestrial nitrogen inputs in the Pearl River Delta (PRD). <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 9875-9883.	3.6	40
1242	Nitrogen removal through different pathways in an aged refuse bioreactor treating mature landfill leachate. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 9225-9234.	3.6	52
1243	Higher diversity of ammonia/ammonium-oxidizing prokaryotes in constructed freshwater wetland than natural coastal marine wetland. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 7015-7033.	3.6	91
1244	More refined diversity of anammox bacteria recovered and distribution in different ecosystems. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 3653-3663.	3.6	47
1245	<i>amoA</i> -encoding archaea in wastewater treatment plants: a review. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 1425-1439.	3.6	88
1246	Dominance of <i>Candidatus Scalindua</i> species in anammox community revealed in soils with different duration of rice paddy cultivation in Northeast China. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 1785-1798.	3.6	77

#	ARTICLE	IF	CITATIONS
1247	Vertical Distribution of Ammonia-Oxidizing Archaea and Bacteria in Sediments of a Eutrophic Lake. <i>Current Microbiology</i> , 2013, 67, 327-332.	2.2	40
1248	Comparison of DNA and RNA, and Cultivation Approaches for the Recovery of Terrestrial and Aquatic Fungi from Environmental Samples. <i>Current Microbiology</i> , 2013, 66, 185-191.	2.2	11
1249	Richness and diversity of bacteria in the Nansha carbonate platform (Core MD05-2896), South China Sea. <i>World Journal of Microbiology and Biotechnology</i> , 2013, 29, 1895-1905.	3.6	1
1250	Investigation of the FeFe-hydrogenase gene diversity combined with phylogenetic microbial community analysis of an anaerobic domestic sewage sludge. <i>World Journal of Microbiology and Biotechnology</i> , 2013, 29, 2003-2014.	3.6	10
1251	Comparison of the diversity of root-associated bacteria in <i>Phragmites australis</i> and <i>Typha angustifolia</i> L. in artificial wetlands. <i>World Journal of Microbiology and Biotechnology</i> , 2013, 29, 1499-1508.	3.6	32
1252	Phylogenetic diversity of prokaryotes associated with the mandibulate nasute termite <i>Cornitermes cumulans</i> and its mound. <i>Biology and Fertility of Soils</i> , 2013, 49, 567-574.	4.3	13
1253	Chemical and Microbiological Characterization of Atmospheric Particulate Matter during an Intense African Dust Event in Southern Spain. <i>Environmental Science & Technology</i> , 2013, 47, 3630-3638.	10.0	43
1254	Abundance and diversity of archaeal <i>accA</i> gene in hot springs in Yunnan Province, China. <i>Extremophiles</i> , 2013, 17, 871-879.	2.3	6
1255	High abundance of heterotrophic prokaryotes in hydrothermal springs of the Azores as revealed by a network of 16S rRNA gene-based methods. <i>Extremophiles</i> , 2013, 17, 649-662.	2.3	54
1256	The prokaryotic community of a historically mining-impacted tropical stream sediment is as diverse as that from a pristine stream sediment. <i>Extremophiles</i> , 2013, 17, 301-309.	2.3	49
1257	Microbial Analysis in Primary and Persistent Endodontic Infections by Using Pyrosequencing. <i>Journal of Endodontics</i> , 2013, 39, 1136-1140.	3.1	107
1258	Community-Analyzer: A platform for visualizing and comparing microbial community structure across microbiomes. <i>Genomics</i> , 2013, 102, 409-418.	2.9	27
1259	MSClust: A Multi-Seeds based Clustering algorithm for microbiome profiling using 16S rRNA sequence. <i>Journal of Microbiological Methods</i> , 2013, 94, 347-355.	1.6	17
1260	Metagenomic analysis of the pinewood nematode microbiome reveals a symbiotic relationship critical for xenobiotics degradation. <i>Scientific Reports</i> , 2013, 3, 1869.	3.3	121
1261	Diversity of bacterioplankton in contrasting Tibetan lakes revealed by high-density microarray and clone library analysis. <i>FEMS Microbiology Ecology</i> , 2013, 86, 277-287.	2.7	41
1262	Temporal variation in airborne microbial populations and microbially-derived allergens in a tropical urban landscape. <i>Atmospheric Environment</i> , 2013, 74, 291-300.	4.1	109
1263	Heuristic optimization for global species clustering of <scp>DNA</scp> sequence data from multiple loci. <i>Methods in Ecology and Evolution</i> , 2013, 4, 961-970.	5.2	2
1264	A comparison of two 16S rRNA gene-based PCR primer sets in unraveling anammox bacteria from different environmental samples. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 10521-10529.	3.6	36

#	ARTICLE	IF	CITATIONS
1265	A newly designed degenerate PCR primer based on pmoA gene for detection of nitrite-dependent anaerobic methane-oxidizing bacteria from different ecological niches. Applied Microbiology and Biotechnology, 2013, 97, 10155-10162.	3.6	54
1266	16S rRNA metagenome clustering and diversity estimation using locality sensitive hashing. BMC Systems Biology, 2013, 7, S11.	3.0	19
1267	Comparison of cumulative drip sampling with whole carcass rinses for estimation of Campylobacter species and quality indicator organisms associated with processed broiler chickens. Poultry Science, 2013, 92, 218-224.	3.4	7
1268	Exploring the Capabilities of the Geobiosphere's Microbial Genome. AIChE Journal, 2013, 59, 688-698.	3.6	5
1269	Bacterial and archaeal communities in the acid pit lake sediments of a chalcopyrite mine. Extremophiles, 2013, 17, 941-951.	2.3	22
1270	Alignment-free supervised classification of metagenomes by recursive SVM. BMC Genomics, 2013, 14, 641.	2.8	33
1271	Phylogenetically Diverse Denitrifying and Ammonia-Oxidizing Bacteria in Corals Alcyonium gracillimum and Tubastraea coccinea. Marine Biotechnology, 2013, 15, 540-551.	2.4	41
1272	Viable methanotrophic bacteria enriched from air and rain can oxidize methane at cloud-like conditions. Aerobiologia, 2013, 29, 373-384.	1.7	33
1273	Microbiota associated with the migration and transformation of chlorinated aliphatic hydrocarbons in groundwater. Environmental Geochemistry and Health, 2013, 35, 535-549.	3.4	19
1274	Diversity of cyanobacterial species and phylotypes in biofilms from the littoral zone of Lake Baikal. Journal of Microbiology, 2013, 51, 757-765.	2.8	12
1275	Molecular diversity of protozoa in rumen of Indian buffalo (Bubalus bubalis). Agricultural Research, 2013, 2, 360-366.	1.7	4
1276	An efficient and scalable graph modeling approach for capturing information at different levels in next generation sequencing reads. BMC Bioinformatics, 2013, 14, S7.	2.6	7
1277	Organic loading rate and food-to-microorganism ratio shape prokaryotic diversity in a demo-scale up-flow anaerobic sludge blanket reactor treating domestic wastewater. Antonie Van Leeuwenhoek, 2013, 104, 993-1003.	1.7	20
1278	Rhizosphere bacterial communities associated with healthy and Heterodera glycines-infected soybean roots. European Journal of Soil Biology, 2013, 58, 32-37.	3.2	13
1279	A User's Guide to Quantitative and Comparative Analysis of Metagenomic Datasets. Methods in Enzymology, 2013, 531, 525-547.	1.0	28
1280	Advancing Our Understanding of the Human Microbiome Using QIIME. Methods in Enzymology, 2013, 531, 371-444.	1.0	553
1281	Mariana Forearc Serpentine Mud Volcanoes Harbor Novel Communities of Extremophilic Archaea. Geomicrobiology Journal, 2013, 30, 430-441.	2.0	28
1282	A Map-Reduce Framework for Clustering Metagenomes. , 2013, , .		13

#	ARTICLE	IF	CITATIONS
1283	Soil bacteria and archaea found in long-term corn (<i>Zea mays</i> L.) agroecosystems in Quebec, Canada. Canadian Journal of Soil Science, 2013, 93, 45-57.	1.2	12
1284	Temporal change in the gut community of rats fed high amylose cornstarch is driven by endogenous urea rather than strictly on carbohydrate availability. Journal of Applied Microbiology, 2013, 114, 1516-1528.	3.1	37
1285	The Effects of Different Substrates on Ammonium Removal in Constructed Wetlands: A Comparison of Their Physicochemical Characteristics and Ammonium-Oxidizing Prokaryotic Communities. Clean - Soil, Air, Water, 2013, 41, 283-290.	1.1	31
1286	Salinity Impact on Bacterial Community Composition in Five High-Altitude Lakes from the Tibetan Plateau, Western China. Geomicrobiology Journal, 2013, 30, 462-469.	2.0	36
1287	Pulp mill wastewater sediment reveals novel methanogenic and cellulolytic populations. Water Research, 2013, 47, 683-692.	11.3	2
1288	Growth of <i>Carnobacterium</i> spp. from permafrost under low pressure, temperature, and anoxic atmosphere has implications for Earth microbes on Mars. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 666-671.	7.1	78
1289	Combination of high throughput cultivation and <i>dsrA</i> sequencing for assessment of sulfate-reducing bacteria diversity in sediments. FEMS Microbiology Ecology, 2013, 83, 26-37.	2.7	26
1290	Impact of arbuscular mycorrhizal fungal inoculants on subsequent arbuscular mycorrhizal fungi colonization in pot-cultured field pea (<i>Pisum sativum</i> L.). Mycorrhiza, 2013, 23, 45-59.	2.8	47
1291	Removal of alachlor in anoxic soil slurries and related alteration of the active communities. Environmental Science and Pollution Research, 2013, 20, 1089-1105.	5.3	16
1292	Diversity analyses of microbial communities in petroleum samples from Brazilian oil fields. International Biodeterioration and Biodegradation, 2013, 81, 57-70.	3.9	84
1293	Microbial epibionts of the colonial ascidians <i>Didemnum galacteum</i> and <i>Cystodytes</i> sp.. Symbiosis, 2013, 59, 57-63.	2.3	10
1294	Microbial community structures of methane hydrate-bearing sediments in the Ulleung Basin, East Sea of Korea. Marine and Petroleum Geology, 2013, 47, 136-146.	3.3	43
1295	Leaf litter is the main driver for changes in bacterial community structures in the rhizosphere of ash and beech. Applied Soil Ecology, 2013, 72, 150-160.	4.3	45
1296	Abundance, diversity and spatio-temporal dynamics of <i>nirS</i> gene-harbouring denitrifiers in a potato field over the course of a growth season. Systematic and Applied Microbiology, 2013, 36, 112-115.	2.8	4
1297	Abundance and diversity of ammonia-oxidizing archaea in response to various habitats in Pearl River Delta of China, a subtropical maritime zone. Journal of Environmental Sciences, 2013, 25, 1195-1205.	6.1	12
1298	Bacterial community structures associated with a natural spring phytoplankton bloom in the Yellow Sea, China. Deep-Sea Research Part II: Topical Studies in Oceanography, 2013, 97, 85-92.	1.4	13
1299	Structural changes of gut microbiota in a rat non-alcoholic fatty liver disease model treated with a Chinese herbal formula. Systematic and Applied Microbiology, 2013, 36, 188-196.	2.8	83
1300	Responses of ammonia-oxidizing archaeal and betaproteobacterial populations to wastewater salinity in a full-scale municipal wastewater treatment plant. Journal of Bioscience and Bioengineering, 2013, 115, 424-432.	2.2	32

#	ARTICLE	IF	CITATIONS
1301	Robust estimation of microbial diversity in theory and in practice. ISME Journal, 2013, 7, 1092-1101.	9.8	321
1302	Temporal dynamics in the free-living bacterial community composition in the coastal North Sea. FEMS Microbiology Ecology, 2013, 83, 413-424.	2.7	31
1303	Biodiversity of Actinomycetes Associated with Caribbean Sponges and Their Potential for Natural Product Discovery. Marine Biotechnology, 2013, 15, 413-424.	2.4	38
1304	Bacterial diversity in the rhizosphere of maize and the surrounding carbonate-rich bulk soil. Microbial Biotechnology, 2013, 6, 36-44.	4.2	120
1305	Characterisation of Antarctic cyanobacteria and comparison with New Zealand strains. Hydrobiologia, 2013, 711, 139-154.	2.0	21
1306	Enrichment and dynamics of novel syntrophs in a methanogenic hexadecane-degrading culture from a Chinese oilfield. FEMS Microbiology Ecology, 2013, 83, 757-766.	2.7	48
1307	Broad Diversity and Newly Cultured Bacterial Isolates from Enrichment of Pig Feces on Complex Polysaccharides. Microbial Ecology, 2013, 66, 448-461.	2.8	12
1308	Metagenome analysis of bacterial diversity in Tibetan kefir grains. European Food Research and Technology, 2013, 236, 549-556.	3.3	41
1309	Community structure and transcript responses of anammox bacteria, AOA, and AOB in mangrove sediment microcosms amended with ammonium and nitrite. Applied Microbiology and Biotechnology, 2013, 97, 9859-9874.	3.6	51
1310	Phylogenetic Diversity and Community Structure of the Symbionts Associated with the Coralline Sponge <i>Astrosclera willeyana</i> of the Great Barrier Reef. Microbial Ecology, 2013, 65, 740-752.	2.8	11
1311	Bacterial and archaeal diversities in <i>Yunnan</i> and <i>Tibetan</i> hot springs, <i>China</i> . Environmental Microbiology, 2013, 15, 1160-1175.	3.8	121
1312	Characterization of rhizosphere prokaryotic diversity in a horizontal subsurface flow constructed wetland using a PCR cloning-sequencing based approach. Applied Microbiology and Biotechnology, 2013, 97, 4221-4231.	3.6	18
1313	The <i>Montastraea faveolata</i> microbiome: ecological and temporal influences on a Caribbean reef-building coral in decline. Environmental Microbiology, 2013, 15, 2082-2094.	3.8	80
1314	Intra- and Intergenomic Variation of Ribosomal RNA Operons in Concurrent <i>Alteromonas macleodii</i> Strains. Microbial Ecology, 2013, 65, 720-730.	2.8	5
1315	Bacterial succession in Antarctic soils of two glacier forefields on Larsemann Hills, East Antarctica. FEMS Microbiology Ecology, 2013, 85, 128-142.	2.7	113
1316	Microbial diversity in the coralline sponge <i>Vaceletia crypta</i> . Antonie Van Leeuwenhoek, 2013, 103, 1041-1056.	1.7	14
1317	Roots from beech (<i>Fagus sylvatica</i> L.) and ash (<i>Fraxinus excelsior</i> L.) differentially affect soil microorganisms and carbon dynamics. Soil Biology and Biochemistry, 2013, 61, 23-32.	8.8	55
1318	Molecular indicators of microbial diversity in oolitic sands of <i>Highborne Cay</i> , <i>Bahamas</i> . Geobiology, 2013, 11, 234-251.	2.4	39

#	ARTICLE	IF	CITATIONS
1319	Microbial Community Compositional Shifts in Bleached Colonies of the Brazilian Reef-Building Coral <i>Siderastrea stellata</i> . <i>Microbial Ecology</i> , 2013, 65, 205-213.	2.8	22
1320	Identification of acetate-oxidizing bacteria in a coastal marine surface sediment by RNA-stable isotope probing in anoxic slurries and intact cores. <i>FEMS Microbiology Ecology</i> , 2013, 84, 373-386.	2.7	41
1321	Effects of oxygen on biodegradation of fuels in a corroding environment. <i>International Biodeterioration and Biodegradation</i> , 2013, 81, 114-126.	3.9	32
1322	Molecular richness and biotechnological potential of bacteria cultured from Irciniidae sponges in the north-east Atlantic. <i>FEMS Microbiology Ecology</i> , 2013, 85, 519-536.	2.7	76
1323	Comparative analysis of midgut bacterial communities of <i>Aedes aegypti</i> mosquito strains varying in vector competence to dengue virus. <i>Parasitology Research</i> , 2013, 112, 2627-2637.	1.6	44
1324	Arsenite modifies structure of soil microbial communities and arsenite oxidization potential. <i>FEMS Microbiology Ecology</i> , 2013, 84, 270-279.	2.7	25
1325	Arsenite oxidase gene diversity among <i>Candidatus Chloroflexi</i> and <i>Candidatus Roteobacteria</i> from El Tatio Geyser Field, Chile. <i>FEMS Microbiology Ecology</i> , 2013, 83, 745-756.	2.7	53
1326	A phylogenetic analysis of the phylum Fibrobacteres. <i>Systematic and Applied Microbiology</i> , 2013, 36, 376-382.	2.8	24
1327	Soil moisture effect on bacterial and fungal community in Beilu River (Tibetan Plateau) permafrost soils with different vegetation types. <i>Journal of Applied Microbiology</i> , 2013, 114, 1054-1065.	3.1	90
1328	Mass effects meet species sorting: transformations of microbial assemblages in epiphreatic subsurface karst water pools. <i>Environmental Microbiology</i> , 2013, 15, 2476-2488.	3.8	42
1329	Analysis of the Attached Microbial Community on Mucilaginous Cyanobacterial Aggregates in the Eutrophic Lake Taihu Reveals the Importance of Planctomycetes. <i>Microbial Ecology</i> , 2013, 66, 73-83.	2.8	100
1330	Bacterial communities associated with three Brazilian endemic reef corals (<i>Mussismilia</i> spp.) in a coastal reef of the Abrolhos shelf. <i>Continental Shelf Research</i> , 2013, 70, 135-139.	1.8	4
1332	The Discovery of Stromatolites Developing at 3570 m above Sea Level in a High-Altitude Volcanic Lake Socompa, Argentinean Andes. <i>PLoS ONE</i> , 2013, 8, e53497.	2.5	118
1333	Bacterioplankton communities turn unstable and become small under increased temperature and nutrient-enriched conditions. <i>FEMS Microbiology Ecology</i> , 2013, 84, 614-624.	2.7	16
1335	Shifts in soil bacterial communities associated with the potato rhizosphere in response to aromatic sulfonate amendments. <i>Applied Soil Ecology</i> , 2013, 63, 78-87.	4.3	11
1336	Increased microbial activity and nitrogen mineralization coupled to changes in microbial community structure in the rhizosphere of Bt corn. <i>Applied Soil Ecology</i> , 2013, 68, 46-56.	4.3	13
1337	Structural and functional study in the rhizosphere of <i>Oryza sativa</i> L. plants growing under biotic and abiotic stress. <i>Journal of Applied Microbiology</i> , 2013, 115, 218-235.	3.1	26
1338	Archaeal and bacterial diversity in two hot spring microbial mats from a geothermal region in Romania. <i>Extremophiles</i> , 2013, 17, 523-534.	2.3	66

#	ARTICLE	IF	CITATIONS
1339	Robustness of Gut Microbiota of Healthy Adults in Response to Probiotic Intervention Revealed by High-Throughput Pyrosequencing. <i>DNA Research</i> , 2013, 20, 241-253.	3.4	272
1340	From molecules to dynamic biological communities. <i>Biology and Philosophy</i> , 2013, 28, 241-259.	1.4	12
1341	Mn(II)-oxidizing Bacteria are Abundant and Environmentally Relevant Members of Ferromanganese Deposits in Caves of the Upper Tennessee River Basin. <i>Geomicrobiology Journal</i> , 2013, 30, 779-800.	2.0	99
1342	Suppressive effects of seed-applied fungicides on arbuscular mycorrhizal fungi (AMF) differ with fungicide mode of action and AMF species. <i>Applied Soil Ecology</i> , 2013, 72, 22-30.	4.3	50
1343	Impact of aquaculture on benthic virus–prokaryote interactions in the Mediterranean Sea. <i>Water Research</i> , 2013, 47, 1156-1168.	11.3	27
1344	Using ¹³ C-Stable Isotope Probing to Identify MTBE- and TBA-Degrading Microorganisms in Contaminated Groundwater. <i>Ground Water Monitoring and Remediation</i> , 2013, 33, 57-68.	0.8	15
1345	Abundance and Novel Lineages of Thraustochytrids in Hawaiian Waters. <i>Microbial Ecology</i> , 2013, 66, 823-830.	2.8	33
1346	Abundance and Diversity of Ammonia-Oxidizing Bacteria and Archaea in Cold Springs on the Qinghai-Tibet Plateau. <i>Geomicrobiology Journal</i> , 2013, 30, 530-539.	2.0	10
1347	Methanogen genotypes involved in methane formation during anaerobic decomposition of <i>Microcystis</i> blooms at different temperatures. <i>World Journal of Microbiology and Biotechnology</i> , 2013, 29, 373-377.	3.6	5
1348	MC-MinH: Metagenome Clustering using Minwise based Hashing. , 2013, , .		13
1349	Bacterial Community Composition of South China Sea Sediments through Pyrosequencing-Based Analysis of 16S rRNA Genes. <i>PLoS ONE</i> , 2013, 8, e78501.	2.5	79
1350	Environment-Dependent Distribution of the Sediment <i>nifH</i> -Harboring Microbiota in the Northern South China Sea. <i>Applied and Environmental Microbiology</i> , 2013, 79, 121-132.	3.1	39
1351	Effect of East Asian aerosol enrichment on microbial community composition in the South China Sea. <i>Journal of Plankton Research</i> , 2013, 35, 485-503.	1.8	14
1352	Differences in the Structure of the Gut Bacteria Communities in Development Stages of the Chinese White Pine Beetle (<i>Dendroctonus armandi</i>). <i>International Journal of Molecular Sciences</i> , 2013, 14, 21006-21020.	4.1	43
1353	Scrapheap Challenge: A novel bulk-bone metabarcoding method to investigate ancient DNA in faunal assemblages. <i>Scientific Reports</i> , 2013, 3, 3371.	3.3	72
1354	Diversity of Carbon Monoxide-Oxidizing Bacteria in Five Lakes on the Qinghai-Tibet Plateau, China. <i>Geomicrobiology Journal</i> , 2013, 30, 758-767.	2.0	17
1355	Developing a Novel Approach of rpoB Gene as a Powerful Biomarker for the Environmental Microbial Diversity. <i>Geomicrobiology Journal</i> , 2013, 30, 108-119.	2.0	1
1356	Thaumarchaeotal Signature Gene Distribution in Sediments of the Northern South China Sea: an Indicator of the Metabolic Intersection of the Marine Carbon, Nitrogen, and Phosphorus Cycles?. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2137-2147.	3.1	58

#	ARTICLE	IF	CITATIONS
1357	Comparative Quantitative Analysis of Gene Expression Profiles of Glycoside Hydrolase Family 10 Xylanases in the Sheep Rumen during a Feeding Cycle. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1212-1220.	3.1	13
1358	Normal Operating Range of Bacterial Communities in Soil Used for Potato Cropping. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1160-1170.	3.1	33
1359	A Comparison of Methods for Clustering 16S rRNA Sequences into OTUs. <i>PLoS ONE</i> , 2013, 8, e70837.	2.5	171
1360	Distinct Distal Gut Microbiome Diversity and Composition in Healthy Children from Bangladesh and the United States. <i>PLoS ONE</i> , 2013, 8, e53838.	2.5	278
1361	Spatial Distribution and Factors Shaping the Niche Segregation of Ammonia-Oxidizing Microorganisms in the Qiantang River, China. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4065-4071.	3.1	78
1362	Effects of Trophic Status and Temperature on Communities of Sedimentary Ammonia Oxidizers in Lake Taihu. <i>Geomicrobiology Journal</i> , 2013, 30, 886-896.	2.0	10
1363	Insights into Bacterial Community Structure of a Commercial Copper Bioheapleaching Plant: Growth of Heterotrophic Bacteria in the System. <i>Advanced Materials Research</i> , 0, 825, 50-53.	0.3	4
1364	Free-living bacterial communities associated with tubeworm (<i>Ridgeia piscesae</i>) aggregations in contrasting diffuse flow hydrothermal vent habitats at the Main Endeavour Field, Juan de Fuca Ridge. <i>MicrobiologyOpen</i> , 2013, 2, 259-275.	3.0	38
1365	Soil pathogen communities associated with native and non-native <i>Phragmites australis</i> populations in freshwater wetlands. <i>Ecology and Evolution</i> , 2013, 3, 5254-5267.	1.9	41
1366	Temporal succession of putative glycolate-utilizing bacterioplankton tracks changes in dissolved organic matter in a high-elevation lake. <i>FEMS Microbiology Ecology</i> , 2013, 83, 541-551.	2.7	8
1367	Diversity, abundance, and distribution of <i>NO₃⁻</i> -forming nitrite reductase-encoding genes in deep-sea subsurface sediments of the South China Sea. <i>Geobiology</i> , 2013, 11, 170-179.	2.4	25
1368	Abundance and Diversity of Sulfur-Oxidizing Bacteria along a Salinity Gradient in Four Qinghai-Tibetan Lakes, China. <i>Geomicrobiology Journal</i> , 2013, 30, 851-860.	2.0	17
1369	Consumers of 4-chloro-2-methylphenoxyacetic acid from agricultural soil and rhizosphere harbor <i>cadA</i> , <i>r/sdpA</i> , and <i>tfdA</i> -like gene encoding oxygenases. <i>FEMS Microbiology Ecology</i> , 2013, 86, 114-129.	2.7	19
1370	Denitrifying bacterial community in manure compost pellets applied to an Andosol upland field. <i>Soil Science and Plant Nutrition</i> , 2013, 59, 572-579.	1.9	7
1371	Co-Occurring Anammox, Denitrification, and Codenitrification in Agricultural Soils. <i>Applied and Environmental Microbiology</i> , 2013, 79, 168-176.	3.1	162
1372	Oligotyping: differentiating between closely related microbial taxa using 16S rRNA gene data. <i>Methods in Ecology and Evolution</i> , 2013, 4, 1111-1119.	5.2	652
1373	Broad Distribution of Diverse Anaerobic Ammonium-Oxidizing Bacteria in Chinese Agricultural Soils. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6167-6172.	3.1	89
1374	Seasonal Dynamics of the Bacterial Community in Lake Namco, the Largest Tibetan Lake. <i>Geomicrobiology Journal</i> , 2013, 30, 17-28.	2.0	20

#	ARTICLE	IF	CITATIONS
1375	Screening for novel bacteria from the bioenergy feedstock switchgrass (<i>Panicum virgatum</i>). Environmental Technology (United Kingdom), 2013, 34, 1895-1904.	2.2	16
1376	Comparative molecular analysis of the prokaryotic diversity of two salt mine soils in southwest China. Journal of Basic Microbiology, 2013, 53, 942-952.	3.3	26
1377	Benthic communities in the deep Mediterranean Sea: exploring microbial and meiofaunal patterns in slope and basin ecosystems. Biogeosciences, 2013, 10, 4861-4878.	3.3	29
1378	Diffuse flow environments within basalt- and sediment-based hydrothermal vent ecosystems harbor specialized microbial communities. Frontiers in Microbiology, 2013, 4, 182.	3.5	44
1379	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. Genes and Genetic Systems, 2013, 88, 93-103.	0.7	29
1380	DNA from lake sediments reveals the long-term dynamics and diversity of <i>Synechococcus</i> assemblages. Biogeosciences, 2013, 10, 3817-3838.	3.3	42
1381	Short-term effects of biomass burning on soil ammonia-oxidizing bacteria and ammonia-oxidizing archaea. African Journal of Microbiology Research, 2013, 7, 2486-2496.	0.4	2
1382	Impact of Amazon land use on the community of soil fungi. Scientia Agricola, 2013, 70, 59-67.	1.2	25
1383	Identifying bacteria and studying bacterial diversity using the 16S ribosomal RNA gene-based sequencing techniques: A review. African Journal of Microbiology Research, 2013, 7, 5533-5540.	0.4	9
1384	Simulated distribution nitrification: Nitrification Index evaluation and viable AOB. Journal - American Water Works Association, 2013, 105, E242.	0.3	7
1385	Diversity of the candidate phylum Poribacteria in the marine sponge <i>Aplysina fulva</i> . Brazilian Journal of Microbiology, 2013, 44, 329-334.	2.0	6
1386	Culture-independent analysis of endophytic bacterial communities associated with Brazilian sugarcane. Genetics and Molecular Research, 2013, 12, 4549-4558.	0.2	37
1387	Phylogenetically Diverse ureC Genes and Their Expression Suggest the Urea Utilization by Bacterial Symbionts in Marine Sponge <i>Xestospongia testudinaria</i> . PLoS ONE, 2013, 8, e64848.	2.5	38
1388	Base-Calling Algorithm with Vocabulary (BCV) Method for Analyzing Population Sequencing Chromatograms. PLoS ONE, 2013, 8, e54835.	2.5	11
1389	Spatial Variations in Microbial Community Composition in Surface Seawater from the Ultra-Oligotrophic Center to Rim of the South Pacific Gyre. PLoS ONE, 2013, 8, e55148.	2.5	76
1390	Bacterial Communities Associated with the Leaves and the Roots of <i>Arabidopsis thaliana</i> . PLoS ONE, 2013, 8, e56329.	2.5	679
1391	Molecular Detection of <i>Candidatus Scalindua pacifica</i> and Environmental Responses of Sediment Anammox Bacterial Community in the Bohai Sea, China. PLoS ONE, 2013, 8, e61330.	2.5	86
1392	CLUSTOM: A Novel Method for Clustering 16S rRNA Next Generation Sequences by Overlap Minimization. PLoS ONE, 2013, 8, e62623.	2.5	18

#	ARTICLE	IF	CITATIONS
1393	A DNA-Based Registry for All Animal Species: The Barcode Index Number (BIN) System. PLoS ONE, 2013, 8, e66213.	2.5	1,562
1394	Phylogenetic Analysis of a Microbialite-Forming Microbial Mat from a Hypersaline Lake of the Kiritimati Atoll, Central Pacific. PLoS ONE, 2013, 8, e66662.	2.5	160
1395	Microbial Diversity and Its Relationship to Physicochemical Characteristics of the Water in Two Extreme Acidic Pit Lakes from the Iberian Pyrite Belt (SW Spain). PLoS ONE, 2013, 8, e66746.	2.5	76
1396	DNA-SIP Reveals That Syntrophaceae Play an Important Role in Methanogenic Hexadecane Degradation. PLoS ONE, 2013, 8, e66784.	2.5	61
1397	Ectomycorrhizal-Dominated Boreal and Tropical Forests Have Distinct Fungal Communities, but Analogous Spatial Patterns across Soil Horizons. PLoS ONE, 2013, 8, e68278.	2.5	69
1398	Analysis of the Airway Microbiota of Healthy Individuals and Patients with Chronic Obstructive Pulmonary Disease by T-RFLP and Clone Sequencing. PLoS ONE, 2013, 8, e68302.	2.5	90
1399	Metagenomic Insights into Metabolic Capacities of the Gut Microbiota in a Fungus-Cultivating Termite (<i>Odontotermes yunnanensis</i>). PLoS ONE, 2013, 8, e69184.	2.5	69
1400	Phylodynamics of the Emergence of Influenza Viruses after Cross-Species Transmission. PLoS ONE, 2013, 8, e82486.	2.5	5
1401	The Effects of a Probiotic Yeast on the Bacterial Diversity and Population Structure in the Rumen of Cattle. PLoS ONE, 2013, 8, e67824.	2.5	131
1402	amoA-encoding archaea and thaumarchaeol in the lakes on the northeastern Qinghai-Tibetan Plateau, China. <i>Frontiers in Microbiology</i> , 2013, 4, 329.	3.5	34
1403	Temporal Succession of Phytoplankton Assemblages in a Tidal Creek System of the Sundarbans Mangroves: An Integrated Approach. <i>International Journal of Biodiversity</i> , 2013, 2013, 1-15.	0.7	34
1404	Diversity and distribution of <i>amoA</i> -type nitrifying and <i>nirS</i> -type denitrifying microbial communities in the Yangtze River estuary. <i>Biogeosciences</i> , 2014, 11, 2131-2145.	3.3	57
1405	The Freshwater Sponge <i>Ephydatia fluviatilis</i> Harbours Diverse <i>Pseudomonas</i> Species (Gammaproteobacteria, Pseudomonadales) with Broad-Spectrum Antimicrobial Activity. PLoS ONE, 2014, 9, e88429.	2.5	45
1406	A System to Automatically Classify and Name Any Individual Genome-Sequenced Organism Independently of Current Biological Classification and Nomenclature. PLoS ONE, 2014, 9, e89142.	2.5	49
1407	Bacteria and Genes Involved in Arsenic Speciation in Sediment Impacted by Long-Term Gold Mining. PLoS ONE, 2014, 9, e95655.	2.5	26
1408	SSU rDNA Sequence Diversity and Seasonally Differentiated Distribution of Nanoplanktonic Ciliates in Neritic Bohai and Yellow Seas as Revealed by T-RFLP. PLoS ONE, 2014, 9, e102640.	2.5	10
1409	High Phylogenetic Diversity of Glycosyl Hydrolase Family 10 and 11 Xylanases in the Sediment of Lake Dabusu in China. PLoS ONE, 2014, 9, e112798.	2.5	12
1410	Succession of Bacterial Community Structure and Diversity in Soil along a Chronosequence of Reclamation and Re-Vegetation on Coal Mine Spoils in China. PLoS ONE, 2014, 9, e115024.	2.5	70

#	ARTICLE	IF	CITATIONS
1411	Diversity and Distribution of Archaea Community along a Stratigraphic Permafrost Profile from Qinghai-Tibetan Plateau, China. <i>Archaea</i> , 2014, 2014, 1-11.	2.3	17
1412	Comparative Analysis of the Methanogen Diversity in Horse and Pony by Using mcrAGene and Archaeal 16S rRNA Gene Clone Libraries. <i>Archaea</i> , 2014, 2014, 1-10.	2.3	25
1413	Community Analysis of Arbuscular Mycorrhizal Fungi in Roots of <i>Poncirus trifoliata</i> and <i>Citrus reticulata</i> Based on SSU rDNA. <i>Scientific World Journal</i> , The, 2014, 2014, 1-8.	2.1	4
1414	<i>Vibrio</i> diversity and dynamics in the Monterey Bay upwelling region. <i>Frontiers in Microbiology</i> , 2014, 5, 48.	3.5	51
1415	Bioprospecting from Marine Sediments of New Brunswick, Canada: Exploring the Relationship between Total Bacterial Diversity and Actinobacteria Diversity. <i>Marine Drugs</i> , 2014, 12, 899-925.	4.6	40
1416	Microbial responses to chitin and chitosan in oxic and anoxic agricultural soil slurries. <i>Biogeosciences</i> , 2014, 11, 3339-3352.	3.3	34
1417	Bacterial diversity in relatively pristine and anthropogenically-influenced mangrove ecosystems (Goa, Tj ETQq0 0 0,rgBT /Overlock 10 Tf	2.9	40
1418	Exploring the diversity of <i>Acinetobacter</i> populations in river water with genus-specific primers and probes. <i>Journal of General and Applied Microbiology</i> , 2014, 60, 51-58.	0.7	12
1419	A Consumer Perspective on Mobile Service Platforms: A Conjoint Analysis Approach. <i>Communications of the Association for Information Systems</i> , 2014, 34, .	0.9	11
1420	Bacterial diversity in sediments of core MD05-2902 from the Xisha Trough, the South China Sea. <i>Acta Oceanologica Sinica</i> , 2014, 33, 85-93.	1.0	3
1421	Morphospecies <i><i>versus</i></i> Phylospecies Concepts for Evaluating Phytoplankton Diversity: The Case of the Coccolithophores. <i>Cryptogamie, Algologie</i> , 2014, 35, 353-377.	0.9	12
1422	Probiotics and virulent human rotavirus modulate the transplanted human gut microbiota in gnotobiotic pigs. <i>Gut Pathogens</i> , 2014, 6, 39.	3.4	49
1423	Constructing a Boolean implication network to study the interactions between environmental factors and OTUs. <i>Quantitative Biology</i> , 2015, 2, 127-141.	0.5	3
1424	Phylogenetic analysis of epibacterial communities on the surfaces of four red macroalgae. <i>Journal of Ocean University of China</i> , 2014, 13, 1025-1032.	1.2	11
1425	Culture-Independent Analysis of Bacterial Communities in the Gut of Rice Water Weevil (Coleoptera:) Tj ETQq0 0 0,rgBT /Overlock 10 Tf	2.5	6
1426	High abundance and diversity of nitrite-dependent anaerobic methane-oxidizing bacteria in a paddy field profile. <i>FEMS Microbiology Letters</i> , 2014, 360, 33-41.	1.8	69
1427	Diversity of arsenite oxidizing bacterial communities in arsenic-rich deltaic aquifers in West Bengal, India. <i>Frontiers in Microbiology</i> , 2014, 5, 602.	3.5	71
1428	Linking DNRA community structure and activity in a shallow lagoonal estuarine system. <i>Frontiers in Microbiology</i> , 2014, 5, 460.	3.5	121

#	ARTICLE	IF	CITATIONS
1429	Quantification of HTLV-1 Clonality and TCR Diversity. PLoS Computational Biology, 2014, 10, e1003646.	3.2	71
1430	Applications of Next-Generation Sequencing Technologies to the Study of the Human Microbiome. Comprehensive Analytical Chemistry, 2014, , 75-106.	1.3	0
1431	[FeFe]-Hydrogenase Abundance and Diversity along a Vertical Redox Gradient in Great Salt Lake, USA. International Journal of Molecular Sciences, 2014, 15, 21947-21966.	4.1	17
1432	Verrucomicrobia Are Candidates for Polysaccharide-Degrading Bacterioplankton in an Arctic Fjord of Svalbard. Applied and Environmental Microbiology, 2014, 80, 3749-3756.	3.1	170
1433	Infectious Microecology. Advanced Topics in Science and Technology in China, 2014, , .	0.1	5
1434	Distribution patterns of ammonia-oxidizing bacteria and anammox bacteria in the freshwater marsh of Honghe wetland in Northeast China. Ecotoxicology, 2014, 23, 1930-1942.	2.4	20
1435	Bacterial community in alpine grasslands along an altitudinal gradient on the Tibetan Plateau. FEMS Microbiology Ecology, 2014, 87, 121-132.	2.7	120
1436	Stability of airborne microbes in the Louvre Museum over time. Indoor Air, 2014, 24, 29-40.	4.3	31
1437	Hibernation alters the diversity and composition of mucosa-associated bacteria while enhancing antimicrobial defence in the gut of 13-week-old ground squirrels. Molecular Ecology, 2014, 23, 4658-4669.	3.9	62
1438	Sludge bulking impact on relevant bacterial populations in a full-scale municipal wastewater treatment plant. Process Biochemistry, 2014, 49, 2258-2265.	3.7	63
1439	Molecular Characterization of Prokaryotic Communities Associated with Lonar Crater Basalts. Geomicrobiology Journal, 2014, 31, 519-528.	2.0	20
1440	Myxobacterial community is a predominant and highly diverse bacterial group in soil niches. Environmental Microbiology Reports, 2014, 6, 45-56.	2.4	59
1441	A gut microbiota-targeted dietary intervention for amelioration of chronic inflammation underlying metabolic syndrome. FEMS Microbiology Ecology, 2014, 87, 357-367.	2.7	338
1442	Members of the uncultured bacterial candidate division <i>WWE</i> 1 are implicated in anaerobic digestion of cellulose. MicrobiologyOpen, 2014, 3, 157-167.	3.0	114
1443	Deep-sea methane seep sediments in the Okhotsk Sea sustain diverse and abundant anammox bacteria. FEMS Microbiology Ecology, 2014, 87, 503-516.	2.7	44
1444	Microbial community structures in an integrated two-phase anaerobic bioreactor fed by fruit vegetable wastes and wheat straw. Journal of Environmental Sciences, 2014, 26, 2484-2492.	6.1	35
1445	A shift in the archaeal nitrifier community in response to natural and anthropogenic disturbances in the northern Gulf of Mexico. Environmental Microbiology Reports, 2014, 6, 106-112.	2.4	25
1446	Iron-Manganese Nodules Harbor Lower Bacterial Diversity and Greater Proportions of Proteobacteria Compared to Bulk Soils in Four Locations Spanning from North to South China. Geomicrobiology Journal, 2014, 31, 562-577.	2.0	17

#	ARTICLE	IF	CITATIONS
1447	Inhibitory effects of ammonia on methanogen <i>mcrA</i> transcripts in anaerobic digester sludge. FEMS Microbiology Ecology, 2014, 87, 368-377.	2.7	64
1448	Archaeal <i>amoA</i> and <i>ureC</i> genes and their transcriptional activity in the Arctic Ocean. Scientific Reports, 2014, 4, 4661.	3.3	41
1449	Diversity of halophilic bacteria isolated from Rambla Salada, Murcia (Spain). Canadian Journal of Microbiology, 2014, 60, 839-846.	1.7	18
1450	Genetic Diversity of Picocyanobacteria in Tibetan Lakes: Assessing the Endemic and Universal Distributions. Applied and Environmental Microbiology, 2014, 80, 7640-7650.	3.1	16
1451	Impact of inocula and operating conditions on the microbial community structure of two anammox reactors. Environmental Technology (United Kingdom), 2014, 35, 1811-1822.	2.2	43
1452	Bacterial Diversity Assessment in Antarctic Terrestrial and Aquatic Microbial Mats: A Comparison between Bidirectional Pyrosequencing and Cultivation. PLoS ONE, 2014, 9, e97564.	2.5	60
1453	Investigation on bacterial community and diversity in the multilayer aquifer-aquitard system of the Pearl River Delta, China. Ecotoxicology, 2014, 23, 2041-2052.	2.4	18
1454	Cellulolytic Bacteria Associated with the Gut of <i>Dendroctonus arandi</i> Larvae (Coleoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 71	2.1	71
1455	Sampling locality is more detectable than taxonomy or ecology in the gut microbiota of the brood-parasitic Brown-headed Cowbird (<i>Molothrus ater</i>). PeerJ, 2014, 2, e321.	2.0	126
1456	Effective bioremediation strategy for rapid in situ cleanup of anoxic marine sediments in mesocosm oil spill simulation. Frontiers in Microbiology, 2014, 5, 162.	3.5	62
1457	Microbial community structure and nitrogenase gene diversity of sediment from a deep-sea hydrothermal vent field on the Southwest Indian Ridge. Acta Oceanologica Sinica, 2014, 33, 94-104.	1.0	9
1458	Influence of Calcium Nitrate on Microbial Community Structure of Acidophilic Microorganisms. Advanced Materials Research, 0, 955-959, 869-873.	0.3	0
1459	Systematic Design of 18S rRNA Gene Primers for Determining Eukaryotic Diversity in Microbial Consortia. PLoS ONE, 2014, 9, e95567.	2.5	218
1460	Effects of Elevated Carbon Dioxide and Salinity on the Microbial Diversity in Lithifying Microbial Mats. Minerals (Basel, Switzerland), 2014, 4, 145-169.	2.0	11
1461	Lipid and DNA Evidence of Dominance of Planktonic Archaea Preserved in Sediments of the South China Sea: Insight for Application of the TEX86 Proxy in an Unstable Marine Sediment Environment. Geomicrobiology Journal, 2014, 31, 360-369.	2.0	2
1462	<i>Chironomus plumosus</i> larvae increase fluxes of denitrification products and diversity of nitrate-reducing bacteria in freshwater sediment. Systematic and Applied Microbiology, 2014, 37, 51-59.	2.8	29
1463	Comparison of microbial diversity during column bioleaching of chalcopyrite at different temperatures. Journal of Basic Microbiology, 2014, 54, 491-499.	3.3	9
1464	Dynamics of communities of bacteria and ammonia-oxidizing microorganisms in response to simazine attenuation in agricultural soil. Science of the Total Environment, 2014, 472, 502-508.	8.0	35

#	ARTICLE	IF	CITATIONS
1465	Influence of setup and carbon source on the bacterial community of biocathodes in microbial electrolysis cells. <i>Enzyme and Microbial Technology</i> , 2014, 61-62, 67-75.	3.2	58
1466	“Core species”™ in three sources of indoor air belonging to the human micro-environment to the exclusion of outdoor air. <i>Science of the Total Environment</i> , 2014, 485-486, 508-517.	8.0	23
1467	Variation of rhizosphere bacterial community in watermelon continuous mono-cropping soil by long-term application of a novel bioorganic fertilizer. <i>Microbiological Research</i> , 2014, 169, 570-578.	5.3	92
1468	Interactions in the microbiome: communities of organisms and communities of genes. <i>FEMS Microbiology Reviews</i> , 2014, 38, 90-118.	8.6	174
1469	Molecular diversity of arbuscular mycorrhizal fungi associated with two co-occurring perennial plant species on a Tibetan altitudinal gradient. <i>Mycorrhiza</i> , 2014, 24, 95-107.	2.8	73
1470	In search of genome annotation consistency: solid gene clusters and how to use them. <i>3 Biotech</i> , 2014, 4, 331-335.	2.2	5
1471	Shotgun metagenomics indicates novel family A DNA polymerases predominate within marine viroplankton. <i>ISME Journal</i> , 2014, 8, 103-114.	9.8	51
1472	The effect of corrosion inhibitors on microbial communities associated with corrosion in a model flow cell system. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 907-918.	3.6	32
1473	Effects of submerged macrophytes on the abundance and community composition of ammonia-oxidizing prokaryotes in a eutrophic lake. <i>Environmental Science and Pollution Research</i> , 2014, 21, 389-398.	5.3	36
1474	Molecular Techniques Revealed Highly Diverse Microbial Communities in Natural Marine Biofilms on Polystyrene Dishes for Invertebrate Larval Settlement. <i>Microbial Ecology</i> , 2014, 68, 81-93.	2.8	28
1475	Diversity, Abundance, and Spatial Distribution of Ammonia-Oxidizing β -Proteobacteria in Sediments from Changjiang Estuary and Its Adjacent Area in East China Sea. <i>Microbial Ecology</i> , 2014, 67, 788-803.	2.8	27
1476	Composition and variation of sediment bacterial and nirS-harboring bacterial communities at representative sites of the Bohai Gulf coastal zone, China. <i>World Journal of Microbiology and Biotechnology</i> , 2014, 30, 1291-1300.	3.6	13
1477	When is Sampling Complete? The Effects of Geographical Range and Marker Choice on Perceived Diversity in <i>Nitzschia palea</i> (Bacillariophyta). <i>Protist</i> , 2014, 165, 245-259.	1.5	38
1478	Molecular evidence for nitrite-dependent anaerobic methane-oxidising bacteria in the Jiaojiang Estuary of the East Sea (China). <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 5029-5038.	3.6	62
1479	<i>Environmental Microbiology. Methods in Molecular Biology</i> , 2014, , .	0.9	14
1480	Fungal but not bacterial soil communities recover after termination of decadal nitrogen additions to boreal forest. <i>Soil Biology and Biochemistry</i> , 2014, 72, 35-43.	8.8	49
1481	Phylogenetic and Functional Analysis of Gut Microbiota of a Fungus-Growing Higher Termite: Bacteroidetes from Higher Termites Are a Rich Source of β -Glucosidase Genes. <i>Microbial Ecology</i> , 2014, 68, 416-425.	2.8	46
1482	Community structure and abundance of ammonia-oxidizing archaea and bacteria after conversion from soybean to rice paddy in albic soils of Northeast China. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 2765-2778.	3.6	27

#	ARTICLE	IF	CITATIONS
1483	Microbial diversity in Los Azufres geothermal field (Michoacán, Mexico) and isolation of representative sulfate and sulfur reducers. <i>Extremophiles</i> , 2014, 18, 385-398.	2.3	27
1484	Abundance, Activity, and Diversity of Archaeal and Bacterial Communities in Both Uncontaminated and Highly Copper-Contaminated Marine Sediments. <i>Marine Biotechnology</i> , 2014, 16, 230-242.	2.4	27
1485	Ammonia oxidizers and denitrifiers in response to reciprocal elevation translocation in an alpine meadow on the Tibetan Plateau. <i>Journal of Soils and Sediments</i> , 2014, 14, 1189-1199.	3.0	19
1486	Changes in the Soil Bacterial Communities in a Cedar Plantation Invaded by Moso Bamboo. <i>Microbial Ecology</i> , 2014, 67, 421-429.	2.8	62
1487	Distribution and Diversity of Nitrite-Dependent Anaerobic Methane-Oxidising Bacteria in the Sediments of the Qiantang River. <i>Microbial Ecology</i> , 2014, 67, 341-349.	2.8	98
1488	Biochar addition affected the dynamics of ammonia oxidizers and nitrification in microcosms of a coastal alkaline soil. <i>Biology and Fertility of Soils</i> , 2014, 50, 321-332.	4.3	158
1489	Composition of bacterial communities in sand dunes of subtropical coastal forests. <i>Biology and Fertility of Soils</i> , 2014, 50, 809-814.	4.3	18
1490	Bacterial communities in trace metal contaminated lake sediments are dominated by endospore-forming bacteria. <i>Aquatic Sciences</i> , 2014, 76, 33-46.	1.5	28
1491	Bacterial metal resistance genes and metal bioavailability in contaminated sediments. <i>Environmental Pollution</i> , 2014, 189, 143-151.	7.5	123
1492	Aerobic biodegradation of bisphenol A in river sediment and associated bacterial community change. <i>Science of the Total Environment</i> , 2014, 470-471, 1184-1188.	8.0	66
1493	Archaeal diversity and the extent of iron and manganese pyritization in sediments from a tropical mangrove creek (Cardoso Island, Brazil). <i>Estuarine, Coastal and Shelf Science</i> , 2014, 146, 1-13.	2.1	18
1494	Nonylphenol biodegradation in river sediment and associated shifts in community structures of bacteria and ammonia-oxidizing microorganisms. <i>Ecotoxicology and Environmental Safety</i> , 2014, 106, 1-5.	6.0	45
1495	Molecular and lipid biomarker analysis of a gypsum-hosted endoevaporitic microbial community. <i>Geobiology</i> , 2014, 12, 62-82.	2.4	22
1496	Bacterioplankton communities in a high-altitude freshwater wetland. <i>Annals of Microbiology</i> , 2014, 64, 1405-1411.	2.6	48
1497	Aerobic and Anaerobic Ammonia-Oxidizing Microorganisms in Low-Temperature Hydrothermal Fe-Si-rich Precipitates of the Southwestern Pacific Ocean. <i>Geomicrobiology Journal</i> , 2014, 31, 42-52.	2.0	3
1498	Bacterial structure and spatiotemporal distribution in a horizontal subsurface flow constructed wetland. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 3191-3203.	3.6	30
1499	Pyrosequencing analysis of bacterial community and assembly in activated sludge samples from different geographic regions in China. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 9119-9128.	3.6	55
1500	Abundance and Diversity of Ammonia-Oxidizing Microorganisms in the Sediments of Jinshan Lake. <i>Current Microbiology</i> , 2014, 69, 751-757.	2.2	31

#	ARTICLE	IF	CITATIONS
1501	Evidence for the Cooccurrence of Nitrite-Dependent Anaerobic Ammonium and Methane Oxidation Processes in a Flooded Paddy Field. <i>Applied and Environmental Microbiology</i> , 2014, 80, 7611-7619.	3.1	108
1502	A comparison of pelagic, littoral, and riverine bacterial assemblages in Lake Bangongco, Tibetan Plateau. <i>FEMS Microbiology Ecology</i> , 2014, 89, 211-221.	2.7	22
1503	Microbial diversity in formation water and enrichment cultures from the Gangxi bed of the Dagang terrigenous oilfield (PRC). <i>Microbiology</i> , 2014, 83, 616-633.	1.2	3
1504	Preliminary comparison of quantification efficiency between DNA-derived dataset and cell-derived dataset of mixed diatom sample based on rDNA-ITS sequence analysis. <i>Biochemical Systematics and Ecology</i> , 2014, 57, 183-190.	1.3	3
1505	Ammonia- and methane-oxidizing microorganisms in high-altitude wetland sediments and adjacent agricultural soils. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 10197-10209.	3.6	24
1506	Archaeal and bacterial diversity in five different hydrothermal ponds in the Copahue region in Argentina. <i>Systematic and Applied Microbiology</i> , 2014, 37, 429-441.	2.8	43
1507	Genetic diversity and expression profiles of cysteine phytases in the sheep rumen during a feeding cycle. <i>Letters in Applied Microbiology</i> , 2014, 59, 615-620.	2.2	5
1508	Niche specificity of ammonia-oxidizing archaeal and bacterial communities in a freshwater wetland receiving municipal wastewater in Daqing, Northeast China. <i>Ecotoxicology</i> , 2014, 23, 2081-2091.	2.4	9
1509	Identifying response groups of soil nitrifiers and denitrifiers to grazing and associated soil environmental drivers in Tibetan alpine meadows. <i>Soil Biology and Biochemistry</i> , 2014, 77, 89-99.	8.8	75
1510	Distribution of Naphthalene Dioxygenase Genes in Crude Oil-Contaminated Soils. <i>Microbial Ecology</i> , 2014, 68, 785-793.	2.8	35
1511	Conducting a Microbiome Study. <i>Cell</i> , 2014, 158, 250-262.	28.9	625
1512	Endophytic fungal symbionts associated with gypsophilous plants. <i>Botany</i> , 2014, 92, 295-301.	1.0	26
1513	Methods for understanding microbial community structures and functions in microbial fuel cells: A review. <i>Bioresource Technology</i> , 2014, 171, 461-468.	9.6	145
1514	Fungal and Bacterial Community Succession Differs for Three Wood Types during Decay in a Forest Soil. <i>Microbial Ecology</i> , 2014, 68, 212-221.	2.8	49
1515	Characterization of Chasmoendolithic Community in Miers Valley, McMurdo Dry Valleys, Antarctica. <i>Microbial Ecology</i> , 2014, 68, 351-359.	2.8	77
1516	Abundance and community structure of ammonia-oxidizing microorganisms in reservoir sediment and adjacent soils. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 1883-1892.	3.6	55
1517	Depth-related changes of sediment ammonia-oxidizing microorganisms in a high-altitude freshwater wetland. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 5697-5707.	3.6	48
1518	Indigenous oil-degrading bacteria in crude oil-contaminated seawater of the Yellow sea, China. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 7253-7269.	3.6	120

#	ARTICLE	IF	CITATIONS
1519	Comparison of soil bacterial communities in a natural hardwood forest and coniferous plantations in perhumid subtropical low mountains. , 2014, 55, 50.		20
1520	Structure of hydrocarbonoclastic nitrate-reducing bacterial communities in bioturbated coastal marine sediments. FEMS Microbiology Ecology, 2014, 89, 580-593.	2.7	27
1521	Analysis of diversity of chromophytic phytoplankton in a mangrove ecosystem using <i>rbcL</i> gene sequencing. Journal of Phycology, 2014, 50, 328-340.	2.3	37
1522	The soil carbon/nitrogen ratio and moisture affect microbial community structures in alkaline permafrost-affected soils with different vegetation types on the Tibetan plateau. Research in Microbiology, 2014, 165, 128-139.	2.1	112
1523	Molecular diversity of the ammonia-oxidizing bacteria community in disused tin-mining ponds located within Kampar, Perak, Malaysia. World Journal of Microbiology and Biotechnology, 2014, 30, 757-766.	3.6	5
1524	Vertical distribution of ammonia-oxidizing archaea (AOA) in the hyporheic zone of a eutrophic river in North China. World Journal of Microbiology and Biotechnology, 2014, 30, 1335-1346.	3.6	13
1525	Molecular diversity of the methanotrophic bacteria communities associated with disused tin-mining ponds in Kampar, Perak, Malaysia. World Journal of Microbiology and Biotechnology, 2014, 30, 2645-2653.	3.6	4
1526	Response of an Arctic Sediment Nitrogen Cycling Community to Increased CO ₂ . Estuaries and Coasts, 2014, 37, 724-735.	2.2	31
1527	A genomic perspective on a new bacterial genus and species from the Alcaligenaceae family, Basilea psittacipulmonis. BMC Genomics, 2014, 15, 169.	2.8	10
1528	Investigating Microbial Eukaryotic Diversity from a Global Census: Insights from a Comparison of Pyrotag and Full-Length Sequences of 18S rRNA Genes. Applied and Environmental Microbiology, 2014, 80, 4363-4373.	3.1	70
1529	Wastewater Irrigation Increases the Abundance of Potentially Harmful Gammaproteobacteria in Soils in Mezquital Valley, Mexico. Applied and Environmental Microbiology, 2014, 80, 5282-5291.	3.1	80
1530	Policy, phylogeny, and the parasite. Trends in Parasitology, 2014, 30, 274-281.	3.3	33
1531	Bacterial community associated with traps of the carnivorous plants Utricularia hydrocarpa and Genlisea filiformis. Aquatic Botany, 2014, 116, 8-12.	1.6	21
1532	Long-term batch brewing accumulates adaptive microbes, which comprehensively produce more flavorful Chinese liquors. Food Research International, 2014, 62, 894-901.	6.2	45
1533	Spatial variability of winter bacterioplankton community composition in the Gulf of Finland (the Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 1	2.1	15
1534	A trait based perspective on the biogeography of common and abundant marine bacterioplankton clades. Marine Genomics, 2014, 15, 17-28.	1.1	69
1535	Replicating the microbial community and water quality performance of full-scale slow sand filters in laboratory-scale filters. Water Research, 2014, 61, 141-151.	11.3	44
1536	Interactive effects of hypoxia and polybrominated diphenyl ethers (PBDEs) on microbial community assembly in surface marine sediments. Marine Pollution Bulletin, 2014, 85, 400-409.	5.0	9

#	ARTICLE	IF	CITATIONS
1537	The responses of the taxa composition of particle-attached bacterial community to the decomposition of Microcystis blooms. Science of the Total Environment, 2014, 488-489, 236-242.	8.0	67
1538	Dynamic processes of indigenous microorganisms from a low-temperature petroleum reservoir during nutrient stimulation. Journal of Bioscience and Bioengineering, 2014, 117, 215-221.	2.2	25
1539	Sequence analysis of marine nematodes based on 18S rRNA gene in intertidal sediments of Hiroshima, Seto Inland Sea. Nippon Suisan Gakkaishi, 2014, 80, 16-20.	0.1	3
1540	Evolution in the <i>Bacillaceae</i> . Microbiology Spectrum, 2014, 2, .	3.0	4
1541	Molecular Methods To Study Complex Microbial Communities. , 2014, , 323-345.		0
1542	Ammonia availability shapes the seasonal distribution and activity of archaeal and bacterial ammonia oxidizers in the Puget Sound Estuary. Limnology and Oceanography, 2014, 59, 1321-1335.	3.1	37
1543	Pyrosequencing analysis of a bacterial community associated with lava-formed soil from the G otjawal forest in J eju, K orea. MicrobiologyOpen, 2015, 4, 301-312.	3.0	11
1544	Species, Abundance and Function of Ammonia-oxidizing Archaea in Inland Waters across China. Scientific Reports, 2015, 5, 15969.	3.3	49
1545	Modulation of gut microbiota by berberine and metformin during the treatment of high-fat diet-induced obesity in rats. Scientific Reports, 2015, 5, 14405.	3.3	499
1546	Functional diversity and dynamics of bacterial communities in a membrane bioreactor for the treatment of metal-working fluid wastewater. Journal of Water and Health, 2015, 13, 1006-1019.	2.6	8
1547	Contrasting soil bacterial community structure between the phyla Acidobacteria and Proteobacteria in tropical Southeast Asian and temperate Japanese forests. Genes and Genetic Systems, 2015, 90, 61-77.	0.7	41
1548	Microbial "social networks". BMC Genomics, 2015, 16, S6.	2.8	52
1550	Microbial Community Analysis Using High-Throughput Amplicon Sequencing. , 2015, , 2.4.2-1-2.4.2-26.		4
1551	Abundance and Diversity of Bacterial Nitrifiers and Denitrifiers and Their Functional Genes in Tannery Wastewater Treatment Plants Revealed by High-Throughput Sequencing. , 2015, , 101-123.		1
1552	Effect of CO2 and N2 on microbial community changes during column bioleaching of low-grade high pyrite-bearing chalcocite ore. Journal of Central South University, 2015, 22, 4528-4535.	3.0	3
1553	Rearing and foraging affects bumblebee (<i>Bombus terrestris</i>) gut microbiota. Environmental Microbiology Reports, 2015, 7, 634-641.	2.4	15
1554	Microbial diversity in tanning wastewaters treatment reactors. Environmental Progress and Sustainable Energy, 2015, 34, 401-410.	2.3	8
1555	Differences in major bacterial populations in the intestines of mature broilers after feeding virginiamycin or bacitracin methylene disalicylate. Journal of Applied Microbiology, 2015, 119, 1515-1526.	3.1	35

#	ARTICLE	IF	CITATIONS
1556	Bacterial Diversity Analysis during the Fermentation Processing of Traditional Chinese Yellow Rice Wine Revealed by 16S rDNA 454 Pyrosequencing. <i>Journal of Food Science</i> , 2015, 80, M2265-71.	3.1	41
1557	Effects of microclimate on soil bacterial communities across two contrasting timberline ecotones in southeast Tibet. <i>European Journal of Soil Science</i> , 2015, 66, 1033-1043.	3.9	7
1558	High Genetic Diversity of Microbial Cellulase and Hemicellulase Genes in the Hindgut of <i>Holotrichia parallela</i> Larvae. <i>International Journal of Molecular Sciences</i> , 2015, 16, 16545-16559.	4.1	15
1559	Trehalose promotes <i>Rhodococcus</i> sp. strain YYL colonization in activated sludge under tetrahydrofuran (THF) stress. <i>Frontiers in Microbiology</i> , 2015, 6, 438.	3.5	7
1560	Bacteria in the injection water differently impacts the bacterial communities of production wells in high-temperature petroleum reservoirs. <i>Frontiers in Microbiology</i> , 2015, 6, 505.	3.5	19
1561	The effect of D123 wheat as a companion crop on soil enzyme activities, microbial biomass and microbial communities in the rhizosphere of watermelon. <i>Frontiers in Microbiology</i> , 2015, 6, 899.	3.5	30
1562	Diversity and Habitat Preferences of Cultivated and Uncultivated Aerobic Methanotrophic Bacteria Evaluated Based on <i>pmoA</i> as Molecular Marker. <i>Frontiers in Microbiology</i> , 2015, 6, 1346.	3.5	408
1563	Carbon-Fixation Rates and Associated Microbial Communities Residing in Arid and Ephemeral Wet Antarctic Dry Valley Soils. <i>Frontiers in Microbiology</i> , 2015, 6, 1347.	3.5	25
1564	Comparative Gut Microbiota of 59 Neotropical Bird Species. <i>Frontiers in Microbiology</i> , 2015, 6, 1403.	3.5	216
1565	Bioinformation and α -Omic Approaches for Characterization of Environmental Microorganisms. , 2015, , 483-505.		4
1566	Variations in Microbial Community Structure through the Stratified Water Column in the Tyrrhenian Sea (Central Mediterranean). <i>Journal of Marine Science and Engineering</i> , 2015, 3, 845-865.	2.6	12
1567	Metagenomics: Tools and Insights for Analyzing Next-Generation Sequencing Data Derived from Biodiversity Studies. <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S12462.	2.0	317
1568	Microbial community composition of a household sand filter used for arsenic, iron, and manganese removal from groundwater in Vietnam. <i>Chemosphere</i> , 2015, 138, 47-59.	8.2	84
1569	Fecal menaquinone profiles of overweight adults are associated with gut microbiota composition during a gut microbiota-targeted dietary intervention. <i>American Journal of Clinical Nutrition</i> , 2015, 102, 84-93.	4.7	42
1570	Leprous lesion presents enrichment of opportunistic pathogenic bacteria. <i>SpringerPlus</i> , 2015, 4, 187.	1.2	14
1571	Predicting Clinical Phenotype Using OTU-Based Metagenome Representation. , 2015, , .		1
1572	An Improved K-Means Algorithm for DNA Sequence Clustering. , 2015, , .		6
1573	Effect of Different Solvent Extractants on the Activity and Community Structure of Acidophilic Microorganisms. <i>Advanced Materials Research</i> , 2015, 1130, 222-225.	0.3	1

#	ARTICLE	IF	CITATIONS
1574	Metagenomics as a Tool for Enzyme Discovery: Hydrolytic Enzymes from Marine-Related Metagenomes. <i>Advances in Experimental Medicine and Biology</i> , 2015, 883, 1-20.	1.6	35
1575	MtHc: a motif-based hierarchical method for clustering massive 16S rRNA sequences into OTUs. <i>Molecular BioSystems</i> , 2015, 11, 1907-1913.	2.9	21
1576	The study of metabonomics combined with diversity of intestinal flora in LDP intervention in kidney-yin deficiency hyperthyroid rats. <i>RSC Advances</i> , 2015, 5, 57975-57983.	3.6	9
1577	Exploration of Microbial Cells: The Storehouse of Bio-wealth Through Metagenomics and Metatranscriptomics. , 2015, , 7-27.		2
1578	Diversity and Infection Frequency of Symbiotic Bacteria in Different Populations of the Rice Brown Planthopper in China. <i>Journal of Entomological Science</i> , 2015, 50, 47-66.	0.3	10
1579	Anaerobic treatment of p-acetamidobenzene sulfonyl chloride (p-ASC)-containing wastewater in the presence or absence of ethanol in a UASB reactor. <i>International Biodeterioration and Biodegradation</i> , 2015, 98, 81-88.	3.9	8
1580	Occurrence and importance of anaerobic ammonium-oxidising bacteria in vegetable soils. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 5709-5718.	3.6	35
1581	Contribution of arbuscular mycorrhizal fungi of sedges to soil aggregation along an altitudinal alpine grassland gradient on the <sc>T</sc>ibetan <sc>P</sc>lateau. <i>Environmental Microbiology</i> , 2015, 17, 2841-2857.	3.8	64
1582	Depth-specific distribution and importance of nitrite-dependent anaerobic ammonium and methane-oxidising bacteria in an urban wetland. <i>Soil Biology and Biochemistry</i> , 2015, 83, 43-51.	8.8	81
1583	Dynamic of sulphate-reducing microorganisms in petroleum-contaminated marine sediments inhabited by the polychaete <i>Hediste diversicolor</i> . <i>Environmental Science and Pollution Research</i> , 2015, 22, 15273-15284.	5.3	12
1584	Microbial Analysis and Efficiency of Biofiltration Packing Systems for Hydrogen Sulfide Removal from Wastewater Off Gas. <i>Environmental Engineering Science</i> , 2015, 32, 121-128.	1.6	19
1585	Contribution of enrichments and resampling for sulfate reducing bacteria diversity assessment by high-throughput cultivation. <i>Journal of Microbiological Methods</i> , 2015, 110, 92-97.	1.6	1
1586	Infectivity and community composition of arbuscular mycorrhizal fungi from different soil depths in intensively managed agricultural ecosystems. <i>Journal of Soils and Sediments</i> , 2015, 15, 1200-1211.	3.0	15
1587	Methanogenic food web in the gut contents of methane-emitting earthworm <i>Eudrilus eugeniae</i> from Brazil. <i>ISME Journal</i> , 2015, 9, 1778-1792.	9.8	34
1589	Investigation of Methanogenic Community Structures in Rural Biogas Digesters from Different Climatic Regions in Yunnan, Southwest China. <i>Current Microbiology</i> , 2015, 70, 679-684.	2.2	14
1590	Marine fungal communities in water and surface sediment of a sea cucumber farming system: habitat-differentiated distribution and nutrients driving succession. <i>Fungal Ecology</i> , 2015, 14, 87-98.	1.6	22
1591	Microbial diversity of the Soldhar hot spring, India, assessed by analyzing 16S rRNA and protein-coding genes. <i>Annals of Microbiology</i> , 2015, 65, 1323-1332.	2.6	15
1592	Effects of warming on microbial communities in the coastal waters of temperate and subtropical zones in the Northern Hemisphere, with a focus on Gammaproteobacteria. <i>Journal of Oceanography</i> , 2015, 71, 91-103.	1.7	11

#	ARTICLE	IF	CITATIONS
1593	Crude oil degradation by bacterial consortia under four different redox and temperature conditions. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 1451-1461.	3.6	14
1594	Minimum entropy decomposition: Unsupervised oligotyping for sensitive partitioning of high-throughput marker gene sequences. <i>ISME Journal</i> , 2015, 9, 968-979.	9.8	530
1595	Vertical distribution of nitrite-dependent anaerobic methane-oxidising bacteria in natural freshwater wetland soils. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 349-357.	3.6	60
1596	Comparison of the microbial communities of hot springs waters and the microbial biofilms in the acidic geothermal area of Copahue (Neuqu�n, Argentina). <i>Extremophiles</i> , 2015, 19, 437-450.	2.3	49
1597	A comparison of DNA extraction methods for biodiversity studies of eukaryotes in marine sediments. <i>Aquatic Microbial Ecology</i> , 2015, 75, 15-25.	1.8	19
1598	Comparative analysis of two 16S rRNA gene-based PCR primer sets provides insight into the diversity distribution patterns of anammox bacteria in different environments. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 8163-8176.	3.6	21
1599	Integron diversity in marine environments. <i>Environmental Science and Pollution Research</i> , 2015, 22, 15360-15369.	5.3	17
1600	Ruminal Bacterial Community Composition in Dairy Cows Is Dynamic over the Course of Two Lactations and Correlates with Feed Efficiency. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4697-4710.	3.1	249
1601	Short-term response of nitrifier communities and potential nitrification activity to elevated CO ₂ and temperature interaction in a Chinese paddy field. <i>Applied Soil Ecology</i> , 2015, 96, 88-98.	4.3	49
1602	Distribution of Arsenite-Oxidizing Bacteria and its Correlation with Temperature in Hot Springs of the Tibetan-Yunnan Geothermal Zone in Western China. <i>Geomicrobiology Journal</i> , 2015, 32, 482-493.	2.0	7
1603	Anaerobic ammonium oxidation in traditional municipal wastewater treatment plants with low-strength ammonium loading: Widespread but overlooked. <i>Water Research</i> , 2015, 84, 66-75.	11.3	168
1604	Altitudinal distribution patterns of AM fungal assemblages in a Tibetan alpine grassland. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv078.	2.7	55
1605	Is Planktonic Diversity Well Recorded in Sedimentary DNA? Toward the Reconstruction of Past Protistan Diversity. <i>Microbial Ecology</i> , 2015, 70, 865-875.	2.8	55
1606	Further Analysis of Anammox Bacterial Community Structures Along an Anthropogenic Nitrogen-Input Gradient from the Riparian Sediments of the Pearl River Delta to the Deep-Ocean Sediments of the South China Sea. <i>Geomicrobiology Journal</i> , 2015, 32, 789-798.	2.0	30
1607	Snapshot of methanogen sensitivity to temperature in Zoige wetland from Tibetan plateau. <i>Frontiers in Microbiology</i> , 2015, 6, 131.	3.5	41
1608	Characterization of shed medicinal leech mucus reveals a diverse microbiota. <i>Frontiers in Microbiology</i> , 2014, 5, 757.	3.5	14
1609	Distribution and Diversity of Aerobic Carbon Monoxide-Oxidizing Bacteria in Geothermal Springs of China, the Philippines, and the United States. <i>Geomicrobiology Journal</i> , 2015, 32, 903-913.	2.0	19
1610	Impact of preferential methane flow through soil on microbial community composition. <i>European Journal of Soil Biology</i> , 2015, 69, 8-16.	3.2	15

#	ARTICLE	IF	CITATIONS
1611	Microbial communities in dark oligotrophic volcanic ice cave ecosystems of Mt. Erebus, Antarctica. <i>Frontiers in Microbiology</i> , 2015, 6, 179.	3.5	120
1612	The influence of vent systems on pelagic eukaryotic micro-organism composition in the Nordic Seas. <i>Polar Biology</i> , 2015, 38, 547-558.	1.2	7
1613	Archaeal communities associated with roots of the common reed (<i>Phragmites australis</i>) in Beijing Cuihu Wetland. <i>World Journal of Microbiology and Biotechnology</i> , 2015, 31, 823-832.	3.6	12
1614	RIEMS: a software pipeline for sensitive and comprehensive taxonomic classification of reads from metagenomics datasets. <i>BMC Bioinformatics</i> , 2015, 16, 69.	2.6	73
1615	Microbiotaâ€™implications for immunity and transplantation. <i>Nature Reviews Nephrology</i> , 2015, 11, 342-353.	9.6	47
1616	The integration of sequencing and bioinformatics in metagenomics. <i>Reviews in Environmental Science and Biotechnology</i> , 2015, 14, 357-383.	8.1	13
1617	Temperature impacts differentially on the methanogenic food web of celluloseâ€™supplemented peatland soil. <i>Environmental Microbiology</i> , 2015, 17, 720-734.	3.8	60
1618	Candidatus <i>Brocadia</i> and Candidatus <i>Kuenenia</i> predominated in anammox bacterial community in selected Chinese paddy soils. <i>Journal of Soils and Sediments</i> , 2015, 15, 1977-1986.	3.0	29
1619	Unusually low TEX86 values in the transitional zone between Pearl River estuary and coastal South China Sea: Impact of changing archaeal community composition. <i>Chemical Geology</i> , 2015, 402, 18-29.	3.3	42
1620	The response of root-associated bacterial community to the grafting of watermelon. <i>Plant and Soil</i> , 2015, 391, 253-264.	3.7	29
1621	Environmental diversity of bacteria in a warm monomictic tropical freshwater lake. <i>Annals of Microbiology</i> , 2015, 65, 2099-2108.	2.6	2
1622	Restoration of a <scp>M</scp>editerranean forest after a fire: bioremediation and rhizoremediation fieldâ€™scale trial. <i>Microbial Biotechnology</i> , 2015, 8, 77-92.	4.2	28
1623	Shift of anammox bacterial community structure along the <scp>P</scp>earl <scp>E</scp>stuary and the impact of environmental factors. <i>Journal of Geophysical Research: Oceans</i> , 2015, 120, 2869-2883.	2.6	28
1624	The human gut microbiome, a taxonomic conundrum. <i>Systematic and Applied Microbiology</i> , 2015, 38, 276-286.	2.8	113
1625	A Filifactor alocis-centered co-occurrence group associates with periodontitis across different oral habitats. <i>Scientific Reports</i> , 2015, 5, 9053.	3.3	78
1626	The diversity of coral associated bacteria and the environmental factors affect their community variation. <i>Ecotoxicology</i> , 2015, 24, 1467-1477.	2.4	47
1627	Pyrosequencing analysis of bacterial communities in biofilms from different pipe materials in a city drinking water distribution system of East China. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 10713-10724.	3.6	77
1628	Clone Libraries of Ribosomal RNA Gene Sequences for Characterization of Microbial Communities. <i>Springer Protocols</i> , 2015, , 127-154.	0.3	2

#	ARTICLE	IF	CITATIONS
1629	Antimicrobial and Biocatalytic Potential of Haloalkaliphilic Actinobacteria. Sustainable Development and Biodiversity, 2015, , 29-55.	1.7	11
1630	Taxonomic profiling of bacterial community structure from coastal sediment of Alangâ€Sosiya shipbreaking yard near Bhavnagar, India. Marine Pollution Bulletin, 2015, 101, 736-745.	5.0	11
1631	GSWABE: faster GPUâ€accelerated sequence alignment with optimal alignment retrieval for short DNA sequences. Concurrency Computation Practice and Experience, 2015, 27, 958-972.	2.2	25
1632	The dynamics of the bacterial diversity in the redox transition and anoxic zones of the Cariaco Basin assessed by parallel tag sequencing. FEMS Microbiology Ecology, 2015, 91, fiv088.	2.7	13
1633	Bio-desilication of rutile concentrate and analysis of community structure in bio-desilication reactor. Transactions of Nonferrous Metals Society of China, 2015, 25, 2398-2406.	4.2	7
1634	The links between ecosystem multifunctionality and above- and belowground biodiversity are mediated by climate. Nature Communications, 2015, 6, 8159.	12.8	471
1635	Evaluation of feed grade sodium bisulfate impact on gastrointestinal tract microbiota ecology in broilers via a pyrosequencing platform. Poultry Science, 2015, 94, 3040-3047.	3.4	14
1636	Improved OTU-picking using long-read 16S rRNA gene amplicon sequencing and generic hierarchical clustering. Microbiome, 2015, 3, 43.	11.1	77
1637	Variation in abundance and community structure of particle-attached and free-living bacteria in the South China Sea. Deep-Sea Research Part II: Topical Studies in Oceanography, 2015, 122, 64-73.	1.4	20
1638	Integron diversity in bacterial communities of freshwater sediments at different contamination levels. FEMS Microbiology Ecology, 2015, 91, fiv140.	2.7	23
1639	Comparative analysis of alkaline phosphatase-encoding genes (<i>phoX</i>) in two contrasting zones of Lake Taihu. Canadian Journal of Microbiology, 2015, 61, 227-236.	1.7	15
1640	Effects of nutrients and warming on <i>P</i> dynamics and diversity: a palaeolimnological view based on sedimentary <i>DNA</i> and <i>RNA</i>. Freshwater Biology, 2015, 60, 31-49.	2.4	34
1641	Bacterial composition and spatiotemporal variation in sediments of Jiaozhou Bay, China. Journal of Soils and Sediments, 2015, 15, 732-744.	3.0	32
1642	Bioaugmentation of overloaded anaerobic digesters restores function and archaeal community. Water Research, 2015, 70, 138-147.	11.3	84
1643	Effect of inoculum sources on the enrichment of nitrite-dependent anaerobic methane-oxidizing bacteria. Applied Microbiology and Biotechnology, 2015, 99, 939-946.	3.6	53
1644	Enrichment and Identification of Cellulolytic Bacteria from the Gastrointestinal Tract of Giant African Snail, Achatina fulica. Applied Biochemistry and Biotechnology, 2015, 175, 1971-1980.	2.9	34
1645	Microbial diversity in the hydrate-containing and -free surface sediments in the Shenhu area, South China Sea. Geoscience Frontiers, 2015, 6, 627-633.	8.4	29
1646	Genomic insights into the uncultivated marine <i>Zetaproteobacteria</i> at Loihi Seamount. ISME Journal, 2015, 9, 857-870.	9.8	69

#	ARTICLE	IF	CITATIONS
1647	<i>Paratrechina longicornis</i> ants in a tropical dry forest harbor specific Actinobacteria diversity. Journal of Basic Microbiology, 2015, 55, 11-21.	3.3	12
1648	Ammonia-oxidizing bacteria and archaea in sediments of the Gulf of Mexico. Environmental Technology (United Kingdom), 2015, 36, 124-135.	2.2	25
1649	Investigation of microbial community structure of a shallow lake after one season copper sulfate algacide treatment. Microbiological Research, 2015, 170, 105-113.	5.3	37
1650	Unraveling free-living marine nematode community structure from a biodiversity-rich tropical coastal setting based on molecular approaches. Marine Biodiversity, 2015, 45, 537-547.	1.0	7
1651	Composition and diversity of the bacterial community in snow leopard (<i>Uncia uncia</i>) distal gut. Annals of Microbiology, 2015, 65, 703-711.	2.6	5
1652	Bacterial community change through drinking water treatment processes. International Journal of Environmental Science and Technology, 2015, 12, 1867-1874.	3.5	18
1653	Variation in diazotrophic community structure in forest soils reflects land use history. Soil Biology and Biochemistry, 2015, 80, 1-8.	8.8	15
1654	Comparison of bacterial communities in soil between nematode-infected and nematode-uninfected <i>Pinus massoniana</i> pinewood forest. Applied Soil Ecology, 2015, 85, 11-20.	4.3	19
1655	Evolution in the <i>Bacillaceae</i> , 0, , 21-58.		3
1656	Probing the diversity of healthy oral microbiome with bioinformatics approaches. BMB Reports, 2016, 49, 662-670.	2.4	39
1657	Influence of Starvation on the Structure of Gut-Associated Bacterial Communities in the Chinese White Pine Beetle (<i>Dendroctonus armandi</i>). Forests, 2016, 7, 126.	2.1	3
1658	Vertical Segregation and Phylogenetic Characterization of Ammonia-Oxidizing Bacteria and Archaea in the Sediment of a Freshwater Aquaculture Pond. Frontiers in Microbiology, 2015, 6, 1539.	3.5	37
1659	Diversity, Abundance, and Niche Differentiation of Ammonia-Oxidizing Prokaryotes in Mud Deposits of the Eastern China Marginal Seas. Frontiers in Microbiology, 2016, 7, 137.	3.5	40
1660	Phylogenetic Diversity, Distribution, and Cophylogeny of Giant Bacteria (<i>Epulopiscium</i>) with their Surgefish Hosts in the Red Sea. Frontiers in Microbiology, 2016, 7, 285.	3.5	41
1661	Environmental Controls Over Actinobacteria Communities in Ecological Sensitive Yanshan Mountains Zone. Frontiers in Microbiology, 2016, 7, 343.	3.5	28
1662	Dietary Shifts May Trigger Dysbiosis and Mucous Stools in Giant Pandas (<i>Ailuropoda melanoleuca</i>). Frontiers in Microbiology, 2016, 7, 661.	3.5	60
1663	The Architecture of Iron Microbial Mats Reflects the Adaptation of Chemolithotrophic Iron Oxidation in Freshwater and Marine Environments. Frontiers in Microbiology, 2016, 7, 796.	3.5	100
1664	The Dark Side of the Mushroom Spring Microbial Mat: Life in the Shadow of Chlorophototrophs. I. Microbial Diversity Based on 16S rRNA Gene Amplicons and Metagenomic Sequencing. Frontiers in Microbiology, 2016, 7, 919.	3.5	123

#	ARTICLE	IF	CITATIONS
1665	Diversity and Distribution of Prokaryotes within a Shallow-Water Pockmark Field. <i>Frontiers in Microbiology</i> , 2016, 7, 941.	3.5	27
1666	Environmental Conditions Outweigh Geographical Contiguity in Determining the Similarity of nifH-Harboring Microbial Communities in Sediments of Two Disconnected Marginal Seas. <i>Frontiers in Microbiology</i> , 2016, 7, 1111.	3.5	14
1667	A Genetic and Chemical Perspective on Symbiotic Recruitment of Cyanobacteria of the Genus <i>Nostoc</i> into the Host Plant <i>Blasia pusilla</i> L. <i>Frontiers in Microbiology</i> , 2016, 7, 1693.	3.5	46
1668	Potential Impacts of PCBs on Sediment Microbiomes in a Tropical Marine Environment. <i>Journal of Marine Science and Engineering</i> , 2016, 4, 13.	2.6	1
1669	Assessing Bacterial Diversity in the Rhizosphere of <i>Thymus zygis</i> Growing in the Sierra Nevada National Park (Spain) through Culture-Dependent and Independent Approaches. <i>PLoS ONE</i> , 2016, 11, e0146558.	2.5	47
1670	Diversity of Cultivated Fungi Associated with Conventional and Transgenic Sugarcane and the Interaction between Endophytic <i>Trichoderma virens</i> and the Host Plant. <i>PLoS ONE</i> , 2016, 11, e0158974.	2.5	51
1671	Estimating and comparing microbial diversity in the presence of sequencing errors. <i>PeerJ</i> , 2016, 4, e1634.	2.0	73
1672	A multiproxy approach to evaluate biocidal treatments on biodeteriorated majolica glazed tiles. <i>Environmental Microbiology</i> , 2016, 18, 4794-4816.	3.8	33
1673	Methanogenic abundance and changes in community structure along a rice soil chronosequence from east <scp>C</scp>hina. <i>European Journal of Soil Science</i> , 2016, 67, 443-455.	3.9	12
1674	The diversity and distribution of anammox bacteria in the marine aquaculture zones. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 8943-8953.	3.6	21
1675	Formateâ€derived H₂, a driver of hydrogenotrophic processes in the rootâ€zone of a methaneâ€emitting fen. <i>Environmental Microbiology</i> , 2016, 18, 3106-3119.	3.8	12
1676	Comparative analysis of midgut bacterial communities in three aedine mosquito species from dengueâ€endemic and nonâ€endemic areas of Rajasthan, India. <i>Medical and Veterinary Entomology</i> , 2016, 30, 264-277.	1.5	9
1677	Soil microorganisms behave like macroscopic organisms: patterns in the global distribution of soil euglyphid testate amoebae. <i>Journal of Biogeography</i> , 2016, 43, 520-532.	3.0	43
1678	CAMIL: Clustering and Assembly with Multiple Instance Learning for phenotype prediction. , 2016, , .		3
1680	Application of horizontal-flow anaerobic immobilized biomass reactor for bioremediation of acid mine drainage. <i>Journal of Water and Health</i> , 2016, 14, 399-410.	2.6	12
1681	DACE: a scalable DP-means algorithm for clustering extremely large sequence data. <i>Bioinformatics</i> , 2017, 33, 834-842.	4.1	12
1682	Diversity of the aerobic anoxygenic phototrophy gene <i>pufM</i> in Arctic and Antarctic coastal seawaters. <i>Acta Oceanologica Sinica</i> , 2016, 35, 68-77.	1.0	4
1683	BiMat: a MATLAB package to facilitate the analysis of bipartite networks. <i>Methods in Ecology and Evolution</i> , 2016, 7, 127-132.	5.2	58

#	ARTICLE	IF	CITATIONS
1684	Inhabitancy of active Nitrosopumilus-like ammonia-oxidizing archaea and Nitrospira nitrite-oxidizing bacteria in the sponge Theonella swinhoei. Scientific Reports, 2016, 6, 24966.	3.3	56
1685	Integrated analysis of root microbiomes of soybean and wheat from agricultural fields. Scientific Reports, 2016, 6, 28084.	3.3	198
1686	The impact of zinc oxide nanoparticles on the bacterial microbiome of activated sludge systems. Scientific Reports, 2016, 6, 39176.	3.3	32
1688	Metagenomic Profiling, Interaction of Genomics with Meta-genomics. Translational Bioinformatics, 2016, , 241-267.	0.0	0
1689	Diversity, abundance and community structure of ammonia-oxidizing archaea and bacteria in riparian sediment of Zhenjiang ancient canal. Ecological Engineering, 2016, 90, 447-458.	3.6	23
1690	Laboratory maintained and wild populations of Hydra differ in their microbiota. Annals of Microbiology, 2016, 66, 931-935.	2.6	2
1691	Spatiotemporal dynamics of bacterial and archaeal communities in household biogas digesters from tropical and subtropical regions of Yunnan Province, China. Environmental Science and Pollution Research, 2016, 23, 11137-11148.	5.3	3
1692	Anaerobic methane oxidation coupled to nitrite reduction can be a potential methane sink in coastal environments. Applied Microbiology and Biotechnology, 2016, 100, 7171-7180.	3.6	58
1693	Pyrosequencing analysis of bacterial diversity in soils contaminated long-term with PAHs and heavy metals: Implications to bioremediation. Journal of Hazardous Materials, 2016, 317, 169-179.	12.4	118
1694	Spatial variation of microbial community structure in the Zijinshan commercial copper heap bioleaching plant. Minerals Engineering, 2016, 94, 76-82.	4.3	29
1695	Environmental factors affecting the presence of Acidimicrobiaceae and ammonium removal under iron-reducing conditions in soil environments. Soil Biology and Biochemistry, 2016, 98, 148-158.	8.8	88
1696	Characterization of the bacterial and fungal microbiome in indoor dust and outdoor air samples: a pilot study. Environmental Sciences: Processes and Impacts, 2016, 18, 713-724.	3.5	74
1697	Bioturbation of Tubificid worms affects the abundance and community composition of ammonia-oxidizing archaea and bacteria in surface lake sediments. Annals of Microbiology, 2016, 66, 1065-1073.	2.6	10
1698	Abundance and Diversity of Methanotrophs and Propanotrophs in Soils above Yangxin Oil Reservoir, China. Geomicrobiology Journal, 2016, 33, 661-670.	2.0	4
1699	Ribosomal Tag Pyrosequencing of DNA and RNA Reveals "Rare" Taxa with High Protein Synthesis Potential in the Sediment of a Hypersaline Lake in Western Australia. Geomicrobiology Journal, 2016, 33, 426-440.	2.0	22
1700	Optimization of cold-active CMCase production by psychrotrophic Sphingomonas sp. FLX-7 from the cold region of China. Cellulose, 2016, 23, 1335-1347.	4.9	21
1701	Intricacies of assessing the human microbiome in epidemiologic studies. Annals of Epidemiology, 2016, 26, 311-321.	1.9	46
1702	Soil biochar amendment shapes the composition of N ₂ O-reducing microbial communities. Science of the Total Environment, 2016, 562, 379-390.	8.0	117

#	ARTICLE	IF	CITATIONS
1703	pH affects bacterial community composition in soils across the Huashan Watershed, China. Canadian Journal of Microbiology, 2016, 62, 726-734.	1.7	6
1704	Performance assessment and microbial diversity of two pilot scale multi-stage sub-surface flow constructed wetland systems. Journal of Environmental Sciences, 2016, 46, 38-46.	6.1	10
1705	Diversity and distribution of catechol 2, 3-dioxygenase genes in surface sediments of the Bohai Sea. FEMS Microbiology Letters, 2016, 363, fnw086.	1.8	14
1706	Effects of <i>Saccharomyces cerevisiae</i> fermentation products on dairy calves: Ruminal fermentation, gastrointestinal morphology, and microbial community. Journal of Dairy Science, 2016, 99, 5401-5412.	3.4	85
1707	Dominance of ammonia-oxidizing archaea community induced by land use change from Masson pine to eucalypt plantation in subtropical China. Applied Microbiology and Biotechnology, 2016, 100, 6859-6869.	3.6	10
1708	The Symbiotic Bacteria <i>Nardonella</i> in Rice Water Weevil (Coleoptera: Curculionidae): Diversity, Density, and Associations With Host Reproduction. Annals of the Entomological Society of America, 2016, 109, 415-423.	2.5	11
1709	Phylogenetic analysis of bacterial community composition in sediments with organic contaminants from the Jiaojiang estuary in China. Marine Pollution Bulletin, 2016, 109, 558-565.	5.0	12
1710	Network analysis reveals seasonal variation of co-occurrence correlations between Cyanobacteria and other bacterioplankton. Science of the Total Environment, 2016, 573, 817-825.	8.0	101
1711	Functional Nucleic Acids Detection in Food Safety. , 2016, , .		10
1712	Characterization of Microbial Diversity in Food Chain: A Molecular Review. , 2016, , 365-382.		0
1713	DNA barcodes for bio-surveillance: regulated and economically important arthropod plant pests. Genome, 2016, 59, 933-945.	2.0	57
1714	Infection state of <i>Pantoea agglomerans</i> in the rice water weevil <i>Lissorhoptrus oryzophilus</i> (Coleoptera: Curculionidae). Applied Entomology and Zoology, 2016, 51, 561-569.	1.2	6
1715	Abundance and Community Structure of Bacteria on Asian Dust Particles Collected in Beijing, China, during the Asian Dust Season. Biological and Pharmaceutical Bulletin, 2016, 39, 68-77.	1.4	27
1716	Diversity, Community Composition and Abundance of Anammox Bacteria in Sediments of the North Marginal Seas of China. Microbes and Environments, 2016, 31, 111-120.	1.6	17
1717	Nonparametric Regularized Regression for Phenotype-Associated Taxa Selection and Network Construction with Metagenomic Count Data. Journal of Computational Biology, 2016, 23, 877-890.	1.6	0
1718	Improved PCR primers to amplify 16S rRNA genes from NC10 bacteria. Applied Microbiology and Biotechnology, 2016, 100, 5099-5108.	3.6	32
1719	Diversity of ammonia-oxidising bacteria and archaea in seven different estuarine sediments from Poyang Lake. Marine and Freshwater Research, 2016, 67, 1897.	1.3	6
1720	Comparative Analysis of Microbial Communities in Iron-Dominated Flocculent Mats in Deep-Sea Hydrothermal Environments. Applied and Environmental Microbiology, 2016, 82, 5741-5755.	3.1	26

#	ARTICLE	IF	CITATIONS
1721	The upper respiratory tract microbiome and its potential role in bovine respiratory disease and otitis media. <i>Scientific Reports</i> , 2016, 6, 29050.	3.3	83
1722	Driving forces of soil bacterial community structure, diversity, and function in temperate grasslands and forests. <i>Scientific Reports</i> , 2016, 6, 33696.	3.3	308
1723	Sedimentary archaeal amoA gene abundance reflects historic nutrient level and salinity fluctuations in Qinghai Lake, Tibetan Plateau. <i>Scientific Reports</i> , 2016, 5, 18071.	3.3	52
1725	Response of performance and ammonia oxidizing bacteria community to high salinity stress in membrane bioreactor with elevated ammonia loading. <i>Bioresource Technology</i> , 2016, 216, 714-721.	9.6	46
1726	Identification and evaluation of cultivable gut bacteria associated with peach fruit fly, <i>Bactrocera zonata</i> (Diptera: Tephritidae). <i>Phytoparasitica</i> , 2016, 44, 165-176.	1.2	20
1727	<i>Quercus</i> species control nutrients dynamics by determining the composition and activity of the forest floor fungal community. <i>Soil Biology and Biochemistry</i> , 2016, 98, 186-195.	8.8	14
1728	Differential distribution patterns of ammonia-oxidizing archaea and bacteria in acidic soils of Nanling National Nature Reserve forests in subtropical China. <i>Antonie Van Leeuwenhoek</i> , 2016, 109, 237-251.	1.7	16
1729	Elevation gradient of soil bacterial communities in bamboo plantations. , 2016, 57, 8.		7
1730	Abundance and community composition of ammonia oxidizers in rhizosphere sediment of two submerged macrophytes. <i>Journal of Freshwater Ecology</i> , 2016, 31, 407-419.	1.2	10
1731	Cultivable endophytic bacteria from heavy metal(loid)-tolerant plants. <i>Archives of Microbiology</i> , 2016, 198, 941-956.	2.2	30
1732	Phytoplankton assemblage during the North Atlantic spring bloom assessed from functional gene analysis. <i>Journal of Plankton Research</i> , 2016, 38, 1135-1150.	1.8	8
1733	Biofilm formation on RO membranes: the impact of seawater pretreatment. <i>Desalination and Water Treatment</i> , 2016, 57, 4741-4748.	1.0	14
1734	Peat: home to novel syntrophic species that feed acetate- and hydrogen-scavenging methanogens. <i>ISME Journal</i> , 2016, 10, 1954-1966.	9.8	62
1735	Distribution and activity of anaerobic ammonium-oxidising bacteria in natural freshwater wetland soils. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 3291-3300.	3.6	41
1736	Phytoplankton community diversity is influenced by environmental factors in the coastal East China Sea. <i>European Journal of Phycology</i> , 2016, 51, 107-118.	2.0	19
1737	Bioremediation technologies for polluted seawater sampled after an oil-spill in Taranto Gulf (Italy): A comparison of biostimulation, bioaugmentation and use of a washing agent in microcosm studies. <i>Marine Pollution Bulletin</i> , 2016, 106, 119-126.	5.0	60
1738	Bacterial communities of an agricultural soil amended with solid pig and dairy manures, and urea fertilizer. <i>Applied Soil Ecology</i> , 2016, 103, 61-71.	4.3	56
1739	Estimates of Soil Bacterial Ribosome Content and Diversity Are Significantly Affected by the Nucleic Acid Extraction Method Employed. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2595-2607.	3.1	28

#	ARTICLE	IF	CITATIONS
1740	Differences in nitrite-oxidizing communities and kinetics in a brackish environment after enrichment at low and high nitrite concentrations. <i>Journal of Environmental Sciences</i> , 2016, 42, 41-49.	6.1	8
1741	Diversity of gene cassettes and the abundance of the class 1 integron-integrase gene in sediment polluted by metals. <i>Extremophiles</i> , 2016, 20, 283-289.	2.3	11
1742	Open-Source Sequence Clustering Methods Improve the State Of the Art. <i>MSystems</i> , 2016, 1, .	3.8	155
1743	bioOTU: An Improved Method for Simultaneous Taxonomic Assignments and Operational Taxonomic Units Clustering of 16s rRNA Gene Sequences. <i>Journal of Computational Biology</i> , 2016, 23, 229-238.	1.6	11
1744	Characterization of the gut microbiome in epidemiologic studies: the multiethnic cohort experience. <i>Annals of Epidemiology</i> , 2016, 26, 373-379.	1.9	42
1745	Specificity and selectivity of arbuscular mycorrhizal fungal polymerase chain reaction primers in soil samples by clone library analyses. <i>Acta Agriculturae Scandinavica - Section B Soil and Plant Science</i> , 2016, 66, 333-339.	0.6	3
1746	Distinct compositions of free-living, particle-associated and benthic communities of the <i>Roseobacter</i> group in the North Sea. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv145.	2.7	18
1747	Microbial community in a pilot-scale bioreactor promoting anaerobic digestion and sulfur-driven denitrification for domestic sewage treatment. <i>Bioprocess and Biosystems Engineering</i> , 2016, 39, 341-352.	3.4	50
1748	<i>Defluviitalea phaphyphila</i> sp. nov., a Novel Thermophilic Bacterium That Degrades Brown Algae. <i>Applied and Environmental Microbiology</i> , 2016, 82, 868-877.	3.1	43
1749	The interaction between iron nutrition, plant species and soil type shapes the rhizosphere microbiome. <i>Plant Physiology and Biochemistry</i> , 2016, 99, 39-48.	5.8	182
1750	Distribution characteristics of ammonia oxidizing microorganisms in rhizosphere sediments of cattail. <i>Ecological Engineering</i> , 2016, 88, 99-111.	3.6	13
1751	Diversity and distribution patterns of root-associated fungi on herbaceous plants in alpine meadows of southwestern China. <i>Mycologia</i> , 2016, 108, 281-291.	1.9	29
1752	Illumina high-throughput sequencing and comparative analysis of bacterial communities in cherry orchard soil. <i>Toxicological and Environmental Chemistry</i> , 2016, 98, 462-478.	1.2	1
1753	Effect of self-alkalization on nitrite accumulation in a high-rate denitrification system: Performance, microflora and enzymatic activities. <i>Water Research</i> , 2016, 88, 758-765.	11.3	91
1754	Microbial Distribution in a Hydrothermal Plume of the Southwest Indian Ridge. <i>Geomicrobiology Journal</i> , 2016, 33, 401-415.	2.0	18
1755	First report on the bacterial diversity in the distal gut of dholes (<i>Cuon alpinus</i>) by using 16S rRNA gene sequences analysis. <i>Journal of Applied Genetics</i> , 2016, 57, 275-283.	1.9	11
1756	Microbial Diversity in Soil, Sand Dune and Rock Substrates of the Thar Monsoon Desert, India. <i>Indian Journal of Microbiology</i> , 2016, 56, 35-45.	2.7	33
1757	Effects of Environmental Factors on Anammox Bacterial Community Structure in Sediments of a Freshwater Aquaculture Farm, Yangcheng Lake. <i>Geomicrobiology Journal</i> , 2016, 33, 479-487.	2.0	7

#	ARTICLE	IF	CITATIONS
1758	Five-Year Monitoring of Bacterial Communities in Dripping Water from the Heshang Cave in Central China: Implication for Paleoclimate Reconstruction and Ecological Functions. Geomicrobiology Journal, 2016, 33, 1-11.	2.0	46
1759	Nitrogen loss by anaerobic ammonium oxidation in unconfined aquifer soils. Scientific Reports, 2017, 7, 40173.	3.3	31
1760	Astrobiological implications of dim light phototrophy in deep-sea red clays. Life Sciences in Space Research, 2017, 12, 39-50.	2.3	3
1761	Diversity of culturable bacteria in deep-sea water from the South Atlantic Ocean. Bioengineered, 2017, 8, 572-584.	3.2	29
1762	Capturing Compositional Variation in Denitrifying Communities: a Multiple-Primer Approach That Includes Epsilonproteobacteria. Applied and Environmental Microbiology, 2017, 83, .	3.1	9
1763	Structural modulation of gut microbiota during alleviation of antibiotic-associated diarrhea with herbal formula. International Journal of Biological Macromolecules, 2017, 105, 1622-1629.	7.5	73
1764	Abundance and diversity of ammonia-oxidizing archaea and bacteria in the rhizosphere soil of three plants in the Ebinur Lake wetland. Canadian Journal of Microbiology, 2017, 63, 573-582.	1.7	21
1765	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. MSystems, 2017, 2, .	3.8	1,339
1766	The bovine colostrum microbiome and its association with clinical mastitis. Journal of Dairy Science, 2017, 100, 3031-3042.	3.4	76
1767	Comparison of Archaeal Populations in Soil and Their Encapsulated Iron-Manganese Nodules in Four Locations Spanning from North to South China. Geomicrobiology Journal, 2017, 34, 811-822.	2.0	3
1768	Seen once or more than once: applying Goodâ€™Turing theory to estimate species richness using only unique observations and a species list. Methods in Ecology and Evolution, 2017, 8, 1221-1232.	5.2	31
1769	A New Primer to Amplify pmoA Gene From NC10 Bacteria in the Sediments of Dongchang Lake and Dongping Lake. Current Microbiology, 2017, 74, 908-914.	2.2	7
1770	Community composition and assembly processes of the free-living and particle-attached bacteria in Taihu Lake. FEMS Microbiology Ecology, 2017, 93, .	2.7	52
1771	Nature and origin of the violet stains on the walls of a Roman tomb. Science of the Total Environment, 2017, 598, 889-899.	8.0	10
1772	Improving runoff behavior resulting from direct inoculation of soil micro-organisms. Soil and Tillage Research, 2017, 171, 35-41.	5.6	47
1773	Molecular diversity patterns among various phytoplankton size-fractions in West Greenland in late summer. Deep-Sea Research Part I: Oceanographic Research Papers, 2017, 121, 54-69.	1.4	30
1774	Emergent macrophytes modify the abundance and community composition of ammonia oxidizers in their rhizosphere sediments. Journal of Basic Microbiology, 2017, 57, 625-632.	3.3	4
1775	DMclust, a Densityâ€“based Modularity Method for Accurate OTU Picking of 16S rRNA Sequences. Molecular Informatics, 2017, 36, 1600059.	2.5	15

#	ARTICLE	IF	CITATIONS
1776	Illumina-based analysis of endophytic bacterial diversity of tree peony (<i>Paeonia</i> Sect. <i>Moutan</i>) roots and leaves. <i>Brazilian Journal of Microbiology</i> , 2017, 48, 695-705.	2.0	90
1777	Antioxidant status and gut microbiota change in an aging mouse model as influenced by exopolysaccharide produced by <i>Lactobacillus plantarum</i> YW11 isolated from Tibetan kefir. <i>Journal of Dairy Science</i> , 2017, 100, 6025-6041.	3.4	106
1778	Bioaerosol sampling and detection methods based on molecular approaches: No pain no gain. <i>Science of the Total Environment</i> , 2017, 599-600, 2095-2104.	8.0	54
1779	Prevalence of ammonia-oxidizing bacteria over ammonia-oxidizing archaea in sediments as related to nutrient loading in Chinese aquaculture ponds. <i>Journal of Soils and Sediments</i> , 2017, 17, 1928-1938.	3.0	17
1780	Structure and function of the bacterial communities during rhizoremediation of hexachlorobenzene in constructed wetlands. <i>Environmental Science and Pollution Research</i> , 2017, 24, 11483-11492.	5.3	28
1781	Enrichment of dissimilatory Fe(III)-reducing bacteria from groundwater of the SiklÃ³s BTEX-contaminated site (Hungary). <i>Folia Microbiologica</i> , 2017, 62, 63-71.	2.3	18
1782	Methods for Microbiome Analysis. <i>Translational Medicine Research</i> , 2017, , 269-298.	0.0	1
1783	The Microbiome and Human Biology. <i>Annual Review of Genomics and Human Genetics</i> , 2017, 18, 65-86.	6.2	266
1784	Ferrous iron and ammonium-rich diffuse vents support habitat-specific communities in a shallow hydrothermal field off the Basiluzzo Islet (Aeolian Volcanic Archipelago). <i>Geobiology</i> , 2017, 15, 664-677.	2.4	17
1786	Diversity and Abundance of the Denitrifying Microbiota in the Sediment of Eastern China Marginal Seas and the Impact of Environmental Factors. <i>Microbial Ecology</i> , 2017, 73, 602-615.	2.8	14
1787	Methane fates in the benthos and water column at cold seep sites along the continental margin of Central and North America. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2017, 120, 122-131.	1.4	7
1788	Expression of mitogen-activated protein kinase double-stranded RNA in cucumber has no apparent effect on the diversity of rhizosphere archaea. <i>Journal of Integrative Agriculture</i> , 2017, 16, 2239-2245.	3.5	1
1789	Bioinformatics for Microbiome Research: Concepts, Strategies, and Advances. , 2017, , 111-123.		3
1790	Spatial and temporal distribution of nitrite-dependent anaerobic methane-oxidizing bacteria in an intertidal zone of the East China Sea. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 8007-8014.	3.6	28
1791	Small-scale variation of ammonia oxidisers within intertidal sediments dominated by ammonia-oxidising bacteria <i>Nitrosomonas</i> sp. amoA genes and transcripts. <i>Scientific Reports</i> , 2017, 7, 13200.	3.3	15
1792	Evidence of cryptic incidence in childhood diseases. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20171268.	2.6	8
1793	Novel arsenic-transforming bacteria and the diversity of their arsenic-related genes and enzymes arising from arsenic-polluted freshwater sediment. <i>Scientific Reports</i> , 2017, 7, 11231.	3.3	98
1794	Assessment of molecular detection of anaerobic ammonium-oxidizing (anammox) bacteria in different environmental samples using PCR primers based on 16S rRNA and functional genes. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 7689-7702.	3.6	21

#	ARTICLE	IF	CITATIONS
1796	Isolation and characterization of aerobic anoxygenic phototrophs from exposed soils from the Sør Rondane Mountains, East Antarctica. <i>Systematic and Applied Microbiology</i> , 2017, 40, 357-369.	2.8	69
1797	The novel <i>mef</i> (C)– <i>mph</i> (G) macrolide resistance genes are conveyed in the environment on various vectors. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 10, 47-53.	2.2	25
1798	Reprint of: Contribution of enrichments and resampling for sulfate reducing bacteria diversity assessment by high-throughput cultivation. <i>Journal of Microbiological Methods</i> , 2017, 138, 100-105.	1.6	1
1799	OptiClust, an Improved Method for Assigning Amplicon-Based Sequence Data to Operational Taxonomic Units. <i>MSphere</i> , 2017, 2, .	2.9	365
1800	Community Composition and Abundance of Anammox Bacteria in Cattail Rhizosphere Sediments at Three Phenological Stages. <i>Current Microbiology</i> , 2017, 74, 1349-1357.	2.2	8
1801	A clinician's guide to microbiome analysis. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2017, 14, 585-595.	17.8	124
1802	Effects of macrobenthic bioturbation on the abundance and community composition of ammonia-oxidizing prokaryotes under different temperatures. <i>Journal of Freshwater Ecology</i> , 2017, 32, 405-414.	1.2	3
1803	Metagenomic Insights into Herbivore Gut: An Application-Based Perspective. , 2017, , 201-215.		1
1804	Assessing the impact of rumen microbial communities on methane emissions and production traits in Holstein cows in a tropical climate. <i>Systematic and Applied Microbiology</i> , 2017, 40, 492-499.	2.8	33
1805	Bacterial community radial-spatial distribution in biofilms along pipe wall in chlorinated drinking water distribution system of East China. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 749-759.	3.6	21
1806	Microbial communities within the water column of freshwater Lake Radok, East Antarctica: predominant 16S rDNA phylotypes and bacterial cultures. <i>Polar Biology</i> , 2017, 40, 823-836.	1.2	14
1807	Fungus-associated bacteriome in charge of their host behavior. <i>Fungal Genetics and Biology</i> , 2017, 102, 38-48.	2.1	30
1808	Identification of new bacteria harboring <i>qnrS</i> and <i>aac</i> (6- Ib/cr) and mutations possibly involved in fluoroquinolone resistance in raw sewage and activated sludge samples from a full-scale WWTP. <i>Water Research</i> , 2017, 110, 27-37.	11.3	32
1809	Effect of Synbiotic-Assisted Modulation of Gastrointestinal Microbiota on Human Health. , 2017, , 223-236.		1
1810	Identifying spatially concordant evolutionary significant units across multiple species through DNA barcodes: Application to the conservation genetics of the freshwater fishes of Java and Bali. <i>Global Ecology and Conservation</i> , 2017, 12, 170-187.	2.1	23
1811	Two Efficient Hashing Schemes for High-Dimensional Furthest Neighbor Search. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2017, 29, 2772-2785.	5.7	14
1812	From reads to operational taxonomic units: an ensemble processing pipeline for MiSeq amplicon sequencing data. <i>GigaScience</i> , 2017, 6, 1-10.	6.4	47
1813	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. <i>Genes and Genetic Systems</i> , 2017, 92, 1-20.	0.7	11

#	ARTICLE	IF	CITATIONS
1814	Archaea Dominate the Ammonia-Oxidizing Community in Deep-Sea Sediments of the Eastern Indian Ocean from the Equator to the Bay of Bengal. <i>Frontiers in Microbiology</i> , 2017, 8, 415.	3.5	23
1815	Global Diversity of Desert Hypolithic Cyanobacteria. <i>Frontiers in Microbiology</i> , 2017, 8, 867.	3.5	61
1816	Phylogenetic Diversity of T4-Type Phages in Sediments from the Subtropical Pearl River Estuary. <i>Frontiers in Microbiology</i> , 2017, 8, 897.	3.5	19
1817	Oxidative Weathering and Microbial Diversity of an Inactive Seafloor Hydrothermal Sulfide Chimney. <i>Frontiers in Microbiology</i> , 2017, 8, 1378.	3.5	28
1818	Analysing Microbial Community Composition through Amplicon Sequencing: From Sampling to Hypothesis Testing. <i>Frontiers in Microbiology</i> , 2017, 8, 1561.	3.5	265
1819	Diversity and Structure of Diazotrophic Communities in Mangrove Rhizosphere, Revealed by High-Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 2032.	3.5	49
1820	Geochemical Influence on Microbial Communities at CO ₂ -Leakage Analog Sites. <i>Frontiers in Microbiology</i> , 2017, 8, 2203.	3.5	17
1821	Genomic features of <i>Candidatus Venteria ishoeyi</i> , a new sulfur-oxidizing macrobacterium from the Humboldt Sulfuretum off Chile. <i>PLoS ONE</i> , 2017, 12, e0188371.	2.5	12
1822	Bacterial community in the rumen of Tibetan sheep and Gansu alpine fine-wool sheep grazing on the Qinghai-Tibetan Plateau, China. <i>Journal of General and Applied Microbiology</i> , 2017, 63, 122-130.	0.7	26
1823	Relations among epiphytic microbial communities from soil, leaves and grapes of the grapevine. <i>Frontiers in Life Science: Frontiers of Interdisciplinary Research in the Life Sciences</i> , 2017, 10, 73-83.	1.1	19
1824	Isolation and characterization of extremely halotolerant <i>Bacillus</i> species from Dead Sea black mud and determination of their antimicrobial and hydrolytic activities. <i>African Journal of Microbiology Research</i> , 2017, 11, 1303-1314.	0.4	12
1825	hc-OTU: A Fast and Accurate Method for Clustering Operational Taxonomic Units Based on Homopolymer Compaction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 441-451.	3.0	10
1826	Comparing Alkaline Phosphatase PhoX-Encoding Genes in Two Contrasting Habitats of the Large Eutrophic Lake Taihu, China. <i>Geomicrobiology Journal</i> , 2018, 35, 528-536.	2.0	7
1827	Characteristic of filamentous fungal diversity and dynamics associated with wheat Qu and the traditional fermentation of Chinese rice wine. <i>International Journal of Food Science and Technology</i> , 2018, 53, 1611-1621.	2.7	35
1828	Gammaproteobacterial Diversity and Carbon Utilization in Response to Salinity in the Lakes on the Qinghai-Tibetan Plateau. <i>Geomicrobiology Journal</i> , 2018, 35, 392-403.	2.0	19
1829	Denitrifying anaerobic methane oxidizing in global upland soil: Sporadic and non-continuous distribution with low influence. <i>Soil Biology and Biochemistry</i> , 2018, 119, 90-100.	8.8	19
1830	Self-organized Bacterial Evolutionary Dynamics: Fractal Characteristics. <i>Advances in Intelligent Systems and Computing</i> , 2018, , 229-237.	0.6	0
1831	Low-dissolved-oxygen nitrification in tropical sewage: an investigation on potential, performance and functional microbial community. <i>Water Science and Technology</i> , 2018, 77, 2274-2283.	2.5	31

#	ARTICLE	IF	CITATIONS
1832	Nitrification and the ammonia-oxidizing communities in the central Baltic Sea water column. Estuarine, Coastal and Shelf Science, 2018, 202, 280-289.	2.1	6
1833	Shifts of methanogenic communities in response to permafrost thaw results in rising methane emissions and soil property changes. Extremophiles, 2018, 22, 447-459.	2.3	23
1834	Stimulating ammonia oxidizing bacteria (AOB) activity drives the ammonium oxidation rate in a constructed wetland (CW). Science of the Total Environment, 2018, 624, 87-95.	8.0	28
1835	Discovering novel enzymes from marine ecosystems: a metagenomic approach. Botanica Marina, 2018, 61, 161-175.	1.2	7
1836	Dietary changes during weaning shape the gut microbiota of red pandas (<i>Ailurus fulgens</i>). , 2018, 6, cox075.		30
1837	Abundance and Diversity of Aerobic/Anaerobic Ammonia/Ammonium-Oxidizing Microorganisms in an Ammonium-Rich Aquitard in the Pearl River Delta of South China. Microbial Ecology, 2018, 76, 81-91.	2.8	11
1838	Salinity and DOC Influence the Distribution of Free-living and Particle-attached Aerobic Anoxygenic Phototrophic Bacteria in the Qinghai-Tibetan Lakes. Geomicrobiology Journal, 2018, 35, 247-254.	2.0	5
1839	Investigating monsoon and post-monsoon variabilities of bacterioplankton communities in a mangrove ecosystem. Environmental Science and Pollution Research, 2018, 25, 5722-5739.	5.3	33
1840	A Microbial Analysis Primer for Biogeochemists. , 2018, , 599-609.		3
1841	Comparative Analyses of Methanogenic and Methanotrophic Communities Between Two Different Water Regimes in Controlled Wetlands on the Qinghai-Tibetan Plateau, China. Current Microbiology, 2018, 75, 484-491.	2.2	11
1842	Origin of abundant moonmilk deposits in a subsurface granitic environment. Sedimentology, 2018, 65, 1482-1503.	3.1	22
1843	Diversity of Free-Living Environmental Bacteria and Their Interactions With a Bactivorous Amoeba. Frontiers in Cellular and Infection Microbiology, 2018, 8, 411.	3.9	29
1844	Microbial Community Composition and Predicted Functional Attributes of Antarctic Lithobionts Using Targeted Next-Generation Sequencing and Bioinformatics Tools. Methods in Microbiology, 2018, , 243-290.	0.8	3
1845	Characterization of the bacterial communities on recent Icelandic volcanic deposits of different ages. BMC Microbiology, 2018, 18, 122.	3.3	15
1846	Bioinformatic Analysis of Microbiome Data. ICSA Book Series in Statistics, 2018, , 1-27.	0.2	6
1847	Gill chamber and gut microbial communities of the hydrothermal shrimp <i>Rimicaris chacei</i> Williams and Rona 1986: A possible symbiosis. PLoS ONE, 2018, 13, e0206084.	2.5	24
1848	Niche differentiation of ammonia and nitrite oxidizers along a salinity gradient from the Pearl River estuary to the South China Sea. Biogeosciences, 2018, 15, 5169-5187.	3.3	44
1849	Abundant and Rare Bacterioplankton in Freshwater Lakes Subjected to Different Levels of Tourism Disturbances. Water (Switzerland), 2018, 10, 1075.	2.7	18

#	ARTICLE	IF	CITATIONS
1850	Abundance and community structure of ammonia-oxidizing bacteria in activated sludge from different geographic regions in China. <i>Water Science and Technology</i> , 2018, 77, 1698-1705.	2.5	2
1851	Mapping the transition from pre-European settlement to contemporary soil conditions in the Lower Hunter Valley, Australia. <i>Geoderma</i> , 2018, 329, 27-42.	5.1	19
1852	Definition of two new symbiovars, sv. lupini and sv. mediterraneense, within the genera <i>Bradyrhizobium</i> and <i>Phyllobacterium</i> efficiently nodulating <i>Lupinus micranthus</i> in Tunisia. <i>Systematic and Applied Microbiology</i> , 2018, 41, 487-493.	2.8	18
1853	<i>Analytic Methods in Microbiome Studies.</i> , 2018, , 29-42.		0
1854	Linking abundance and community of microbial N ₂ O-producers and N ₂ O-reducers with enzymatic N ₂ O production potential in a riparian zone. <i>Science of the Total Environment</i> , 2018, 642, 1090-1099.	8.0	51
1855	Genetic Diversity and Cooccurrence Patterns of Marine Cyanopodoviruses and Picocyanobacteria. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	5
1856	Biogeography and environmental conditions shape bacteriophage-bacteria networks across the human microbiome. <i>PLoS Computational Biology</i> , 2018, 14, e1006099.	3.2	45
1857	Sustainable Agriculture: Role of Metagenomics and Metabolomics in Exploring the Soil Microbiota. , 2018, , 183-199.		19
1858	In Silico Approach for Sustainable Agriculture. , 2018, , .		1
1859	Fungal Community and Ligninolytic Enzyme Activities in <i>Quercus deserticola</i> Trel. Litter from Forest Fragments with Increasing Levels of Disturbance. <i>Forests</i> , 2018, 9, 11.	2.1	15
1860	Diversity and population density of methanogens in the large intestine of pigs fed diets of different energy levels. <i>Animal Science Journal</i> , 2018, 89, 1468-1474.	1.4	3
1861	Linking serpentinization, hyperalkaline mineral waters and abiotic methane production in continental peridotites: an integrated hydrogeological-bio-geochemical model from the Cabeço de Vide CH ₄ -rich aquifer (Portugal). <i>Applied Geochemistry</i> , 2018, 96, 287-301.	3.0	15
1862	Temporal heterogeneity of prokaryotic micro-organism communities in sediment of traditional freshwater cultured fish ponds in Southwest China. <i>Biotechnology and Biotechnological Equipment</i> , 2018, 32, 102-108.	1.3	2
1863	A pulse of summer precipitation after the dry season triggers changes in ectomycorrhizal formation, diversity, and community composition in a Mediterranean forest in California, USA. <i>Mycorrhiza</i> , 2018, 28, 665-677.	2.8	24
1864	Dynamics of phosphorus and bacterial <i>phoX</i> genes during the decomposition of <i>Microcystis</i> blooms in a mesocosm. <i>PLoS ONE</i> , 2018, 13, e0195205.	2.5	13
1865	The gut microbiome of nonhuman primates: Lessons in ecology and evolution. <i>American Journal of Primatology</i> , 2018, 80, e22867.	1.7	100
1866	Diversity and distribution of anammox bacteria in water column and sediments of the Eastern Indian Ocean. <i>International Biodeterioration and Biodegradation</i> , 2018, 133, 52-62.	3.9	32
1867	A case study for late Archean and Proterozoic biogeochemical iron and sulphur cycling in a modern habitat—the Arvadi Spring. <i>Geobiology</i> , 2018, 16, 353-368.	2.4	5

#	ARTICLE	IF	CITATIONS
1868	High contribution of ammonia-oxidizing archaea (AOA) to ammonia oxidation related to a potential active AOA species in various arable land soils. <i>Journal of Soils and Sediments</i> , 2019, 19, 1077-1087.	3.0	23
1869	Diversity and Dynamics of “Candidatus Endobugula” and Other Symbiotic Bacteria in Chinese Populations of the Bryozoan, <i>Bugula neritina</i> . <i>Microbial Ecology</i> , 2019, 77, 243-256.	2.8	4
1870	A parallel computational framework for ultra-large-scale sequence clustering analysis. <i>Bioinformatics</i> , 2019, 35, 380-388.	4.1	8
1871	MicroPro: using metagenomic unmapped reads to provide insights into human microbiota and disease associations. <i>Genome Biology</i> , 2019, 20, 154.	8.8	29
1872	Metagenomic insights into the diversity and functions of microbial assemblages in lakes. , 2019, , 175-223.		3
1873	TADA: phylogenetic augmentation of microbiome samples enhances phenotype classification. <i>Bioinformatics</i> , 2019, 35, i31-i40.	4.1	9
1874	Metagenomics for Utilizing Herbivore Gut Potential. , 2019, , 3-15.		0
1875	K-strategic ammonia-oxidizing bacteria capitalize on biological nitrogen fixation in a flooded, unfertilized rice soil. <i>Biology and Fertility of Soils</i> , 2019, 55, 713-722.	4.3	5
1876	Biodiversity of <i>Photobacterium</i> spp. Isolated From Meats. <i>Frontiers in Microbiology</i> , 2019, 10, 2399.	3.5	32
1877	Variations of bacterial community during the decomposition of <i>Microcystis</i> under different temperatures and biomass. <i>BMC Microbiology</i> , 2019, 19, 207.	3.3	9
1878	A critical analysis of state-of-the-art metagenomics OTU clustering algorithms. <i>Journal of Biosciences</i> , 2019, 44, 1.	1.1	5
1879	Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis. <i>Nature Communications</i> , 2019, 10, 5029.	12.8	1,007
1880	TreeCluster: Clustering biological sequences using phylogenetic trees. <i>PLoS ONE</i> , 2019, 14, e0221068.	2.5	99
1881	New insights into environmental controls on the occurrence and abundance of Group I alkenones and their paleoclimate applications: Evidence from volcanic lakes of northeastern China. <i>Earth and Planetary Science Letters</i> , 2019, 527, 115792.	4.4	17
1882	Diversity of Archaea and Its Correlation with Environmental Factors in the Ebinur Lake Wetland. <i>Current Microbiology</i> , 2019, 76, 1417-1424.	2.2	10
1883	Distribution Characteristics of Anammox Bacteria in Ancient Canal (Guyun River) Riparian Sediment of Zhenjiang, China. <i>Geomicrobiology Journal</i> , 2019, 36, 243-250.	2.0	4
1884	Anammox and denitrification separately dominate microbial N-loss in water saturated and unsaturated soils horizons of riparian zones. <i>Water Research</i> , 2019, 162, 139-150.	11.3	78
1885	The Structure and Function of Aquatic Microbial Communities. <i>Advances in Environmental Microbiology</i> , 2019, , .	0.3	2

#	ARTICLE	IF	CITATIONS
1886	Isolation and Cultivation of Bacteria. <i>Advances in Environmental Microbiology</i> , 2019, , 313-351.	0.3	21
1887	Nitrate Consumers in Arctic Marine Eukaryotic Communities: Comparative Diversities of 18S rRNA, 18S rRNA Genes, and Nitrate Reductase Genes. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	14
1888	Diversity and community of methanogens in the large intestine of finishing pigs. <i>BMC Microbiology</i> , 2019, 19, 83.	3.3	16
1889	Biogeography of Cyanobacterial <i>isiA</i> Genes and Their Link to Iron Availability in the Ocean. <i>Frontiers in Microbiology</i> , 2019, 10, 650.	3.5	7
1890	Research Techniques Made Simple: Profiling the Skin Microbiota. <i>Journal of Investigative Dermatology</i> , 2019, 139, 747-752.e1.	0.7	49
1891	<i>Bombyx mori</i> bidensovirus infection alters the intestinal microflora of fifth instar silkworm (<i>Bombyx</i>) Tj ETQq1 1 0.784314 rgBT /Overbo	3.2	22
1892	Spatiotemporal distributions and environmental drivers of diversity and community structure of nosZ-type denitrifiers and anammox bacteria in sediments of the Bohai Sea and North Yellow Sea, China. <i>Journal of Oceanology and Limnology</i> , 2019, 37, 1211-1228.	1.3	6
1893	Stimulation of <i>Smithella</i> â€dominating propionate oxidation in a sediment enrichment by magnetite and carbon nanotubes. <i>Environmental Microbiology Reports</i> , 2019, 11, 236-248.	2.4	52
1894	Metabarcoding free-living marine nematodes using curated 18S and CO1 reference sequence databases for species-level taxonomic assignments. <i>Ecology and Evolution</i> , 2019, 9, 1211-1226.	1.9	66
1895	Watershed hydrology and salinity, but not nutrient chemistry, are associated with arid-land stream microbial diversity. <i>Freshwater Science</i> , 2019, 38, 77-91.	1.8	5
1896	Microbial Community Analyses Associated with Nine Varieties of Wine Grape Carposphere Based on High-Throughput Sequencing. <i>Microorganisms</i> , 2019, 7, 668.	3.6	37
1897	Factors affecting performance and functional stratification of membrane-aerated biofilms with a counter-diffusion configuration. <i>RSC Advances</i> , 2019, 9, 29337-29346.	3.6	15
1898	Nitrogen release and its influence on anammox bacteria during the decay of <i>Potamogeton crispus</i> with different values of initial debris biomass. <i>Science of the Total Environment</i> , 2019, 650, 604-615.	8.0	13
1899	The impact of OTU sequence similarity threshold on diatom-based bioassessment: A case study of the rivers of Mayotte (France, Indian Ocean). <i>Ecology and Evolution</i> , 2019, 9, 166-179.	1.9	55
1900	Factors driving the distribution and role of AOA and AOB in <i>Phragmites communis</i> rhizosphere in riparian zone. <i>Journal of Basic Microbiology</i> , 2019, 59, 425-436.	3.3	13
1901	Effects of deforestation on microbial diversity in a Siberian larch (<i>Larix sibirica</i>) stand in Mongolia. <i>Journal of Forestry Research</i> , 2019, 30, 1885-1893.	3.6	2
1902	Phenotype Prediction from Metagenomic Data Using Clustering and Assembly with Multiple Instance Learning (CAMIL). <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 828-840.	3.0	5
1903	OBSOLETE: Bioinformatic Platforms for Metagenomics. , 2020, , .		0

#	ARTICLE	IF	CITATIONS
1904	Insight into biodegradation of cellulose by psychrotrophic bacterium <i>Pseudomonas</i> sp. LKR-1 from the cold region of China: optimization of cold-active cellulase production and the associated degradation pathways. <i>Cellulose</i> , 2020, 27, 315-333.	4.9	20
1905	An adaptive independence test for microbiome community data. <i>Biometrics</i> , 2020, 76, 414-426.	1.4	5
1906	Purified plant cell walls with adsorbed polyphenols alter porcine faecal bacterial communities during <i>in vitro</i> fermentation. <i>Food and Function</i> , 2020, 11, 834-845.	4.6	15
1907	Elucidating the biomineralization of low-temperature hydrothermal precipitates with varying Fe, Si contents: Indication from ultrastructure and microbiological analyses. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2020, 157, 103208.	1.4	8
1908	Mycobiota in Chilean chilli <i>Capsicum annuum</i> L. used for production of Merck®n. <i>International Journal of Food Microbiology</i> , 2020, 334, 108833.	4.7	11
1909	Species Boundaries and Molecular Markers for the Classification of 16S rRNA Phytoplasmal Inferred by Genome Analysis. <i>Frontiers in Microbiology</i> , 2020, 11, 1531.	3.5	25
1910	Insight into cold-active xylanase production and xylan degradation pathways in psychrotrophic <i>Acinetobacter</i> sp. HC4 from the cold region of China. <i>Cellulose</i> , 2020, 27, 7575-7589.	4.9	10
1911	Data-Driven Modeling for Species-Level Taxonomic Assignment From 16S rRNA: Application to Human Microbiomes. <i>Frontiers in Microbiology</i> , 2020, 11, 570825.	3.5	12
1912	The Composition of Microbial Communities in Six Streams, and Its Association With Environmental Conditions, and Foodborne Pathogen Isolation. <i>Frontiers in Microbiology</i> , 2020, 11, 1757.	3.5	13
1913	Distribution and expression of virulence genes in potentially pathogenic bacteria isolated from seafood in Thailand. <i>CYTA - Journal of Food</i> , 2020, 18, 753-763.	1.9	4
1914	NetCoMi: network construction and comparison for microbiome data in R. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	222
1915	Weak Influence of Paleoenvironmental Conditions on the Subsurface Biosphere of Lake Ohrid over the Last 515 ka. <i>Microorganisms</i> , 2020, 8, 1736.	3.6	9
1916	BIOCOM-PIPE: a new user-friendly metabarcoding pipeline for the characterization of microbial diversity from 16S, 18S and 23S rRNA gene amplicons. <i>BMC Bioinformatics</i> , 2020, 21, 492.	2.6	16
1917	Dissecting the effect of continuous cropping of potato on soil bacterial communities as revealed by high-throughput sequencing. <i>PLoS ONE</i> , 2020, 15, e0233356.	2.5	25
1918	Modeling the ecological status response of rivers to multiple stressors using machine learning: A comparison of environmental DNA metabarcoding and morphological data. <i>Water Research</i> , 2020, 183, 116004.	11.3	27
1919	Bacterioplankton abundance and community structure during post-monsoon in mangrove dominated estuaries of the Indian Sundarbans; An insight to biogeochemical processes. <i>Estuarine, Coastal and Shelf Science</i> , 2020, 243, 106895.	2.1	3
1920	The effect of ultra-processed very low-energy diets on gut microbiota and metabolic outcomes in individuals with obesity: A systematic literature review. <i>Obesity Research and Clinical Practice</i> , 2020, 14, 197-204.	1.8	26
1921	Analysis of Marine Planktonic Cyanobacterial Assemblages From Mooriganga Estuary, Indian Sundarbans Using Molecular Approaches. <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	8

#	ARTICLE	IF	CITATIONS
1922	Bdellovibrio and Like Organisms in Lake Geneva: An Unseen Elephant in the Room?. <i>Frontiers in Microbiology</i> , 2020, 11, 98.	3.5	23
1923	The Computational Diet: A Review of Computational Methods Across Diet, Microbiome, and Health. <i>Frontiers in Microbiology</i> , 2020, 11, 393.	3.5	32
1924	Screening of folate-producing lactic acid bacteria and modulatory effects of folate-biofortified yogurt on gut dysbacteriosis of folate-deficient rats. <i>Food and Function</i> , 2020, 11, 6308-6318.	4.6	31
1925	C41 methyl and C42 ethyl alkenones are biomarkers for Group II Isochrysidales. <i>Organic Geochemistry</i> , 2020, 147, 104081.	1.8	14
1926	Combustion behavior and fire security of storage grains before and after mildew. <i>Journal of Fire Sciences</i> , 2020, 38, 395-411.	2.0	8
1927	16S rRNA gene sequencing reveals an altered composition of the gut microbiota in chickens infected with a nephropathogenic infectious bronchitis virus. <i>Scientific Reports</i> , 2020, 10, 3556.	3.3	10
1928	Microbial communities and biogenic Mn-oxides in an on-site biofiltration system for cold Fe-(II)- and Mn(II)-rich groundwater treatment. <i>Science of the Total Environment</i> , 2020, 710, 136386.	8.0	31
1929	Investigating Algal Communities in Lacustrine and Hydro-Terrestrial Environments of East Antarctica Using Deep Amplicon Sequencing. <i>Microorganisms</i> , 2020, 8, 497.	3.6	8
1930	Comammox bacterial abundance, activity, and contribution in agricultural rhizosphere soils. <i>Science of the Total Environment</i> , 2020, 727, 138563.	8.0	57
1931	Reintroducing mothur: 10 Years Later. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	160
1932	High-effectively degrade the di-(2-ethylhexyl) phthalate via biochemical system: Resistant bacterial flora and persulfate oxidation activated by BC@Fe ₃ O ₄ . <i>Environmental Pollution</i> , 2020, 262, 114100.	7.5	18
1933	Diversity of bacteria in different life stages and their impact on the development and reproduction of <i>Zeugodacus tau</i> (Diptera: Tephritidae). <i>Insect Science</i> , 2021, 28, 363-376.	3.0	40
1934	Performance evaluation and microbial community analysis of the biofilter for removing grease and volatile organic compounds in the kitchen exhaust fume. <i>Bioresource Technology</i> , 2021, 319, 124132.	9.6	15
1935	Mechanisms of the phytomicrobiome for enhancing soil fertility and health. , 2021, , 1-14.		5
1936	Optimizing the quality of clinical studies on oral microbiome: A practical guide for planning, performing, and reporting. <i>Periodontology 2000</i> , 2021, 85, 210-236.	13.4	51
1937	An assessment of the persistence of putative pathogenic bacteria in chloraminated water distribution systems. <i>Water Research</i> , 2021, 190, 116677.	11.3	11
1938	Cultivation of anaerobic ammonium oxidizing bacteria (AnAOB) using different sewage sludge inoculums: process performance and microbial community analysis. <i>Journal of Chemical Technology and Biotechnology</i> , 2021, 96, 454-464.	3.2	8
1939	Nanopore based sequencing enables easy and accurate identification of yeasts in breweries. <i>Journal of the Institute of Brewing</i> , 2021, 127, 160-166.	2.3	4

#	ARTICLE	IF	CITATIONS
1940	Using nanoselenium to combat Minamata disease in rats: the regulation of gut microbes. <i>Environmental Science: Nano</i> , 2021, 8, 1437-1445.	4.3	2
1941	Distribution of ammonia-oxidizing archaea and bacteria along an engineered coastal ecosystem in subtropical China. <i>Ecotoxicology</i> , 2021, 30, 1769-1779.	2.4	2
1942	Bioinformatic Platforms for Metagenomics. , 2021, , 91-112.		0
1943	Microbial analyses of blood spot surfaces collected from a laboratory and the bathroom of a female single-person household under different environmental conditions. <i>FEMS Microbiology Letters</i> , 2021, 368, .	1.8	1
1944	Seasonal Dynamics of Abundance, Structure, and Diversity of Methanogens and Methanotrophs in Lake Sediments. <i>Microbial Ecology</i> , 2021, 82, 559-571.	2.8	14
1945	Abundance and Functional Importance of Complete Ammonia Oxidizers and Other Nitrifiers in a Riparian Ecosystem. <i>Environmental Science & Technology</i> , 2021, 55, 4573-4584.	10.0	38
1946	Comparison of Methods for Picking the Operational Taxonomic Units From Amplicon Sequences. <i>Frontiers in Microbiology</i> , 2021, 12, 644012.	3.5	21
1947	The pattern of sedimentary bacterial communities varies with latitude within a large eutrophic lake. <i>Limnologia</i> , 2021, 87, 125860.	1.5	7
1948	Influence of Temperature and Sulfate Concentration on the Sulfate/Sulfite Reduction Prokaryotic Communities in the Tibetan Hot Springs. <i>Microorganisms</i> , 2021, 9, 583.	3.6	8
1949	Methods for exploring the faecal microbiome of premature infants: a review. <i>Maternal Health, Neonatology and Perinatology</i> , 2021, 7, 11.	2.2	3
1951	Early establishment of spruce (<i>Picea glehnii</i> [Fr. Schm.] Masters) seedlings on disturbed soil with the aim of assisted natural regeneration. <i>Scandinavian Journal of Forest Research</i> , 2021, 36, 126-134.	1.4	1
1952	Development of a Rapid and Accurate Nanopore-based Sequencing Platform for on-Field Identification of Beer-Spoilage Bacteria in the Breweries. <i>Journal of the American Society of Brewing Chemists</i> , 2021, 79, 240-248.	1.1	4
1953	Seagrass (<i>Zostera marina</i>) promotes nitrification potential and selects specific ammonia oxidizers in coastal sediments. <i>Journal of Soils and Sediments</i> , 2021, 21, 3259-3273.	3.0	12
1954	A primer on metagenomics and next-generation sequencing in fish gut microbiome research. <i>Aquaculture Research</i> , 2021, 52, 4574-4600.	1.8	12
1955	Microbiome and colorectal cancer: A review of the past, present, and future. <i>Surgical Oncology</i> , 2021, 37, 101560.	1.6	7
1956	Co-occurrence and patterns of phosphate solubilizing, salt and metal tolerant and antibiotic-resistant bacteria in diverse soils. <i>3 Biotech</i> , 2021, 11, 356.	2.2	4
1957	Mesocosm Experiments Reveal Global Warming Accelerates Macrophytes Litter Decomposition and Alters Decomposition-Related Bacteria Community Structure. <i>Water (Switzerland)</i> , 2021, 13, 1940.	2.7	7
1958	Swarm v3: towards tera-scale amplicon clustering. <i>Bioinformatics</i> , 2021, 38, 267-269.	4.1	40

#	ARTICLE	IF	CITATIONS
1959	The Nitrogen-Cycling Network of Bacterial Symbionts in the Sponge <i>Spheciospongia vesparium</i> . <i>Journal of Ocean University of China</i> , 2021, 20, 999-1012.	1.2	2
1960	Combined foliar and soil selenium fertilizer improves selenium transport and the diversity of rhizosphere bacterial community in oats. <i>Environmental Science and Pollution Research</i> , 2021, 28, 64407-64418.	5.3	9
1961	Multiomic Approach to Analyze Infant Gut Microbiota: Experimental and Analytical Method Optimization. <i>Biomolecules</i> , 2021, 11, 999.	4.0	3
1962	The Novel Interplay between Commensal Gut Bacteria and Metabolites in Diet-Induced Hyperlipidemic Rats Treated with Simvastatin. <i>Journal of Proteome Research</i> , 2021, , .	3.7	5
1964	Microbial interaction promotes desulfurization efficiency under high pH condition. <i>Environmental Research</i> , 2021, 200, 111423.	7.5	15
1965	An accurate and exact clustering algorithm for next generation sequencing metagenomic sequences. <i>Mathematical Methods in the Applied Sciences</i> , 0, , .	2.3	1
1966	Microbiota-Macroalgal Relationships at a Hawaiian Intertidal Bench Are Influenced by Macroalgal Phyla and Associated Thallus Complexity. <i>MSphere</i> , 2021, 6, e0066521.	2.9	3
1967	Diversity and Distribution of Culturable <i>Thermus</i> Species in Terrestrial Hot Springs of Southwestern Yunnan Province in China. <i>Diversity</i> , 2021, 13, 455.	1.7	0
1968	Molecular diversity of arbuscular mycorrhizal fungi associated with two alpine plant species in the Tibetan Plateau. <i>Rhizosphere</i> , 2021, 19, 100384.	3.0	2
1970	Occurrence and abundance of ammonia-oxidizing archaea and bacteria from the surface to below the water table, in deep soil, and their contributions to nitrification. <i>MicrobiologyOpen</i> , 2017, 6, e00488.	3.0	25
1971	Overview of the Gastrointestinal Microbiota. <i>Advances in Experimental Medicine and Biology</i> , 2008, 635, 29-40.	1.6	35
1972	Microbial Communities, Structure, and Function. <i>Encyclopedia of Earth Sciences Series</i> , 2011, , 592-595.	0.1	7
1973	Pyrosequencing of Chaperonin-60 (cpn60) Amplicons as a Means of Determining Microbial Community Composition. <i>Methods in Molecular Biology</i> , 2011, 733, 143-158.	0.9	23
1974	Next Generation Barcode Tagged Sequencing for Monitoring Microbial Community Dynamics. <i>Methods in Molecular Biology</i> , 2014, 1096, 101-110.	0.9	2
1975	Metagenomic Analysis of Low-Temperature Environments. , 2017, , 389-421.		4
1976	Characterizing Microbial Population Structures through Massively Parallel Sequencing. <i>Microbiology Monographs</i> , 2009, , 278-292.	0.6	3
1977	Finding Biologically Accurate Clusterings in Hierarchical Tree Decompositions Using the Variation of Information. <i>Lecture Notes in Computer Science</i> , 2009, , 400-417.	1.3	10
1978	Compost Microbial Populations and Interactions with Plants. , 2010, , 231-251.		9

#	ARTICLE	IF	CITATIONS
1979	CRISPy-CUDA: Computing Species Richness in 16S rRNA Pyrosequencing Datasets with CUDA. Lecture Notes in Computer Science, 2011, , 37-49.	1.3	4
1980	Metagenomics: The Exploration of Unculturable Microbial World. , 2014, , 105-115.		1
1981	Life on a Leaf: Bacterial Epiphytes of a Salt-Excreting Desert Tree. Cellular Origin and Life in Extreme Habitats, 2010, , 393-406.	0.3	4
1982	Microbial Diversity in Modern Stromatolites. Cellular Origin and Life in Extreme Habitats, 2011, , 383-405.	0.3	33
1983	Morphology and composition of the midgut bacterial community of <i>Scaptocoris castanea</i> Perty, 1830 (Hemiptera: Cydnidae). Cell and Tissue Research, 2020, 382, 337-349.	2.9	5
1984	Seasonal epiphytic microbial dynamics on grapevine leaves under biocontrol and copper fungicide treatments. Scientific Reports, 2020, 10, 681.	3.3	35
1988	Thermal Environments and Biodiversity. , 0, , 11-29.		13
1989	Cd1d-dependent regulation of bacterial colonization in the intestine of mice. Journal of Clinical Investigation, 2009, 119, 1241-1250.	8.2	146
1990	Molecular Biology and Ecology of the Rhizobiaâ€“Legume Symbiosis. Books in Soils, Plants, and the Environment, 2007, , 237-266.	0.1	9
1991	Pyrosequencing Analysis Reveals Abundance and Community Composition of Denitrifying Bacteria in Xilin River Sludge. Advances in Microbiology, 2014, 03, 70-78.	0.0	1
1992	An Automated Phylogenetic Tree-Based Small Subunit rRNA Taxonomy and Alignment Pipeline (STAP). PLoS ONE, 2008, 3, e2566.	2.5	44
1993	Contrasting Microbial Community Assembly Hypotheses: A Reconciling Tale from the RÃo Tinto. PLoS ONE, 2008, 3, e3853.	2.5	34
1994	Integron Gene Cassettes and Degradation of Compounds Associated with Industrial Waste: The Case of the Sydney Tar Ponds. PLoS ONE, 2009, 4, e5276.	2.5	46
1995	Molecular Taxonomy of Phytopathogenic Fungi: A Case Study in <i>Peronospora</i> . PLoS ONE, 2009, 4, e6319.	2.5	186
1996	Comparative Analysis of Pyrosequencing and a Phylogenetic Microarray for Exploring Microbial Community Structures in the Human Distal Intestine. PLoS ONE, 2009, 4, e6669.	2.5	719
1997	Disordered Microbial Communities in Asthmatic Airways. PLoS ONE, 2010, 5, e8578.	2.5	1,436
1998	Spatial Structure and Activity of Sedimentary Microbial Communities Underlying a <i>Beggiatoa</i> spp. Mat in a Gulf of Mexico Hydrocarbon Seep. PLoS ONE, 2010, 5, e8738.	2.5	117
1999	Bacterial Gut Symbionts Contribute to Seed Digestion in an Omnivorous Beetle. PLoS ONE, 2010, 5, e10831.	2.5	68

#	ARTICLE	IF	CITATIONS
2000	18S rDNA Sequences from Microeukaryotes Reveal Oil Indicators in Mangrove Sediment. PLoS ONE, 2010, 5, e12437.	2.5	47
2001	Species Delimitation in Taxonomically Difficult Fungi: The Case of <i>Hymenogaster</i> . PLoS ONE, 2011, 6, e15614.	2.5	32
2002	High Genetic Diversity and Different Distributions of Glycosyl Hydrolase Family 10 and 11 Xylanases in the Goat Rumen. PLoS ONE, 2011, 6, e16731.	2.5	17
2003	jMOTU and Taxonator: Turning DNA Barcode Sequences into Annotated Operational Taxonomic Units. PLoS ONE, 2011, 6, e19259.	2.5	180
2004	Sunlight-Exposed Biofilm Microbial Communities Are Naturally Resistant to Chernobyl Ionizing-Radiation Levels. PLoS ONE, 2011, 6, e21764.	2.5	63
2005	Comparative Analysis of Salivary Bacterial Microbiome Diversity in Edentulous Infants and Their Mothers or Primary Care Givers Using Pyrosequencing. PLoS ONE, 2011, 6, e23503.	2.5	128
2006	Changes in N-Transforming Archaea and Bacteria in Soil during the Establishment of Bioenergy Crops. PLoS ONE, 2011, 6, e24750.	2.5	119
2007	Cellulosomics, a Gene-Centric Approach to Investigating the Intraspecific Diversity and Adaptation of <i>Ruminococcus flavefaciens</i> within the Rumen. PLoS ONE, 2011, 6, e25329.	2.5	28
2008	Comparing the Bacterial Diversity of Acute and Chronic Dental Root Canal Infections. PLoS ONE, 2011, 6, e28088.	2.5	114
2009	Prokaryotic and Eukaryotic Community Structure in Field and Cultured Microbialites from the Alkaline Lake Alchichica (Mexico). PLoS ONE, 2011, 6, e28767.	2.5	111
2010	Dirichlet Multinomial Mixtures: Generative Models for Microbial Metagenomics. PLoS ONE, 2012, 7, e30126.	2.5	653
2011	Host Plant Induced Variation in Gut Bacteria of <i>Helicoverpa armigera</i> . PLoS ONE, 2012, 7, e30768.	2.5	173
2012	The Influence of Intense Chemical Pollution on the Community Composition, Diversity and Abundance of Anammox Bacteria in the Jiaojiang Estuary (China). PLoS ONE, 2012, 7, e33826.	2.5	32
2013	Phylogenetic Diversity and Environment-Specific Distributions of Glycosyl Hydrolase Family 10 Xylanases in Geographically Distant Soils. PLoS ONE, 2012, 7, e43480.	2.5	15
2014	Production of Organic Acids by Probiotic Lactobacilli Can Be Used to Reduce Pathogen Load in Poultry. PLoS ONE, 2012, 7, e43928.	2.5	178
2015	Impact of Oil on Bacterial Community Structure in Bioturbated Sediments. PLoS ONE, 2013, 8, e65347.	2.5	61
2016	Diversity and Spatial Distribution of Hydrazine Oxidoreductase (hzo) Gene in the Oxygen Minimum Zone Off Costa Rica. PLoS ONE, 2013, 8, e78275.	2.5	61
2017	Temperature Responses of Ammonia-Oxidizing Prokaryotes in Freshwater Sediment Microcosms. PLoS ONE, 2014, 9, e100653.	2.5	35

#	ARTICLE	IF	CITATIONS
2018	Bacterial Communities in the Gut and Reproductive Organs of <i>Bactrocera minax</i> (Diptera: Tephritidae) Based on 454 Pyrosequencing. PLoS ONE, 2014, 9, e106988.	2.5	121
2019	Abundance and Diversity of Bacterial Nitrifiers and Denitrifiers and Their Functional Genes in Tannery Wastewater Treatment Plants Revealed by High-Throughput Sequencing. PLoS ONE, 2014, 9, e113603.	2.5	120
2020	Ubiquity and Diversity of Heterotrophic Bacterial <i>nasA</i> Genes in Diverse Marine Environments. PLoS ONE, 2015, 10, e0117473.	2.5	15
2021	Estimating Bacterial Diversity for Ecological Studies: Methods, Metrics, and Assumptions. PLoS ONE, 2015, 10, e0125356.	2.5	89
2022	CLUSTOM-CLOUD: In-Memory Data Grid-Based Software for Clustering 16S rRNA Sequence Data in the Cloud Environment. PLoS ONE, 2016, 11, e0151064.	2.5	9
2023	K-shuff: A Novel Algorithm for Characterizing Structural and Compositional Diversity in Gene Libraries. PLoS ONE, 2016, 11, e0167634.	2.5	8
2024	DUDE-Seq: Fast, flexible, and robust denoising for targeted amplicon sequencing. PLoS ONE, 2017, 12, e0181463.	2.5	47
2025	Change of Sponge(<i>Axinella</i> sp.)-Associated Bacterial Community during the Cultivation with Hexabromobenzene. Journal of Marine Bioscience and Biotechnology, 2014, 6, 76-83.	0.1	1
2026	DNA Sequencing: Strategies for Soil Microbiology. Soil Science Society of America Journal, 2007, 71, 592-600.	2.2	28
2027	A Comparison of Bacterial Composition in Diabetic Ulcers and Contralateral Intact Skin. Open Microbiology Journal, 2010, 4, 8-19.	0.7	122
2028	Comparative microbial ecology of the water column of an extreme acidic pit lake, Nuestra Señora del Carmen, and the R��o Tinto basin (Iberian Pyrite Belt). International Microbiology, 2014, 17, 225-33.	2.4	9
2029	Effect of DNA Extraction Methods on the Apparent Structure of Yak Rumen Microbial Communities as Revealed by 16S rDNA Sequencing. Polish Journal of Microbiology, 2015, 64, 29-36.	1.7	31
2030	Diversity of planktonic cyanobacteria and microcystin occurrence in Polish water bodies investigated using a polyphasic approach. Aquatic Microbial Ecology, 2008, 51, 223-236.	1.8	9
2031	Mesopelagic protists: diversity and succession in a coastal Arctic ecosystem. Aquatic Microbial Ecology, 2009, 56, 25-39.	1.8	50
2032	Periodic sulfide irruptions impact microbial community structure and diversity in the water column of a hypersaline lake. Aquatic Microbial Ecology, 2010, 60, 97-108.	1.8	3
2033	Seasonal dynamics of bacterial biofilms on the kelp <i>Laminaria hyperborea</i> . Aquatic Microbial Ecology, 2010, 60, 71-83.	1.8	141
2034	Phylogenetic diversity and community structure of sponge-associated bacteria from mangroves of the Caribbean Sea. Aquatic Microbial Ecology, 2011, 62, 231-240.	1.8	18
2035	Nitrogen fixation within the water column associated with two hypoxic basins in the Southern California Bight. Aquatic Microbial Ecology, 2011, 63, 193-205.	1.8	126

#	ARTICLE	IF	CITATIONS
2036	Response of a summertime Antarctic marine bacterial community to glucose and ammonium enrichment. <i>Aquatic Microbial Ecology</i> , 2011, 64, 205-220.	1.8	23
2037	Abundance and diversity of Planctomycetes in a Tyrrhenian coastal system of central Italy. <i>Aquatic Microbial Ecology</i> , 2011, 65, 129-141.	1.8	33
2038	Effects of salinity and nutrients on sedimentary bacterial communities in oligosaline Lake Bosten, northwestern China. <i>Aquatic Microbial Ecology</i> , 2013, 69, 123-134.	1.8	31
2039	Spatial variability of microbial communities of the coralline demosponge <i>Astrosclera willeyana</i> across the Indo-Pacific. <i>Aquatic Microbial Ecology</i> , 2015, 74, 143-156.	1.8	3
2040	Remarkably diverse and contrasting archaeal communities in a large arctic river and the coastal Arctic Ocean. <i>Aquatic Microbial Ecology</i> , 2006, 44, 115-126.	1.8	105
2041	Microbial community composition of black band disease on the coral host <i>Siderastrea siderea</i> from three regions of the wider Caribbean. <i>Marine Ecology - Progress Series</i> , 2008, 362, 85-98.	1.9	111
2042	Spatial and temporal variability in nitrogenase activity and diazotrophic community composition in coastal microbial mats. <i>Marine Ecology - Progress Series</i> , 2010, 417, 13-25.	1.9	10
2043	Microbial distribution in different spatial positions within the walls of a black sulfide hydrothermal chimney. <i>Marine Ecology - Progress Series</i> , 2014, 508, 67-85.	1.9	6
2044	Diarrhoea-predominant irritable bowel syndromedistinguishable by 16S rRNA gene phylotype quantification. <i>World Journal of Gastroenterology</i> , 2009, 15, 5936.	3.3	157
2045	Deciphering Diversity Indices for a Better Understanding of Microbial Communities. <i>Journal of Microbiology and Biotechnology</i> , 2017, 27, 2089-2093.	2.1	578
2046	Endomicrobial Community Profiles of Two Different Mealybugs: <i>Paracoccus marginatus</i> and <i>Ferrisia virgata</i> . <i>Journal of Microbiology and Biotechnology</i> , 2020, 30, 1013-1017.	2.1	3
2047	Bayesian Phylogenetic Analysis of Rhizobia Isolated From Root-Nodules of Three Tunisian Wild Legume Species of the Genus <i>Sulla</i> . <i>Journal of Phylogenetics & Evolutionary Biology</i> , 2015, 03, .	0.2	2
2048	Phylogeny of Bacteria from Steelmaking Wastes and Their Acidic Enrichment Cultures. <i>Advances in Microbiology</i> , 2014, 04, 816-828.	0.6	1
2049	Feeding Strategies for Enrichment and Characterization of Anammox Biomass in a Sequencing Batch Reactor. <i>American Journal of Analytical Chemistry</i> , 2014, 05, 891-900.	0.9	2
2050	Molecular and Chemical Analyses of Cyanobacterial Blooms in Tropical Lagoons from Southeast Brazil. <i>Journal of Water Resource and Protection</i> , 2015, 07, 50-71.	0.8	2
2051	The Effects of Ocean Acidity and Elevated Temperature on Bacterioplankton Community Structure and Metabolism. <i>Open Journal of Ecology</i> , 2014, 04, 434-455.	1.0	12
2052	Microbial diversity in the larval gut of field and laboratory populations of the sugarcane weevil <i>Sphenophorus levis</i> (Coleoptera, Curculionidae). <i>Genetics and Molecular Research</i> , 2011, 10, 2679-2691.	0.2	24
2053	Sustained Anthropogenic Impact in Carter Saltpeter Cave, Carter County, Tennessee and the Potential Effects on Manganese Cycling. <i>Journal of Cave and Karst Studies</i> , 2013, 75, 189-204.	0.6	9

#	ARTICLE	IF	CITATIONS
2054	Microbial Community Analysis using RDP II (Ribosomal Database Project II):Methods, Tools and New Advances. Environmental Engineering Research, 2009, 14, 3-9.	2.5	10
2055	Productivity-diversity relationships from chemolithoautotrophically based sulfidic karst systems. International Journal of Speleology, 2009, 38, 27-40.	1.0	67
2056	Comparative microbial community composition from secondary carbonate (moonmilk) deposits: implications for the Cansiliella servadeii cave hygropetric food web. International Journal of Speleology, 2013, 42, 181-192.	1.0	32
2057	Diversity and distribution of nitrogen fixation genes in the oxygen minimum zones of the world oceans. Biogeosciences, 2020, 17, 5953-5966.	3.3	15
2062	Effect of different plant densities on the diversity of arbuscular mycorrhizal fungi community in a long-term maize monocrop system. Spanish Journal of Agricultural Research, 2010, 8, 123.	0.6	7
2063	Diversity of <i>Butyrivibrio</i> Group Bacteria in the Rumen of Goats and Its Response to the Supplementation of Garlic Oil. Asian-Australasian Journal of Animal Sciences, 2014, 27, 179-186.	2.4	13
2064	Microbial Biodiversity and Biogeography on the Deep Seafloor. , 0, , .		1
2065	RICHEST - a web server for richness estimation in biological data. Bioinformation, 2009, 3, 296-298.	0.5	22
2066	A heritability-based comparison of methods used to cluster 16S rRNA gene sequences into operational taxonomic units. PeerJ, 2016, 4, e2341.	2.0	41
2067	Agricultural land-use change in a Mexican oligotrophic desert depletes ecosystem stability. PeerJ, 2016, 4, e2365.	2.0	13
2068	Microbial communities in the reef water at Kham Island, lower Gulf of Thailand. PeerJ, 2017, 5, e3625.	2.0	9
2069	Accuracy of microbial community diversity estimated by closed- and open-reference OTUs. PeerJ, 2017, 5, e3889.	2.0	138
2070	MetaBoot: a machine learning framework of taxonomical biomarker discovery for different microbial communities based on metagenomic data. PeerJ, 2015, 3, e993.	2.0	13
2071	Emerging Evidence on the Effects of Dietary Factors on the Gut Microbiome in Colorectal Cancer. Frontiers in Nutrition, 2021, 8, 718389.	3.7	19
2072	Molecular signatures of Janthinobacterium lividum from Trinidad support high potential for crude oil metabolism. BMC Microbiology, 2021, 21, 287.	3.3	2
2075	Benthic Bacterial Diversity Based on Cloning and Sequencing of 16S rRNA Genes. , 2009, , .		0
2076	Analysis of microbial communities under long-term conventional and reduced-input management of tillage soil. , 2010, , .		1
2079	Comparison of bacterial diversity in large intestine of Xiangxi yellow cattle (Bos taurus) associated with different diet: Fresh Miscanthus sinensis and mixed forage. African Journal of Microbiology Research, 2012, 6, .	0.4	1

#	ARTICLE	IF	CITATIONS
2080	Application of Amplicon Pyrosequencing in Soil Microbial Ecology. Han'guk T'oyang Piryo Hakhoe Chi Han'guk T'oyang Piryo Hakhoe, 2012, 45, 1073-1085.	0.9	0
2083	Bioinformatics for Genomes and Metagenomes in Ecology Studies. Advanced Topics in Science and Technology in China, 2014, , 203-226.	0.1	0
2084	To Develop Strain Specific Molecular Marker for Easy and Proper Identification of Fungal Species Based on Molecular Characters: A Review. Journal of Molecular Biomarkers & Diagnosis, 2014, 05, .	0.4	1
2085	Bioinformatic Tools in the Analysis of Determinants of Pathogenicity and Ecology of Entomopathogenic Fungi Used as Microbial Insecticides in Crop Protection. , 2014, , 215-234.		0
2087	Measuring Diversity. , 0, , 131-151.		1
2088	Seasonal Variations in the Bacterial Community of Gwangyang Bay Seawater. Journal of Life Science, 2014, 24, 522-531.	0.2	5
2090	Denitrification in municipal waste landfill by Pseudomonas stutzeri P-1-5. , 2016, , .		0
2092	The Abundance and Community Composition of Ammonia-Oxidizing Prokaryotes in Small-Reservoir Sediments in China's Huashan Watershed. Polish Journal of Environmental Studies, 2016, 25, 2665-2673.	1.2	0
2093	Response of the Coral Associated Nitrogen Fixing Bacteria Toward Elevated Water Temperature. Journal of Water Resources and Ocean Science, 2017, 6, 98.	0.4	2
2094	Change of Soil Bacteria Diversity between Desertification and Restoration. IOSR Journal of Pharmacy and Biological Sciences, 2017, 12, 74-87.	0.1	0
2098	Effects of feed intake on the diversity and population density of homoacetogens in the large intestine of pigs. Asian-Australasian Journal of Animal Sciences, 2019, 32, 1907-1913.	2.4	0
2099	Authors need to be prudent when assigning names to microbial isolates. Archives of Microbiology, 2021, 203, 5845-5848.	2.2	6
2100	The endophytome (plant-associated microbiome): methodological approaches, biological aspects, and biotech applications. World Journal of Microbiology and Biotechnology, 2021, 37, 206.	3.6	7
2102	Actinobacterial Communities of Chosen Extreme Habitats in China. Polish Journal of Ecology, 2020, 68, .	0.2	2
2103	Differential Toxicological Outcome of Corn Oil Exposure in Rats and Mice as Assessed by Microbial Composition, Epithelial Permeability, and Ileal Mucosa-Associated Immune Status. Toxicological Sciences, 2021, 180, 89-102.	3.1	6
2104	Long-term P fertilization significantly altered the diversity, composition and mycorrhizal traits of arbuscular mycorrhizal fungal communities in a wheat-maize rotation. Applied Soil Ecology, 2022, 170, 104261.	4.3	16
2105	Protein profiling as a tool for identifying environmental aerobic endospore-forming bacteria. Open Journal of Bacteriology, 2020, 4, 001-007.	0.3	1
2106	Isolation of Plant Growth Promoting Bacteria from the Rhizosphere of Different Plants and Assessment of Their Plant Growth Promotion Potential. Pakistan Biomedical Journal, 2021, 3, .	0.1	0

#	ARTICLE	IF	CITATIONS
2107	Abundance and Diversity of Microbiota. , 2013, , 23-40.		1
2108	Rhizospheric bacterial community structure of <i>Triticum</i> and <i>Aegilops</i> revealed by pyrosequencing analysis of the 16S rRNA gene: dominance of the A genome over the B and D genomes. <i>Genes and Genetic Systems</i> , 2020, 95, 249-268.	0.7	4
2111	Using DGGE and 16S rRNA gene sequence analysis to evaluate changes in oral bacterial composition. <i>Chinese journal of dental research: the official journal of the Scientific Section of the Chinese Stomatological Association (CSA)</i> , The, 2011, 14, 95-103.	0.2	1
2112	Estimation of Personal Environment Via Fingertip Microbiome and Mobile Phone Surfaces. <i>Iranian Journal of Biotechnology</i> , 2021, 19, e2696.	0.3	0
2113	Authors Need to be Prudent When Assigning Names to Microbial Isolates. <i>Current Microbiology</i> , 2021, 78, 4005-4008.	2.2	4
2114	Phylogeny, alkenone profiles and ecology of Isochrysidales subclades in saline lakes: Implications for paleosalinity and paleotemperature reconstructions. <i>Geochimica Et Cosmochimica Acta</i> , 2022, 317, 472-487.	3.9	16
2115	The Clinical Utility of Two High-Throughput 16S rRNA Gene Sequencing Workflows for Taxonomic Assignment of Unidentifiable Bacterial Pathogens in Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry. <i>Journal of Clinical Microbiology</i> , 2022, 60, JCM0176921.	3.9	13
2116	Authors need to be prudent when assigning names to microbial isolates. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 1-5.	1.7	4
2118	Characterization of Tobacco Microbiome by Metagenomics Approach. <i>Methods in Molecular Biology</i> , 2022, 2413, 229-244.	0.9	1
2119	Influence of Fermentation Conditions (Temperature and Time) on the Physicochemical Properties and Bacteria Microbiota of Amasi. <i>Fermentation</i> , 2022, 8, 57.	3.0	7
2120	ASAP 2: a pipeline and web server to analyze marker gene amplicon sequencing data automatically and consistently. <i>BMC Bioinformatics</i> , 2022, 23, 27.	2.6	6
2121	Phytoplankton diversity and ecology through the lens of high throughput sequencing technologies. , 2022, , 353-413.		8
2122	Response of bacterial communities in saline-alkali soil to different pesticide stresses. <i>Environmental Science and Pollution Research</i> , 2022, 29, 42709-42719.	5.3	4
2123	Microbiome Changes of Endemic Lake Baikal Sponges during Bleaching Syndrome Development. <i>Diversity</i> , 2021, 13, 653.	1.7	3
2124	Reconstitution and Transmission of Gut Microbiomes and Their Genes between Generations. <i>Microorganisms</i> , 2022, 10, 70.	3.6	17
2125	A critical analysis of state-of-the-art metagenomics OTU clustering algorithms. <i>Journal of Biosciences</i> , 2019, 44, .	1.1	0
2126	Variation in the Structure and Composition of Bacterial Communities within Drinking Water Fountains in Melbourne, Australia. <i>Water (Switzerland)</i> , 2022, 14, 908.	2.7	2
2127	Effect of Nitrate Concentration on the Coupling Process of Electricity Generation and Nitrate Removal in Biocathode Microbial Fuel Cells. <i>Journal of Environmental Engineering, ASCE</i> , 2022, 148, .	1.4	2

#	ARTICLE	IF	CITATIONS
2128	Isolation, characterization and complete genome sequencing of fish pathogenic <i>Aeromonas veronii</i> from diseased <i>Labeo rohita</i> . <i>Aquaculture</i> , 2022, 553, 738085.	3.5	11
2129	Analysis of the intestinal microbial community altered during rotavirus infection in suckling mice. <i>Virology Journal</i> , 2021, 18, 254.	3.4	9
2130	How clear is our current view on microbial dark matter? (Re-)assessing public MAG & SAG datasets with MDMcleaner. <i>Nucleic Acids Research</i> , 2022, 50, e76-e76.	14.5	19
2131	The Coupling Response between Different Bacterial Metabolic Functions in Water and Sediment Improve the Ability to Mitigate Climate Change. <i>Water (Switzerland)</i> , 2022, 14, 1203.	2.7	6
2132	Molecular Identification of <i>Bacillus</i> Isolated from Korean Water Deer (<i>Hydropotes inermis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587 Td Marker. <i>Animals</i> , 2022, 12, 979.	2.3	3
2133	Microbiomes of Urine and the Prostate Are Linked to Human Prostate Cancer Risk Groups. <i>European Urology Oncology</i> , 2022, 5, 412-419.	5.4	21
2158	Microbially promoted calcite precipitation in the pelagic redoxcline: Elucidating the formation of the turbid layer. <i>Geobiology</i> , 2022, 20, 498-517.	2.4	5
2159	Context-Aware Phylogenetic Trees for Phylogeny-Based Taxonomy Visualization. <i>Frontiers in Genetics</i> , 2022, 13, .	2.3	1
2160	Nitrogen Cycling Microbial Diversity and Operational Taxonomic Unit Clustering: When to Prioritize Accuracy Over Speed. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	0
2161	Impacts of land-use change on soil microbial communities and their function in the Amazon Rainforest. <i>Advances in Agronomy</i> , 2022, , 179-258.	5.2	3
2162	Phylogeny-guided microbiome OTU-specific association test (POST). <i>Microbiome</i> , 2022, 10, .	11.1	2
2163	Bacterial Metabolic Potential in Response to Climate Warming Alters the Decomposition Process of Aquatic Plant Litterâ€™In Shallow Lake Mesocosms. <i>Microorganisms</i> , 2022, 10, 1327.	3.6	0
2166	Presence and habitats of bacterial fish pathogen relatives in a marine salmon post-smolt RAS. <i>Aquaculture Reports</i> , 2022, 26, 101312.	1.7	1
2167	Tools to Study Gut Microbiome. , 2022, , 253-270.		0
2168	Comprehensive Evaluation of Shotgun Metagenomics, Amplicon Sequencing and Harmonization of Said Platforms for Epidemiological Studies Using the Large Multi-Center HCHS/SOL Cohort. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
2169	Metagenomic approaches for understanding microbial communities in contaminated environments: Bioinformatic tools, case studies and future outlook. , 2023, , 103-156.		1
2170	Identification of Bacterial Isolates Recovered from the Surface of Cleanroom Operatorsâ€™™ Garments following Wear. <i>European Journal of Parenteral and Pharmaceutical Sciences</i> , 0, , .	1.0	0
2171	Niche differentiation and symbiotic association among ammonia/nitrite oxidizers in a full-scale rotating biological contactor. <i>Water Research</i> , 2022, 225, 119137.	11.3	3

#	ARTICLE	IF	CITATIONS
2172	Machine learning and deep learning applications in microbiome research. ISME Communications, 2022, 2, .	4.2	44
2173	Effects of Preservation and Propagation Methodology on Microcosms Derived from the Oral Microbiome. Microorganisms, 2022, 10, 2146.	3.6	1
2174	Potential autotrophic carbon-fixer and Fe(II)-oxidizer Alcanivorax sp. MM125-6 isolated from Wocan hydrothermal field. Frontiers in Microbiology, 0, 13, .	3.5	2
2175	Combining deep sequencing and conventional molecular approaches reveals broad diversity and distribution of fleas and Bartonella in rodents and shrews from Arctic and Subarctic ecosystems. Parasites and Vectors, 2022, 15, .	2.5	2
2176	GUT BACTERIAL DIVERSITY BETWEEN POLYGRID LAND SNAILS REFLECT ENVIRONMENTAL DIFFERENCES. Texas Journal of Science, 2022, 74, .	0.2	0
2177	Is There a Universal Endurance Microbiota?. Microorganisms, 2022, 10, 2213.	3.6	2
2178	Novel database and cut-off value for bacterial amoA gene revealed a spatial variability pattern of the ammonia-oxidizing bacteria community from river to sea. Marine Pollution Bulletin, 2022, 185, 114351.	5.0	2
2179	Analysis and Interpretation of metagenomics data: an approach. Biological Procedures Online, 2022, 24, .	2.9	16
2180	Polycystic Ovary Syndrome and Gut Microbiota: Phenotype Matters. Life, 2023, 13, 7.	2.4	1
2181	Ciliate Morpho-Taxonomy and Practical Considerations before Deploying Metabarcoding to Ciliate Community Diversity Surveys in Urban Receiving Waters. Microorganisms, 2022, 10, 2512.	3.6	2
2182	Assessment of diversity of archaeal communities in Algerian chott. Extremophiles, 2023, 27, .	2.3	2
2183	Microbial diversity gradients in the geothermal mud volcano underlying the hypersaline Urania Basin. Frontiers in Microbiology, 0, 13, .	3.5	2
2184	Laboratory Investigations in Infectious Uveitis. Ocular Immunology and Inflammation, 2023, 31, 1405-1415.	1.8	1
2185	Comprehensive evaluation of shotgun metagenomics, amplicon sequencing, and harmonization of these platforms for epidemiological studies. Cell Reports Methods, 2023, 3, 100391.	2.9	5
2186	Characterization of Boxwood Shoot Bacterial Communities and Potential Impact from Fungicide Treatments. Microbiology Spectrum, 2023, 11, .	3.0	2
2188	Spatiotemporal distribution of free-living marine nematodes in the tidal flats of Nakatsu and Yokohama Umino-Koen. Japanese Journal of Benthology, 2022, 77, 10-19.	0.1	0
2189	Conjunctival sac microbiome in anophthalmic patients: Flora diversity and the impact of ocular prosthesis materials. Frontiers in Cellular and Infection Microbiology, 0, 13, .	3.9	3
2190	Unveiling the role of emerging metagenomics for the examination of hypersaline environments. Biotechnology and Genetic Engineering Reviews, 0, , 1-39.	6.2	2

#	ARTICLE	IF	CITATIONS
2194	Clustering Sequences into OTUs. , 2023, , 147-159.		0
2195	Moving Beyond OTU Methods. , 2023, , 227-288.		0
2196	Natural durability and fungal diversity of five wood species in a field-test site in Jeongseon, Korea. Holzforschung, 2023, .	1.9	1
2197	Characterization of the Oral Microbiota in Captive Sichuan Golden Snub-nosed Monkeys (<i>Rhinopithecus roxellana</i>) of Different Ages. International Journal of Primatology, 0, , .	1.9	0
2198	Immediate impacts of soybean cover crop on bacterial community composition and diversity in soil under long-term <i>Saccharum</i> monoculture. PeerJ, 0, 11, e15754.	2.0	0
2199	Biocontrol potential and molecular characterization of lipopeptides producing <i>Bacillus subtilis</i> against <i>Sclerotinia sclerotiorum</i> . Journal of Biological Control, 0, , 215-221.	0.2	1
2200	Spatial and temporal variation in the diet of introduced sambar deer (<i>Cervus unicolor</i>) in an alpine landscape. Wildlife Research, 2023, , .	1.4	0
2201	Effect of Different Plant Growth-Promoting Rhizobacteria on Biological Soil Properties, Growth, Yield and Quality of Oregano (<i>Origanum onites</i> L.). Agronomy, 2023, 13, 2511.	3.0	1
2202	Aspirin inhibits rotavirus replication and alters rat gut microbial composition. Virology Journal, 2023, 20, .	3.4	0
2203	A toolbox of machine learning software to support microbiome analysis. Frontiers in Microbiology, 0, 14, .	3.5	0
2204	The Impact of Warming on Assembly Processes and Diversity Patterns of Bacterial Communities in Mesocosms. Microorganisms, 2023, 11, 2807.	3.6	0
2205	Changes in Diversity and Abundance of Ammonia-Oxidizing Archaea and Bacteria along a Glacier Retreating Chronosequence in the Tianshan Mountains, China. Microorganisms, 2023, 11, 2871.	3.6	0
2206	Ready Reckoner for Using Bioinformatics Tools in Fish and Shellfish Microbiome Analysis. , 2023, , 93-120.		0
2207	Polar lake microbiomes have distinct evolutionary histories. Science Advances, 2023, 9, .	10.3	4
2208	The combination of multiple environmental stressors strongly alters microbial community assembly in aquatic ecosystems. Journal of Environmental Management, 2024, 350, 119594.	7.8	3
2209	Assessing the diet and seed dispersal ability of non-native sambar deer (<i>Rusa unicolor</i>) in native ecosystems of south-eastern Australia. Ecology and Evolution, 2023, 13, .	1.9	0
2210	Effect of biochar in soil on microbial diversity: a meta-analysis. IOP Conference Series: Earth and Environmental Science, 2023, 1263, 012047.	0.3	0
2211	Novel database for accA gene revealed a vertical variability pattern of autotrophic carbon fixation potential of ammonia oxidizing archaea in a permeable subterranean estuary. Marine Environmental Research, 2024, 194, 106342.	2.5	0

#	ARTICLE	IF	CITATIONS
2212	Nematodes living on the leaves of <i>Zostera marina</i> in Kiritappu Cove, Hokkaido, Japan. Japanese Journal of Benthology, 2023, 78, 37-41.	0.1	0
2213	Responses of Natural Microorganisms to Land Reclamation and Applications of Functional Microorganisms in Biorestation of Coal Mining Area. Diversity, 2024, 16, 86.	1.7	0
2214	Taxonomic and functional α -diversity patterns reveal stochastic assembly rules in microbial communities of seagrass beds. Frontiers in Plant Science, 0, 15, .	3.6	0
2215	Study of drosophila kinship from three regions in East Java, Indonesia. IOP Conference Series: Earth and Environmental Science, 2024, 1312, 012050.	0.3	0